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Monday 24 June 2013

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Change in the early life-history of Indo-Pacific fishes

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Perceptions of the pelagic, early life-history stages of Indo-Pacific fishes have changed greatly in the 40 years since my first publication on fish larvae. This is appropriate, because the pelagic larval phase is all about change. It is a period of growth and development, so what the larvae do and how they changes with time. It is also a period of dispersal, and one that requires the ability not only to survive, but also to find an entirely different, and not previously experienced habitat at the end. The transition to this challenging new habitat requires new abilities plus major morphological transitions. Perhaps not surprisingly, it is also period that few individuals survive, so it is a period of strong selection. Different taxa have found different solutions to the problems of the pelagic phase: there is no single larval strategy or behaviour. Indo-Pacific larval-fishes used to be studied almost exclusively from the deck of a ship by towing plankton nets, in effect, treating larvae as little more than feeble, biological drift cards with little influence over their dispersal. Larvae are now more likely to be studied in the lab or in the ocean and on a broad range of subjects: this has revealed the larvae to be real animals doing lots of interesting things very well. But, these things all develop and change during the larval phase. The larvae clearly have the ability to strongly influence their dispersal, to interact with other species in their environment, and to make an extensive, yet rapid transition from being pelagic animals to being demersal ones. This understanding has contributed to a paradigm change in marine ecology: from an assumption that marine fish populations are largely 'open' due to extensive larval dispersal to the realization that larval dispersal can be more restricted than previously thought, and in fact includes both self-recruitment and wide dispersal. This talk reviews these characteristics of change, the challenges of studying them, and how we got to this level of understanding. In retrospect, we should not be surprised by these findings.

The center of Indo-Pacific reef fish diversity

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Although it is widely accepted that the "Coral Triangle", particularly Indonesia and the Philippines, is the global center of reef fish diversity, there has been considerable conjecture regarding the exact location of the epicenter. The development of new mapping software has facilitated an updated, comprehensive analysis of the distribution patterns of more than 4,000 Indo-Pacific species. Comparative diversity data is presented for the entire Indo-Pacific with special emphasis on the "Coral Triangle" and adjacent areas. The study reveals important new data related to localized areas of endemism and the richest areas for overall diversity. The current study is based on an extensive literature review and ongoing field work by the author and colleagues.

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Phylogeny and tempo of diversification in the superradiation of acanthomorph fishes

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Acanthomorphs, or spiny-rayed fishes, comprise nearly one third of all living vertebrate species, but despite a dominant role in aquatic ecosystems their phylogenetic relationships and evolutionary history are poorly understood. The reasons for the lack of well-resolved phylogenetic hypotheses of acanthomorphs include the extensive diversity of the clade and a paucity of morphological characters to infer relationships among the major lineages. Molecular phylogenetic studies published over the past 10 to 15 years have resolved several unexpected and interesting clades within acanthomorphs. These recently discovered lineages include a clade containing Gadiformes, *Stylephorus*, and Zeiformes, a clade containing Lophiiformes and Tetraodontiformes, and the recently described Ovalentaria. In this talk I present a set of phylogenetic analyses of acanthomorphs using a nuclear gene supermatrix that includes 10 genes sampled from more than 600 species. This new molecular phylogeny challenges existing taxonomic classifications, supports the unexpected resolutions discovered in earlier molecular phylogenetic analyses, and resolves several additional novel clades. A relaxed molecular clock time tree was inferred using 36 well-justified age constraint priors from the teleost fossil record. The temporal analysis indicates acanthomorphs originated in the Early Cretaceous, with no changes in lineage diversification across the Cretaceous-Paleogene (K-Pg) mass extinction event 66 million years ago. A decrease in lineage diversification 50 mya is associated with a saturation of morphospace occupation, indicating that the early Paleogene was the zenith of acanthomorph evolutionary innovation. The hyper-diversity of living acanthomorphs is highlighted by several rapidly radiating lineages including tunas, gobies, blennies, snailfishes, and cichlids that collectively invaded diverse aquatic habitats.

Is ocean acidification a threat to marine fishes?

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Ocean acidification, caused by the uptake of additional CO_2 from the atmosphere, is a serious threat to marine ecosystems. In general, marine fishes are thought to be relatively tolerant to rising CO_2 levels and ocean acidification because they have well developed physiological mechanisms for acid-base regulation. However, it was recently discovered that near-future CO_2 levels interfere with a range of sensory functions and behaviours of marine fishes. Behavioural changes include increased activity and boldness, loss of lateralization in movement, altered auditory preferences, and impaired olfactory function. In this talk I describe the consequences of these sensory and behavioural changes to predator-prey interactions, homing ability and habitat selection in reef fishes, all of which influence the replenishment and sustainability of fish populations. I then describe the underlying mechanism responsible for these diverse sensory and behavioural effects, and how it relates to the exceptional acid-base regulatory abilities of marine fish. New experiments show that exposure to elevated CO_2 interferes with brain neurotransmitter function in marine fish, and possibly other organisms, a previously unrecognized threat of ocean acidification. I conclude by examining the necessity to test the potential for acclimation and adaptation in ocean acidification research. Short-term experiments have identified many of the ecological impacts of ocean acidification, but an evolutionary perspective is now required to predict the long-term consequences for marine ecosystems.

Pelagic Indo-Pacific reef fishes: Remarkable animals doing remarkable things

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Nearly all teleost fishes that live on coral reefs as adults spend their early life history in the pelagic environment before finding settlement habitat and adopting a demersal life style. These pelagic reef fishes look different from the adults (often with highly specialized morphology), live in different places, eat different things and have different behaviours. Our ability to identify larval fishes from the Indo-Pacific has expanded greatly, and study of larval morphology and ontogeny has played an important role in determining relationships in several groups. Once identification obstacles are [partially] overcome, it becomes possible to investigate the ecology and behaviour of the larvae. Behaviours and capabilities of Indo-Pacific larval-fishes have surprised us, yet they have important implications for reef-fish demography, population connectivity and evolution. The otoliths of larval fishes can reveal much about the their pelagic sojourn, allowing inferences not only about pelagic larval duration, but also growth, origin and dispersal trajectory. The small, pelagic larvae of demersal fishes are excellent swimmers, are able to orientate their swimming in the seemingly featureless pelagic environment, and are highly successful, specialized feeders. Larval reef-fish physiology is astonishing: the larvae can not only to swim at high speeds (20-30 body lengths per sec) over long distances (10s of km), but also readjust their physiology rapidly upon settlement. Plus, they have well-developed sensory systems that seem to be able to do things we humans can't. What we now know about the remarkable larvae of Indo-Pacific fishes, along with what we don't know, are reviewed. This talk examines whether the warm-water larvae of the Indo-Pacific are substantially different in these issues from those of temperate waters. It will also speculate on how larval-fish studies will change, and describe some threatening changes that lie ahead.

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Sex, Hues & Ecological Roles: how natural selection drives incipient divergence despite continuous gene flow in sympatric color morphs of the arceye hawkfish

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The role of sympatric speciation in generating marine biodiversity is a long-standing controversy. Despite a growing body of empirical evidence, many examples remain hotly debated due to the challenges of dis-proving past phases of allopatry. The approach here is to utilize a unique case of speciation-in-action in the arceye hawkfish to examine the earliest stages of divergence, where the factors causing the split are still evident and testable. Here, we provide evidence suggesting that disruptive natural selection on color pattern in combination with color-based assortative mating may be driving divergence in sympatric populations of the color polymorphic arceye hawkfish (*Paracirrhites arcatus*) in Hawai'i. First, results from ecological surveys indicate that color morphs exist in adjacent, yet divergent niches. Second, behavioral observations have shown that even in zones of overlap morphs tend to segregate assortatively, thereby reinforcing reproductive isolation. Third, genetic analysis of 30 microsatellite loci shows divergent patterns of genetic variation across morphs that are likely linked to areas under natural selection. To gain further resolution, we are currently using RAD sequencing to perform genome scans of thousands of SNPs (single nucleotide polymorphisms) to identify genomic regions that show signatures of natural selection and elucidate the relative roles of both neutral and selective processes on genomic differentiation. Taken together, these results suggest that reproductive isolation between morphs may be arising as a by-product of divergent selection on ecological differences and enhanced by the isolating effects of assortative mating. This research provides the first evidence of a marine fish diverging within Hawai'i and one of the few case studies of ongoing sympatric divergence in any marine fish. We argue that divergence with continuous gene flow is not only possible, but may be a potentially significant mechanism of divergence in species-rich communities like coral reefs.

Range-wide phylogeography of goatfishes of the genus *Mulloidichthys*

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The genus *Mulloidichthys* comprises seven species of goatfishes that inhabit coral reefs throughout the tropics. Recent morphological work suggested the presence of cryptic species within the genus and a need for a taxonomic revision. We constructed a molecular phylogeny with mtDNA cytochrome b, ATPase8 and ATPase6 sequences. Initial divergence of the genus dates to the Pliocene (*M. pflugeri*, *M. flavolineatus* and *M. vanicolensis* clade), but the rest of the members of the genus split during the Pleistocene (*M. vanicolensis*, *M. dentatus, M. martinicus* and *M. mimicus*). Whereas the origin of the Tropical Eastern Pacific *M. dentatus* and the Tropical Western Atlantic *M. martinicus* is consistent with a history of allopatric isolation following rare dispersal events across the biogeographic barriers, we hypothesize that adaptation to predation avoidance might have played a prominent role in the split of the sympatric sister species *M. mimicus* and *M. vanicolensis*. We undertook range-wide phylogeographic surveys of *M. flavolineatus and M. vanicolensis,* in the Indo-Pacific, *M. dentatus,* in the Tropical Eastern Pacific, and *M. martinicus,* in the the Tropical Western Atlantic. Within-species examinations of *M. vanicolensis* and *M. flavolineatus* indicated a history of colonization in the Red Sea consistent with the complex biogeography of this region, and little genetic structure throughout the rest of the range. Similarly, we did not find any genetic partitions within *M. dentatus* in the Tropical Eastern Atlantic and *M. martinicus* in the Tropical Western Atlantic. Our work constitutes an unprecedented revision of the molecular taxonomy of *Mulloidichthys* and highlights the potential of this system to study speciation mechanisms in reef fishes.

"Phylogeography and evolution of butterflyfish in the subgenus *Corallochaetodon*: *Chaetodon lunulatus*, *Chaetodon trifasciatus*, *Chaetodon austriacus*, *Chaetodon melapterus*"

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Butterflyfishes are diverse pan-tropical fish that have stunning coloration, high levels of ecological and morphological diversity, and are important members of coral reef communities. Research has shown that butterflyfishes, because of their distinct specialist diets and geographical range, are an ideal model group for studying ecological specialization. The subgenus *Corallochaetodon* consists of four parapatric species that are specialized corallivores: *Chaetodon lunulatus, Chaetodon trifasciatus, Chaetodon austriacus,* and *Chaetodon melapterus*. The varying size of their distribution ranges, colorations, and dietary specializations species suggest that distinct patterns of genetic diversity and population structure may arise within this subgenus. We hypothesize that habitat requirements and geographic isolation may both influence evolutionary patterns in these species. To examine the population connectivity and determine if there is a difference in population genetic structure between the sister species, a genetic comparison is underway consisting of microsatellite loci and mtDNA sequences. Previous studies suggest that the size of the distribution range is a good predictor of population subdivision in reef fishes; therefore we expect a low level of genetic structure in the widespread Pacific *C. lunulatus*. However, preliminary data from the Hawaiian archipelago indicate strong population subdivision with at least two distinct management units. Evaluating gene flow within this subgenus will determine populations that can be defined as distinct management units and indicate how these specialists will react to declining resource availability. A pattern of contrasting gene flow in a dietary specialist versus a habitat specialist can facilitate management of other reef fish species and contribute to our understanding of biodiversity on Indo-Pacific coral reefs.

Reef fish hybridisation at biogeographic boundaries: butterflyfish hybrids at Christmas Island

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Natural hybridisation is widespread among coral reef fishes. However, the ecological promoters and evolutionary consequences of reef fish hybridisation have not been thoroughly evaluated. Butterflyfishes form a high number of hybrids and represent an appropriate group to investigate hybridisation in reef fishes. This study provides a rare test of terrestrially derived hybridisation theory in the marine environment by examining hybridisation between *Chaetodon trifasciatus* and *C. lunulatus* at Christmas Island. Overlapping spatial and dietary ecologies enable heterospecific encounters. Non-assortative mating and local rarity of both parent species appear to permit heterospecific breeding pair formation. Microsatellite loci and mtDNA confirmed the status of hybrids, which displayed the lowest genetic diversity in the sample and used a reduced suite of resources, suggesting decreased adaptability. Maternal contribution to hybridisation was unidirectional, and no introgression was detected, suggesting limited, localised evolutionary consequences of hybridisation. Comparisons to other reef fish hybridisation studies revealed that different evolutionary consequences emerge, despite being promoted by similar factors, possibly due to the magnitude of genetic distance between hybridizing species. This study highlights the need for further enquiry aimed at evaluating the importance and long-term consequences of reef fish hybridisation.

Hybridization and extensive introgression in Indo-Pacific sister species of surgeonfish

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Sister species can provide valuable insights into evolutionary processes through their ecology, distribution, and the history of recent divergence recorded in their genomes. In the Indo-Pacific, many reef fishes are divided into sister species split between the Indian Ocean and Pacific Ocean, with a broad zone of contact in the eastern Indian Ocean. It is unclear whether hybridization in this contact zone represents incomplete speciation, secondary contact, an evolutionary dead-end (for hybrids), or some combination of the above. To address these issues, we conducted a range-wide survey of sister surgeonfish species, *Acanthurus leucosternon* (N = 110) and *Acanthurus nigricans* (N = 344), with mtDNA cytochrome *b* sequences and ten microsatellite loci. These surgeonfish are found primarily in the Indian and Pacific Oceans respectively, but overlap extensively, including hybrid zones at Christmas Island and Cocos-Keeling Islands in the eastern Indian Ocean. Our results indicate little genetic structure within-species, evidence of recent population expansion across their range, and a separation between species that dates to the Pleistocene (600,000 years ago). We also found between-species sharing of some mtDNA haplotypes and extensive hybridization based on microsatellite alleles, consistent with (later generation) hybrids within and outside of the suture zone. Here we highlight the introgression in reef fish complexes that goes undetected at oceanic islands.

Hybridization between the endemic Hawaiian Sergeant Major, *Abudefduf abdominalis*, and a recent immigrant, *A. vaigiensis*

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The ecological impact of the introduction of non-native species has been extensively studied; however the evolutionary implications of these introductions on endemic populations have received little attention. The Hawaiian Archipelago is the most remote island chain on earth, where over a quarter of the marine species are endemic. In the early 1990's the Indo-Pacific Sergeant Major, *Abudefduf vaigiensis*, was reported in Hawaii waters for the first time, believed to have arrived via flotsam. In 2007 reports of interspecific spawning and the presence of an intermediate color morph of *A. vaigiensis* and the endemic Hawaiian Sergeant Major, *A. abdominalis,* indicated the possibility of hybrid offspring. Using molecular techniques, this study aimed to: 1) Determine whether interspecific spawning was successful and if the intermediate morphs are indeed hybrids, 2) evaluate if there is introgression, and 3) describe the frequency of hybridization (numerically and geographically) across the Hawaiian Archipelago. We analyzed 328 and 225 samples of *A. abdominalis* and *A. vaigiensis*, respectively, from across the Hawaiian Archipelago and assessed mtDNA and nDNA sequence data to infer maternal and parental species lineages for each individual. Hybridization frequency across the archipelago ranged from 6.92-9.91%, and 5.42% of the population classified as an F2 or BC1 backcross. A higher frequency of hybridization was observed in the Main Hawaiian Islands than in the Northwestern Hawaiian Islands and may be attributed to higher population densities of both species in that region. These findings show that, ~20 years after the initial introduction, *A. vaigiensis* has fully colonized the Hawaiian Archipelago and is producing hybrid offspring with *A. abdominalis*. If hybridization frequency increases the formation of hybrid swarms may prove a threat to the evolutionary integrity of the endemic *A. abdominalis.*

Do endemic and widespread species exhibit different patterns of genetic connectivity? A phylogeographic comparison of Hawaiian endemic and Indo-Pacific damselfish species in the Hawaiian Archipelago

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Remote islands and archipelagoes are known for exhibiting high rates of endemism in marine taxa. The Hawaiian Archipelago is one of the most isolated archipelagoes in the world. Over 20% of its reef fishes are endemic to the archipelago, making Hawaii a global hotspot for reef fish endemism and therefore an ideal system for studying endemics. With respect to connectivity, endemic species essentially represent closed systems that are maintained by local larval production. Conversely, widespread species, which possess much broader geographic distributions and higher dispersal potential, can theoretically receive propagules from distant populations. This study addresses the question of whether these characteristics result in endemic and widespread species exhibiting different patterns of genetic connectivity, particularly within the Hawaiian Archipelago. Genetic surveys were conducted for two Hawaiian endemic (*Abudefduf abdominalis* and *Chromis ovalis*) and two Indo-Pacific (*A. vaigiensis* and *C. vanderbilti*) damselfish species throughout the archipelago. Levels of connectivity were evaluated based on sequences from two mitochondrial markers: cytochrome *b* and the control region. Because they contribute to biodiversity value, endemic species are of special interest to the designation of marine protected areas. Furthermore, the limited range size of endemics places them at greater risk of extinction and thus at greater need of protection. Knowledge on how endemic and widespread species differ in terms of connectivity could have significant implications for conservation. Additionally, the results of this study will be useful in assessing how much connectivity is exchanged between the Main Hawaiian Islands and the Northwestern Hawaiian Islands, which constitute the Papahānaumokuākea Marine National Monument. This topic has been highlighted as a research priority by the management of the Monument and may provide valuable data for other marine protected areas in the tropical Pacific.

A Review of multispecies connectivity

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The exchange of individuals across populations, termed connectivity, is most readily studied in the marine ecosystem using genetic markers, which allow researchers to infer patterns of pelagic dispersal for marine taxa. However, genetic connectivity provides a composite picture of the multiple effects of oceanography, ecology, as well as historic and demographic effects on genetic diversity. Hence, despite hundreds of studies on singular exemplar species across the globe, it is still unclear whether coherent patterns across species emerge within a given location or ecosystem. Aside from piecemeal evidence for the roles of oceanography and habitat quality in shaping general trends at a given location, there is little understanding of the key drivers of community-level cohesion and the factors governing connectivity for entire suites of species. In the Hawaiian Archipelago, we find four concordant barriers to dispersal across a broad and diverse range of 27 marine species (from cnidarians to elasmobranchs and marine mammals) that are not detected using single-species approaches. The present review will examine the potential bases for such shared genetic restrictions within the general context of multispecies connectivity, as well as explore the methodologies under development useful towards such meta-analyses across multiple genetic loci at the archipelagic scale. Understanding the mechanisms underlying multispecies connectivity has broad application towards both multispecies fisheries and ecosystem-based management initiatives, while providing a novel perspective in modeling the flow of genetic information across ecosystems.

Comparative anatomy of *Biwia* and *Microphysogobio* (Cypriniformes, Cyprinidae, Gobioninae)

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The genera *Biwia* and *Microphysogobio* include 29 species and are typical bottom-dwellers that inhabit various waters in Eastern Asia. Though previous studies have been focusing on the generic relationship between *Biwia* and *Microphysogobio*, the interrelationships and evolutionary process at species level remain unclear. In the present study, we investigated the anatomical characters such as osteology, cephalic lateral line systems, intestines and air bladders in all *Biwia* species and some related *Microphysogobio* species. Relevant comparative anatomy clarified some derived characters among these groups. (1) All the species belonging to *Biwia* and *Microphysogobio* share the long rostral branch. (2) *Biwia* and *M. linghensis* share disjunction of the infraorbital from the supraorbital and preopercle canals, and each supratemporal canal. (3) In Korean *Microphysogobio* except *M. jeoni*, the mandibular canal is absent in association with the development of the lower lip and papillae. (4) *Microphysogobio* that lacks a mandibular canal, reciprocally has a very complicated intestine. (5) *Biwia* and *M. linghensis* share middle-sized air bladders. (6) In most *Microphysogobio* species, air bladders are very small, as has been previously described. These findings lead us to reconfirm the sister-group relationship between *Biwia* and *Microphysogobio*, such as character (1). *Biwia* is so unique that they have paedomorphic characters such as disjunction of each cephalic lateral (2), while *Microphysogobio* has strong autapomorphies such characters as (3) and (4). Although *Microphysogobio* was regarded as a paraphyletic group because of the absence of definitive autapomorphies in relationship with *Biwia* (Hosoya, 1988), this genus was indicated as a monophyletic group in this study. Some taxonomic problems were also highlighted on the basis of our phylogeny. *Microphysogobio linghensis* shares (2) and (5) with *Biwia,* but does not have the autapomorphies of *Microphysogobio* in (3) and (4). Therefore, we conclude *M. linghensis* should be transferred to *Biwia*. Furthermore, *Microphysogobio jeoni* shares the characters (1) and (6), but does not have the autapomorphies of either *Biwia* or *Microphysogobio*. Hence, we speculate that *M. jeoni* is the most ancestral species of both genera.

Phylogenetic insights into the evolution of Ostariophysi (Gonorynchiformes, Cypriniformes, Characiformes, Siluriformes, and Gymnotiformes) using ultraconserved elements

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Ostariophysi is a superorder containing over 8,000 species (roughly 25% of all known bonyfishes and 75% of all freshwater fishes) in 1100 genera and 70 families. This superorder is divided into five major lineages: Gonorynchiformes (milkfishes and sandfishes), Cypriniformes (carps and minnows), Characiformes (tetras), Siluriformes (catfishes), and Gymnotiformes (Neotropical electric knifefishes). The relationships among these major groups remain poorly understood. Molecular and morphological analyses have yet to result in a consensus phylogeny except that most previous analyses distinguish Anotophysi (Gonorhynchiformes) from the remaining four lineages (grouped together in Otophysi). The Otophysi lineage is united based on a number of unique features including a Weberian apparatus (a particular arrangement of vertebral structures that connect the swimbladder to the auditory system) and the production of a unique chemical alarm substance (Schreckstoff). In this analysis we use massively parallel sequencing techniques in a next-generation framework that utilizes the phylogenetically informative flanking regions of ultraconserved elements (UCE) to produce a phylogeny of thirty representative ostariophysan taxa. The UCE approach results in a highly supported and well-resolved phylogeny from several hundred genetic loci in one the most data-rich analyses of its kind.

Taxonomy and distribution pattern of Japanese grenadiers (Gadiformes: Macrouridae)

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The family Macrouridae, commonly known as grenadiers or rattails, is one of the most diverse and dominant deep demarsal fishes in the world ocean. In the northwestern Pacific around Japan, extensive trawl surveys have been conducted over the past century, resulting in numerous grenadier specimens in museum collections. Taxonomy and distribution pattern of Japanese grenadiers were reviewed based on more than 9,400 specimens collected at depths between 78 to 6,450 m (*Bathygadus* and *Gadomus* were excluded in this study). Literature records were evaluated mostly from voucher specimens. Total 69 species representing 2 subfamilies and 16 genera were found, including at least 4 undescribed species and 4 new records. Twenty of these are currently known only from Japanese waters. The genus *Coelorinchus* is the most specious with 25 species (36.2%), followed by *Coryphaenoides* with 16 (23.2%), *Ventrifossa* with 7 (10.1%), and *Nezumia* with 6 (8.7%). These four genera comprise about 3/4 of the total fauna. While a few species are widespread, most have southerly or northerly distributions. Additionally, the number of species generally decreases towards the northeast: 50 from the East China Sea (including 9 known only from northern Taiwan); 53 from off the Pacific coasts of southern Japan; 18 from off the Pacific coasts of northern Japan; 7 from the Okhotsk Sea; 9 from the Sea of Japan (including 3 known only from Korea); 13 from the Kyushu-Palau Ridge. While the dispersal ability of grenadiers is largely uncertain, these trends suggest that the distribution of each species might be affected by water temperature as well as ocean currents, particularly the warm waters of Kuroshio and the cold waters of Oyashio.

Molecular systematics and biogeography of the Sciaenidae (Teleostei: Perciformes)

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The family Sciaenidae contains approximately 66 genera and 295 species. Most of the species are ecologically and economically important fishes found throughout warm temperate to tropical coastal waters and estuaries. Only a few species from five genera inhabit restrictedly freshwater. Previous phylogenetic studies of the Sciaenidae were conducted using morphological and/or mitochondrial DNA data and most of these studies have focused on a few taxa in a unitary area. An overall phylogenetic hypothesis for the Sciaenidae is still lacking, making difficult to reconstruct and discuss the biogeography of this group. The aim of this study was to infer the phylogenetic relationships of 99 globally sampled sciaenid species in 51 genera using a phylogenomic approach. Our character sampling included two mitochondrial and four nuclear genes for a total of 6,618 base pairs. Three perciform taxa from Moronidae, Lethrinidae, and Sparidae were chosen as outgroups for the analyses. The results show that the family Sciaenidae forms a monophyletic group. Within the family, several strongly supported clades are found, including a large clade containing only species found in the Indo-Western Pacific region. The widely distributed genus *Argyrosomus* (from Eastern Atlantic and Mediterranean to Western Pacific), the western African endemic genera, *Pseudotolithus* and *Pteroscion*, and the American endemic *Totoaba macdonaldi* (in the Gulf of California in Mexico) are close allies of the sciaenids from Indo-Western Pacific clade. The genera *Argyrosomus*, *Larimichthys*, *Pennahia*, *Nibea*, and *Johnius* represented with multiple species sampled in this study appear to be monophyletic while *Umbrina*, *Cynoscion, Scianea* and *Pseudotolithus* are not. The South-American freshwater sciaenids sampled in this study form a monophyletic group and they are not related to the North-American freshwater sciaenid, *Aplodinotus grunniens*. This result suggests at least two independent transitions from marine to freshwater environments. As far as we know, this is the most comprehensive phylogenetic study of the family Sciaenidae. Our phylogenetic hypothesis provides a framework to further investigate the global sciaenid biogeography.

Comparative morphology and molecular based intrarelationships of sanddivers (Perciformes: Trichonotidae)

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The family Trichonotidae (*sensu* Nelson, 2006) is composed of the single genus *Trichonotus* with 12 species and 6 undescribed species. All species of the genus are protogynous showing remarkable sexual dimorphism, which was the cause of their taxonomic confusion. Excluding the unique *T. filamentosus,* the genus is divided into three morphological groups: *Trichonotus setiger* group (5 species) previously misidentified as a wide ranging species, "*T. setiger*", *Trichonotus cyclograptus* group (3 species) without elongated dorsal-fin spines in male, and *T. elegans* group (3 species) having slender body, free-pterygiophores under interdorsal space, and scaleless portion on body. In this study, we tentatively estimate the relationships among *T. setiger* and *T. elegans* groups, and *T. filamentosus* by using morphological and partial mtDNA data. The present molecular analysis supports the monophyly of *Trichonotus* species examined and each group, except for the placement of one species, and the uniquness of *T. filamentosus*. As in other recent studies, our data implies that the percophid Hemerocoetinae and Creediidae is closely related to *Trichonotus,* and that the Hemerocoetinae is the sister group of *Trichonotus*. Further, we discuss the systematics of the family Trichonotidae and the evolution of some morphological characters of *Trichonotus* species.

The species of the clinin genus *Springeratus* and their distribution (Blennioidei: Clinidae)

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The Indo-west Pacific clinin *Springeratus* is the only genus with a broadly tropical distribution. Like other Clinini it is a live bearer. Work on gene flow patterns of some South African clinids and the dearth of larvae in plankton samples suggest that a short planktonic existence curtails dispersal abilities of Indo-west Pacific clinid species.This paper looks at the putative species of *Springeratus*, which are difficult to distinguish morphologically, and explores some preliminary ideas about their biogeography.

Molecular identification of fish eggs in the Korean waters: focus on *Trichiurus japonicus*

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Morphology-based identification of fish eggs has been regarded ambiguous because of their microscopic size and deficiency of taxonomic information. In order to resolve the difficulty, several molecular techniques have been adopted. We identified fish eggs using molecular markers for estimating spawning period and area. Fish eggs were collected from 2009 to 2012 around the Korean Peninsula, including adjacent waters of Jeju Island, the Korean Strait and the East Sea using ichthyoplankton sampling gears (conical net, Bongo net, IKMT net). Many types of fish eggs were divided according to morphological characters such as egg shape, size and membrane structure, subsequently were identified to the species level using DNA barcoding. A variety of fish eggs were identified (i.e. family Trichiuridae, Moronidae, Aulopodidae, Labridae and Uranoscopidae species). We newly found *Trichiurus japonicus* spawns from coastal area of south sea to offshore, even to the southern Jeju Island during May-November.

Distributional and habitat characteristics of a rare hypogean gobiid, *Luciogobius pallidus* from Jeju Island, Korea (Perciformes: Gobiidae)

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From the Korean waters, only four species of the worm-like gobiid genus Luciogobius have been recognized as follows: L. grandis, L. guttatus, L. koma, and L. saikaiensis. Recently we collected another Luciogobius species with a unique coloration of yellowish orange from the southern coastal waters of Jeju Island, Korea during the Excavation Project of Korean Indigenous Species by chance. It was subsequently identified as L. pallidus on the basis of comparison with type specimens of the species. L. pallidus has been recognized as a rare hypogean fish lives primarily in groundwater or spring in the western part of Honshu Island, Japan until now. The present record of the species in Korea is not only the first record out of the Japanese waters but also the westernmost record of the world of L. pallidus. To establish the fundamental information for conservation of the species in Korea, we conducted the field survey focused on clarification of distributional and habitat characteristics of L. pallidus along the coastal region (mainly on intertidal zones) of the island during the ebb tide from January to December in 2012. Fish fauna of the intertidal zone of the island occurring Luciogobius species were also investigated. As a result, it was revealed that L. pallidus occurs from the northwestern and southwestern coastal regions of Jeju Island, whereas its similar species L. guttatus was found from almost all surveyed intertidal regions of the island. Totally 40 species belong to 14 families were also collected from the surveyed area of the island. The family Gobiidae comprising 18 species was the most abundant followed by the family Stichaeidae consisting three species. In addition, four gobiid fishes comprising L. elongatus, L. platycephalus, Clariger cosmurus, and Bathygobius hongkongensis were also found as new to Korea. Especially, L. pallidus was found throughout the year from the intertidal zone located at Haye region of the island and was ranged from 17.6 mm o 58.6 mm in standard length. The species was inhabited mainly on gravel substrate composed of coarse sands and pebbles under the boulders or rocks where freshwater spring is flowing from gaps between pebbles.

Gradient variation of quantitative traits among flatfish species (Teleostei: Pleuronectidae): testing different adaptive hypotheses

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Clinal variation in quantitative morphological traits associated with a temperature gradient or with geographical latitude is well described for fishes. Different species from the northern cold waters, including several righteye flounders (Pleuronectidae), usually have a higher number of vertebrae and fin rays than their southern conspecifics. However, many flounder species that share similar latitude-temperature regimes also differ by the same quantitative traits demonstrating evolutionary change in their mean phenotypes. Furthermore, some sister species have the opposite direction of interspecific variation, showing lower character values in the north and higher in the south, which may indicate some adaptive response confounded with ecological heterogeneity. Therefore, factors involved in inter-species variation among righteye flounders are more complex than previously thought. In the present study, different morphometric and meristic characters of sixteen species of righteye flounders from the Northern Pacific and two from the Western Atlantic coast were analyzed using principal components (PC) and then were tested for different selective regimes in the R package OUCH (Butler and King, 2004). Maximum likelihood phylogenetic trees were reconstructed from cytochrome *b* and cytochrome oxidase I partial sequences (~1750 bp in total). The variation between the group means in PC1 (fin ray counts) and PC2 (body shape) was analyzed against spatial and depth distribution ranges of the species. Four distinct benthic groups of flounders significantly correlated with the gradient change in PC1 ($F = 71.22$, $d.f. = 3$, $p = 0.0001$): nearshore (0–50 m), sublittoral (0–200 m), epibathyal (100–400 m) and mesobathyal (200–1000 m). A significant difference was also observed between geographic locations by PC2 ($F = 5.02$, $d.f. = 3$, $p = 0.01$). The best-supported model for variation in PC1 was the adaptation to depth, and for variation in PC2 was the geographic model with northern, southern and ubiquitous species. A comparison of different phenotypic optima revealed a gradient increase in fin ray numbers with oceanic depth and the increase in body depth with the geographical latitude. These results provide new insights into the variation, and responsivity to selection pressures, of quantitative traits among flatfishes.

Sources and sinks of larvae among reefs of the Great Barrier Reef

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The persistence of reef fish populations depends on reproductive output, larval survival, pathways of connectivity and postsettlement processes. Historically, it has been assumed that the genetic robustness of populations among reefs that are closely spaced would be on temporal scales of tens of years or much longer. Here we present data on an apogonid *Ostorhinchus doederleini* from a group of four reefs separated by kilometers to tens of kilometers on the southern Great Barrier Reef. Over a nine year period we have demonstrated significant differences in the population genetics of fish among reefs. Some reefs have shown a relatively persistent genetic composition, while others have varied greatly. We provide evidence that the size of source populations is important. Reefs with large lagoons have exhibited small changes in genetics among years. In contrast reefs with little lagoonal habitat showed greatest changes among years. We have demonstrated that larval apogonids are capable of detecting olfactory cues from their natal reef and this contributes to genetically distinct populations. There is also a vulnerability for *O. doederleini* that would contribute to population change in that few fish live beyond 6 months and age maxima are less than one year and, therefore, spawning failure could result in a population collapse. Further, residents can also influence successful settlement by chasing non-member reef recruits. Persistence of distinct genetic populations is likely to vary with demography, the size of spawning stock, larval processes and priority effects at settlement. In conclusion, reefs that are closely spaced can have populations that are genetically distinct and can be a geographic unit of speciation

Reverse-assembly of a large-scale larval dispersal model

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Genetic isolation by distance (IBD) estimates are useful starting points for the study of ecologically important parameters pertaining to population connectivity. The twoband anemonefish *Amphiprion bicinctus* in the Red Sea represents an ideal study system for IBD research by incorporating a highly sedentary organism with an intermediate pelagic larval duration among a linear coastline with nearly continuous habitat. The restricted size of the basin allows for an integrated modeling approach, based on oceanography and genetic patterns. We genotyped 991 individuals from 19 locations spanning over 1400 km of the Saudi Arabian coastline of the Red Sea over 38 polymorphic microsatellite loci. We then compare observed patterns of genetic structure to the predictions of a spatially explicit genetic framework informed by a 3-D model of oceanographic currents. We are thus able to reconstruct a realistic scenario that describes connectivity across the whole Red Sea basin for *A. bicinctus*. This approach allows for the fine-tuning of different larval characteristics (e.g., vertical migration, ontogenetic changes in attraction to reefs, mortality) according to model fit. Our approach may outline a blueprint of how large-scale population genetic datasets, in conjunction with detailed oceanographic models, can be used to infer larval behaviour and its effects on metapopulation connectivity. Our genetic data reveals a noticeable break between the southernmost and central and northern populations of *A. bicinctus* in the Red Sea, a pattern that oceanography and behaviour alone cannot fully explain. The genetic disruption concurs with a marked shift in environmental conditions in the southern Red Sea compared to central and northern sites. Mismatches of phenotypes adapted to origin conditions settling in a non-suitable environment might thus cause selection against immigrants at the southern sites, resulting in a disparity of larval dispersal and reproductive connectivity. This study underlines the importance of a holistic approach to connectivity research and denotes the potential importance of post-settlement selection in shaping patterns of large-scale genetic structure.

Importance of reproductive mode, PLD and local abundance on larval dispersal

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There is a growing body of evidence indicating that larval connectivity can be influenced by species-specific life history traits (e.g. mode of spawning, PLD, sensorial capabilities), oceanography and geographic settings. However, a comprehensive understanding of how these factors, and their interactions, influence the extent of larval dispersal in marine populations remains poorly understood. Here, we compared genetic variation inferred from microsatellite markers (between 12 and 18 loci per species) among three coral reef fish species (*Cheatodon vagabundus, Amphiprion percula* and *Amphiprion polymnus*), along seven sampling sites separated between 30 and 140 Km in Papua New Guinea. *C. vagabundus* is a pelagic spawner with a ~38 day PLD, while both *Amphiprion* species are benthic spawners with a ~11 day PLD). In turn, *A. polymnus* and *A. percula* have similar reproductive strategies and PLD but differ in their local abundances. While *A. polymnus* is rather rare, found in small patches of sandy substrate, *A. percula* occurs commonly in reefs within the study area. These settings provide a unique opportunity to evaluate the relative importance of spawning mode, pelagic larval duration and species relative abundance on the extent of larval dispersal (genetic structure), while controlling for differences in geographic settings. The results from this work will provide valuable information for conservation management of Indo-Pacific coral reef fish.

Integrating larval behaviour, dispersal, habitat selection, and recruitment dynamics in a temperate reef fish metapopulation: identifying drivers of resilience in a changing ocean

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The replenishment of benthic marine populations is the culmination of many processes that influence the production, dispersal, settlement and survival of larvae to maturity. Although there have been recent advances in our understanding of dispersal and its importance to population connectivity, to date no study has attempted to evaluate all early life-history processes to assess their relative importance in the maintenance and stability of marine metapopulations. Using a model temperate reef fish species, the southern hulafish (*Trachinops caudimaculatus*), we present data on larval vertical distributions, larval dispersal patterns from otolith microchemistry, larval settlement from behavioural choice experiments, and population vital rates from longitudinal surveys and integrate these empirical results into a coupled biophysical dispersal model and a stage-structured metapopulation model. Integrating field and lab-based data with a spatially explicit metapopulation model allowed us to map the emergent patterns in population persistence and metapopulation dynamics. Our results highlight the importance of using ecologically realistic frameworks that incorporate the complex dynamics of real metapopulations in conservation planning and fisheries management.

Winners and Losers: Effects of dispersal on larval fish phenotypes and stability of a reef fish metapopulation

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Many fishes produce excess offspring, and most individuals will die before they can reproduce. Such reproductive "losers" may persist in populations for extended periods, to shape evolution and exact unknown costs on individuals that successfully breed (i.e., winners). The importance of "survival of the fittest" is well recognized across biological disciplines, but what are the consequences of losers, which can compete for resources, attract predators, and alter the fates of winners? Since Darwin's seminal work, existing paradigms have been preoccupied with winners; reproductive losers are rarely a focus of investigation. Our previous research on a small marine fish, the common triplefin (*Forsterygion lapillum*), indicates that losers may be created when young individuals experience unfavourable conditions during larval development. We use LA-ICPMS and image analysis to unlock the "environmental fingerprints" and demographic records preserved within fish otoliths, to infer that: (i) larval fish developing in offshore waters acquire distinct traits that transform them into losers; (ii) losers regularly recruit to reefs alongside winners; and (iii) losers may be more readily shuffled between distant populations. We present results from empirical studies and mathematical modeling, which together, reveal how the presence of multiple phenotypes (i.e., winners and losers) can affect local population structure and the stability of a reef fish metapopulation.

Sound propagation in the ocean: A case study in the North coast of Moorea, French Polynesia

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Underwater sound emanating from reef crest is known to attract fish and crustacean larvae, but the distance at which it propagates as a valuable orientation cue for the larvae is not yet know. In our present study, we aimed to estimate the distance at which the crest sound gradient is overlapped by ocean sound. Environmental underwater sound recordings were taken at three sites on the North coast of Moorea Island (French Polynesia) at day, dusk and night time, at distances ranging from the crest to two kilometers in the ocean, and were compared to simultaneous recordings taken at the crest. No variation in sound intensity and spectrum was observed at the crest with day time and site, but sound propagation in the ocean varied with site. At the site situated in the middle of the crest, we observed a cylindrical loss of sound pressure with distance until one kilometer, a result congruent with previous calculations based on acoustical particle velocity of reef sound. The larval fishes would then not be able to orientate themselves through the crest sound gradient at distances greater than a kilometer. Our results also highlight a "pass effect" in front of fast-flowing pass, where sound intensity pressure in the ocean on great distances is higher than expected due to water flow turbulence, which might increase the distance of sound detection by fishes. To better estimate the real distances over which larval fishes can detect reef sound, studies on acoustic pressure and particle motion effects on larval fish hearing are needed, as well as a better understanding of relation between reef crest topography and sound propagation.

Orientation abilities and sensory cue hierarchy in reef-fish larvae using visual orientation

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Most reef fishes spend part of their early development as larvae in the pelagic environment. As many species are site-attached as adults it is during this phase that spatial dynamics of populations are determined. Dispersal of larvae was previously thought to be dictated by physical processes such as ocean currents alone, however we now know that orientation and swimming abilities in larval fishes may be sufficient to influence their dispersal to habitat. It is not clear which sensory cues are utilised for this behaviour in an environment where visual landmarks are scarce. This study, carried out at Lizard Island Research Station on the Great Barrier Reef in January 2013, investigated the use of celestial cues for orientation in settlement-stage larvae of a pomacentrid, the black-axil chromis (*Chromis atripectoralis*) by simulating changes in sun position and polarised light patterns to assess the ability of larvae to detect these cues and what trade-offs may be involved between them. The effects on orientation abilities in this species and the relative importance of these sensory cues were investigated: the results and their implications will be presented. A better understanding of orientation behaviour in larval fishes is critical for accurate modelling of population connectivity and therefore fisheries management and conservation.

Preference of fish larvae for coral above algal water cues: Potential implications in the context of coral reef degradation

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The biodiversity is declining, and habitat degradation is now commonplace. The degradation in coral ecosystems is usually characterized by coral mortality from natural and anthropogenic stressors. This decrease of coral cover causes substantial increases in macroalgal cover which, in turn, limits the recovery of coral populations and thus modifies fish and invertebrates communities. Thus, areas experiencing perturbance often exhibit declines in adult populations, leading to a higher rate of extirpation than in pristine habitat, and the persistence of species in the area becomes reliant on the rescue effect of recruitment. While evidence is mounting that larval fish are active participants in the process of dispersal and recruitment, the sensory and behavioural mechanisms by which larvae disperse and return from their oceanic phase to appropriate recruitment habitat remains unknown, especially in the context of habitat degradation. Our study aimed to test the preference of fish larvae for coral vs. algal water cues at Rangiroa Island. Many reefs in French Polynesia have changed from coral to algal dominate states, and the abundance and species richness of dominant corals, sea-urchins, parrotfishes, and surgeonfishes that provide either direct chemical cues or indirect auditory cues vary according to reef state (coral vs. algal dominance). Therefore, the potential of French Polynesian reefs to attract larvae may have decreased, with profound consequences on the number of larvae arriving, potentially disconnecting the recruitment potential of an island from the availability of larvae in the surrounding water column.Our study aimed to test the *a priori* prediction; larval fish will orientate themselves towards water from reefs dominated by coral compared to water from reefs dominated by algae. Our experiments with 2-channel choice chambers showed that during the recruitment stage, seven of the 10 fish species studied preferred water from reefs dominated by coral compared to reefs dominated by algae (e.g. *Aulostomus chinensis, Sargocentron spiniferum*). Only one fish species (*Zebrasoma veliferum*) preferred water from reefs dominated by algae. Overall, our study showed that olfactory cues could play an important role in directing pelagic larval stage fishes to a suitable reef in which they can settle on.

Ontogenetic vertical migration of deep-sea fish revealed by oxygen isotopic analysis using secondary ion mass spectrometry

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This study evaluated the possibility to use Pacific bluefin tuna otolith (*Thunnus orientalis)* as working standard for δ18O analysis by secondary ion mass spectrometer. High lateral resolution analysis was conducted by 10-μm diameter primary 133Cs+ beam and secondary negative ions were extracted for mass analysis using an accelerating voltage of 10 kV. The multi-collector system was adjusted to detect 16O (by Faraday cup), 17O (by Electron Multiplier) and 18O (FC) ions at the same time. Repeated analysis on the same growth increments of tuna otolith showed spot to spot reproducibility better than 0.17‰ (1σ, standard error), indicating the feasibility of high precision analysis for fish otoliths. The same analytical approaches and parameters were applied to deep-sea fish to disclose their mysterious migratory life history by trans-life analysis from otolith core to the edge. Dramatic increases up to 4-6‰ of δ18Ootolith were detected in the juvenile stage of deep-sea eels (*Synaphobranchus kaupii*) and at the middle of blind cusk eel (*Barathronus maculatus*) otolith. These results clearly distinguished the fish's life history into planktonic stage in the mixed layer of the ocean and benthic life on the deep-sea floors. The signal of habitat shift was recorded within 150 μm width of otolith growth zone, which was too narrow to be clearly detected by mechanical drilling and conventional isotopic ratio mass spectrometer. However, considerable variations down to -5‰ were found when the Cs2+ beams sputtering at otolith core and larval stage. Carbon mapping by electron probe microanalyzer and staining by Toluidine Blue solution suggested the abundant organic matters e.g., proteins existed in the areas with large negative δ18Ootolith values. These findings implied careful design of analytical areas or tracks on the heterogeneous otolith was important for high accurate and precision analysis.

Sex with the lights on: the evolution of the deep-sea swallowers (Chiasmodontidae: Acanthomorphata)

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The processes of deep-sea fish diversification are poorly understood because the geographic barriers are not very clear, vast areas of the oceans remain poorly sampled, and several groups still need taxonomy and phylogeny revisions. The chiasmodontids, however, serve as good models for biogeography because the taxonomy is fairly well solved, there are little gaps in known species distribution, the family is monophyletic, and there is a phylogenetic hypothesis available for species interrelationships. Chiasmodontidae is a family of exclusively deep-sea fishes that includes four genera: two mesopelagic, *Chiasmodon* Johnson (seven species) and *Pseudoscopelus* Lütken (17 species); and two bathypelagic *Dysalotus* Mac Gilchrist (two species) and *Kali* Lloyd (seven species). *Kali* and *Dysalotus* are widely distributed in all oceans and occur sympatrically; although some species usually occurs in higher latitudes than others. In other hand, *Chiasmodon* and *Pseudoscopelus* have a high level of endemism. Overlaying the cladograma on the distribution maps, it becomes evident that the actual species range was caused by vicariant events: closely related species have disjunctive distributions with little or no range overlapping, while members of distant-related clades can be found sympatrically. Consistent patterns among different species of *Pseudoscopelus* and *Chiasmodon* indicate that the mechanisms of isolation were similar and include plate tectonics, marine currents, temperature variation and zones of oxygen depletion. Intrinsic biological characteristics also have a hole in the process: half of family diversity is composed of species of *Pseudoscopelus*. Compared to the other chiasmodontid genera, the species of *Pseudoscopelus* have a novel structure: photophores – absent in only two species. The photophores are arranged in species-specific patterns on head and body, with tenuous variation among the closely related species, but more significant variation among the distant related species. The photophores of deep-sea organism are extremely important for the colonization of that twilight zone: in most cases they serve as a mechanism of counter illumination for camouflage or individual species recognition, but in other fish families can also form structures such as lanterns and baits for predation.

Fishes of the families Bathylagidae and Microstomatidae in the exclusive economic zone of New Zealand

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The fish families Bathylagidae and Microstomtidae include meso- and bathypelagic species found in all oceans. Species of these families are difficult to identify because they are morphologically similar and due to their soft bodies are frequently damaged in trawls. This is evident from the uncertain identifications in the key to species of the Bathylagidae (including Microstoma and Nansenia) in Paulin et al. (1989). Fishery surveys that followed the declaration of New Zealand's Exclusive Economic Zone (EEZ) and the development of the orange roughy commercial trawl fishery resulted in a considerable collection of bathylagid and microstomatids species held at the fish collection of the National Museum of New Zealand. While working on this collection for a new book on the fishes of New Zealand's EEZ we found several new records for the region. We also uncovered a synonymy and, as a consequence, a new species. Vertebral counts emerged as a key character for correct identification of species of both families, but this character has been underutilized in the past. The EEZ material included specimens of larger size than previously reported for several species, particularly of the genus Bathylagichthys. Species of the Bathylagidae usually did not mix with each other and plots of their distribution within the EEZ suggest that it corresponds with frontal zones within the EEZ. Microstomatids apparently are less common as they were represented by much fewer specimens.

Gobioid Fishes of the World – A Photo-Guide

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After many years of two of us holding knowledge of gobioid species in a large database as well as in our heads, notes and filing cabinets, we have joined with the third author to produce a summary of what we know of gobioid fishes to date. The intention is to produce a photo-guide to all described gobioid species, within a classification. Sections will include history, taxonomy, discussion of various classifications, species lists, distribution, habitat information and conservation. Key features will be described and illustrated. Most of the book will be devoted to photographs, maps and brief information for each species. It is hoped that most species will be illustrated in colour.

The Systematics and Diversity of Eel Gobies (Gobioidei: Amblyopinae): Status Report for 2013

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Gobies of the gobioid subfamily Amblyopinae are elongate, mud-dwelling fishes of the Indo-West Pacific region that are commonly referred to as “eel gobies” or “worm gobies”. In life, these gobies are pink, purple, or red. In contrast to the majority of gobies, amblyopine gobies have a continuous dorsal fin; the spinous (first) and soft (second) dorsal fins are connected by membrane. Because they live in turbid water habitats, the eyes of amblyopines are reduced in size and may have limited function. The authors recognize the following two features as synapomorphies for the monophyletic Amblyopinae (i.e. ‘Taenioides’ Group + ‘Trypauchen’ Group): fin element to vertebra ratio of 2:1; and ultimate dorsal- and anal-fin pterygiophores supporting only a single ray. Currently, 15 genera and 29 species, including 3 undescribed genera and 2 undescribed species, are recognized, although recent molecular studies indicate the existence of additional cryptic species within the Amblyopinae. This presentation provides a general framework of the systematics and diversity of the Amblyopinae, updating our previous presentations.

A preliminarily revision of the eel goby, genus *Trypauchenopsis* (Gobiidae, Amblyopinae), with molecular approach

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The genus *Trypauchenopsis* is a mud-dwelling eel-like goby, inhabiting rivers and estuaries, including mangrove forests, in the Indian and West Pacific Oceans. It is a monotypic genus consisting of *Trypauchenopsis intermedia* Volz, 1903, in which two nominal eel gobies, *Taenioides jacksoni* J.L.B. Smith, 1943 and *Ta. limicola* C.L. Smith, 1964, were synonymized with *T. intermedia* in the recent redescription of *Trypauchenopsis* based on morphological characters. In contrast to generic assignment, there are many complications involved in the classification of eel gobies at the species-level based only on morphology. Thus, we applied a classic combination approach of molecular and morphology to the classification of this genus. On the basis of partial mitochondrial 16S rRNA gene sequences, two diverged lineages were detected in samples from the Ryukyu Archipelago, Japan (uncorrected p distance = 3.9%: hereafter tentatively referred to as sp. A and sp. B). As a result of the morphological examination, differences in the numbers of segmented dorsal-fin rays (sp. A, 28–31 vs. sp. B, 31–34), anal-fin rays (27–29 vs. 30–33), pectoral-fin rays (17–19 vs. 13, 16, and 17), and caudal vertebrae (16 vs. 17 and 18) between the two were clearly observed. With respect to the morphometric characters, we could not obtain any obvious key for distinguishing them. Range and denseness of black pigments on the caudal peduncle and caudal fin were also different between them. Since these genetically and morphologically distinguishable groups were distributed in sympatric, it is suggested that they are separate species. Most of the meristic characters of the holotype of *Trypauchenopsis intermedia* were assigned to sp. B, but the vertebral count, clearly different between two species in our samples, is within the range of sp. A. Since geographical variation in the combination of the counts of the morphological characters may exist, further analyses are required for samples from Southeast Asian and South African regions to clarify the taxonomical status of the members of the genus *Trypauchenopsis*.

Ontogenetic shifts in mechanisms of competitive coexistence between coral-dwelling gobies

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Coral-dwelling gobies from the genus *Gobiodon* compete for *Acropora* coral colonies, which they require for shelter, breeding sites and food. Previous research has suggested that a competitive lottery for space among juveniles promotes coexistence between two ecologically similar coral-dwelling gobies, *Gobiodon histrio* and *Gobiodon erythrospilus*. However, not all the assumptions of lottery competition have been tested and patterns of habitat use by adults suggest that niche partitioning may occur in larger size classes. We investigated the hypothesis that the mechanism of competitive coexistence changes with ontogeny, with a lottery for space operating at settlement and niche partitioning occurring in adults. To test this hypothesis, a series of field surveys and laboratory experiments were performed. First, patterns of resource use in the field were compared for juveniles and adults of each species. Habitat preference and size-based competitive ability was then tested for juveniles and adults in laboratory experiments. Finally, pelagic larval duration (PLD) and size-at-settlement of each species was estimated from otoliths to determine if differences in size at settlement could affect the outcome of competitive interactions among juveniles. Juveniles of the two species exhibited more similar patterns of habitat use in the field than did adults. Juveniles also had similar size-based competitive abilities, which is consistent with a lottery mechanism of competitive coexistence. However, the PLD of *G. histrio* (20.7 days) was over two days longer that *G. erythrospilus* (18.5 days) suggesting that differences in size at settlement could affect competitive outcomes among juveniles. Adults of each species preferred colonies of *Acropora nasuta*, however *G. histrio* was a superior competitor in laboratory experiments and prevented *G. erythrospilus* for using *A. natuta* in more them 60% of the trials. These results suggest that the mechanism of coexistence between the two *Gobiodon* species shifts from a lottery to niche-partitioning mechanisms with ontogeny and that size-based and species-specific competitive ability could affect the outcome of competitive interactions at different life stages.

Diversity of sand or sandy mud-dwelling gobiine genera in brackish estuaries and adjacent areas in southern Japan

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A large diversity of small-sized (up to 70 mm in standard length, 30 mm or less in many species), bottom-dwelling gobies of the subfamily Gobiinae is found on sandy or sandy-mud bottoms in estuaries and adjacent areas in southern Japan, including the Ryukyu Islands. Although they can be very common locally the taxonomy of many of these Japanese (JPN) species is still not well resolved. This presentation reviews some examples, including the genera *Favonigobius* (JPN species: *F. gymnauchen*, *F. melanobranchus*, *F. opalescens*, *F. reichei* and 3 undescribed species), *Heteroplopomus* (JPN species: *H. barbatus* and 2 undescribed species), *Silhouettea* (JPN species: *S. capitolineata*, *S. dotui* and 3 undescribed species) and *Drombus* (JPN species: 2 undescribed species), as well as an undescribed genus (JPN species: 1 undescribed species). Typically, the gobies of these genera have a dull, sandy-colored body, and their identification in the field is often difficult. Morphological diagnoses and geographic distributions of all 18 JPN species of these 5 genera are provided.

Review of the current state of knowledge of the systematics of gobioid fishes

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As background to a book on the gobioid fishes of the world we present an analysis of the existing classification of the group at all levels. Currently slightly over 3100 species of gobioid fishes have been described with around 1800 of those recognised as distinct species in 307 genera. Rates of descriptions of new species have increased from about 15 species a year to over 27 after 1990. Much of that increase has resulted from sampling of new habitats and increased taxonomic research on the group. Geographical color forms are frequently being described as new species without comprehensive revisionary work or genetic studies. The rate of taxonomic revisions has not increased and currently only a quarter of the genera have had a major taxonomic revision and about a quarter regarded as monotypic. It is common for the incorrect names to be applied to species and species often believed to be new have previously been described. The poor condition of many type specimens hampers some revisionary work. With so many species, the generic classification has always been highly subjective and increasingly genera are being defined with little phylogenetic analysis. The higher classification of the group is currently unresolved. Morphological approaches are dominated by loss of primitive features often suggesting paraphyly of existing primitive groups. Molecular approaches often differ from morphological classifications and change as new genes are examined. A special problem at the generic level and above is the existence of highly specialized groups, which may have evolved rapidly within an existing group.

The Chondrichthyan Tree of Life Project

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The Chondrichthyan Tree of Life Project is a five year, multi-disciplinary multi-institutional, project funded by the US National Science Foundation. Its mission is to document both extant and extinct chondrichthyan diversity and to provide an evolutionary framework for the interpretation of variation within the group. There are four components to the project (A) An up-to-date taxonomic accounting of all extant species including scientific illustrations for each species (B) An estimate of evolutionary relationships based on comparisons of DNA sequences and skeletal anatomy (C) Up-to-date range maps for all described extant species (D) CT scans for representatives of the major lineages for comparative anatomy. In pursuing the project, we have developed new technologies for high throughput DNA sequencing targeted toward phylogenetics and population genetics, technology for the interactive display of geographic range information, technology for the interactive display of comparative anatomy over the world wide web and new methods for phylogenetic analysis of DNA sequence data.

Jaws for the Tree of Life: Taxon-rich estimates of chondrichthyan phylogeny based on mitochondrial and nuclear DNA markers

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The chondrichthyan fishes are a particularly interesting group to study from an evolutionary perspective. Having undergone two major adaptive radiations, and survived several mass extinction events, they are one of the oldest and most successful vertebrate lineages. They diverge at the base of the vertebrate tree, are sister to Oestichthyes, but also show similarities with mammals in terms of genome organization. As such, understanding the relationships among chondrichthyan fishes could not only reveal their own evolutionary history, but also provide relevant insights across the broader vertebrate tree of life. To date, molecular based reconstructions of chondrichthyan phylogeny have mostly been based on mitochondrial DNA sequence data. Although useful, these estimates essentially constitute a single gene tree, which may, or may not, accurately depict true species level relationships. Highly discordant gene trees have also emerged from the few studies where independent nuclear gene markers were used, most likely due to sparse taxon and gene sampling. Consequently, the chondrichthyan phylogeny is the most poorly resolved of all the major vertebrate groups. Here, we present the most current and comprehensive estimate of chondrichthyan phylogeny to date. We analysed data from eight independent protein coding loci (7 nuclear, 1 mitochondrial), from an excellent taxon sampling that spans the diversity of chondrichthyan fishes (including representatives of 98% of extant families and 79% of extant genera). The most salient points emerging from the overall tree will be discussed, as well as some particularly noteworthy findings pertaining to specific groups of interest.

Gould and Me and the Tree of Life: Illustrating the world's shark and ray species

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The Tree of Life project is a large international collaborative project that aims to catalog the diversity and genealogy of the world's chondrichthyans (Sharks, Rays and Chimeras). As the natural history artist for the project, my work represents the major visual component of the Tree of Life project and marks the first attempt by any artist to illustrate all of the extant chondrichthyan fishes. Given the many parallels between natural history illustration and taxonomy, this talk will outline the process involved in the "cradle to grave" completion of high quality natural history artworks. This includes the processes involved in specimen selection, the close relationship with taxonomy and demonstrating how modern advances in technology have improved the field of natural history illustration. As natural history illustrations can provide the first point of reference to biological and ecological studies, it is imperative that accurate illustrations continue to be incorporated into scientific works. Given that many chondrichthyan species are facing the threat of extinction due to overfishing and habitat destruction, some species are only now being discovered just before they are potentially lost. Natural history art provides a way to preserve a record of species diversity in time for future generations.

Scanning and Segmentation of Chondrichthyan Skeletons for the Tree of Life: a Progress Report

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An ambitious project is underway to document the cartilaginous endoskeleton in modern chondrichthyan fishes (sharks, rays and chimaeras) by means of scanning and 3-D segmentation, and to make the digitized data available on-line. Specimens are scanned using a combination of medical and high-resolution tomography scanners, depending on the size and ontogenetic age of individual specimens. Segmentation analysis of the scan slices is performed using proprietary software, including Mimics and VG Studio Max running on Dell Precision Work Stations at the American Museum and the Hollings Marine Laboratory. Components of the endoskeleton are analyzed separately and each segmented structure is saved as an individual STL file. Entire suites of endoskeletal components (e.g., chondrocranium, upper and lower jaws, hyoid and branchial arch elements, axial skeleton, appendicular skeleton, etc) are thus accumulating in a digital library. When this is eventually placed on-line, users will be able to view the entire collection of chondrichthyan isosurface renderings and to compare homologous components across taxa or to combine files and recreate entire skeletons (which can be modeled using 3-D printers). The information gleaned from this exercise thus has tremendous scientific and educational potential and will form a valuable resource for future systematic, phylogenetic and evolutionary studies. In addition to modern chondrichthyans, data from fossils will eventually be incorporated, thus broadening the scientific and educational value of the digital library. This project is now in its second year and will continue with NSF support (Award # 1036488) for a further three years.

Molecular phylogeny of Squaliformes: targeted gene capturing methods allow insights into the phylogeny and evolution of dogfish sharks

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Squaliform sharks comprise a variety of mostly deep-dwelling elasmobranchs such as the giant *Somniosus microcephalus* or the dwarf lantern shark, *Etmopterus perryi*. Further, the group contains the only known sharks capable of bioluminescence. Their fossil record dates back to the Upper Jurassic 163 - 140 Ma ago. Despite their long evolutionary history and unique traits, our knowledge of the phylogeny and evolution of this diverse group of elasmobranchs is limited. Such information would not only be interesting from an evolutionary biology perspective but also for conservation purposes since many squaliform species are adversely impacted by targeted commercial fisheries as well as by-catch. Recent molecular phylogenetic approaches neither clarify the intrafamiliar relationships within Squaliformes nor support the monophyly of the order as a whole, if the bramble sharks (family: Echinorhinidae) are considered as squaliform sharks. It is likely, however, that the sequence datasets analyzed so far were lacking enough signal to reconstruct a reliable molecular phylogeny of squaliforms. Here, we present a new phylogenetic analysis for the Squaliformes that was derived from a large number of nuclear loci gained through targeted gene capture methods and subsequent next generation sequencing.

Capturing protein-coding genes across divergent species and its implication in evolutionary biology

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With the development of next-generation sequencing (NGS), high-throughput sequence data now are available at relatively low cost and can be collected in a short time. Sequencing whole genomes, however, is still costly and unnecessary in most evolution studies. Gene capture with subsequent NGS that targeting a subset of the genome has been used in many aspect of evolutionary biology, such as reconstructing phylogeny and detecting genetic disorders in human populations. Currently, gene capture has been applied mainly to different individuals of the same species or closely related species. In this study, we optimized the conditions for the capture methods to enable targeting protein-coding genes across highly diverged taxa. We tested our approach in capturing single-copy protein-coding sequences across 10 vertebrates representing major vertebrate lineages. We also applied our optimized methods in 13 chondrichthyans, including elephant shark (*C. milii*), five skates and rays (*Aetobatus narinari*, *Leucoraja erinacea*, *Neotrygon cf kuhlii*, *Rhinobatos schlegelii*, *Torpedo formosa*) and seven sharks (*Carcharhinus amblyrhynchos*, *Chlamydoselachus anguineus*, *Etmopterus joungi*, *Heterodontus portusjacksoni*, *Isurus oxyrinchus*, *Orectolobus halei*, *Squatina nebulosa*). The maximum divergence between the baits and the target sequence successfully captured was 39%. The conditions that affect the efficacy of gene capture and the potential limiting factors of gene capture across species are listed. The implications of our approach in different aspects of evolutionary biology are discussed.

Phylogenetic relationships among major groups of living elasmobranchs: a morphological perspective

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Morphological data bearing on the higher-level relationships of major elasmobranch groups are revised, and new sources of morphological data affecting the placement of these groups are discussed. We bring to light evidence from comparative studies of the skeleton, mandibular and hyoid arch muscles, and afferent branchial vessels that support the placement of rays (Batoidea) high within squalomorphs as part of the hypnosqualean group (alongside angelsharks and sawsharks), supporting current morphological phylogenies. These data contradict an all-inclusive shark clade that stands equal in rank to the rays. No morphological data appear to support the monophyly of sharks, a topology universally recovered, however, in molecular phylogenetic studies based on different genes. This discrepancy is not seen as a conflict *per se*, only as a "different way of seeing" based on vastly disparate sources of data, and is by no means unreasonable or indicative that one is "right" while the other is "wrong". We do see a problem, however, in accepting a molecular theory of relationships to explain morphological evolution when resolved morphological phylogenies exist, or allowing molecular analyses to guide taxonomic decisions *pro forte*, trends currently popular (the former even among paleontologists). These trends derive from *tree-thinking*, whereas in morphology we are dominated by *character-thinking* – a quest to understand homology. Our morphological theories, whether phylogenetic or taxonomic, should be based on morphological data. That is, we should be interested in describing and exploring the contribution of morphology whether it agrees or conflicts with molecular data. Molecular analyses can be of great aid in taxonomic revisions, but not by strictly imposing species limits (e.g. a single species may present relatively ample genetic variation while being morphologically indistinct, or *vice-versa*). Morphology, after all, is essentially what we are trying to explain; comprehending an organism and its many levels of relationships (i.e. its hierarchically distributed homologies) are complex endeavors that require the formation of specialists, themselves perhaps facing extinction during the tree-thinking domination of systematics.

Rays: a guide to the world's fauna

Peter Last

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The batoid fishes, which have received increasing taxonomic attention in recent decades, are now confirmed to be more diverse than their close relatives, the sharks. A working checklist, generated for the chondrichthyan Tree of Life project, presently contains about 621 valid described species, and about 50 undescribed species. However, the composition of this list is likely to change slightly as the group is examined in more detail by a team of specialists preparing a long-overdue, guide to the rays of the world, to be published in 2014. The largest group of rays, the skates, collectively comprise almost half (49%) of all ray species, with almost 10% of them undescribed. While many ray groups are taxonomically stable, issues exist across all base levels of the classification, from families through to species. The ray guide project, its content and objectives, and some of the main taxonomic challenges and impediments to this research, are discussed in the light of new molecular insights.

Cranial morphology of *Cirrhigaleus asper* (Merrett, 1973) and its implications for the systematics of the family Squalidae (Chondrichthyes: Squaliformes)

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Recent studies of external morphology, morphometrics, and vertebral counts of the genus *Cirrhigaleus* have called attention to the morphological differences between *Cirrhigaleus asper* and its congeners as well as to its similarities to species of *Squalus*. However, skeletal morphology has never been compared between these taxa in detail. Investigation of the cranial morphology of *C. asper* is provided herein in comparison with other squalids. The results demonstrate that the neurocranium is typically squaliform with a spoon-shaped rostrum, prominent basal angle, inconspicuous preorbital processes and evident supraorbital crest. Elevated intraspecific variation exists, however, among specimens of *C. asper* from the Southwestern Atlantic and Indian Oceans, such as, respectively: broad precerebral fenestra vs. straight precerebral fenestra, broad postorbital processes vs. slender postorbital processes, presence of conspicuous cartilaginous processes on basal plate vs. their absence, and prominent glossopharyngeal base vs. discrete glossopharyngeal base. Cranial measurements of specimens from the Southwestern Atlantic Ocean are proportionally greater than those from the Indian Ocean, especially concerning rostrum length (23.6% vs. 34.3%-34.6% of CL), width across postorbital processes (68.3% vs. 52.0%-63.7% of CL), width across hyomandibular facets (56.4% vs. 40.5%-50.0% of CL), and basal plate length (51.9% vs. 43.8%-44.1% of CL). Rostral appendages are not usually found in *C. asper*, although lateral rostral appendages are evident in one specimen from the Indian Ocean. In general, *C. asper* and *C. barbifer* share a short and wide rostrum, large preorbital canal and a well-defined antorbital cartilage. Supraethmoidal processes are evident in *C. asper* from the Southwestern Atlantic Ocean whereas in *C. barbifer* there are two short similar processes and an epiphysial pit that is continuous to the precerebral fenestra. The neurocranium of *Cirrhigaleus* differs from that of *Squalus* by the shape of the rostrum, lateral concavity of the supraorbital crest, greater prominence of the postorbital processes and presence of two foramina for the carotid artery on the basal plate. Our observations show that the intraspecific variation among specimens of *C. asper* indicate potential taxonomic characters for separating species as well as new morphological characters for supporting the monophyly of *Squalus* and *Cirrhigaleus*.

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Resolving taxonomic confusion in the sea chubs (F. Kyphosidae)

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Sea chubs are widespread reef inhabitants of tropical and temperate reefs, but the relationships and taxonomy of the 16 valid species (*Hermosilla, Kyphosus, Neoscorpis and Sectator*) are confused because of problems with character differentiation. We undertook a molecular phylogenetic study using complete taxon sampling from these fishes, and species delimitation was determined on the basis of congruence between monophyletic groupings in the molecular phylogeny combined with comparison of morphological variation in type material. The results overall indicate that our understanding of species diversity and higher level relationships require revision. Topologies including a range of outgroup taxa consistently failed to retrieve a monophyletic Kyphosidae *sensu* Nelson (2006), i.e. *Kyphosus* + *Girella* + *Scorpis*. Our work thus supports previous phylogenetic studies in suggesting that Kyphosidae, Scorpididae and Girellidae be considered separate families. Both *Hermosilla* and *Sectator* are now considered junior synonyms of *Kyphosus*. The distribution of *Kyphosus* species was reconsidered based on the taxonomic revision, indicating that four species (*K. bigibbus*, *K. cinerascens*, *K. sectatrix* and *K. vaigiensis*) are found in both the Atlantic and Indo-Pacific regions. The Hawaiian *K. sandwicensis* was found to be a junior synonym of east Pacific *K. elegans*. The Atlantic endemic *Kyphosus incisor* and the eastern Pacific *K. analogus* were found to be conspecific with the Indo-Pacific *K. vaigiensis*. *Kyphosus gallveii*, only known from Saint Helena, and the Pacific *K. pacificus* and *K. lutescens*, the latter endemic to the Revillagigedo Islands in the east Pacific, were found to be conspecific with *K. sectatrix*, previously considered an Atlantic endemic. A higher number of gill rakers was found to be characteristic of all tropical species, suggesting this character changed in response to the invasion of low latitude reefs – perhaps as a response to a change in diet from large sub-tropical macroalgae to smaller algal growth on tropical reefs. Furthermore, careful examination of multiple molecular markers and a re-examination of morphological variation confirmed that a previously unrecognised species (*Kyphosus gladius* sp. nov.) had been clumped with *Kyphosus sydneyanus* in Western Australia. Overall, the family contains fewer species (12) than previously thought, but four of these species are considerably more widespread than expected.

The origins of herbivory in kyphosids (F. Kyphosidae) and related taxa

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Sea chubs, family Kyphosidae, have a global distribution and are consumers of macroalgae in some temperate and all tropical reef systems. We determined phylogenetic relationships of the ingroup and related outgroup taxa using partial fragments from mitochondrial markers (*12s*, *16s*, *cytb*, *tRNA -Pro*, *-Phe*, *-Thr* and *-Val*) and three nuclear markers (*rag1*, *rag2*, *tmo4c4*), in total comprising 5960 bp from 118 individuals. The basal taxa in the kyphosid topology, *Neoscorpis lithophilus* (eastern South Africa to southern Mozambique), *Kyphosus cornelii* (Western Australia) and *Hermosilla azurea* (southern California to Baja), are all herbivorous, and have a subtropical to temperate distribution. This, together with a sister-group relationship to the temperate, omnivorous scorpidids, implies that the common ancestor of kyphosids was herbivorous or omnivorous, and inhabited the subtropical Indo-Pacific. A chronogram using several outgroup fossil calibrations revealed that kyphosids originated in the sub-tropical Indo-Pacific during the late Eocene or early Oligocene, and rapidly colonized subtropical seas. *Kyphosus* originated relatively recently, in the early Miocene. The temperate clade of *Kyphosus*, represented by the Australasian *K. sydneyanus* and *K. gladius*, diverged from the common ancestor of the tropical kyphosids between the late Miocene and the early Pliocene. The tropical kyphosids diversified on low latitude reefs much more recently in the Pliocene and Pleistocene, when they speciated rapidly and evolved new dietary preferences. Diversification into low latitude reef systems was geographically comprehensive and occurred during a period of marked environmental fluctuation in tropical oceans. Herbivory is a basal trait and originated in temperate environments, while zooplanktivory in the tropical, autapomorphic *Sectator ocyurus* is derived.

Geographic and evolutionary patterns in the demography of scarine labrids, parrotfishes

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The parrotfishes, strongly reef associated perciform fishes have a recent history of diversification . Although initial divergence of the parrot fishes commenced during the Oligocene diversification resulting in the present day assemblages occurred in the Pliocene and early Pleistocene. In this interval parrotfishes colonized the world's tropical reefs and today represent a numerically dominant assemblage of grazing fishes. Colonization occurred differentially resulting in distinctive taxonomic and functional assemblages in the tropical Atlantic vs the Indo-Pacific and in clearly partitioned faunas within the Indo-Pacific. Phylogenetic analysis retrieves two major clades of parrotfishes the Sparisomatinines with the greatest diversity in the Atlantic ocean and the scarinnines with limited representation in the Atlantic but the dominant group in the Indo-Pacific. Demographic analysis reveals that members of the Atlantic sparisomatinines manifest faster growth rates and generally shorter life spans than the scarinines of the Indo-Pacific, suggesting that for this group the demographic clocks are running faster in the Atlantic. Resolution of this issue requires taking phylogenetic influences, ocean basin history and biogeographic and habitat configurations into account. Given the broad distribution of this group it is possible to evaluate a hypothesis of demographic differentiation in all the major clades on a biogeographic scale. To achieve this representatives of all major clades from the Atlantic, East Pacific and the entire Indo-West Pacific will be analysed for demographic and life history trends taking into account phylogeny, ocean basin history and habitat configuration.

Darwin's fishes: Marine speciation in the Galápagos Archipelago

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Island populations have played a pivotal role in the elucidation of allopatric speciation, with the Galápagos finches as the most notable example. The study of the origin of species is currently experiencing renewed interest with theoretical and empirical advances, yet while much attention has been devoted to terrestrial and freshwater systems, comparatively little is known about speciation in marine environments. In particular, scientists have not capitalized on the potentially important island systems. In this study we worked in the Galápagos Islands and surrounding areas where we examined the relationship between population structure, a precursor to speciation, in species of reef fishes that exhibit three types of distributions: endemic, insular, and Panamic. Using a combination of population structure and coalescent approaches, we assessed the degree of genetic population structure in the three groups of fish species. In addition, we evaluated the level of inter-island genetic diversity in endemic species to determine if Galápagos fishes, like their terrestrial counterparts, could be used as a model for allopatric speciation in the sea.

Phylogeography of the Manybar Goatfish, *Parupeneus multifasciatus*, reveals isolation of the Hawaiian archipelago and a cryptic endemic lineage in the Marquesas

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To assess genetic connectivity in a common and abundant goatfish (family Mullidae), we surveyed 637 specimens of *Parupeneus multifasciatus* from 22 locations across the Pacific Ocean with a focus on the Hawaiian Islands. Based on mtDNA cytochrome *b* sequences we found no evidence of population structure across Hawai'i and the North Pacific, however we observed genetic structuring between northern and southern Pacific locations with the equator-straddling Line Islands affiliated with the southern population. The Marquesas sample in the South Pacific was highly divergent (d = 4.12% average sequence divergence) possibly indicating a cryptic species. Preliminary morphological examination, however, did not yield any obvious characters to distinguish these two evolutionary lineages. These findings demonstrate that this goatfish is capable of extensive dispersal, consistent with early life history in the Mullidae, and indicate that the Marquesan archipelago is highly isolated from the adjacent Society Islands.

Marine lakes in Palau are "Islands" for marine species

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Little is known about evolution of marine species in geographically isolated-environments, because ocean currents often facilitate gene flow among populations. We focused on marine lakes of Palau Islands that are oceanic islands located in western Pacific. A large number of these islands are composed of limestonederived from hard corals,and there are 70 marine lakes in the islands. Meromictic marine lakes particularly harbor unique marine fauna that have been isolated since the formation of the lakes after the Last Glacial Maximum (ca. 12,000 years ago). Therefore, marine lakes are considered to be isolated marine environments like terrestrial islands for marine species. To examine evolutionary processes in marine lakes, we conducted population genetic analyses on marine lake populations of orbiculate cardinalfish, *Sphaeramia* orbicularis, coastal cardinalfish, *Apogon lateralis*, and striped silverside, *Atherinomorus endrachtensis*, using molecular markers: mitochondrial DNA (mtDNA)and comparative genomederived simple sequence repeats (CG-SSRs). The results showed that level of genetic diversity of marine lake populations is considerably lower than that of lagoon populations, suggesting that the marine lake populations clearly experienced strong bottleneck event (founder effect). Furthermore, marine lake populations have different genetic structure from each other, even in the same island. This result could be ascribed to differences of their formation age. So far, such high genetic divergences in extreme narrow geographical ranges (ca. 150–250 m) have scarcely been reported for marine organisms. Our studies showed that almost all marine lake populations have been completely isolated each other and have been differentiated from lagoon populations, and each marine lake population has been experienced different evolutionary processes. These findings clearly demonstrate that marine lakes are excellent model for the evolutionary study of marine species.

The role of peripheral endemism in species diversification

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We examined how peripherally isolated endemic species may have contributed to the biodiversity of the Indo-Australian Archipelago biodiversity hotspot by reconstructing the evolutionary history of the wrasse genus *Anampses*. We identified three alternate models of diversification: the vicariance-based 'successive division' model, and the dispersal-based 'successive colonisation' and 'peripheral budding' models. The genus was well suited for this study given its relatively high proportion (42%) of endemic species, its reasonably low diversity (12 species), which permitted complete taxon sampling, and its widespread tropical Indo-Pacific distribution. Monophyly of the genus was strongly supported by three phylogenetic analyses: maximum parsimony, maximum likelihood, and Bayesian inference based on mitochondrial CO1 and 12S rRNA and nuclear S7 sequences. Estimates of species divergence times from fossil-calibrated Bayesian inference suggest that *Anampses* arose in the mid-Eocene and subsequently diversified throughout the Miocene. Evolutionary relationships within the genus, combined with limited spatial and temporal concordance among endemics, offer support for all three alternate models of diversification. Finally, we compared the patterns and age estimates of species within this genus to those of other peripherally isolated island endemics from closely related coral reef fish genera. Overall our findings emphasise the importance of peripherally isolated locations in creating and maintaining endemic species and their contribution to the biodiversity of the Indo-Australian Archipelago.

Origins of tropical marine biodiversity

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The enigma of speciation in the sea stands as one of the primary challenges in evolutionary biology. Central to this issue is whether biodiversity hotspots such as the Coral Triangle are producing and exporting new species, or accumulating species that arose elsewhere. Phylogeographic and evolutionary studies yield conflicting results on this issue, but have overturned three fundamental paradigms about marine biodiversity: 1) *Speciation is driven by physical isolation*. In contrast, phylogenetic studies show that many closely-related species occupy the same or adjacent habitats, diminishing the likelihood of physical isolation (allopatry) for speciation in the sea; 2) *Peripheral habitats such as oceanic archipelagos are evolutionary graveyards that contribute little to overall biodiversity*. New studies show that oceanic archipelagos and marginal seas can export biodiversity to other regions; 3) *Speciation in the sea follows the same patterns as in terrestrial systems.* Evolutionary pathways above and below the waterline follow markedly different trajectories, due in large part to the higher dispersal capability of most marine organisms. The realignment of these principles allows for a new understanding of biodiversity production in the sea. Marine speciation is proceeding along ecological boundaries rather than physical barriers in many cases. New species forged under intense competition at biodiversity hotspots can radiate out to depauperate areas, where they may evolve novel functions under the "ecological opportunity" scenario proposed by G.G. Simpson. In this reconciliation of "center of speciation" and "center of accumulation", both hotspots and peripheral ecosystems benefit fromthis exchange in a process called biodiversity feedback.

Shifts in the biological structure of coral reef habitats and effects on reef fishes

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Scleractinian corals are the key habitat-forming species on coral reefs and contribute greatly to the diversity of coral reef fishes. Removal or destruction of corals will therefore profoundly alter the structure and dynamics of coral-reef habitats, with potentially significant effects on abundance and diversity of coral reef fishes. It is predicted, for example, reef systems that are devoid of corals will support 60-70% fewer species of the fishes compared to reefs with healthy coral growth, which has obvious ramifications for reef-based fisheries. It is unlikely however, that climate change will in itself cause global extinction of all scleractinian corals. More likely is that coral ecosystems will come to be dominated by a restricted suite of coral species that are either resistant to, or capable of rapid recovery in the aftermath of, major disturbances. Coral assemblages may shift to become more dominated by fast growing, mostly branching, "weedy" species (e.g., *Acropora*) or more resistant massive corals (e.g., *Porites*). The ultimate structure of coral assemblages will depend upon the severity versus frequency of disturbances, but either way changes in coral assemblages are likely to lead to more depauperate fish assemblages.

The effect of habitat biodiversity on fish community structure: does the species pool matter?

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A fundamental goal of ecology is to understand key processes that establish and maintain patterns of biodiversity, and thus how biodiversity may be affected by environmental perturbations. Although increased habitat diversity has been argued to promote diversity of fish communities, few experiments have been conducted to directly explore this relationship. We tested the effect of coral species richness and composition on the abundance, diversity and community structure of their associated fish communities. The same experimental design was employed in three locations: two in the western Pacific (Lizard Island, Great Barrier Reef, Australia and Kimbe Bay, Papua New Guinea) on the high end of the Indo-Pacific gradient in species diversity and one site in the south central Pacific (Moorea, French Polynesia) where background species richness is much lower. Small patch reefs were constructed with different combinations of six coral types; each reef was composed of one, three or all six corals. The total species richness of the assemblages that formed on the patch reefs was much higher at Lizard Island (150 species) and Kimbe Bay (122) than at Moorea (67). The patch reefs at the western Pacific sites averaged up to 25 species and there was a positive relationship between coral species richness and the number of fish species on the reefs. By contrast, in Moorea individual reefs contained on average only about 11 species of fish and species richness was not affected by habitat (coral) species richness. In no case was overall abundance of fish positively associated with habitat diversity, but species composition of fish varied according to the types of coral present. The experiments revealed that the particular species of habitat-providing coral had a stronger influence on local richness of fish assemblages than did local habitat diversity, a pattern that was robust across the geographic diversity gradient of corals and fishes.

Cross-scale patterns of habitat structure and fish foraging behaviour

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Reef fish and the functional roles they provide, have been recognized as critical for the resilience of reefs within coral-dominated states. However, there are still considerable gaps in our knowledge regarding the spatial scales at which fish interact with reefs and provide functional impact. In this study we, 1) Used fractal techniques to characterize patterns of cross-scale habitat complexity, and examine how this relates to body-depth abundance distributions of associated fish assemblages over corresponding spatial scales, 2) Assessed the allometric relationship between foraging movements and fish body length, and 3) Evaluated the influence of habitat condition on the scale of foraging movements. We found that the availability of potential refuges at different scales correlates with patterns in fish body depth distributions, the scale of functional impact is positively related to body size, and habitat condition modifies foraging behaviour. These outcomes have significant implications for the ability of fish assemblages to continue to deliver their functional role in the face of increasingly large-scale anthropogenic impacts. However, identification of the scales at which fish communities are susceptible to disturbance, provides managers with the knowledge needed to design management strategies to support resilience of coral-dominated reefs, by enhancing function at the identified spatial scales

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Macroalgal-driven feedbacks and the role of herbivorous fishes of coral reefs

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Habitat structure is a fundamental property of all ecological systems. The physical structure of a habitat interacts with ecological processes in a variety of ways, and can have significant effects on the composition, structure and function of fish communities. Understanding the potential effects of habitat structure on ecosystem processes is becoming increasingly important as climate change and anthropogenic stressors are fundamentally changing the physical and ecological structure of ecosystems worldwide. Coral reefs are one of the onothmosthreatenedecosystemtclimatchangandhave experienced unprecedented declines in the cover of live coral over the past three decades, with many being overgrown by large fleshy macroalgae. Such shifts from coral- to macroalgal-dominance are fundamentally changing the physical structure and functioning of these reefs. While the causes of such reef degradation is relatively well established, there is a clear need to understand how key ecological processes respond to proliferation of macroalgae. The purpose of this talk is to describe the likely effects of macroalgal expansion and associated habitat structure on a critical ecosystem process on coral reefs; herbivory. In particular, the potential effects of macroalgae on the recruitment, foraging behavior and role of herbivorous fishes on coral reefs will be examined. In doing so, this talk will identify potential feedbacks that may lead to the stability and expansion of macroalgal stands on corals reefs.

Different herbivorous fish assemblages remove *Sargassum* bioassays on reefs covered in coral vs. macroalgae

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Macroalgae-feeding fishes are considered to be a key functional group on coral reefs due to their role in preventing and potentially reversing phase shifts to macroalgae. However, research to date has shown that systems have limited functional redundancy at local scales, with high variability even within one system (e.g. the Great Barrier Reef, Australia, where most of the work has been done). This study expands our knowledge of macroalgal-feeding fishes to include species that can tackle macroalgae in the Western Indian Ocean; an area that was devastated by the 1998 mass bleaching event, with many reefs now covered in macroalgae. Moreover, we compared reefs in two conditions -those that had high live coral cover (20-46%), and those that had high macroalgae cover (57-82%) – to investigate the influence of macroalgal density on the ability and identity of species to remove macroalgae. Using filmed *Sargassum* bioassays, we found significantly different *Sargassum* removal rates with mean assay weight loss due to herbivory ranging from 27.9 $\pm$ 4.9 % on reefs with high coral cover, to 2.2 $\pm$ 1.1 % on reefs with high macroalgae cover. The assemblage of macroalgal-assay feeders differed between the two conditions; 23 fish species were observed to consume the assays, 8 of which were recorded only from reefs with high coral cover, and 1 only from reefs with high macroalgae cover. However, only 7 species dominated *Sargassum* consumption, 4 from high coral cover reefs, and 3 from high macroalgae cover reefs, highlighting the low functional redundancy and high vulnerability of the function, especially because many of these species are important fishing targets.

Demographic and numerical responses of parrotfishes to landscape-scale destruction of reef-forming corals

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Stony coral on the fore reef of Moorea, French Polynesia, was reduced from ~ 50% to ~ 2% cover by an outbreak of predatory Crown-of-Thorns Seastars (*Acanthaster planci*, COTS) in 2007-09. There was a compensatory increase in the cover of turfing algae, which is consumed by herbivores, and within a year the biomass of roving herbivorous fishes, particularly bullethead parrotfish (*Chlorurus sordidus*) and palenose parrotfish (*Scarus psittacus*), increased several fold on the fore reef. Experiments reveal that intense grazing by these roving species prevented the widespread establishment of macroalgae following death of coral on the fore reef. The COTS outbreak did not appreciably change the cover of live coral in lagoon habitats, including the nursery habitat for parrotfishes in Moorea (the mounding coral *Porites rus*). The six-fold increase in biomass of parrotfishes on the fore reef arose from a doubling in the average mass of individual fish and a four-fold increase in density. The increase in density offshore resulted from a numerical response and not just a redistribution of existing fishes; we estimate that the sizes of bullethead and palenose parrotfish populations increased on the order of 50% island-wide in the year following the widespread death of coral on the fore reef. This impressive numerical response was facilitated by the presence of intact nursery habitat (*P. rus*) in the lagoon. Parrotfish settle to *P. rus* and migrate to the fore reef as they grow during their first year. The numerical response resulted from enhanced recruitment to the offshore adult life stage, and this and the increase in individual body mass resulted from significantly greater age-specific growth rates of individuals in response to increases in their food supply, turfing algae. These results indicate the importance to reef resilience of protecting critical nursery habitat in addition to preventing overfishing of key herbivorous fishes. They also indicate that for Moorea at least, parrotfish populations are food limited, a state that enhances the resilience of the system.

Using functional characteristics of herbivorous fish communities to infer the vulnerability of coral reefs to phase shifts

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Human actions continue to erode the capacity of many ecosystems to resist degradation. This has motivated searches for more effective approaches to management such as the application of concepts of ecosystem resilience. Conservation of biodiversity is fundamental to modern resource management but it is not species richness per se that promotes resilience but the functional contribution of species to important ecosystem processes. Measures of function that have a strong theoretical basis for their use may prove valuable indicators of ecosystem resilience. Here we explore the idea that resilience is positively related to the diversity within and among important functional groups of organisms. Specifically we infer the relative vulnerability of different reef environments to undesirable coral-macroalgal phase shifts based on the functional characteristics of the local herbivorous fishes that are perceived to be primarily responsible for their prevention. Reef slopes on 92 reefs were surveyed annually in three zones of the continental shelf within eight latitudinal sectors of Australia's Great Barrier Reef (GBR) for up to 15 years. Spatial variation in measures of herbivore functional diversity, functional redundancy and abundance was high, particularly among shelf zones. Values tended to be higher offshore and lower inshore in close association with gradients of water clarity. Turbid inshore subregions were considered most vulnerable based on very low measures of herbivore function. This assessment was supported by the occurrence of a phase shift on one turbid inshore reef following major coral declines. However, a few equally disturbed reefs with similarly low measures of herbivore function did not undergo phase shifts in other subregions. This shows that phase shifts do not necessarily occur when grazing capacity is very low; presumably other factors may compensate to alter phase shift thresholds. Using measures of herbivore function to indicate phase shift vulnerability may thus prove conservative in some cases but caution is appropriate as compensatory factors are not well understood and could be inadvertently eroded by human actions. Our results also highlight the need for spatially targeted management strategies and maintenance of water quality to broadly preserve herbivore functions and enhance resilience in coral reef ecosystems.

Sediments suppress the functional roles of herbivorous fishes on coral reefs

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Feeding by herbivorous reef fishes is of critical importance to coral reefs, and maintaining healthy herbivore populations is widely regarded as a key management technique to maintain reef resilience. Abundant herbivores, however, may not be enough; reef sediments appear to play an important ecological role in mediating herbivory. This presentation summarises several recent studies that demonstrate that sediments bound within algal turfs directly and deleteriously affect herbivory and bioerosion. Initial sediment reduction experiments resulted in considerably increased herbivory, with low sediment turfs appearing more palatable. Even very small sediment reductions had significant effects. A subsequent sediment addition study compared the responses of algal turfs on reefs to increased benthic sediments and/or herbivore exclusion. Algal turfs grew rapidly following both sediment addition and herbivore exclusion, furthermore they remained longer for at least three months, well after the benthic sediments had recovered. These long-lasting increases driven by sediments were directly comparable to herbivore exclusion. Thus, a reef with high sediment loads may be as vulnerable as a reef with no herbivores. Some herbivores and detritivores actively 'clean' reefs and so offer a level of sediment resilience to reefs. However, on reefs with chronically high sediment this function may be overwhelmed, undermining reef resilience. These studies together highlight that benthic sediments alter reef fish behaviour and suppress the key functional roles they play.

Feeding in pairs: an ecological perspective

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In feeding on the benthos, herbivorous reef fishes alter the ecological and physical structure of coral reefs. However, different herbivorous taxa have considerably different effects on reefs. Rabbitfishes (f. Siganidae) differ from other herbivorous coral reef fishes in their tendency to form pairs rather than schools. While this behaviour is commonly linked to reproduction, possible effects of pairing on the ecology of rabbitfishes are poorly understood. To explore pairing behaviour and its consequences for the ecological niche of rabbitfishes, we quantified the frequency of this behaviour, explored pair fidelity and investigated the possible role of reproductive pairing. Using visual censuses, acoustic telemetry and gonad histology, we found that in the rabbitfish *Siganus doliatus*, pairing is the most prevalent social association and that pair members continuously maintain close contact. While these characteristics are commonly associated with monogamous mating, we found a relatively high prevalence of homosexual pairs (25%) suggesting that ecological factors are likely to play a role in rabbitfish pairing. We investigated the feeding behaviour of pairing rabbitfishes and compared the observed patterns to other reef herbivores. Our observations revealed that pairing rabbitfishes differ from other reef herbivores in exploiting micro-topographically complex environments such as reef crevices and interstices. Rabbitfishes penetrated the reef-substratum more often and to a greater extent, took fewer bites and swam larger distances between forays, suggesting that the functional role of rabbitfishes may differ from other herbivores. Therefore, pairing rabbitfishes appear to exploit a unique feeding niche and consequently, the loss of pairing rabbitfishes may have fundamental effects on coral reef ecosystems and lead to severe alterations in the habitat structure of coral reefs.

Relationships between the areas of seagrass, mangroves and saltmarshes with commercial finfish catch in various types of NSW Estuaries

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Seagrass is well known to provide habitat and food items for fish and prawns in estuaries. The area of seagrass in estuaries has been suggested to be related to the commercial fish catch (McArthur et. al., 2003). NSW Fisheries (Williams et. al., 2006) have surveyed the areas of seagrass, mangroves and saltmarshes in estuaries and this data has been used to examine the relationship of these habitats with the commercial finfish catch. The nine estuaries assessed by Gillson et. al. (2008) was used to investigate these relationships. Commercial fish catch is traditionally used to assess the health of estuaries. Investigating how these three habitats relate to the finfish catch data may provide a useful additional means of assessing the health of estuaries. Subject to further investigation, the potential benefits of this approach for estuary management include: Estimation of the potential effects on fish catch due to mangrove, seagrass and saltmarsh area degradation; Identification of habitat areas efficiently providing support to the fishery; Optimisation of fishery management with regard to catch and protection of appropriate areas. The close-fitting relationship between commercial and predicted fish catch for eight of the nine estuaries assessed indicates the linkage between habitat and fish production over a range of estuary types. Port Stephens/Karuah River had a lower commercial catch than predicted, apparently due to fishing area closures under the Port Stephens-Great Lakes Marine Park Plan. The relationship of seagrass area to fish catch in the highly urbanised Tuggerah Lakes and Lake Illawarra estuaries was found to be the same as operating in the other estuaries.

Spawning ecology of black bream (*Acanthopagrus butcheri*, Sparidae: Munro 1949) in a changing environment

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Many estuaries around the world are experiencing prolonged drought resulting in significant decreases in freshwater input. Although previous research has found a link between freshwater flows and strong year classes of commercially caught estuarine fish and crustaceans, the causal link between flows and recruitment is still unclear. Many of these species utilise estuaries as spawning and larval habitats. Freshwater flow plays an important role in estuarine productivity and the timing and amount of flow could impact larval distribution and survival. This study focussed on the eggs and larvae of a commercially and recreationally significant fishery species black bream, *Acanthopagrus butcheri*. Black bream have a long pelagic larval stage estimated to be 40-60 days and are exposed to the naturally high variability of the physico-chemical structure of the estuary. We surveyed 23 sites over two spawning seasons in the Gippsland Lakes and found that although fish spawned in both the lake and river estuarine reaches, more than 99% of larvae were collected in the rivers and in particular the upper sections towards the salt front. Fine scale sampling in the Mitchell River revealed that there was a distinct spatial coupling between larval distribution and high prey abundances with the salt front. The results from this study indicate that the salt front forms an important habitat for larval black bream that is under threat from drought and anthropogenic impacts decreasing freshwater input into estuaries.

Good fences make good neighbours: experimental rehabilitation of the spawning habitat of *Galaxias maculatus*

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Numerous stressors from agriculture, urbanisation and natural disturbances affect coastal margins and the species that rely on riparian habitats to complete their life-histories. One effect of changes to riparian vegetation is that the ground-level light, temperature and humidity environment has also been altered. *Galaxias maculatus*, one of the most widely distributed fishes of the southern hemisphere, lays eggs almost exclusively beneath riparian vegetation in tidally influenced reaches of rivers and streams. These eggs develop terrestrially for up to 4 weeks. Sink populations have resulted from alterations to spatially explicit "gateways" in the early life history of this diadromous species, principally through reductions in the quantity and quality of spawning habitat. This could exacerbate population declines by creating life-history bottlenecks in many rivers. In rural areas, livestock grazing is presumed to be one of the primary stressors affecting spawning sites. We will present the effects of removal of livestock grazing on riparian vegetation, physical variables and subsequent spawning including egg densities and egg survival. The pathways of impacts associated with vegetational changes through human-induced disturbances are complex yet potentially devastating. We demonstrate that even a wide-ranging species with many robust adult populations can be compromised if a stage-specific habitat required to complete a life-history is degraded by localised or more diffuse impacts, but that targeted intervention and management might readily improve this.

Evidence for endocrine disruption in two fisheries species from the Great Barrier Reef region

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In this study, we examine the potential reproductive impacts of endocrine disrupting compounds (EDCs) derived from agricultural sources on wild fisheries populations. In the catchments surrounding the Great Barrier Reef (GBR) region such impacts are plausible given that: (i) low chronic levels of herbicide residues are present in the GBR throughout the year, (ii) triazine concentrations exceed GBR and national water quality guidelines in some freshwater and marine locations, and (iii) labile sex determination is common amongst tropical fish. First, we collected juvenile (putatively male) barramundi (*Lates calcarifer)* and juvenile (putatively female) coral trout (*Plectropomus leopardus* and *P. maculatus)* across the GBR region during the 2011 and 2012 wet seasons. Collections were conducted after floodwaters had discharged into the GBR lagoon, potentially exposing juvenile fish to agricultural run-off and associated EDCs. Second, we conducted dose-response experiments with juvenile barramundi in controlled laboratory experiments, using environmentally relevant concentrations of the agricultural herbicide atrazine. For both field and laboratory fish, we quantified expression levels of two genes, vitellogenin (egg yolk protein which is normally expressed only in sexually mature females) and aromatase (converts testosterone to estrogen and is linked to sex change) on liver and brain samples via qPCR. For barramundi, we see frequent up-regulation of vitellogenin in juveniles collected from a variety of river basins in the GBR, suggesting the potential for wide spread exposure to endocrine active compounds. Preliminary results from the laboratory experiments suggest that atrazine may be one of the endocrine disrupting compounds responsible for this up-regulation. For coral trout, we also see up-regulation of vitellogenin albeit at much lower levels than those documented in barramundi. We discuss our results in the context of potential implications for wild fisheries, and make recommendations for future research.

Recent status of the freshwater fishes of Babeldaob Island, Palau

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Very few works dealt with the freshwater fishes of Palau. Though not published, in1960, Fehlmann listed 95 species, consisting from 67 genera of 36 families in his dissertation thesis. In recent years, Bight and June (1981) and Tighe (1994) reported 47 species, about half of Fehlmann. However, in the last two decades, we have observed drastic environmental change in freshwater fish habitat in the main Island, Babeldaob. One of the reasons of drastic environmental change is construction of the main road, named Compact Road, and because of it, mudslide has been occurred easily when the heavy rain comes. After that, we observe some riverbeds are covered with mud and sand. It causes the habitat destruction and degeneration of algal flora in the river. The most recent study of the freshwater fish fauna of the island reported only 19 species (Jenkins, 1999), less than one quarter of that in 1960. After the construction of the road finished, we have reinvestigated the freshwater fish fauna of the island from 2011 using underwater camera, hand nets and cast nets. In a result, we recognized 61 species. We will discuss the change in freshwater fish fauna in relation to environmental change caused by the road construction.

Fish fauna investigated by four methods in eastern coastal waters off Korea

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The coastline of eastern Korea is very simple and has a narrow continental shelf. The sea is average depth 1350m, with maximum depth over 3500m. The Tsushima warm current and North Korea cold current affects the fish assemblage and dynamics of fisheries production. The objective of this study is to describe the fish fauna at eastern coastal waters off Korea and to identify the changes in fish distribution and composition. Fish fauna was investigated using four methods, trawl, Danish seine net, set net and gill net since 2009. A total of 227 fish species belonging 79 families were investigated. (1) Trawl; total 72 species were collected and dominant species were *Clupea pallasii, Arctoscopus japonicus, Glyptocephalus stelleri* and *Gadus macrocephalus*. (2) Danish seine net; total 106 species appeared and dominant species were dermersal fishes, for example, *Arctoscopus japonicus, Glyptocephalus stelleri, Dasycottus setiger* and *Hippoglossoides dubius.* (3) Set net; total 141 species were investigated and dominant species were mainly pelagic fishes, i.e., *Scomber japonicus, Thamnaconus modestus, Clupea pallasii* and *Seriola quinqueradiata.* (4) Gill net; total 83 species were investigated and dominant species were *Glyptocephalus stelleri, Dasycottus setiger, Hippoglossoides dubius* and *Liparis ochotensis.* Owing to the climate change, about 30 subtropical fish species appeared at 37-38°N of east coasts of Korea during summer to autumn, such as, *Plectorhynchus cinctus, Etrumeus teres,Decapterus macrosoma, Acanthocybium solandri* etc. In addition, about 25 species were newly recorded in eastern part of Korea since 2005.

Attempt to reconstruct the past fish fauna of the Shubuto River System, SW Hokkaido, Japan using museum specimens and interviews

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In order to reconstruct the past fish fauna of the Shubuto River System, fish specimens collected from the river system were investigated at the Bihoro Museum, Hokkadio, Japan (BIHM), the Hakodate City Museum, Hokkaido, Japan (HCM), the Fisheries Science Center of the Hokkaido University Museum, Hokkaido, Japan (HUMZ), and the National Museum of Nature and Science, Ibaraki, Japan (NSMT). Eighteen local members of the Fisheries Cooperative of the Shubuto River and other related organizations were interviewed regarding the past fish fauna of the river system and changes in the abundance of each fish species. Thirteen fish species were re-examined, but it was not possible to re-examine the Sakhalin taimen (*Hucho perryi*; Itou), which was captured in the Shubuto River in July 1886 and registered at the Hakodate Museum (now HCM). Among a total of 42 fish species that had been collected or observed by the interviewees, 34 species were assumed to be reliably identified. The interviewees were concerned about changes in the abundance of protected species that had been identified by regional fishing cooperatives. In particular, reductions in the fish species of floodplain wetlands such as the Arctic lamprey (*Lethenteron camtschaticum*; Kawa-yatsume), were of concern. Indications of the extinction of the Sakhalin taimen (*Hucho perryi*; Itou) population and the rapid decline of the Arctic lamprey (*Lethenteron camtschaticum*; Kawa-yatsume) supported the validity of the action plan in the Kuromatsunai Town Biodiversity Strategy, which targets restoration of floodplain wetlands of the river system. The present study suggested that interviews can provide useful information regarding the decline of fish species that are familiar to many citizens and can complement museum data and literature.

Lessepsian (Red Sea to Mediterranean) fish migration: From DNA to taxonomy

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The phenomenon of Red Sea fish species migrating via the Suez Canal and their subsequent population establishment and westward distribution in the Mediterranean Sea, known as "Lessepsian migration", shows no sign of ceasing. In fact, in the last two decades, Lessepsian fish migration has dramatically increased and has become the subject of many molecular studies, which have increased our knowledge of the origin, parasites, founder effect and rate of invasion of these species. DNA analysis has revealed that several of these successful invasive species, previously considered as having a wide Indo-Pacific distribution, are actually members of a distinct taxon and confined to the Red Sea and now in the Mediterranean. Examples of such cases are *Antherinomorus forskalii*, formerly considered *A. lacunosus* and *Etrumeus golanii* in the Red Sea and Mediterranean, previously considered the cosmopolitan *E. teres*. Other changes are likely in *Saurida* (Synodontidae), *Sillago* (Sillaginidae), *Pempheris* (Pempheridae) and *Pomadasys* (Haemulidae). Molecular and taxonomic studies together will deepen our understanding of biodiversity and ecosystems affected by the phenomenon of fish migration.

Genetic isolation among gizzard shad *Nematalosa japonica* (Clupeidae) populations

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Genetic population structure of Japanese gizzard shad *Nematalosa japonica* Regan was studied using nucleotide sequence analysis of the mitochondrial DNA D-loop region. A total of 247 individuals from five localities; Japan (Kochi of mainland, and Haneji Inland Sea and Nakagusuku Bay in Okinawajima Island), Taiwan (Taichung) and Vietnam (Hai Phong) were surveyed. 106 variable sites and 117 different haplotypes were detected among localities. Genetic diversities (haplotype diversity and nucleotide diversity %) within locality ranged from 0.77 (three in Japanese localities) to 0.99 (Taiwan and Vietnam) and from 0.23% (Haneji) to 2.75% (Taiwan), respectively. Taiwan and Vietnam hold high genetic diversity than Japanese localities. Analysis of molecular variance (AMOVA) revealed high genetic differentiation among localities (Φ.41; P<0.001), which were also supported by the significant pairwise Fst comparisons. These results suggested a restricted gene flow and genetic differentiation among all populations. Also it is important to survey the early life history and the reproductive season of different genetic units. Our data support the treatment of habitat areas as separate management units.

Higher genetic diversity in an extinct Okinawajima Island population of Ryukyu-ayu than endangered Amami-oshima Island populations

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Comparison of Ryukyu-ayu's (*Plecoglossus altivelis ryukyuensis* Nishida, 1988) genetic diversity of an extinct Okinawajima Island population fixed on formalin in 1971 (42 years ago) and endangered Amami-oshima Island populations was conducted, using nucleotide sequence analysis of the mitochondrial DNA control region. A total of 91 individuals from three localities; Kawauchi River and Yakugachi River (Amami-oshima Island, collected in 2006) and Yona River (Okinawajima Island) were surveyed. Crude DNA was extracted from muscles of formalin samples using a DNA extraction kit for Paraffin Samples. Out of the 130 bp in the mtDNA control region sequences, 9 variable sites and 11 different haplotypes were detected among individuals. Genetic diversities (haplotype diversity and nucleotide diversity %) within the locality ranged from 0.40 (Yakugachi) to 0.77 (Yona) and from 0.41% (Yakugachi) to 1.12% (Yona), respectively. An extinct Okinawajima Island locality showed higher genetic diversity than Amami-oshima Island localities. Analysis of molecular variance (AMOVA) revealed high genetic differentiation among localities ($\Phi st=0.53$; $P<0.001$), which were also supported by the significant pairwise *F*st comparisons. The present study showed for the first time the level of genetic diversity of an extinct Okinawajima Island population fixed on formalin in 1971 by using recently developed DNA technique. The result indicates how important to conserve wild organisms, endangered Amami-oshima Island populations in this case, with as much effort as possible, because the exact same population will never be resurged.

Structure and diversity of the *Mugil cephalus* species complex in the Indo-Pacific Ocean

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Vicariance and biogeographic barriers may have deeply contributed to the isolation and the diversification of the marine fauna of the Indo-Pacific region. It is important to assess their importance in the present distributions of species and in their phylogeographic structure. The flathead mullet (*Mugil cephalus*) species complex has representatives in many coastal regions of the tropical and temperate Indo-Pacific. Nine distinct mitochondrial lineages have been uncovered in flathead mullets in the Indo-Pacific, which are thought to be as many distinct biological species. To further describe the genetic diversity and structure of the *M. cephalus* species complex in the Indo-Pacific, a phylogeographic analysis has been undertaken using mitochondrial and nuclear markers. Different lineages generally present allopatric distributions, except for the northwestern and the southwestern tropical Pacific, where different lineages occur in sympatry. The importance of Pleistocene sea level variation and present sea surface temperature are invoked to explain the geographic structure of the *M. cephalus* species complex in the Indo-Pacific.

Historical divergence followed by secondary contact in *Sebastes trivittatus* (Scorpaeniformes: Sebastidae)

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The species-rich genus *Sebastes* includes several recently diverged sibling species pairs with little or no morphological (meristic and morphometric) differentiation, having been documented by molecular genetic analyses. *Sebastes trivittatus* is a common coastal species in the western North Pacific, including the Sea of Japan and the Sea of Okhotsk. We tested for the possibility of sibling species within *S. trivittatus* utilizing mitochondrial DNA (mtDNA) sequencing and microsatellite (MS) analyses of specimens collected from the coasts of Northern Japan, such representing a large part of the area included within the overall geographical distribution of the species. The minimum spanning tree of the mtDNA sequences showed two highly divergent lineages, both occurring throughout the sampling area, suggestive of the presence of sibling species. However, the pairwise *F*st between these two lineages, based on seven MS loci, was negative and statistically insignificant. In addition, the Bayesian-based individual assignment using MS divided the specimens into genetic groups according to geographical areas (the Pacific Ocean, the Sea of Japan and the Sea of Okhotsk), but not to the mtDNA lineages. We suggest that the historical population separation of *S. trivittatus* led to the differentiation of the two mtDNA lineages, followed by secondary contact and gene flow, thereby shaping the contemporary patterns of genetic diversity within the species. Possible causes for the historical population separation were also considered on the basis of the geographic distribution of the observed genetic variations and estimates of historical demographic parameters.

Revisiting latitudinal diversity gradients in the Indo-West Pacific: Phylogeography of the flathead fishes (Platycephalidae)

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Latitudinal Diversity Gradients (LDGs) represent a well-established model for explaining species diversity and distribution in the Indo-West Pacific (IWP). We make use of flathead fishes endemic to the IWP tropical and temperate zones to explore mechanisms and timing of speciation to understand the influence of LDGs on the evolution of this group. Nuclear and mitochondrial phylogenies were inferred from 44 out of 77 nominal Platycephalidae species representing 17 of the 18 currently recognized genera as well as 16 additional cryptic OTUs. A relaxed molecular clock approach was applied to estimate the main climatic and geological events responsible for diversification in flathead fishes. Subfamilies Onigociinae and Platycephalinae diverged in the Eocene into predominately tropical and temperate assemblages of species. Onigociins appear to have remained in the tropics since this time and diversified across the region in the Miocene. Platycephalins remained isolated in the temperate regions with only a few derived taxa successfully infiltrating the tropics through the Miocene. The subsequent introduction of platycephalins from the Australian continent into the tropical IWP was likely facilitated via tectonic rafting and subsequent dispersal throughout the shallow-water environments, which formed along the Sunda Arc margin following the collision of the Australian Plate with the Eurasian Plate. An 'out of the deep south' evolutionary trajectory in contrast to the 'out of the tropics' LDG paradigm is apparent across Platycephalinae while centrifugal speciation has apparently shaped diversity in both subfamilies across tropical regions. In this context, molecular phylogenies coupled with molecular clock approximations, have proved to be powerful tools for exploring the influence of palaeoclimatic changes and geological episodes responsible for the distribution of species in tropical and temperate regions. Given the commercial importance of flatheads and the taxonomic instability within this family, our results have considerable implications for future management and conservation strategies for these fishes. Furthermore, our results provide a comprehensive framework for exploring evolutionary processes in marine taxa with similar distribution patterns.

Molecular phylogeny and zoogeography of marine sculpins in the genus *Gymnocanthus* (Teleostei; Cottidae) based on mitochondrial DNA sequences

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The genus *Gymnocanthus* has the most extensive distribution of all members of the Cottidae, with six species distributed the high latitude in northern hemisphere. They distribute in North Pacific Ocean, the Arctic Ocean and North Atlantic Ocean. Five species (*G. herzensteini*, *G. detrisus*, *G. galeatus*, *G. intermedius* and *G. pistilliger*) distribute in Pacific Ocean and *G. pistilliger* also appears in Atlantic Ocean separately, and *G. tricuspis* distributes the Arctic Ocean and the surrounding area. To clarify the molecular phylogeny and zoogeography, and to estimate the divergence times of the species within this genus, 2,548 bp of the partial sequences of the 12-16S rRNA, cytchrome oxidase subunit I and cytchrome *b* gene were analyzed. Total numbers of samples were 108 individuals, collected from Chukchi Sea, Alaska, Vladivostok and Hokkaido in 2007-2010. Maximum likelihood and Bayesian inference were explored to estimate the molecular phylogeny. We used a geographic event: an opening of the Bering Strait [5.5-4.8 Million years ago (Ma)] to estimate the divergence time. The monophyletic genus, which arose in the Aleutian Archipelago, was divided into shallow-water group and deep-water group 8.1 Ma and this molecular tree was conformed to the morphological tree. *G. tricuspis* of shallow-water group firstly migrated from the Pacific Ocean to the Arctic Ocean about 5.0 Ma when the Bering Strait first opened. The divergence time of *G. herzensteini* from the other two deep-water species was 5.3 Ma, and the divergence time of *G. detrisus* and *G. galeatus* was 4.3 Ma. On the other hands, the divergence time of *G. intermedius* and *G. pistilliger*, which occurred after *G. tricuspis* divergence, was 3.9 Ma. The second migration to the Arctic Ocean occurred late Pliocene to early Pleistocene after which *G. pistilliger* and *G. intermedius* diverged at 3.9 Ma via Bering Strait, and moved to southward when cool period started. Therefore, the two cases of sympatric distribution: *G. herzensteini* and *G. intermedius* (Far East) and *G. galeatus* and *G. pistilliger* (circum North Pacific), were considered to met secondary after speciation.

Population genetic structure of a pelagic marine fish, cobia (*Rachycentron canadum*)

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Cobia (*Rachycentron canadum*) is a coastal pelagic fish which is pantropical in distribution, with the exception of the Pacific coast of the Americas. Despite their attractiveness to the aquaculture industry, little is known about its population genetic structure. Mitochondrial sequence variations within a 688 bp fragment ranging from the 3' end of *cytochrome b* to the 5' end of the control region were used to evaluate population genetic structure of cobia distributed in the Gulf of Thailand, Andaman Sea, and the Western Bay of Bengal. Cobia shows a high level of haplotype diversity (0.9558±0.0111), but a low level of nucleotide diversity (0.0052±0.0296). The haplotype network showed a star-like shape with 2 nested clades separated by three mutational steps. Haplotype clade I was found in both Thai and Western Bay of Bengal populations whereas clade II was found prominently in the Western Bay of Bengal population. Cobia distributed along the Thai–Malay peninsula shows genetic homogeneity, but reveals a highly significant genetic differentiation to the Western Bay of Bengal population. Tajima's D and Fu's Fs were significantly negative in all populations, indicating that the populations posses a number of rare alleles with singletons. The neutrality tests, mismatch distribution, and the GMRF skyride plot were evident a historic population expansion of cobia in Thai-Malay water. The study demonstrates an exit of population genetic structure of cobia, a marine pelagic fin fish known for an ability to migrate over a long distance. The barriers of gene flow could be due to geographic distance coupling with its site fidelity behavior. Further study on the phylogeography of cobia is on going in order to reach back into its cladistic origin and to evaluate the influences of biogeographic barriers on its population genetic structure, contributing information to aid in aquaculture development and fisheries management.

Two species managed as one stock? Genetic stock structure and a potential cryptic species in the spangled emperor (Lethrinus nebulosus) in the South Western Indian Ocean

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The spangled emperor (*Lethrinus nebulosus*) is common and widespread across the Indo-West Central Pacific and is a major component of artisanal, subsistence, recreational and commercial fisheries across its distribution. Many of these fisheries are at risk and are exploited beyond sustainable levels. Although prior genetic studies of *L. nebulosus* indicated homogeneity over large areas, differences in size, growth patterns and rate, and sex ratios across its distribution raise the possibility of the existence of discrete, independent stocks. In this study, the genetic stock structure of *L. nebulosus* was assessed across the South Western Indian Ocean (SWIO), where anecdotal accounts suggest the presence of two morphotypes. Genetic diversity of and spatial genetic structure among 242 individuals from eight sampling regions were assessed with DNA sequence data from a 422 bp fragment of the mitochondrial control region and genotypic data from 14 highly-polymorphic (nuclear) microsatellite loci. *Lethrinus nebulosus* in the SWIO is characterized by high genetic diversity, and two distinct and divergent genetic stocks were identified through the analysis of each marker set. The first stock was widespread throughout the SWIO, while the second was restricted to southern Mozambique and South Africa. Although regions experiencing slightly reduced gene flow and connectivity were identified, geographic distance does not limit gene flow and the former stock can largely be considered panmictic. The distribution of both stocks necessitates trans-boundary fisheries management efforts, while the presence of mixed stocks underscores the importance of accurate biological and population/stock dynamic information for each stock. This is dependent on the accurate identification of individuals of each. To this end, the taxonomic status of each of the stocks was assessed through the analysis of additional sequence data (from the 16S, COI and RAG-1 gene fragments), analysis of 28 morphometric and six meristic characters, and morphological examinations. All data confirmed the substantial differentiation of individuals of the two stocks. This evidence, particularly the marked sequence divergence among the two morphotypes and the paraphyly of *Lethrinus nebulosus s. l.* with respect to other *Lethrinus* species included in the genetic analysis, indicates a possible novel, cryptic species within *L. nebulosus* in the SWIO.

Phylogenetic analysis and biogeographic history of nearshore fishes that increase in diversity when moving away from the East Indies Triangle (Sparidae: *Acanthopagrus*)

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Many groups of Indo-West Pacific nearshore fishes exhibit greatest taxonomic diversity in the East Indies Triangle (EIT), and several hypotheses have been constructed to explain these patterns (e.g. centres of origin, accumulation, or overlap). However, other fish groups exhibit greater diversity when moving away from this region, to the North, South, and West, but reasons why they show a conflicting pattern have not been widely investigated. Here we reconstruct phylogenetic relationships among 15 representatives of *Acanthopagrus* based on mitochondrial and nuclear DNA sequences to test whether their spatial patterns of diversity reflect multiple centres of radiation outside the EIT, or peripheral reliction of lineages that could have previously occupied or dispersed out of the EIT, as has been proposed for the development of antitropical distributions. Inferred phylogenies differed between mitochondrial and nuclear genes. The nuclear topology was more compatible with radiation outside the EIT, with sister-taxon relationships observed for both temperate Australian and subtropical-temperate North Pacific species. Furthermore, one of the two lineages represented in the EIT persisted throughout the radiation of contemporary lineages without contributing. The mitochondrial topology was more equivocal in its support of radiation centres outside the EIT, and in both topologies elevated extinction rates of tropical lineages would conceal diversification and subsequent dispersal from this region.

Testing the core-periphery hypothesis: genetic signatures across the latitudinal range of the neon damselfish, *Pomacentrus coelestis*

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Genetic patterns are expected to vary across a species'distribution according to range position. The 'core-periphery hypothesis'predicts that genetic diversity will be higher within the core of the species range than in the periphery and that peripheral populations will be more genetically divergent. The demographic processes leading to such patterns could be both historical and contemporary (e.g. range expansion, population age, population isolation/connectivity etc.). Range-wide genetic patterns have rarely been investigated in marine systems, particularly in tropical organisms that are distributed across the equator. Our study investigates genetic patterns of the neon damselfish, *Pomacentrus coelestis*, a fish common to shallow coral reef habitat throughout much of the Indo-Pacific. We collected fish from around Australia, parts of the Coral Triangle, and the West Pacific to produce 354 *de novo* sequences (mtDNA, control region). Our sequences were combined with previously published sequences from fish collected throughout the Coral Triangle, Taiwan and Japan (540 sequences total), thus covering the latitudinal extremes of the species range (35° N in Japan to 37° S in Australia). We found nucleotide diversity was significantly higher in the core of the species range than in both the northern periphery and southern periphery. This result was robust to the exclusion of divergent clades that only existed within the core of the species range. We found no significant difference in haplotype diversity across the species range, however there were informative differences in the 'nestedness'(i.e. differences due to diversity) and 'turnover' (i.e. differences due to divergence or evolutionary novelty) components of haplotype richness. Evolutionary novelty (turnover) contributed most to haplotype richness in the northern periphery of the range, whereas in the southern periphery there was very little evolutionary novelty, and the haplotypes were almost entirely a subset of those found in the core of the species range. Our study reveals that despite the environmental similarity of the northern and southern periphery of the neon damselfish's range, these regions have had divergent population histories. The northern periphery resembles what might be expected according to the 'core-periphery hypothesis', the southern periphery likely reflects high levels of contemporary immigration from the core.

Connectivity of *Amphiprion akallopisos* (Skunk Clown Fish) in the Indian Ocean

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Like many coral reef associated organisms, *Amphiprion akallopisos*, which lives in mutualistic symbiosis with two species of giant sea anemones, is unable to migrate from one coral reef to another during its adult life stage. Dispersal between reefs in the patchy coral reef environment is assured during the pelagic larval stage. Because small pelagic larvae are extremely difficult to track in the open ocean, population genetics is a useful technique to evaluate gene flow and connectivity between populations of coral reef associated organisms. *Amphiprion akallopisos* has a disjunct distribution, occurring in the Western Indian Ocean (WIO) and the Eastern Indian Ocean (EIO) but not in the Central Indian Ocean (CIO), leaving a gap of more than 4.500 km. In this study, a 337 base pair long sequence of the Control Region of the mitochondrial DNA is used as a genetic marker to study connectivity both between and within the WIO and EIO populations. A total of 263 samples from 17 different sites in the WIO and the EIO have been analysed. Strong population structure ($\phi st=0.28$; $P<0.001$), strong differentiation ($\phi ct=0.61$; $P<0.001$), and low gene flow between the EIO and the WIO populations was observed. A total of 76 haplotypes were identified, none of which simultaneously occurred in individuals sampled in the EIO and WIO. Within both the WIO and EIO populations, low population structure was observed. Selective neutrality tests indicate that the WIO population underwent a recent expansion. The EIO population was identified as the source population based on higher genetic diversity. With a pelagic larval duration of less than 2 weeks, it is improbable that the WIO was directly colonized from the EIO and our results indicate low gene flow between WIO and EIO populations. Suitable sea anemone habitat occurs in the CIO, making stepwise migration towards the WIO possible, but is occupied here by another species, *Amphiprion nigripes*. The reason for the absence of *A. akallopisos* in the CIO, competition or speciation, could not be defined.

Population genetics of a deep-sea demersal fish genus *Lycodes* in the Japan Sea and adjacent areas

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For most marine organisms, present patterns of distribution and composition of populations are the products of historical climatic and hydrographic changes. We examine the phylogeographic patterns of two *Lycodes* fishes, a group of deep-sea bottom-dwelling teleost with little or no larval/egg dispersal ability, by performing population genetic analysis using nucleotide sequences of mitochondrial control region and cytochrome *b* gene. *L.tanakae* and *L.matsubarai* were collected from two marginal seas of the northwestern Pacific, the Japan Sea and the Okhotsk Sea, which was disconnected each other during the last glacial period. We also reconstructed their population history using Bayesian inference on effective population size and coalescent theory-based analysis of migration rate between local populations. For both of two fishes, several haplotypes were shared between local samples of the Japan Sea and the Okhotsk Sea, though the test of *F*st values and the exact tests altogether suggested significant genetic differentiation between local samples. Bayesian Skyline plot revealed specific difference in population dynamics at the last glacial period, also supported by the neutrality tests and the mismatch distribution analysis. Simulated migration rates between local populations showed rapid increase after the last glacial maximum in two species. Rapid population mixing of the deep-sea bottom-dwellers without larval/egg dispersal were shown to have occurred after the last glacial maximum. We are analyzing phylogeography of other *Lycodes* fishes and will discuss factors which have influenced population formation of this deep-sea demersal fish community in the Japan Sea.

Complex evolutionary history of marine fishes in tropical Indo-West Pacific region revealed by comparative phylogeography of emperor breams (Percomorpha: Lethrinidae)

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The origin of the Coral Triangle's extreme concentration of marine biodiversity, in relation to geological, climate and evolutionary events, has been under discussion for many years. Advanced comparative phylogeographic surveys of species from various zoological groups are still needed to reach conclusions on the major evolutionary patterns and processes at play. In this study, we investigated the population structure and phylogeography of multiple species within a single family of marine fishes that share a similar pattern of distribution across the Indo-West Pacific. The model-species being studied were the longface emperor (*Lethrinus olivaceus*), the spangled emperor (*L. nebulosus*), and the spotcheek emperor (*L. rubrioperculatus*). Sequences of the three genetic markers (one mitochondrial and two nuclear genes) were obtained from more than 70 individuals of each species, which were sampled in the Indian Ocean (Zanzibar, Mayotte, Mauritius and Maldives), the Coral Triangle (Taiwan, Vietnam, Bali, West Papua and Papua New Guinea) and the Pacific Ocean (Marshall Is., New Caledonia, Fiji and Moruroa). The analyses of the mitochondrial locus revealed species-specific patterns for each species: (1) a genetically homogeneous population for *L. rubrioperculatus*; (2) a definite genetic break between an Indian Ocean population and all the other populations in *L. nebulosus*; and (3) three deeply divided lineages for *L. olivaceus* represented by the samples from the Indian Ocean, the Coral Triangle, and the Pacific Ocean, respectively. While the results at nuclear markers were generally congruent with mitochondrial sequences in all three species, divergence between nuclear lineages within a species was less significant, and some lineages that were defined by mitochondrial sequences were not detected with nuclear markers. All species/lineages were found to have experienced similar population expansion. However, estimated coalescence times differed between species/lineage. This reveals different timings of contraction-expansion, themselves possibly linked to different episodes of sea-level fluctuation or environmental change in the Pleistocene.

Contrasting population genetic structures among three species of *Acentrogobius* around the Japanese archipelago

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Gobiidae, a species-rich, ecologically divergent family, is an excellent subject for investigating mechanisms of population genetic structure formation in association with ecological characteristics. We focused on three sister species of *Acentrogobius* (*Acentrogobius* sp. A, *Acentrogobius* sp. B and *Acentrogobius* sp. C), all being widely distributed around the Japanese archipelago. The three species have similar life histories (including pelagic larval duration, life span and net reproductive rate), although their distribution patterns in bays differ as a result of restrictions to differing habitat environments; *Acentrogobius* sp. A occurs on the shallow bottoms of riverine estuaries, mainly tidal flats, *Acentrogobius* sp. B, on the shallow bottoms of the inner parts of bays, and *Acentrogobius* sp. C, on much deeper bottoms in the middle of bays. To elucidate the relationships between common patterns of population genetic subdivisions within the three species and their distribution patterns, a total of 411 specimens of the three species were collected (largely sympatrically) from 21 sites around the Japanese archipelago, and partial sequences (800bp) of their mitochondrial cytochrome *b* (cyt*b*) gene determined. AMOVAs and maximum parsimony haplotype networks indicated strong phylogeographical structuring in *Acentrogobius* sp. A and *Acentrogobius* sp. B, there being no significant evidence for such in *Acentrogobius* sp. C (*F*ST: 0.207, 0.127, 0.013, respectively). This suggests that the degree of intraspecific gene flow differs among the three species depending upon their distribution patterns, being more limited in species inhabiting shallower and inner parts of bays, possibly due to the lesser effects of water currents on larval dispersal. In the presentation, we will also discuss the formation of population genetic structures from a phylogeographical viewpoint.

Finding panmixia and uncovering species boundaries: the case of sister unicornfishes (Naso hexacanthus and Naso caesius)

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Phylogeographic studies have shown that many coral reef fish species lack population structure at oceanic scales and some at inter-oceanic scales. However, conventional phylogeographic methods frequently fail to distinguish between long-term panmictic populations and large metapopulations connected by gene flow. Furthermore, large effective population sizes and high genetic diversity make it difficult to detect population structure if it exists. Therefore, at what spatial scale coral reef fish populations experience independent evolutionary trajectories is still a matter of debate. One solution to this problem is to test phylogeographic data against a model. Model-based phylogeography can correctly reject a model of panmixia even if intrinsic patterns in the data fail to do so. In this presentation I show that populations of a cosmopolitan Indo-Pacific surgeonfish, the sleek unicornfish (*Naso hexacanthus*), are best described by a model of long-term panmixia. Yet, if the sleek unicornfish comprises a single evolutionary unit across the Indo-Pacific how and when did it diverge from its closely related and broadly-sympatric sister species, *Naso caesius*? Data from both species are most consistent with a scenario of allopatric divergence, followed by a period of secondary contact that did not result in species collapse. Therefore, even highly dispersive species appear to have experienced isolation, by some historical condition, sufficient for divergence.

Relationships within the surgeonfish genus *Prionurus* with comments on biogeography and evolutionary history

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The surgeonfish family Acanthuridae contains six genera with approximately 80 species. One of these genera, *Prionurus*, has a notabledistribution and is poorly studied. While the vast majority of surgeonfishes are tropical, most species within *Prionurus* have anti-tropical distributions, or are restricted to cold-water upwelling areas. Within *Prionurus* there are six species distributed in the Indian and Pacific Oceansand one species, *P. biafraensis*, in the Eastern Atlantic. There have been several previous studies examining the relationships among genera within Acanthuridae, however most of these studies have only included one or two species within the genus *Prionurus*. Here we present the evolutionary relationships within this genus using both mitochondrial and nuclear DNA to discuss this lineages biogeographic and phylogenetic history.

Hybridisation of allopatrically distributed sister species, *N. elegans – N. lituratus*, in the east Indian Ocean

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Population genetic structure of the allopatrically distributed coral reef sister species (*N. lituratus – N. elegans*; family Acanthuridae) was examined. Whilst these sister taxa are largely segregated by Ocean basin (Indian Ocean vs. Pacific Ocean), they overlap at Cocos Keeling- and Christmas Islands in the eastern Indian Ocean. In addition to sampling the sister taxa extensively across both ocean basins, we collected 3 hybrid individuals identified by intermediate colouration from the contact zone. Three hundred and twenty three fish from 14 locations were amplified using species-specific mtDNA control region primers. A subset of 38 samples were also examined using two nuclear (ETS2, S7I1) and one additional mtDNA (CO1) locus. Standard population structure analyses were performed on the full dataset, the control region (n=323). Additional phylogenetic analyses (MCMC Bayesian, maximum likelihood and maximum parsimony) were performed on each locus separately for the reduced dataset (n=38) to substantiate evidence for hybridisation, as opposed to incomplete lineage sorting. Our results suggest bidirectional exchange of mtDNA and nDNA. We confirm hybridisation of the sibling species, *N.elegans – N. lituratus*, using genetic, morphological, distributional and ecological data. This supports the importance of these east Indian Ocean islands as areas of distributional overlap and potential hybridization of allopatric sister species.

Recruitment of tropical fishes in expanding coral habitats on the temperate coasts of Japan

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Tropical reef corals are expanding on Japanese temperate rocky reefs in response to rising sea surface temperature. Many tropical fish juveniles have been routinely observed in such coral-dominated habitats during summer, most of these larvae probably being transported from the subtropical regions (e.g., the Ryukyu Islands) by the Kuroshio Current during their pelagic larval stage. A comparative study of fish assemblage structures between rocky and coral-dominated habitats found a considerably higher density of tropical fishes in the coral-dominated habitats. Species and individual numbers of tropical fishes roughly paralleled 1–2 months after seasonal change of the seawater temperature, with higher numbers being observed during August–October and lower numbers during February–May. The numbers of many tropical species decreased when the seawater temperature decreased below 18 °C; therefore, the temperature of coral-dominated habitats seems to be an important factor in the strong overwinter survival of tropical fishes. The fishes most unique to coral-dominated habitats were planktivores and corallivores, which belong to Pomacentridae and Chaetodontidae. Light trap sampling on rocky and coral-dominated habitats during summer season revealed that the abundance of settlement-stage larvae was considerably higher in coral-dominated habitats than in rocky habitats, suggesting that coral-dominated habitats attract offshore tropical fish larvae. In an underwater visual survey, tropical fish juveniles were observed to be more abundant in coral-dominated habitats than in rocky habitats, and a laboratory habitat choice experiment demonstrated that these larvae showed a preference for corals rather than rocks. Therefore, habitat choice at settlement possibly accounts for the differences in tropical fish distribution patterns between rocky and coral-dominated habitats. Overall, the findings suggest that coral intrusion on the temperate coasts will lead to an increase in the numbers of coral-associated tropical fishes and will change the fish community composition of the temperate coasts.

Little fishes and big tides: Larval fish assemblages over a macro-tidal, tropical, continental shelf off the Kimberley, north-western Australia

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The Kimberley region of north-western Australia is characterized by huge tides (>10 m), a wide continental shelf and highly variable coastal topography. Although fish diversity is high (>800 neritic species), little is known about larval fishes in the region. This study investigated the pelagic ecosystem (four cross-shelf transects from coastal to oceanic waters) at different temporal scales (hours, days, weeks) to ascertain the influence of environmental parameters, particularly tidal forcing, on larval fish assemblages. Replicated, depth-integrated Bongo net samples (from 150 m to the surface) captured □ 7,000 fish larvae representing 94 neritic and 21 meso-pelagic teleost families. Oceanic stations were dominated by larvae of Myctophidae, Gonostomatidae and Phosichthyidae, slope and outer shelf stations had fewer meso-pelagic species but more neritic taxa including Scombridae and Lutjanidae, whilst coastal stations were dominated by Engraulidae, Bregmacerotidae, Gobiidae and Apogonidae. The spring-neap tidal cycle was not found to have a significant influence on the larval fish assemblages although meso-pelagic taxa were more abundant over the shelf on the spring tide. PERMANOVA indicated spatial structuring of larval fish assemblages associated with the factors of isobath, transect and subsequent tide (same station sampled 12 h apart) but *post hoc* ANOSIM revealed that there was no significant difference between assemblages on subsequent tides. Sampling over 24 h at a station located on the 200 m isobath showed shallowing of the mixed layer in the water column during high tides and a concomitant increase in mean concentration of larval fishes. Although having low replication, ANOSIM analyses of larval fish assemblages showed tide to return a strongly significant result but with no significant diel effect. The substantial differences in concentrations between high and low tides suggest use of vertical migration to minimize offshore dispersal of neritic larvae. If so, this represents an important behavioural adaptation in the extreme physical conditions of the Kimberley continental shelf ecosystem.

Suspended sediment threatens larval development of a coral reef fish

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Increasing sediment input into coastal marine environments is having a profound influence on shallow marine habitats and their supported species. Coral reef ecosystems appear to be particularly sensitive, with increased sediment deposition and turbidity regimes being associated with declines in the abundance and diversity of coral reef fishes. Recent work has demonstrated that suspended sediment impairs habitat choice, foraging success, and predator-prey interactions in coral reef fishes through a reduction in their ability to distinguish visual and chemical cues. However, it is unknown if suspended sediment affects larval development, which is a factor that could alter recruitment patterns in areas prone to high suspended sediment and flood plume exposure. In this study, we investigated if exposure to suspended sediment impairs larval development of *Amphiprion percula,* a coral reef damselfish. Specifically, larvae were subjected to four experimental concentrations of suspended sediment over four different exposure times. Changes in metamorphosis patterns and development were assessed to categorize the impact of suspended sediment concentration and exposure on larval development. Suspended sediment had a significant effect on time to metamorphosis. The fish in the control experienced an average pelagic larval duration of 10.9 days, compared to ~12 days for the sediment treatments. Fishes in suspended sediment showed increased variation in time to metamorphosis, with 83% of the fishes in the control settling by day 11, compared to only 50% in the sediment treatments. In the highest sediment treatment, some individuals extended their larval phase by 100%. Sediment also had a significant effect on foraging. The fish in the low sediment treatment were significantly heavier than the fish in the control or the medium and high sediment treatment. The results of this study suggest that at low levels, sediment can confer a trophic advantage. However, an extension of the pelagic larval stage is likely to reduce survivorship. A sediment-induced impairment of larval development can have major effects on patterns of fish distribution, abundance and population dynamics.

Factors affecting the occurrence patterns of two anemonefishes: an application of metapoppulation model to marine organisms

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As a mechanism of population persistence, much attention has been paid on the concept of metapopulation in which local populations are connected by dispersal or migration among them. Even if local populations are prone to extinction, new populations are subsequently established by dispersal or migration from other local populations (colonization) in metapopulation. Although most marine organisms are postulated to form metapopulations by larval dispersal or migration, the mechanisms of population persistence in marine organisms are poorly understood. Understanding its mechanism is important for effective management of coastal biodiversity threated by anthropogenic disturbance. In terrestrial ecosystems, the incidence function model has been widely used for this purpose. In this model, the occurrence probability of local populations in metapopulation is assumed to increase with increasing habitat patch size because of the lower extinction risk, and to decrease with increasing patch isolation because of reduced rates of dispersal and colonization. We applied this model to examine occurrence patterns of two anemone-fishes (*Amphiprion frenatus* and *A. perideraraion*) around a sheltered bay of Puerto Galera, the Philippines. We used logistic regression to analyze the occurrence of the anemonefishes in relation to (1) habitat patch size (anemone size), (2) isolation based on distance between patches, (3) the presence or absence of other anemonefish species, and (4) depth. Occurrence of *A. frenatus* was significantly related to habitat patch size, the presence of other species and depth, but that of *A. perideraion* was only affected by the presence of other species. Interspecific competition over habitats was likely to decrease the occurrence of both targeting species. Lack of significant effect of habitat patch size on *A. perideraion* is probably due to the presence of other species preventing the colonization in many habitat patches (16 of 46 patches). Isolation was not significant for both species probably because the rate of dispersal is not directly proportional to geographic distance between patches in the coastal areas. Incorporation of ocean current data into the model may increase the accuracy of model to explain occurrence patterns of marine metapopulations.

Wave-driven water motion affects escape responses in juvenile coral reef fishes

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Escaping predators is critical for survival in most taxa. A number of intrinsic (e.g., size, morphology) and extrinsic (e.g., temperature, hypoxia) factors influence the success of escape responses. Despite its ubiquity in aquatic systems, however, the effect of water motion on fast-start escapes in fish remains completely unexplored. In shallow marine habitats, wave action varies both spatially and temporally, creating unsteady water motion that likely affects swimming behaviour. Here, I examined whether wave-driven, unsteady water motion affects the swimming performance of juvenile coral reef fishes during fast-start escape responses. I compared three species with contrasting body morphologies (deep, intermediate and fusiform). Deep bodies are thought to improve postural control and maneuverability compared to fusiform bodies. Escape responses were elicited by mechanical stimulation under conditions of either no flow or unsteady water flow. When swimming in the unsteady flow treatment, all fish covered a greater distance and achieved a higher speed and acceleration when escaping with rather than against the water motion. Compared to the no flow treatment, however, unsteady flow had no effect on maximum escape performance, although fish took longer to respond to the stimulus (increased latency). This latency effect depended on fish body shape. Fish with a more fusiform body responded slower in unsteady flow than in no flow, but the response time of fish with a deeper body was unaffected. This difference is likely due to fish with a deep body orienting themselves more often into the flow and being less displaced by water motion. Since response latency is a major determinant of escape success, postural disturbances from wave-driven, unsteady water motion might reduce the ability of some coral reef fishes to evade predators during settlement. This could have important implications for the distribution, abundance and recruitment of juveniles to adult populations across both spatial and temporal scales.

Recruitment of fishes to coastal reef habitats after the heavy disturbance by the tsunami in northeast Japan

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Underwater visual census has been conducted in a coastal area once in two months after the heavy disturbance by the tsunami in March 2011. Fish species and abundance were recorded through ten replicates of belt transects at four stations in and around the Moune Bay, Kesennuma, northeast Japan. In May 2011, two months after the tsunami, only a few juveniles of fish were found at each station. Fish species and abundance increased along with the recovery of the *Sargassum* bed in the following months. In September, when the water temperature was the highest in the year (21 °C), warm water species such as jack mackerel *Trachurus japonicus*, flathead mullet *Mugil cephalus* and Bensasi goatfish *Upeneus japonicus* were found. In November, the temperature went down and the warm water species disappeared, yet there were still plenty of gobies; *Pterogobius elapoides* was particularly abundant. In the winter season from January to March, temperature went down to 4 °C and relatively few fish were found. In May 2012 (14 months after the tsunami), although the temperature was still low (12 °C), the number of fish species and abundance in each stations were roughly twice and 20 times of those at the same time of the previous year, respectively, including a few large individuals of rockfishes and flatfishes. In September 2012, temperature went up to 23 °C and fish originating from tropical waters, such as manybar goatfish *Parupeneus multifasciatus* and bluestriped fangblenny *Plagiotremus rhinorhynchos*, were found, both being new records in this area. Relatively low abundance of long-lived predators such as rockfishes *Sebastes* spp. may have enhanced recruitment and survival of short-lived gobies as well as seasonal migrants from southern waters after the disturbance by the tsunami.

Phylogenetics and diversification of Percomorpha—An introduction to the symposium

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Percomorpha contains approximately 17,100 species, which is more than 25% of all living vertebrates. The phylogenetic relationships among the major lineages of this incredibly species-rich clade of teleost fishes is largely unresolved, prompting Gareth Nelson to refer to the percomorphs as the the "bush at the top of the [teleost] tree." Over the past three decades percomorph phylogeny has been inferred in comparative anatomical studies and phylogenetic analyses of molecular data, primarily partial mtDNA sequences. Despite these efforts, relationships among the most inclusive percomorph clades are generally unresolved. Recent studies based on extensive taxon and character sampling from whole mitogenomes and nuclear genes; however, have shed new light on our understanding of percomorph phylogenies. This presentation will provide a brief review of these recent molecular studies and review the current knowledge about phylogeny at the top of the teleost tree.

The evolution and history of fishes on coral reefs

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One of the hardest challenges in coral reef ecology is to understand the role that history has played in shaping the ecology of reefs as we see them today. Our evidence is based on two highly contrasting data sets, the fossil record and phylogenies, particularly molecular phylogenies. By far the most popular research area today is molecular phylogenetics, where increasingly large data sets and sophisticated analytical tools are providing insights into relationships and, more importantly, the timing and rates of diversification of various groups. However, ecological inferences must be made with care as character mapping becomes increasingly problematical towards the base of trees and during periods of rapid diversification; often the periods of greatest interest. At this time, however, fossils offer a striking contrast with clear indications of both form and potential function. From these two disparate lines of evidence a clear picture is emerging of successive waves of piscine innovation that have produced both the complexity and vulnerability of coral reefs that we see today.

Rates of speciation and morphological evolution are correlated across ray-finned fishes

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Several evolutionary theories predict that rates of morphological change should be positively associated with the rate at which new species arise. For example, the theory of punctuated equilibrium proposes that phenotypic change typically occurs in rapid bursts associated with speciation events. However, recent phylogenetic studies have found little evidence linking these processes in nature. Here, we demonstrate that rates of species diversification are highly correlated with the tempo of body size evolution across the 30,000+ living species of actinopterygians that comprise the majority of vertebrate biological diversity. This coupling is a general feature of fish evolution and transcends vast differences in ecology and body-plan organization. Our results suggest that evolvability – the capacity of organisms to evolve – shapes the dynamics of speciation through time and serves as a potent architect of evolutionary trends at the largest phylogenetic scales.

Phylogenomics resolves the sister lineage of Percomorpha

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Percomorph fishes comprise more than one quarter of all living vertebrates, and include several model organisms and species of high economic importance. The higher level phylogenetic relationships of percomorphs is poorly understood. In particular, resolution of the sister lineage to Percomorpha has been contentious with hypotheses ranging from squirrelfishes (Holocentridae), dories (Zeiformes), roughies and flashlightfishes (Beryciformes), or a clade containing Beryciformes and Stephanoberyciformes (pricklefishes and whalefishes). Molecular analyses of ray-finned fish phylogeny based on whole mitochondrial genomes and nuclear genes have consistently supported a monophyletic Beryciformes (with Stephanoberyciformes) as the sister lineage of Percomorpha; however, these analyses were charcterized by limited taxon sampling, and the published and online teleost classifications still place the Beryciformes (*sans* Stephanoberyciformes) as the sister lineage of Percomorpha. Using an anchored hybrid enrichment strategy with next generation sequencing, we sampled 132 loci comprising over 99,000 base pairs for representative beryciform, stephanoberyciform, zeiform, percomorph, percopsiform, and gadiform species. Our phylogenetic analyses strongly support the monophyly of Beryciformes, which includes the traditional Stephanoberyciformes, as sister to Percomorpha. These results challenge not only the currently defined taxonomic status of Stephanoberyciformes, but also the predominant view of percomorph phylogeny. We investigated the timescale of beryciform diversification with relaxed molecular clock analyses based on a comparative dataset of 7 nuclear genes and one mitochondrial gene sampled from more than 90 species. The results of our analyses reveal that despite a Cretaceous origin of living beryciform lineages, the extreme ecological and morphological disparity in the clade has recent origins, with much of the contemporary species diversity originating in the Miocene.

Alone in the family: Phylogeny of monotypic and monogeneric percomorph lineages

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The approximately 17,100 species of Percomorpha are classified into more than 235 taxonomic families, of which at least 23% are monotypic or monogeneric. Many of these families have eluded phylogenetic resolution in morphological based systematic studies and they present challenges in the construction of a rank-free classification of actinopterygians. It is not known if these species-poor lineages nest deeply within major percomorph clades, or if they have more recent origins within traditionally delimited families. The phylogenetic relationships and stem lineage ages of 46 monotypic and monogeneric percomorph families were assessed from analyses of 10 nuclear gene DNA sequence dataset, sampled from more than 550 species. Phylogenetic relationships were inferred using maximum likelihood and lineage ages were estimated using a Bayesian relaxed molecular clock analysis with 36 fossil-based age constraint priors. All sampled species resolved into one of fourteen major lineages within Percomorpha in the new molecular phylogeny. Analyses of clade ages will determine if the monotypic and monogeneric families are young when compared to the age of more species-rich taxonomic families, and if their phylogenetic resolution results in paraphyly of other traditionally recognized percomorph families.

Origin, assembly and diversification of the modern coral reef fish fauna

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Coral reefs harbor spectacular fish diversity but how did the modern assemblage of reef fishes come about and what has been the impact of reefs on fish evolution? We investigated the history of reef invasions using a time-calibrated molecular phylogeny of 579 species representing all major lineages of spiny-rayed fishes, and using Bayesian stochastic mapping to reconstruct the assembly of the modern coral reef fish fauna. This revealed at least 50 transitions onto reefs in the past 100 my to form the modern assemblage. There is a striking pattern of elevated invasion rates between the Cretaceous-Paleogene (K-Pg) mass extinction event 65 mya and 40 mya, followed by a sharp decline in transition rates since then. This pattern is consistent with a scenario of rapid filling of major reef niche space by spiny-rayed fishes through the first half of the Paleogene, followed by saturation and markedly declining transitions. We explored the impact of reefs on ecomorphological diversification in two major reef fish radiations. Over 500 of the approximately 600 labrid species live on reefs, and the group includes spectacular ecological diversity. Patterns of diversification in the iconic labrids were contrasted with Haeumulidae, which, although an important New World group, is more species rich in non-reef habitats and shows modest trophic diversity. Using an analysis pipe-line that accounted for phylogentic relationships among species, the time available for diversification and model uncertainty we found that reef labrids occupy 68.6% more trophic morphospace than non-reef species and have rates of trait evolution that are on average twice as fast as non-reef lineages. Such a pattern might be expected in this quintessential radiation of reef fish, but we found an even stronger pattern in Haemulidae where trophic traits evolve up to 12 times faster in reef lineages, despite no niches unique to reefs having evolved in this group. Together these analyses present a strong case that reef habitats cause a higher rate of morphological diversification in fishes. Exactly why cannot yet be determined, but the high physical and biological complexity on reefs may offer tremendous ecological opportunity that drives diversification.

Paleogene adaptive radiation of tunas and their pelagic relatives revealed by bioinformatic and mitogenomic analyses

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Uncertainties surrounding the evolutionary origin of the epipelagic fish family Scombridae (tunas and mackerels) are symptomatic of the difficulties in resolving suprafamilial relationships within Percomorpha, a hyperdiverse teleost radiation that contains approximately 17,000 species placed in 13 ill-defined orders and 269 families. Here we find that scombrids share a common ancestry with 14 families based on (*i*) bioinformatic analyses using partial mitochondrial and nuclear gene sequences from all percomorphs deposited in the database (10,733 sequences from 5368 species across all 13 suborders, 215 families, and 1558 genera) and *ii*) subsequent mitogenomic analysis based on 57 species from those targeted 15 families and 67 outgroup taxa. Morphological heterogeneity among those 15 families is so extraordinary that they have placed in 6 different perciform suborders. However, members of the 15 families are either coastal or oceanic pelagic in their ecology with diverse modes of life, suggesting that there has been an undetected adaptive radiation in the pelagic realm. Analysis of depth ecology using a time-calibrated phylogeny implies that scombrids originated from a deep-ocean ancestor and began to radiate after the end-Cretaceous when large predatory epipelagic fishes were selective victims of the Cretaceous-Paleogene mass extinction. We name this clade of open-ocean fishes containing Scombridae 'Pelagia' in reference to the common habitat preference that links the 15 families.

Molecular systematics and historical biogeography of the perch-like fishes (Teleostei: Perciformes)

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The perciform or perch-like fishes are the most diversified fish order with more than 10,000 species currently classified in 160 families within 20 suborders. Although they may occur in freshwater habitats, most species are tropical marine. Species from this group are not only a major component of the modern ichthyofauna, but they also support important worldwide subsistence fisheries. In spite of their fundamental importance in both ecosystems and human activities, the classification of this order is still unsettled because of a continuing lack of understanding of the higher-level sister-group relationships among the perciform lineages and their relatedness to other percomorph fishes. In fact, there is no indisputable evidence to support monophyly of the Perciformes and some typical suborders/families such as the Percoidei, Percichthyidae, Serranidae, and many other proposed groups. Most of current efforts (e.g., FISH-BOL) in molecular systematics of the Perciformes have been at lower taxonomic levels and based on mitochondrial gene or genome data. A tremendous amount of data from the nuclear genome has not been easily obtained or readily available for the systematic and evolutionary studies of the group until very recently. In this paper, we examine the phylogenetic relationships of perch-like fishes using 5 nuclear genes (5310 bp) with an attempt to resolve this long-stand higher-level systematic problem. Taxonomic sampling is composed of the taxa from 116 families represented in all suborders, and from a diverse array of other percomorph fishes (257 plus 2 non-percomorph outgroup taxa in total). These taxa/genes were analyzed in partitioned RAxML and Bayesian analyses. The resulting phylogenetic hypothesis of these fishes will be compared with previous hypotheses of relationships and classification of these fishes. The historical biogeography and the cases of phylogenetic niche conservatism will be discussed.

A new rank-free and phylogeny-based classification of Acanthomorpha and Percomorpha, derived from an expanded molecular phylogeny of actinopterygians

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Using DNA sequence data from 10 nuclear genes sampled from more than 700 species of ray-finned fishes, we have inferred a highly resolved phylogeny of acanthomorph fishes. From our phylogeny, a new classification of Acanthomorpha is proposed. The acanthomorph fishes consist of 5 major clades: an unnamed clade containing *Polymixia* and Percopsiformes; Zeoigadiformes (including *Stylephorus*); Lampriformes; Beryciformes; and Percomorpha. Within the Percomorpha we delimit 14 major clades. The two earliest diverging percomorph clades are the Ophidiiformes and Batrachoidiformes. The other clades are: an unnamed clade containing scombroids, bramids, mullids, syngnathoids, and others; Gobiiformes (= gobioids, apogonids, and kurtids); an unnamed clade containing nandids, mastacembelids, anabantoids, indostomids, and synbranchids; Carangomorpha (including carangoids, billfishes, snooks, barracudas, and pleuronectiforms); Ovalentaria (athernomorphs, blennioids, cichlids, pomacentrids, and others); Gerreidae; Labridae; Paratrachinoidei (ammodytids, uranoscopids, pinguipedids); an unnamed clade including centrarchids, percichthyids, kyphosids, girellids, cirrhitids, and others; an unnamed clade including acropomatids, pentacerotids, creediids, *Howella*, *Ostracoberyx*, *Glaucosoma*, polyprionids, pempherids, and others; a revised and much more restricted Perciformes (including serranoids, percids, scorpaeniforms, zoarcoids, and gasterosteoids); and an unnamed clade consisting of moronids, many of the former squamipinnes, lophiiforms, tetradontiforms, acanthuroids, sciaenids, sparoids, haemulids, and lutjanoids. Many of these clades find some degree of support in phylogenetic analyses of whole mtDNA genome sequences. We anticipate that this new phylogenetic perspective on acanthomorph diversity will provide important insights into the history of phenotypic and ecological diversification within the clade.

The evolution and diversification of Percomorpha: a 'deep time' perspective

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Percomorpha—"the bush at the top" of the teleost tree—is represented by a rich fossil record characterized by an abundance of well-preserved skeletons that bear considerable anatomical character information. Despite the quality of this archive, paleontology has made little impact on our understanding of percomorph evolution. Colin Patterson provided the last comprehensive review of the percomorph fossil record two decades ago, but analytical advances made since that time, combined with new fossil discoveries, have yielded novel perspectives on percomorphs in 'deep time'. Here I focus on the unique contributions that paleontology can make to our understanding of the origin of modern percomorph diversity by focusing on three interrelated themes: morphological innovation, timing of major divergences, and rates of anatomical change. Concerning the evolution of novelty, fossils provide unique insights on patterns of trait acquisition because they preserve character combinations not found in extant taxa. Here I show how fossils document the evolution of some of the most bizarre specializations in percomorphs by reviewing examples from Carangimorpha, and illustrate how paleontological data can be integrated with developmental information to provide a more comprehensive understanding of anatomical transformation. With respect to the timing of evolutionary divergences, it is obvious that the first appearances of groups in the fossil record will always postdate their true time of origin. However, new statistical techniques that consider the incompleteness of paleontological archives permit probabilistic estimates of divergence times based on fossil data alone. Here I explore patterns of congruence between this more realistic view of the fossil record with evolutionary timescales for Percomorpha derived from molecular clock analyses. Finally, fossils provide information on rates of phenotypic change in groups over time that can alter perceptions based on recent species alone. Here I examine shifts in the rates of morphological evolution over the history of percomorphs, and ask if any of these patterns might relate to major events in earth system history.

UCE-based sequence capture enables robust phylogeographic reconstruction in fishes

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The identification of markers that are informative at a range of phylogeographic scales and that can be economically targeted and sequenced using next-generation technologies remains elusive. Here we present a novel workflow based upon targeted enrichment of ultra-conserved nuclear DNA elements (UCEs) and their flanking sequence. Our approach allows for efficient and economic generation of phylogenetic data sets with thousands of loci for large numbers of non-model taxa. We show that these markers enable robust phylogeographic reconstruction within several acanthomorph families due to the large number of loci that can be targeted as well as the high degree of rate variability within and across UCE regions. A further advantage of our approach is that UCE loci are broadly conserved across the fish tree of life. Thus data from phylogeographic studies in different taxa and at various scales can easily be integrated to pursue broader-scale phylogenetic questions.

Application of gene capture and next-generation sequencing technologies in the study of phylogenetic relationship of Gobioidei fishes

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Gobioidei is the largest group in Perciformes, comprising 9 families, 270 genera, and about 2,211 species. Because this group of fishes differentiated into many species within an extremely short period of time, it's very difficult to reconstruct their phylogenetic relationship. In the past, only a single or a few mitochondrial genes have been used to study phylogeny of gobioid fishes, which is particularly problematic in resolving the interrelationships in such a fast-evolving group. Next-generation sequencing allows us to collect lots of sequence data efficiently. In the present study, we applied gene capture and next-generation sequencing approaches on 16 representative species of the nine families of Gobioidei. We collected sequence data from ~ 500 nuclear loci. We screened the loci for the ones with clock-like rate and stationary base composition. By applying different species tree methods, we obtained a well-supported phylogeny. Our approach showed the potential of using a large number of nuclear loci in resolving phylogenetic interrelationships of fast-evolving groups.

Population structure of *Stiphodon rutilaureus* (GOBIIFORMES: SICYDIINAE) in the New Georgian Islands, Solomon Islands

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In this study, we use seven microsatellite loci to investigate the population structure of the amphidromous goby species *Stiphodon rutilaureus* in the New Georgian Islands. A total of 220 specimens were collected between June 2010 and August of 2012 on three different trips using backpack electro-fisher, hand nets and aquarium nets. The preliminary AMOVA results reveal that 99% of variation is contained within populations. Pairwise comparisons reveal no significant differences between three different regions (Northern New Georgian islands, Western New Georgian islands and Central New Georgian islands), but a significant difference occurs between Kolobangara and Rendova islands. The findings in this study concur with results from previous studies indicating low or no population structure among populations of amphidromous fish species on different islands within an archipelago. This information is critical for effective management and conservation of this and other island species.

Evolution of microhabitat association and morphology in a diverse group of cryptobenthic coral reeffishes (Teleostei: Gobiidae: *Eviota*)

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Gobies (Teleostei: Gobiidae) are an extremely diverse and widely distributed group and are the second most species rich family of vertebrates. Ecological drivers are key to the evolutionary success of the Gobiidae. However, ecological and phylogenetic data are lacking for many diverse genera of gobies. Our study investigated the evolution of microhabitat association across the phylogeny of 18 species of dwarfgobies (genus *Eviota*), an abundant and diverse group of coral reef fishes. In addition, we also explore the evolution of several morphological characters to determine the relationship between morphological evolution and microhabitat shifts. Our results demonstrate that *Eviota* species switched multiple times from a facultative hard-coral association to inhabiting rubble or mixed sand/rubble habitat. We found no obvious relationship between microhabitat shifts and changes in morphology. We also found evidence of evolution via reduction, simplification or loss in several morphological characters. The relative flexibility in coral-association in *Eviota* combined with the ability to move into non-coral habitats suggests a genetic capacity for ecological release in contrast to the strict obligate coral-dwelling relationship commonly observed in closely related coral gobies, thus promoting co-existence through fine scale niche partitioning. The variation in microhabitat association may facilitate opportunistic ecological speciation, and species persistence in the face of environmental change. This increased speciation opportunity, in concert with a high resilience to extinction, may explain the exceptionally high diversity seen in *Eviota* compared to related genera in the family.

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Assessment of the potential use of morphological and pigmentation characters during larval development for phylogenetic analysis of Gobiidae

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The Gobiidei are a very diverse group of fish comprising nine families with about 270 genera and 2,210 species. There have been a variety of studies undertaken using morphological, osteological and molecular characters of adults to investigate phylogenetic relationships within the group. Larval developmental series collected from southern Australian waters of seven genera of Gobiidae (210 genera, 1,950 spp) *Arenigobius, Afurcagobius, Favonigobius, Gobiopterus, Paedogobius, Psueogobius* and *Redigobius* and two genera of Eleotridae (35 genera 155 sp) *Hypseleotris* and *Philypnodon* were assessed. For the larval development series of these nine genera, ontogenetic changes in body shape and pigmentation patterns and the size at development of fins, notochord flexion and transition to juveniles for each genus were documented. There was considerable variation in these larval characters between the two families and between genera. The larval development characters were assessed to determine similarities and differences between genera and then compared with the proposed lineages for these genera based on adult characters.

Reexamination of commensal goby, *Bryaninops* (Teleostei: Gobiidae) collected from Japan

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The Gobioid genus *Bryaninops*, included within the group of commensal gobies associated with corals (e.g. *Anthipathes, Cirrhipathes, Ellisella, Junceella* and *Acropora*) and sponges, currently includes twelve species from the Indo-Pacific region, nine having been recorded from Japan. However, some species have often been misidentified when observed, owing to a lack of appreciation of their diagnostic life coloration. Recent investigations conducted on *Bryaninops* have disclosed three unidentified species, one sometimes misidentified as *Bryaninops yongei* due to considerable individual variations in the numbers of pectoral, second dorsal and anal fin rays. In fact, an analysis of fin ray numbers revealed two peaks in their frequency distributions, the cryptic (undescribed) species having greater numbers of pectoral, second dorsal and anal fin rays, and unbranched anal fin rays, and a reduced number of scales than *B. yongei*, in addition to a more slender head and body, and different color pattern (dark lateral bands on the body). A second species resembles *B. amplus* and *B. loki* in appearance, but differs from both in having dark lateral bands on the body, and from the former in having oval pelvic fins (from ventral view) with larger lobes and a non-villiform inner edge. It differs from *B. loki* in having the pelvic fin lobe folded, predorsal scales present, a reduced number of lateral and transverse scales, and the gill opening posterior to the preopercle, and different arrangement of cephalic sensory papillae. The third species also resembles *B. loki* in appearance, but differs in having yellowish dorsal, anal and caudal fins, dark lateral bands on the body, the dorsal fin base length less than the fin height, narrower interorbital space, reduced numbers of lateral and transverse scales, and different arrangement of cephalic sensory papillae.

Specific gravity and migratory pattern of two types of amphidromous gobies on Okinawa Island, Japan

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Amphidromy is a type of diadromy. Larvae hatching in freshwater drift to the sea where they spend larval life and migrate back to freshwater to grow and reproduce. There seems to be two types of amphidromy in fish, which have differences in several life history characteristics such as egg and larval sizes. We hypothesized that these differences affect their migratory patterns and migratory distances in the ocean. However, ecology of oceanic larval stages and migratory distances of amphidromous fish are still unclear. To estimate migratory patterns, otoliths of *Tridentiger kuroiwae* (N=20) and *Stenogobius* sp. (N=10) were analyzed with femtosecond laser ablation ICP-MS. The Sr:Ca and Ba:Ca results showed that all of them are amphidromous. Some fish stayed upper/middle reaches and others had several movements between upper and lower reaches in freshwater. During early life stages, aquatic organisms are affected by their own buoyancy (specific gravity: SG). To understand their amphidromous life history, we chose four amphidromous gobies, with large egg type (*Rhinogobius giurinus* and *T. kuroiwae*), and small egg type (*Stenogobius* sp. and *Eleotris acanthopoma*) and examined their SG. Egg clutches were collected in streams on Okinawa Island, Japan and newly hatched larvae were reared in the laboratory. SG was measured every 1-5 days until settlement for *R. giurinus* and *T. kuroiwae*, and 0, 1, 2, 3, 5 and 7 days after hatching for *Stenogobius* sp. and *E. acanthopoma* during daytime (10:00-14:00) and at night (22:00-26:00). SG of 4 species ranged from 1.0159 to 1.0488, with variety among ontogenetic stages, day and night, and species. The ontogenetic changes of SG were relatively similar in *R. giurinus* and *T. kuroiwae*, with lower in early stages of experiments and greater after yolk absorptions. While dial changes were different as *T. kuroiwae* had greater SG in daytime, *R. giurinus* had slightly opposite patterns in their later stages until settlement. SG of *Stenogobius* sp. and *E. acanthopoma* had similar patterns with greater at hatching and getting lower without large differences between day and night. Those results suggest that their migratory patterns were various and may be influenced by several larval traits including SG.

Scratching the surface - a BOL analysis of the *Trimma tevegae* grouping of reef gobies

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This phenetic grouping contains four nominal species, all of which appear to be valid (Winterbottom, 2011), and is made up of at least 11 different, and often widely divergent, haplogroups in our BOL analysis. The species for which the grouping is named, *Trimma tevegae*, was described from Rabaul, New Britain. Our BOL analysis includes specimens identified as *T. gigantum*, despite the fact that these fishes lack a dark caudal spot so typical of *T. tevegae*. Two other nominal species, *T. caudomaculatum* described from Japan, and *T. xanthochrum*, described from the Raja Ampat islands off the Bird's Head of New Guinea, are also included. There are thus four names available for the 11 haplogroups. The minimum distance recovered between any two haplogroups was 2.5% of the CO1 base pairs, and lay between specimens initially identified as *T. xanthochrum* from Raja Ampat + the Fak Fak Peninsula of western Papua New Guinea + Palawan and those from Rabaul, New Britain. The largest minimum distance was between specimens initially identified as *T. tevegae* from Palau (called Group 1 here) and those from Rabaul, New Britain (called Group 6). That distance was 22.4%. The interactions between these 11 haplogroups will be explored in detail, along with morphological congruence where it has been found.

Reproductive biology of four *Lutjanus* fishes (*L. gibbus*, *L. decussatus*, *L. fulvus* and *L. fulviflammus*) around Yaeyama Islands, Okinawa, Japan

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Reproductive biology of four most abundant *Lutjanus* fishes (i.e. *L. gibbus*, *L. decussatus*, *L. fulvus* and *L. fulviflammus*), which are important commercial targets, were investigated using specimens caught around Yaeyama Islands, Okinawa, Japan. Body size was much larger in males (up to ca.41 cm in fork length) than females (32 cm) for *L. gibbus*. On the other hand, females (31-34 cm) were 2 or 3 cm larger than males (29-32 cm) for other three species. Spawning was confirmed from May to October for *L. gibbus*, June to October for *L. decussatus*, June to September for *L. fulvus* and April to August for *L. fulviflammus*. The first maturation sizes (age) of females were estimated to be 24 cm (4-yrs) for *L. gibbus*, 21 cm (3-yrs) for *L. decussatus*, 22 cm (4-yrs) for *L. fulvus* and 21 cm (2-yrs) for *L. fulviflammus*. Those of males were 22 cm (3-yrs) for *L. gibbus*, 20 cm (2-yrs) for *L. decussatus*, 22 cm (4-yrs) for *L. fulvus* and 21 cm (2-yrs) for *L. fulviflammus*. Most of commercial catches were adult sizes. Females of all four species had relatively large ovaries, and gonadosomatic index often exceeded 10 during spawning season. Gonad sizes in males were similar to those in females for *L. fulviflammus* and *L. fulvus*, implying these species exhibit group spawning. On the other hand, gonad sizes were significantly smaller in males than females for *L. gibbus* and *L. decussatus*, and it was particularly prominent for *L. gibbus*. Much larger body size and small testis in male *L. gibbus* may relate its reproductive behavior, as known for many protogynous (= male larger) reef fishes (e.g. part of Labridae, Scaridae and Serranidae) which have smaller testes compared to ovaries and exhibit pair spawning or polygamous mating. *L. decussatus* is a lunar synchronized spawner and has ca. 1 month intervals between each short spawning event, and their testicular size may be sufficient for each of a few spawning days. These differences in life history traits as well as ecological information among *Lutjanus* species may help to understand biodiversity of reef fishes.

Sexual plasticity of gonadal cells in the protogynous wrasse, *Halichoeres trimaculatus*

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It is well known that teleost fish exhibit marked sexual plasticity unlike higher vertebrates. Three-spot wrasse, *Halichoeres trimaculatus*, inhabiting coral reef of Okinawa can change sex from female to male. During the process of gonadal sex change, ovary is substituted with testis along with dramatic histological change. Little, however, is known about what cells enable gonadal sex change. Here, we demonstrate the origin of testicular cells during sex change to identify the cells that enable gonadal sex change and discuss the sexuality of the cells in this species. We first analyzed apoptosis and cell proliferation during the process of gonadal sex change. As a result, it was found that oocytes disappear via apoptosis while gonial germ cells proliferated during degeneration of ovarian tissue. Additionally, it was demonstrated that some types of ovarian somatic cells actively proliferated rather than being induced apoptosis during early stage of sex change. From these results, we hypothesized that these proliferated cells survive during the regression of ovarian tissue. As it affirmed the hypothesis, BrdU pulse-chase analysis showed that the proliferated gonial germ cells might differentiate into sperm, and somatic cells survived in the gonad during sex change. Specifically, it was displayed that proliferative granulosa cells surrounding degenerate oocytes remained in the gonad during sex change and some proliferative somatic cells at the early stage of sex change probably gave origin to Sertoli cells and steroid producing cells in testis. For further investigations, we focused on granulosa cells. Accordingly, it was found that granulosa cells functioned as estrogen-producing cells in the ovary. Therefore, granulosa cells were trucked using steroidogenic enzymes immunohistochemically, indicating that granulosa cells might transform into androgen-producing cells during sex change. In addition, we investigated expression profile of a gene during sex change to identify the origin of Sertoli cells. The result allowed us to presume that supporting cells surrounding gonial germ cells in the ovary were origin of Sertoli cells. From these results, we conclude that some ovarian gonial germ and somatic cells composing ovary exhibit sexual plasticity and this cellular property enables restructuring of the gonad during sex change.

Reproductive characteristics of the Humbug dascyllus, *Dascyllus aruanus* in Chuuk Lagoon, Micronesia

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Reproduction of coral reef fish is varied and quite complex. The spawning of many species in coral reef area was influenced by stimuli of environmental cues, such as lunar cycle and rainfall. The Humbug dascyllus, *Dascyllus aruanus* is one of major components in coral reef fish assemblages of Chuuk Lagoon, Micronesia. In this study, we inve stigated the reproductiv e characteristics of *D. aruanus* in W eno Island of Chuuk Lagoon. Reproductive patterns of *D. aruanus* exhibited multiple spawner characteristics, including coexistence of various maturity stages in maturity process of ovary and testis. However, our knowledge was not clear understanding the relationship between spawning a ctivity and environmental cues. Therefore, it needed to further studies.

Throwing light on the ichthyological work of F. L. de Castelnau – his unpublished notebooks and paintings

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François Louis Nompar de Caumont Laporte, comte de Castelnau, also known as F. L. de Castelnau (1810-1880), was a widely traveled explorer and diplomat and one of the most prolific French naturalists of the 19th Century. In 1843-1847 he led a major expedition to the Matto Grosso, Brazil, and Peru. In 1848-1855, he was the French Consul at Salvador, Bahia, Brazil. In 1855, he returned to France and later travelled via the Red Sea and Reunion to the Cape of Good Hope (South Africa), where he was French Consul at Cape Town from 1856-1858. He was posted as the French Consul to Siam (Thailand) in Bangkok from 1858-1862 and during this time, he also visited Indonesia and Singapore. In 1863, Castelnau was appointed Consul-General for France in Melbourne, Australia, where he remained until his death in 1880. Castelnau was a prolific ichthyologist, who described a total of 469 new species of fishes from Brazil, Peru, South Africa, and Australia. He also collected and painted fishes during his time in Siam, and his notebooks were used by Pieter Bleeker in a series of papers on the fishes of Siam and Singapore. However, for nearly 150 years his collections and notebooks were thought to be lost, until recently uncovered in the Zoology Museum, University of Liège (ZMUL), Belgium. Castelnau's fish collection comprises many dried mounted specimens from South Africa, Siam and Singapore, and an undetermined number of alcohol preserved specimens. His illustrations are contained in five notebooks, and include about 1000 paintings of fishes and notes from Reunion, South Africa, Siam and Singapore. Castelnau's paintings and specimens provide a source of verification and identification for his work on South African fishes and also for publications by Bleeker on the fishes of Siam and Singapore.

Japanese source materials and knowledge used by Cuvier & Valenciennes to describe Japanese fish in the early 19th century

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Even after the acceptance of Linnaeus' scientific classification system based on binominal nomenclature in Europe, it's reach did not extend to the non-European regions. This was aggravated by Japan' s isolation from the west except for Holland at that time. However, Japanese species were eventually integrated into the modern biology classifications through the examination of specimens and other resources which were brought to Europe. The oldest Japanese fish specimens used for the scientific description were brought back by Thunberg, a Swedish scientist and a pupil of Linnaeus, who worked for the Dutch East India Company (VOC). In 1782, based on the Thunberg's specimens, Japanese fishes were first described by Houttuyn, a Dutch naturalist, and Thunberg himself also described new species afterwards. During the Japanese isolationist policy, Japanese natural history was, however, almost unknown to Europe. It was Cuvier and Valenciennes, who could describe Japanese fish species based on the second oldest Japanese fish specimens, as well as non-biological sources. Cuvier and Valenciennens could use Japanese materials brought back by Langsdorff and Tilesius, German natural scientists, who participated in Russia's First Round-the-World Expedition (1803-1806) conducted by Captain Krusenstern. The results of our investigation from 2010 to 2012 have shown that the Japanese ichthyological materials brought back by the Krusenstern Expedition had been widely scattered across Europe. Fish specimens have been stored under the "Langsdorff Collection" at the following three museums: The Natural History Museum in Berlin, Germany (ZMB); The Natural History Museum in Paris (MNHN), and The Zoological Institute of Russian Academy of Sciences, St. Petersburg, Russia (ZIN). Moreover, original drawings by Tilesius, which were used for the Krusenstern's Atlas, have been stored in the Leipzig University, Germany. In addition, Cuvier and Valenciennes used the Japanese printed book called "Umi no sachi," which had been brought to Paris from Holland. In this paper, we would like to discuss the roles of the two types of Japanese materials available to Cuvier and Valenciennes. Focusing on the statuses of the type materials today, we will evaluate their contributions to the progress of Japanese ichthyology in the early 19th century.

How was a new anguillid species *Anguilla luzonensis* discovered in the western North Pacific?

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During a R/V Hakuho Maru research cruise in July 2002, two anguillid leptocephali (46.6, 51.2 mm) with strange mtDNA sequences unlike any known anguillid species were collected in the North Equatorial Current of the western North Pacific close to the spawning areas of *Anguilla japonica* and *Anguilla marmorata*. Initially these new sequences were thought to be caused by introgressions or contamination. However, when three more anguillid leptocephali (29.2–>46.6 mm) were collected in the same region in 2005, 2006 and 2009 that had the same DNA sequences, it became apparent that these larvae must belong to a cryptic species of anguillid eel. The leptocephali were collected in the North Equatorial Current west of Luzon Island of the Philippines, suggesting that the Philippines may be a possible recruitment area of this cryptic species. The morphological characteristics of the leptocephali (102–106 total myomeres and dorsal fin length) suggested the cryptic species was a mottled longfin eel seemingly like *Anguilla celebesensis*, which was thought to recruit to the northern Philippines. Several expeditions were made to the Cagayan River system of northern Luzon Island to search for the cryptic anguillid species, and this led to the collection of yellow eels of a clearly new anguillid eel species, *Anguilla luzonensis*, as reported by Watanabe et al. (2009). This new species was also detected among eels imported as glass eels from northern Luzon and raised in aquaculture ponds in Taiwan (Teng et al. 2009), as well as within other collections of glass eels from the mouth of the Cagayan River. Glass eels from northern Luzon in previous studies (Tabeta et al. 1976) that were thought to be *A. celebesensis* now appear likely to have been *A. luzonensis*. It was 70 years after Ege (1939)'s now well-established taxonomic system of the genus *Anguilla* of 18 species or subspecies that a new species was discovered. It is noteworthy that the first clue to this discovery of a new species of freshwater eels was the collection of its larvae in the open ocean of the Pacific.

Osteology and taxonomy of the opsariichthine cyprinid fishes (Cypriniformes, Cyprinidae)

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The fishes of the opsariichthnes are distributed in East Asia from the Amur River system through the Korean Peninsula to China, Japan, Taiwan and northern Vietnam, inhabiting various habitats in rivers, streams, lakes and ponds. This group has taxonomically been defined by Chen (1982) and contains four genera; *Opsariichthys* Bleeker, 1863, *Zacco* Jordan & Evermann, 1902, *Candidia* Jordan & Richardson, 1909 and *Parazacco* Chen, 1982 placed to a cyprinid subfamily, the Danioninae. However, in this group, generic classification is erratically treated yet. Thus, the phylogenetic relationships within the group are examined herein using the morphological characters mainly by osteology, and inferred based on synapomorphies. The opsariichthines are divided into two monophyletic groups. The first monophyletic group was defined by two synapomorphies: (1) fifth infraorbital bone is remarkably small, (2) anterior tip of cleithrum is extended, and this group was characterized by having irregular cross bars on the side of body such as *O. uncirostris, O. pachycephalus, O. kaopingensis, O. evolans* and *Z. platypus.* The second group was defined by two synapomorphies: (1) having a longitudinal stripe on the flanks, (2) colored in red on the belly of the head; that include *Z. temminckii*, *Z. sieboldii*, *Z. koreanus*, *C. barbata* and *P. spilurus*. In this study, we conclude that each group should be treated as one single genus, and then the first group is taxonomically lumped as *Opsariichthys* Bleeker, 1863, while the second group is *Candidia* Jordan & Richardson, 1909.

"Kunimasu", *Oncorhynchus kawamurae* Jordan and McGregor, 1925 (Salmoniformes: Salmonidae), rescued from extinction!

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Oncorhynchus kawamurae ("Kunimasu"), endemic to Lake Tazawa, Akita Prefecture, but now extinct in that locality, was recently discovered in Lake Saiko, Yamanashi Prefecture, that population having originated from 100,000 eyed eggs introduced from Lake Tazawa in 1935. Biological characteristics of the species, poorly known even before its apparent extinction, have now become apparent, being based on many specimens. Although "Kunimasu" had always been considered to have black body coloration, it is now known to be black only at the spawning stage. Maturing individuals, inhabiting the meso-pelagic zone of the lake, are brownish-gray or brownish-silver in color. Immature individuals, also found in the meso-pelagic zone, are silver in body color, similar to like-sized *O. nerka* ("Himemasu"). These two life stages of "Kunimasu" had been unknown in Lake Tazawa. In addition, although "Kunimasu" had been believed to lack dark spots on the body, a few such spots have been found in some individuals. Although "Kunimasu" has previously been clearly distinguished from a related species ("Himemasu") by a combination of counts of gill-rakers and pyloric caeca, in fact the upper counts of "Kunimasu" pyloric caeca have been found to overlap the lower counts of "Himemasu. On the other hand, gill-raker counts do not overlap between the two species. The specimens of "Kunimasu" and "Himemasu" examined here were separated by a Bayesian-based clustering method using five microsatellite DNA loci.

Diversity and interrelationships of Indo-West Pacific Aulopidae

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In 1989 at the Third Indo-Pacific Fish Conference in Wellington, New Zealand, Takeshi Shimizu and Takeshi Yamakawa presented a poster identifying four genera and four new Western Pacific species in the family Aulopidae. Seventeen years later Bruce Thompson displayed a poster at the 2006 Annual Conference of the American Society of Ichthyology and Herpetology in New Orleans, USA, with a similar view of the family and provided a key to species known at that time. Neither study was published, although one of Shimizu and Yamakawa's four new species has since been described by other authors (Lee and Chao, 1994). An analysis of material now in Australian, New Zealand and Japanese collections using both morphological and genetic techniques supports the recognition of species identified by the former authors and the four genera featuring in the two presentations, as well as additional species that occur in the same overall region that have collectively been misidentified as *Hime japonica* (Tanaka).

Systematics and biology of the oceanic oarfish genus *Regalecus*, Part II

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Part I of this account reviewing the systematic part of his work on the oarfish genus *Regalecus* was presented by the speaker at the 7th Indo-Pacific Fish Congress at Taipei in May 2005. Evidence was provided for two widely distributed species with almost completely allopatric distribution, the coldwater *R. glesne* in the North and South Atlantic and Mediterranean, and the warm-water *R. russellii* in the North Pacific (including Okinawa), South Atlantic, and probably Indian Ocean. Specimens of the two species at all sizes have non-overlapping differences in counts of dorsal fin rays, and abdominal vertebrae. The relatively few available complete specimens of the two species have non-overlapping differences in total vertebrae. Adults have non-overlapping differences in number of gill rakers and of ornamented rays in the second dorsal fin crest. It seems likely that only the warm-water *R. russellii* occurs in the Indian Ocean, but positive species identifications of actual specimens of *Regalecus* from the Indian Ocean are still unavailable as of January 2013. In Part II, at the 9th Indo-Pacific Fish Congress in Okinawa in June 2013, biology of the two species will be discussed, including spawning grounds associated with sea mounts. Large fish expatriated from reproductive populations live out their lives without reproducing in the eastern Pacific and eastern Atlantic. Large *Regalecus* have a paucity of predators and parasites. Self-amputation or autotomy of the posterior part of the body in all fish over 1 or 1.5 m length, was long mistakenly interpreted as due to predation by sharks. Instead of an adaptation to prevent or deter predation, autotomy in *Regalecus* may be an adaptation resulting in metamorphosis from a long-tailed larval form with filamentous caudal fins to an adult consisting mainly of head and abdomen. Autotomy may occur repeatedly in life, finally result being a fish consisting only of head and abdomen, containing all of the vital organs and gonads. The speaker's monograph on *Regalecus* was published as *Memoire de l'MNHN* (Paris) number 202 in September 2012.

Revision of the Indo-West Pacific ophidiid genera *Sirembo* and *Spottobrotula* (Ophidiiformes, Ophidiidae), with two new species

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Currently three of the seven described species of *Sirembo* Bleeker, 1858 and both species of *Spottobrotula* Cohen & Nielsen, 1978 are considered valid. The present revision is based on 64 specimens of *Sirembo* known from the Red Sea to Japan and southwards to northern Australia and 15 specimens of *Spottobrotula* known from the Persian Gulf to Mozambique and from the Andaman Sea. The main characters separating the two genera are number of long rakers on anterior gill arch, presence or absence of distinct sensory papillae on distal part of pelvic fin rays. Newly caught specimens can be identified on their color pattern, which in some species changes with growth. However, they tend to bleach rather fast, but such specimens can be identified by combining number of long gill rakers, pseudobranchial filaments, pectoral fin rays and scales between dorsal fin origin and lateral line, and prepelvic and pelvic fin length in % of SL. *Spottobrotula amaculata* is transferred to *Sirembo* and of the two new species, here described, one is referred to each of the two genera.

Review of deep-sea batfish genus *Halieutopsis* (Lophiiformes: Ogcocephalidae), with descriptions of four new species

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The Indo-Pacific ogcocephalid genus *Halieutopsis* is reviewed with 15 species are recognized. The genus is redefined by using osteological and morphological features. *Dibranchus nudiventer* Lloyd, 1909, *Coelophryne oblonga* Smith and Radcliffe, 1912 and *Dibranchsu nasuta* Alcock, 1891, the later being a senior synonym of *H. vermicularis* Smith and Radcliffe, 1912, are newly assigned to this genus. *Halieutopsis micropa* (Alcock, 1891) is reassigned to *Coelophryne*, and is thus excluded from this work. Four species are now to science: *Halieutopsis* sp.1 from eastern Taiwan and Queensland, northeastern Australia; *Halieutopsis* sp.2 from the southeastern Japan; *Halieutopsis* sp.3 from the Gulf of Aden; and *Halieutopsis* sp.4 from off Taiwan and Indonesia. These species differ from the congeners in the squamation morphology and proportional characters. Comment on the relationship and biogeographic distributions of *Halieutopsis* species are provided.

An undescribed species of the lionfish genus *Pterois* from northeastern Australia (Scorpaenidae: Pteroinae)

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An undescribed species of the genus *Pterois* (Scorpaenidae) is recognized on the basis of 38 specimens from off the northeastern coast of Australia between the Torres Straight and the Cape Moreton. The present species is most similar to *P. russelli* Bennett, 1831 and *P. lunulata* Temminck and Schlegel, 1843 in overall body appearance. However, the undescribed species can be distinguished from the latter two in having numerous small spots on the soft-rayed portions of the dorsal and anal fins and caudal fin (vs. always absent in *P. russelli*; large blotches sometimes present in adults of *P. lunulata* but their shape differs from that of the new species), spots or broken lines on the mandible in large adults (vs. absent at all life stages in the latter two species), and a relatively lower number of scale rows in the longitudinal series 59–68 (vs. 76– 91 in *P. russelli*). The new species is also similar to *P. andover* Allen and Erdmann, 2008 in having 13 pectoral-fin rays and spots on the median fins. The new species differs from the last in several aspects, including counts of scales, body proportions, and coloration. The new species is readily distinguished from *P. volitans* (Linnaeus, 1758) and *P. miles* (Bennett, 1828) in having a lower number of pectoral-fin rays (vs. 14 in the latter two species), and a lower number of scale rows in the longitudinal series (vs. usually more than 90). In addition, the species can be easily distinguished from the remaining congeners, including *P. antennata* (Bloch, 1787), *P. radiata* Cuvier, 1829, *P. sphex* Jordan and Evermann, 1903, *P. mombasae* (Smith, 1957), and *P. brevipectoralis* (Mandrytsa, 2002), in having a lower number of the pectoral-fin rays (vs. more than 16 in the latter), no coronal and tympanic spines (vs. present), and a broad distance between the orbit and suborbital ridge (vs. narrow). The validity of *P. russelli* and *P. lunulata* is also discussed.

Taxonomic revision of the family Hoplichthyidae (Teleostei: Scorpaeniformes)

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The ghost flathead family Hoplichthyidae is characterized by an extremely depressed head, the dorsal surface covered with many spines and serrated ridges, a single row of spines on lateral scutes along the body, and the lowest three to five pectoral-fin rays free. A revision of the family based on more than 500 specimens has resulted in the recognition of 14 species, including 4 that are undescribed: *Hoplichthys langsdorfii*, *H. citrinus*, *H. platophrys*, *H. haswelli*, *H. gilberti*, *H. regani*, *H. ogilbyi*, *H. fasciatus*, *H. pectoralis*, *H. filamentosus*, *Hoplichthys* sp. 1 (Japan and Western Australia), *Hoplichthys* sp. 2 (Western Australia), *Hoplichthys* sp. 3 (Western Australia and New Zealand) and *Hoplichthys* sp. 4 (Western Australia and New Zealand). *Hoplichthys platophrys*, *H. fasciatus* and *H. pectoralis* may be conspecific with other hoplichthyids as they were originally described from juveniles that have not been matched to adults. We treat these species as valid provisionally but acknowledge that we were unable to examine enough specimens of intermediate size in related species. *Hoplichthys citrinus*, currently thought to occur in Hawaii (type locality) and Australia, is considered to be a Hawaiian endemic as no specimens were found in Australian collections. Detailed comparisons of undescribed and valid described species are provided.

An undescribed species of the family Psychrolutidae (Actinopterigii, Scorpaeniformes) from Suruga Bay, Japan

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Two specimens of unknown psychrolutid species were caught in Suruga Bay about 1350-1400 m in depth, by 2 times of accidentally touching down of IKMT (Isaacs-Kidd Midwater Trawl) on the muddy bottom, towed by Bosei Maru, Research and Training Vessel of Tokai University, in October of 2011 and 2012. Both specimens are small, 39.7 and 48.5 mm in SL, having single small urogenital papilla, and presumed adult males. Colors of the bodies and heads are uniformly dark gray, with many dermal granules on the most parts. Their dorsal sides resemble with species of *Dasycottus* of the family Pscyclolutidae, by having of 2 dorsal fins, presences of cirri on head and snout, and presence of osteal projections on occipital region, but the ventral sides are different from them by branchiostegal membranes not forming single fold over isthmus. The specimens are also resembling with species of other psychrolutid genus with 2 dorsal fins, *Malacocottus* spp., by the states of branchiostegal membranes, and absences of prevomerine/ palatine teeth, but different from them by weak preopercular spines under the skin, presences of cirri on head and snout, and presences of osteal projections on occipital region. The specimens are also well distinguished from all psychrolutid species around Japan by fewer numbers of fin rays; D VI–VII, 10; P1 16; A 7–8. Some of their characters look like adapting deep sea area. The broad cephalic and lateral sensory canals are similar with some deep sea cottoid fishes, such as *Gilbertidia* spp., *Cottunculus tubulosus* (Psychrolutidae with single dorsal fin), and *Zesticelus* spp. (Cottidae).

Redescription of *Centrophorus granulosus* (Squaliformes, Centrophoridae), a senior synonym of *C. acus* and *C. niaukang*

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The genus *Centrophorus* is one of the most taxonomically complex and confusing elasmobranch groups and contains some of the more endangered deepwater sharks. *Centrophorus granulosus*, the type species for the genus, has been previously applied to two different morphotypes: a large species >1.5 m TL and a smaller species <1 m TL. *Centrophorus acus* and *C. niaukang* are the most commonly used names applied to the larger morphotype. The original description of *C. granulosus* was based on a large specimen of ~1.5 m TL, but subsequent descriptions were based on both the large and small morphotypes. *Centrophorus granulosus* is clarified and redescribed as a large species of gulper shark and a neotype is designated. *Centrophorus acus* and *C. niaukang* are found to be conspecific and both being junior synonyms of *C. granulosus*. *Centrophorus granulosus* is distinguishable from its congeners by its large size, dermal denticle shape, colouration and a number of morphological and biological characteristics. Ontogenetic changes in morphology, dentition and denticle shape for this species are described in detail.

Taxonomic review of the cookie-cutter sharks, genus *Isistius* Gill, 1865 (Chondrichthyes: Squaliformes: Dalatiidae)

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The genus *Isistius* Gill, 1865 (Dalatiidae), currently is considered to contain three valid species: *Isistius brasiliensis* Quoy & Gaimard, 1824, *I. plutodus* Garrick & Springer, 1964 and *I. labialis* Meng, Zhu & Li, 1985. The most common species, *I. brasiliensis*, has a wide geographic distribution, and can be found in subtemperate and tropical seas. However, a comprehensive comparative analysis of specimens from different localities has never been undertaken. This study proposes to thoroughly study the morphological variation in this species along its distribution, elucidating if it represents a single species or a species-complex. The other two species, *I. plutodus* and *I. labialis*, are known from few specimens, raising doubts about their validity since *I. brasiliensis* is so widely distributed and may occur sympatrically. As *I. labialis* has, purportedly, only two collected specimens, one from the South China Sea and the other from the South Pacific Ocean, a detailed comparative analysis is being undertaken of these individuals to test the validity of this species. The same is being done with the five known specimens of *I. plutodus*, of which three are from the South Pacific Ocean and two from the Western Atlantic Ocean. All valid species of *Isistius* are being studied with the purpose of understanding and describing their morphology in order to define more precise and taxonomically relevant characters. These include characters of external morphology, such as coloration, dentition, dermal denticles, and body proportions, as well as internal morphology, such as the skeleton, musculature, and lateral line canals. This study also aims to better define the genus and provide relevant morphological characters that may integrate future phylogenetic analyses of genera within the family.

Morphology and taxonomy of Southwestern Atlantic species of *Squatina*, with possible implications for the taxonomy of Indo-Pacific angelshark species (Chondrichthyes: Squatiniformes)

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The morphology and taxonomy of species of *Squatina* from the Southwestern Atlantic Ocean are revised. Previous species considered valid, *Squatina argentina* (Marini, 1930), *S. guggenheim* Marini, 1936, and *S. occulta* Vooren and da Silva, 1991 were investigated and described in detail, including an anatomical study. Even though morphologically very similar, the present analysis recognized significant differences among these species in dermal denticles, dorsal coloration, tooth formula and size at maturity, corroborating their validity; the nominal species *S. punctata* Marini, 1936 is a junior synonym of *S. guggenheim* Marini, 1936. Additionally, some skeletal differences between these species are reported and may be helpful for taxonomy, partially corroborating previous work. Morphometric characters proved not to be diagnostic, as well the simple presence or absence of enlarged dermal denticles (=spines or thorns) over the dorsal midline, as previously proposed. Therefore, it is possible that similar characters employed for Indo-Pacific species may not be as helpful as previously thought. The four Northwestern Pacific *Squatina* species have been described as presenting large enlarged dermal denticles (=spines or thorns) over the dorsal midline, although recent publications report this character only for *S. japonica* (Bleeker, 1858). Similarly, the original description of *S. australis* describes the occurrence of a median series of enlarged denticles, while recent descriptions restrict this feature to juvenile specimens and propose the presence of a median row of thorns as diagnostic for *S. pseudocellata* Last and White, 2008. Based on Southwestern Atlantic *Squatina* species, we suspect that morphometric characters should be analyzed from a large amount of specimens in order to be properly employed.

Phylogeny and zoogeography of the genus *Apristurus* (Scyliohinidae)

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The catshark genus *Apristurus* Garman, 1913 comprises deep-sea sharks found globally on continental slopes and submarine elevations at 400– 2000 m depths. This genus is the most diverse genus of extant sharks, with 45 nominal species, of which, currently 36 species are known as valid. However, the distribution and the dispersal of the genus have never been considered because of many unresolved taxonomic confusions, such as presence of many undescribed species and species complexes. We have reviewed the taxonomy of the genus for many years and studied their phylogenetic relationships based on the data of comparative anatomy. As the results, we found (1) the genus was monophyletic group with sister relationship with some species of *Parmaturus*, (2) the species of the genus were grouped into 5 morphotypes (MT), and (3) the genus was composed of 2 major clades (clade 1: MT1,2+3, clade 2: MT4+5) which consist with *Apristurus* subgroups proposed by Nakaya and Sato (1999). The distribution of each *Apristurus* species has been known to be restricted to continental slopes, and some exceptional species have been known from oceanic seamounts. The most *Apristurus* species have very narrow range of distribution, but a few species are found widely from the Indo-Pacific and Atlantic regions. For the supraspecific group of *Apristurus*, each morphotype is characterized by having unique distributional range (MT1: West Pacific to Indian Ocean, MT2: West Pacific, MT3: worldwide, MT4: worldwide, MT5: West Pacific). Those facts indicate both of *Apristurus* clade 1 (MT1,2+3) and clade 2 (MT4+5) include the species from the world, but each clade is further divided into two sister groups of species from West Pacific and from worldwide. The distributional range of common ancestor of *Apristurus* was estimated on the basis of the cladogram presented by this study, and we supposed that the ancestors were distributed in West Pacific regions and dispersed worldwide.

Color patterns and taxonomy of the swellsharks, genus *Cephaloscyllium* (Chondrichthyes: Carcharhiniformes: Scyliorhinidae) from the western North Pacific Ocean

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The sharks of the genus *Cephaloscyllium* Gill, 1862 are called "swell sharks", because they swallow seawater in the stomach and inflate their abdomen. This genus is characterized by the 1st dorsal fin located behind pelvic fin origin, presence of the supraorbital crest on the cranium, smaller 2nd dorsal fin than 1st dorsal and anal fins, 2nd dorsal fin base totally above anal fin base, and absence of the labial furrows from the jaw angles. Species of the genus are known only from the Indo-Pacific Oceans, and twenty species are currently considered as valid (Nakaya, 2011). They are classified based on some morphological characters, but the color patterns are considered to be the most important diagnostic characters in the recognition of the each species. We examined color patterns of the western North Pacific species, and recognized extensive intraspecific color variations. Nominal species from the region can be divided into following three morpho-types (with two subtypes), based on the number of the dorsal saddle bands before first dorsal fin and the patterns of the bands: A) Two-band type: *Cephaloscyllium sarawakensis* Yano, Ahmad & Gambang, 2005 from Malaysia; *C. circulopullum* Yano, Ahmad & Gambang, 2005 from Malaysia; *C. parvum* Inoue & Nakaya, 2006 from the South China Sea; B) Three-band type: *Cephaloscyllium umbratile* Jordan & Fowler, 1903 from Japan; and C) Four-band type: subdivided into—1) reticulated subtype: *Cephaloscyllium fasciatum* Chan, 1966 from Vietnam; *C. pardelotum* Schaaf-da Silva & Ebert, 2008 from Taiwan; *C. maculatum* Schaaf-da Silva & Ebert, 2008 from Taiwan; and 2) blotched subtype: *Cephaloscyllium formosanum* Teng, 1962 from Taiwan.

Gymnura crooki Fowler, 1934: a junior synonym of *G. poecilura* (Shaw, 1804) (Chondrichthyes: Gymnuridae)

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Currently the Indo-Pacific the family Gymnuridae is represented by five valid species: *Gymnura poecilura* (Shaw 1804), *G. tentaculata* Müller & Henle 1841, *G. japonica* (Temminck & Schlegel 1850), *G. zonura* Bleeker 1852 and *G. australis* (Ramsay & Ogilby 1886). Three other nominal species are known in the region: *G. bimaculata* Norman 1925, *Pteroplatea jordani* (Chu 1930) and *G. crooki* Fowler 1934. While the first two species are synonyms of *G. japonica* (Stehmann 1974, Isouchi 1977, Yoshigou et al. 2004), the validity of *G. crooki* needs further scrutiny. The holotype of *G. crooki* (USNM 93388) was analyzed and compared with other species from the Indo-Pacific region. The specimen is an adult male lacking tentacles on spiracles and presenting the tail without spine and dorsal fin. These and other diagnostic characters, such as dorsal coloration (brown uniform) and tail banding pattern, enable this specimen to be identified as *G. poecilura*. The main diagnostic character identifying *G. poecilura* is the tail size, which is proportionally longer than other species and can represent more than ½ disk width. It is worth mentioning that the tail is broken in the holotype, which explains its smaller size. For the realization of a more detailed and comprehensive study, meristic data and comparative morphology of the skeleton are being analyzed. This abstract confirms the occurrence of *G. poecilura* in China.

Distribution of neuromasts in the ventral lateral line canals of freshwater Stingrays (Chondrichthyes: Potamotrygonidae) from the Brazilian Amazon

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The mechanosensory lateral line system of the ventral surface of batoids is employed to detect tactile stimuli generated by buried prey during foraging. This highly developed sensory system possibly compensates the impaired capacity for visual detection of prey underneath the body. The high morphological variation of the lateral line canals in batoids has been described for several species; however, little attention was given to the canal neuromasts. The current study compared the distribution of neuromasts in the lateral line canals (hyomandibular, infraorbital, supraorbital, mandibular, and nasal) of the ventral surface of five sympatric potamotrygonid species (*Potamotrygon motoro*, *P. orbignyi*, *P. schroederi*, *P.* sp. n. and *Paratrygon aiereba*) from the Rio Negro Basin, Brazilian Amazon. These species feed on benthic invertebrates and teleosteans, which have distinct relative importance in their diets. Neuromasts were quantified and their densities per centimeter of canal length were calculated and compared among species, dividing the ventral body surface into three sections [anterior (A), central (C), and posterior (P) portions]. Neuromasts densities were higher in the anterior body portion for *P. motoro* (A=8.4; C=7.8; P=7.2), *P. orbignyi* (A=7.0; C=6.1; P=6.4), and *P.* sp. n. (A=6.4; C=4.6; P=3.7), which may indicate a fine-tuned ability to detect small prey (such as insect larvae and crustaceans) during excavation behavior. On the other hand, there was a lower density and apparently uniform distribution of neuromasts along the three portions of the ventral surface of *P. schroederi* (A=5.6; C=5.7; P=5.1) and *Paratrygon aiereba* (A=4.7; C=4.5; P=4.4). Nevertheless, both species showed a higher concentration of canals around the mouth, indicating their importance to locate and strike at prey. Moreover, the weblike distribution of the infraorbital canal in *Paratrygon aiereba* probably increases its tactile ability when foraging for larger, struggling prey (mainly fish).

Systematics and evolution of the highly diverse and morphologically complex Neotropical freshwater stingrays (Chondrichthyes: Potamotrygonidae)

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Potamotrygonid stingrays presently comprise four genera (*Paratrygon*, *Potamotrygon*, *Plesiotrygon*, *Heliotrygon*) and some 25 valid species, but some 10 new species are in the process of being described (principally in *Potamotrygon*). This elevated diversity is difficult to sort out, requiring large series of specimens and a broad geographic sampling. Intraspecific variation in coloration (and other characters) is pronounced, reinforcing the need for comprehensive collecting. However, coloration is still a very useful feature for diagnosing species once variation is properly understood and when analyzed in combination with other characters (such as extent of labial folds, dorsal spination patterns of disc and tail, dentition, angular cartilage morphology, ventral lateral-line canals). Our recent progress in the systematics of the family is due not only to extensive collecting, but to a directed basin by basin and species by species approach. This effort has permitted the completion of detailed taxonomic revisions of many widespread species (e.g. *Potamotrygon falkneri, P. motoro, P. orbignyi, P. scobina, Paratrygon aiereba, Plesiotrygon iwamae*), resulting in new species being discovered, even in well- sampled basins such as the Paraná-Paraguay, and in the synonymization of previously recognized species (e.g. *Potamotrygon castexi*, *P. dumerilli*). Morphological studies on a system by system basis (e.g. ventral lateral-line canals, teeth, visceral arch skeleton, neurocranium, mandibular, hyoid and pharyngeal muscles, central nervous system) have revealed characters that may be useful not only to identify species but that are of phylogenetic relevance (characters shared by *Paratrygon* and *Heliotrygon* spp., by both species of *Plesiotrygon*, by certain species of *Potamotrygon*, etc.). Ongoing, thorough molecular analyses indicate somewhat different patterns, however, implying that certain morphological characters may have evolved independently in different river basins; the implications of these conflicting patterns are discussed. River systems with elevated potamotrygonid diversity, such as the Negro, Tapajós, and Tocantins basins, have between eight to 10 species, of which at least one is endemic.

Commented list of chondrichthyan fishes from La Reunion (South-western Indian Ocean)

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La Reunion is a small volcanic island in the south-western Indian Ocean. It was recently in the media frontlines because of a series of shark attacks that caused the local authorities to launch a research program on the ecology of two potentially dangerous sharks, the tiger shark and the bull shark. However, other shark species have been recorded in the waters around La Reunion. Another research program, named BIOLAVE, is also under way to study the impact of the volcanic eruptions on the marine habitats and fauna. To complete these actions, it was interesting to undertake a critical inventory of the chondrichthyan fishes occuring around La Reunion. This inventory was established using scientific and grey litterature, specimens in collections, underwater photographies taken by scuba divers, and recent captures that provided new species and records. The occurence of the great white shark and sawfish at La Reunion is discussed.

Status and biodiversity of sharks in the United Arab Emirates

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Data on the artisanal shark fishery and the status of sharks in the United Arab Emirates (UAE) are currently sparse. Preliminary studies at landing sites have shown that the elasmobranch catch is increasingly high which suggests unsustainable levels of fishing. Limited information is available on the composition, abundance, distribution and biology of sharks found in UAE waters. This lack of data limits the development and implementation of management initiatives that could lead to regulations on the exploitation of these stocks and their conservation. Landing sites surveys were conducted from October 2010 to September 2012 in Abu Dhabi, Dubai, Sharjah and Ras Al Khaimah. Data was collected on the fishery characteristics, species composition, seasonal abundance and distribution of sharks. From over 19,000 specimens, 30 species of sharks were morphologically and genetically (DNA barcoding) confirmed from UAE Arabian Gulf waters. Six species represent over 91% of the total catch including the milk shark, *Rhizoprionodon acutus,* and the Spottail shark, *Carcharhinus sorrah.* This data lays the foundations for future studies on sharks in the region as well as provides scientific information to support the development and implementation of new national and regional regulations on the exploitation of these stocks and their conservation.

Inferring population dynamics of reef manta ray, *Manta alfredi*: multi-decadal observation, mark & recapture, and effective population size

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Ecological studies based on multi-decadal, individual-based data series of underwater observations of wildlife population are extremely rare. We present insights from such a study of reef manta ray (*Manta alfredi*) population in Yaeyama, Okinawa, Japan, which has been the subject of direct underwater observations since the mid-1970s, and recently for DNA (microsatellite)-based estimation of its effective population size (*Ne*). Series of mark-recapture analyses using ~11100 sighting records of near-census individuals (n = 305) over 23 years have revealed that the annual survival rate is ~0.95 for adults, ~0.65 for juveniles and longevity is ~40 years. The abundance trend measured across a series of thirteen decadal time-slices indicated an increase in population size from 181 to 242. Matrix population model analyses revealed that increasing population size indicates that the average reproductive cycle of females should be more frequent than one pup for every 2.7 years, assuming no immigration from elsewhere. A genetic *Ne* estimate was 89 (45 –378, 95% CI). I will discuss: (1) how these results match with field observations; (2) what genetic assessments of *Ne* tell us about the population in Yaeyama; and (3) potential promise and pitfalls in using *Ne* as a tool for population assessment for other less intensively studied populations elsewhere.

A novel pharyngeal expansion mechanism in the yellow-spotted fanray, *Platyrhina tangi* (Elasmobranchii: Batoidea), with special reference to the function of the fifth ceratobranchial cartilage in batoids

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Expansion of the 'pharynx' during breathing or capturing prey in fishes generally involves posteroventral retraction of the hyoid arch. However, the hyoid arch structure of batoid fishes (skates, rays, guitarfishes, and sawfishes) is unique, and how they expand the pharyngeal cavity is poorly understood. The hyoid arch of fishes is generally composed of three elements; a basihyal, a ceratohyal, and a hyomandibula (from ventral to dorsal), with the latter connecting to the otic region of the skull. During pharyngeal expansion the pharyngeal muscles pull the basihyal in a posteroventral direction. This enables the ceratohyal to swing ventrally, resulting in expansion of the pharyngeal cavity. However, most batoids 'lack' a ceratohyal, and thus the basihyal has no connection with the other hyoid elements. This strongly suggests that the pharyngeal expansion mechanism of sharks, which is largely driven by rotation of the hyoid apparatus, does not occur in batoids. To investigate the mechanism of pharyngeal expansion during breathing in batoids, we conducted anatomical and kinematic investigations of the pharyngeal region of the yellow-spotted fanray, *Platyrhina tangi*. Ultrasonographic imaging was performed on captive yellow-spotted fanrays at Okinawa Churaumi Aquarium for visualizing internal movement of the fish. Our study revealed that the yellow-spotted fanray and sharks have different skeletal linkage systems for pharyngeal expansion. During pharyngeal expansion in the yellow-spotted fanray the hyoid bar and branchial apparatus rotates ventrally around the hinge joint between the fifth ceratobranchial cartilage and the pectoral girdle. This pharyngeal expansion mechanism appears to be widespread among batoid fishes, and is unique among cartilaginous fishes (sharks, batoids, and holocephalans). Batoid fishes possibly developed this pharyngeal expansion mechanism during early batoid evolution.

Morphological studies on the electric organ of Japanese sleeper ray, *Narke japonica*

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Japanese sleeper ray, *Narke japonica*, a demersal chondrichthyes, possess pair electric organs located within their pectoral fins which can use electric organs discharge for predation and/or defense. It usually hides on sandy seafloor and takes annelids as food. The electric organs are made up by parallel electric bundles which are composed of series electrocytes. A total of 262 males and 277 females were collected weekly at the Dashi fish market, Yilan county from Sep. 2008 to Aug. 2009. Most samples were collected around the waters of Guei-shan Island, Aodi, and Pengjia Islet. The result of paired-samples t-test showed that there was no significant difference ($p > 0.05$) of the electric organ weight (EOW) between two sides for both sexes. The likelihood ratio test indicated the relationships between EOW and total length (TL) was significantly different ($p < 0.05$) by sex, i.e., $EOW = 0.0069TL^{2.7771}$ (n = 238) for female, and $EOW= 0.0167TL^{2.4849}$ (n = 232) for male. The electric bundle became larger when fish grown, but its number did not increased. The multiple nuclei (polykaryocytes, similar to those of the skeletal muscle cells) but no significant A-band and I-band were found in the electrocytes. The electric organs had no significant linkage with reproduction and feeding through compared the monthly variations of gonosomatic index (GSI), hepatosomatic index (HSI) and electrosomatic index (ESI).

The Colombian species of angel sharks (Elasmobranchii: Squatinidae)

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Angel sharks constitutes a natural group of cartilaginous fishes including one genus, *Squatina*, and between15 and 25 tropical and temperate demersal marine species. Colombia is located in the northwester corner of South America, with coasts to the Pacific and Atlantic oceans, therefore marine fauna encompass tropical species of both geographical regions. Based on two mitochondrial genes (16S and COI), Stelbrink et al. (2009) published a phylogenetic tree of 17 species of angel sharks, finding a high correlation of clades to continents. Their tree separates widely the Chilean and the Californian angels sharks, which were generally considered one species. A species of *Squatina* occurs the Colombian Pacific island of Gorgona which differs clearly in coloration from both American Pacific species. Unfortunately no fresh material has been available for molecular analysis, precluding the definition of the taxonomic status of the Colombian Pacific species. On the other hand, the existence of a southern Caribbean angel shark, which distribution extends to the Suriname area, has been reported usually under the name *Squatina dumeril*. Fresh material of this angel shark was collected in mid-2010 off the mouth of the Río Magdalena, Colombian Caribbean. Molecular analysis of the those specimens clearly indicates that the southern Caribbean species has not been described and is the sister taxa to *S. dumeril-S. californica*.

Genetic structure and population connectivity of two shark species among three ocean basins in the Arabian region

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Sharks have long been emphasized as keystone species driving the evolution of marine ecosystems. Their dispersal capacity is limited to adulthood and little is known about the patterns of demographic connectivity between spatially separated populations. This is especially true for the Arabian peninsula, a region that has historically been underrepresented in terms of elasmobranch research. While data pertaining to shark conservation is virtually lacking, ever increasing pressure from unmanaged fisheries are putting large predators at high risk. Here we aim to analyze the genetic structure of two shark species with contrasting biology, *Carcharhinus sorrah* and *Sphyrna lewini* in three ocean basins in the Arabian region. We collected a total of 700 tissue samples at fish markets, landing sites and during longline operations in Saudi Arabia (Red Sea), the United Arab Emirates (Persian Gulf) and Oman (Arabian Sea). Fragments of the mtDNA control region were amplified for both species and all samples were genotyped over a range of species-specific, polymorphic microsatellite markers. We comparatively evaluate the population genetic structure and patterns of gene flow among the two species within and between ocean basins against the background of interspecific differences in reproductive and migratory behavior.

Australian hybrid blacktip sharks *Carcharhinus limbatus* and *C. tilstoni*

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The common blacktip shark, *Carcharhinus limbatus*, and the morphologically similar endemic Australian blacktip shark, *C. tilstoni* dominate the catch of commercial shark fisheries across northern Australia. The two species are closely related but grow to different maximum sizes, have different numbers of vertebrae and are genetically distinct. In 2012 hybrid offspring of the two species were discovered along the eastern Australian coastline. Seven nuclear DNA markers have been developed (targeting single nucleotide polymorphisms and microsatellites) and in combination with mitochondrial DNA screening hybrids can be identified from tissue samples alone. More widespread screening of animals extends the hybrid zone across northern Australia. The frequency and direction of hybridization appears to be spatially determined and is likely driven by differences in local frequencies of the parental species. Although hybrid animals have been found at all sampling locations, first generation (F1) hybrids are rare. The absence of F1 hybrids indicates that hybridization has successfully mixed the species in the past but that modern day crosses are either uncommon, or largely unsuccessful. This may explain why pure parental species are still the most common animals caught. Sustainable management of this species complex requires more information on stock boundaries and the relative impact of hybridization.

Movement, seasonal migration and habitat use of sharks and rays in Ariake Bay on the western coast of Kyushu, Japan

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An increase in some elasmobranch species has been observed in coastal areas of the Kyushu-Okinawa region in southwestern Japan, potentially increasing the pressure on prey species, such as fish, bivalves, and crustaceans. In particular, an increase in the number of eagle rays, *Aetobatus flagellum*, in Ariake Bay has markedly increased the feeding pressure on bivalves in the area, and has seriously affected the local bivalve fisheries. As a result, a predator control program focusing on reducing eagle ray populations has been undertaken in the bay since 2001. Investigations of the life history and movements of this species since 2001 revealed that the size distribution of the eagle rays has decreased recently in response to the increase in fishing pressure. We hypothesize that the drastic changes observed in the Ariake Bay ecosystem, such as the marked increase observed in eagle ray numbers, may have occurred in response to a disruption in the population dynamics of apex predators, such as large sharks. We therefore clarified which fish species inhabited the area and are currently investigating food web structure and ecosystem functioning within the bay. In the absence of accurate information on which elasmobranch species are apex predators in the bay, we are also examining the distribution, seasonal migration patterns, and life histories of the various elasmobranch species in the region. One of the primary aims of this research is to determine which species are resident in the bay seasonally or constantly, and whether they function as apex predators. Surveys conducted to date on movements and seasonal migration patterns have employed Argos satellite transmitters (n = 25) and pop-up satellite archival tags (n = 30) on more than 10 different species, including eagle rays, stingrays, and hammerhead sharks. Here, we present our findings on elasmobranch movements, seasonal migration patterns, and habitat use in Ariake Bay.

Vertical movement and site fidelity of grey reef sharks (*Carcharhinus amblyrhynchos*) at aggregation sites on a coral reef

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We used acoustic telemetry to describe the patterns of vertical movement, site fidelity, and residency of grey reef sharks (*Carcharhinus amblyrhynchos*) on the outer slope of coral reefs in Palau, Micronesia, over a period of two years and nine months. We tagged 39 sharks (mostly adult females) of which 31 were detected regularly throughout the study. Sharks displayed strong inter-annual residency with greater attendance at monitored sites during summer than winter months. More individuals were detected during the day than at night. Mean depths of tagged sharks increased from 35 m in winter to 60 m in spring following an increase in water temperature at 60 m, with maximum mean depths attained when water temperatures at 60 m stabilized around 29°C. Sharks descended to greater depths and used a wider range of depths around the time of the full moon. There were also crepuscular cycles in mean depth, with sharks moving into shallower waters at dawn and dusk each day. We suggest that daily, lunar and seasonal cycles in vertical movement and residency are strategies for optimizing both energetic budgets and foraging behaviour. Cyclical patterns of movement in response to environmental variables might affect the susceptibility of reef sharks to fishing, a consideration that should be taken into account in the implementation of conservation strategies.

Using telemetry to understand the ecology of *Manta* spp. in the eastern Red Sea

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Manta spp. are distributed globally in tropical and sub-tropical waters, but local populations appear small and widely dispersed. Connectivity among populations is largely unknown, but available evidence suggests regional isolation. While recent efforts have initiated investigation of a few populations worldwide, Red Sea *Manta* spp. remain completely enigmatic. We describe short and long-term movements of *Manta* spp. in the southern Saudi Arabian Red Sea using satellite and acoustic telemetry techniques. In addition, we investigate high-resolution dive data for three individuals. These findings enable a better understanding of *Manta* spp. ecology in this poorly-studied region. As prices in Asian markets continue to rise and regional by-catch remains significant, basic information about *Manta* spp. behavior and its applicability to regional management efforts become increasingly urgent. *Manta* spp. harvest and the lucrative ecotourism trade also render this work economically important and could lead to significant local support of conservation efforts.

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Reef fish occupancy dynamics across a disturbed Great Barrier Reef

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With multiple processes occurring at multiple scales, coral reef ecosystems present a challenging system in which to investigate the effects of habitat loss on fish communities. The diversity of reef fish assemblages varies greatly through space and time, stochastically and in response to disturbance events both natural and man-made. Linking change in habitat composition to change in reef fish communities requires accurate assessment of both so that they may be causally linked. Here, we use a dynamic Bayeisan hierarchical occupancy model to quantify changes in reef fish biodiversity through space and time, in response to changes in habitat structure across the Great Barrier Reef, Australia. By structuring uncertainty surrounding the presence and absence of species at a given point in time, we show how changes in habitat affect local immigration and emigration of reef fish during decline and recovery phases of disturbance. We then explore how reef fish biodiversity might change across future habitat scenarios and outline the levels of habitat required to maintain current reef fish biodiversity on the GBR.

Contrasting effects of marine reserves and habitat change on coral reef fishes

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No-take marine reserve networks are being widely implemented throughout the coral triangle as a tool to promote sustainable fishing and protect biodiversity. Increases in the abundance and biomass of exploited species within reserve boundaries have been demonstrated. However, the ability of reserves to protect the majority of species in areas with substantial habitat degradation is less clear. To date, there have been relatively few long-term studies of no-take areas before and after reserves have been implemented. Here we report on decadal changes in fish communities in 4 small coastal reserves and 4 reefs open to fishing in Kimbe Bay, Papua New Guinea. Reef fish densities and benthic cover were monitored for three years before (1997-1999) and 14 years after (2000-2013) reserves were implemented. Substantial reserve effects were recorded for several reef fishes, primarily exploited Surgeonfish species. These effects gradually accumulated, with some evidence that the effect size may have peaked due to only partial compliance. For most small, coral-associated fishes, the long-term dynamics, at both reserves and fished reefs, reflect cycles of decline and recovery in branching coral cover. While fish biodiversity recovered from a low point in 2002, it has never returned to pre-1997 levels. There is evidence of long-term habitat degradation, with increasing macroalgae and sediment cover, which may hinder the ability of reefs to recover after periods of decline. Our results support the view that no-take areas are necessary for coral reef conservation but must be supplemented with effective measures to reduce extrinsic impacts on coral health.

Effectiveness of protection on reef fish assemblages in small Marine Protected Areas in Hong Kong, China

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Tung Ping Chau Marine Park (TPCMP), located in the northeast waters of Hong Kong, China, was designated in 2001 to conserve the coastal coral communities. It is 260 ha in size and includes two core areas that have a total area of 15 ha (0.15 km2). Unlike the rest of the marine park, fishing activities are restricted within these core areas. Reef fish assemblages in these areas during summer/fall season have been monitored by underwater visual census for 15 years from 1998 to 2012, i.e. before and after the designation of the marine park. The total fish density and the density of some indicator species (Labridae, Serrenidae and Chaetodontidae) increased in the first two years after the establishment of the marine park, but dropped back to the pre-protection level since the third year of protection. Causes contributing to the ineffectiveness of this MPA in increasing the density and diversity of fish assemblages may include the small size of the MPA itself, its low habitat complexity, its inability to serve as a source of larval supply or a lack of larval supply from other sources and illegal fishing. Similar ineffectiveness of MPAs nearby was also observed. All these suggest a major re-evaluation of the MPA programme and strategy in Hong Kong is urgently needed if future conservation efforts are going to be more effective.

A comparison of visual and stereo-video based fish community assessment methods in tropical and temperate marine waters of Western Australia

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Robust assessments of abundance and diversity are essential components of research and monitoring programs aimed at detecting changes in marine fish assemblages through space and time. This study examined the comparability of Underwater Visual Census (UVC), and Diver Operated stereo-Video (Stereo-DOV) datasets collected across a wide latitudinal scale (15°) on coral reefs and temperate rocky reefs. Patterns in species richness and overall fish abundance were relatively similar between methods, particularly at temperate locations where richness and abundance measures were lower than tropical locations. Differences in fish assemblage composition are primarily driven by UVC differentiating between scarid and pomacentrid species and detecting more fish that display cryptic behaviour. When examined at higher taxonomic/functional levels however, there was a degree of comparability between the assemblages recorded by each method, with temperate locations again being more similar than tropical locations. The UVC method also recorded higher abundances of species targeted by fishers in tropical locations, and subsequently obtained a much higher proportion of length measurements for these groups. Information collected using stereo-DOV took 2-3 times longer than when using UVC due to extensive post-processing time required by the stereo-DOV method. This study shows that, despite some minor differences, data collected by the two methods are comparable in temperate locations, and in all locations when examined at higher taxonomic/functional levels. However, availability of time, funds and relevant expertise should be primary considerations when determining which method is most appropriate.

Extremes in diversity and distribution: amphidromous fish in small coastal streams

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Large river catchments are almost impossible to completely census for fish species richness due to their vast size, and so decisions must be made regarding the selection of sites, suitable survey methods and the amount of survey effort to be applied. In contrast, small catchments present an opportunity to effectively survey the entire fish community. Snorkel-based surveys were performed along the entire length of three coastal streams from the tidal limit to the mountain source in the Australian Wet Tropics to approximate true gamma fish diversity. Such comprehensive distributional data allowed us to examine changes in fish community composition along the stream continuum (including correlations with altitude, instream barriers, and distance to sea), and investigate if species richness was a function of catchment area. Moreover, by placing our scaled (by catchment area) species richness estimates within a regional and global context, we reveal some surprisingly extreme levels of diversity. We use these two lines of investigation to reinterpret the fish species richness to catchment area paradigm, explore the role of sampling bias, and highlight the specific habitat associations of fishes by surveying to all environmental extremes within streams.

How fish colonised tropical island freshwaters

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Within the open ocean, tropical insular freshwater environments usually represent highly isolated and fragmented habitats. The colonisation of tropical insular rivers, subject to extreme climatic and hydrologic seasonal variations, requires specific adaptations of the life cycle of species occurring in these distinctive habitats. Tropical islands are usually of volcanic origin, so their freshwater systems are initially devoid of any fauna. Their colonisation is interesting in terms of the evolution of the species present, as they can only have come from the marine environment. Diadromy is among the evolutionary answers to the instability of freshwater habitats. Spending part of their life cycle at sea, diadromous species are capable of escaping drought or cyclonic flood events while colonising new environments via oceanic dispersal. This oceanic dispersal of diadromous organisms represents an essential element in the persistence and structuring of populations at both the local (stream, river, archipelago) and regional scales. Amphidromy is a type of diadromy. Amphidromous species (both vertebrate and invertebrate organisms) represent most of island freshwater macrofaunal biodiversity. The adults grow, feed and reproduce in rivers. After hatching, larvae drift downstream to the sea, where they undergo larval development. After this marine dispersal stage, the post-larvae come back to rivers; they recruit in estuaries and from there colonise the adult freshwater habitat. Freshwater species with an amphidromous life cycle therefore exhibit high dispersal abilities and potentially a lower degree of population structure than strictly freshwater species or marine species of low vagility. These species show differences in certain aspects of this life cycle such as, for example, the adult behaviour or the duration of the pelagic larval phase. Among fish species, Sicydiinae gobies represent most of the island freshwater biodiversity and have the highest level of endemism. In addition to being amphidromous, they also developed specific morphological structures enabling them to colonise the entire stream from estuaries to higher reaches, the latter often located at an altitude of several hundred meters. Finally, these species also have developed feeding habits allowing them to exploit as much as possible the small amount of food present in these streams.

Functional diversity in extreme environments: evolutionary mechanisms in waterfall-climbing amphidromous gobiids

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Functional diversity is an important aspect of biodiversity, and extreme environments can place strong demands on functional performance. What range of functional diversity should be expected under extreme environmental pressures, and what mechanisms constrain or help generate this diversity? To examine these questions, we have conducted studies of several species, populations, and age classes of waterfall-climbing gobiid fishes, ranging from measurements of climbing and adhesive performance to experiments evaluating selection on climbing performance and predator evasion. We identified two distinct styles of climbing: one a slow-but-steady "inching" style using alternate adhesion of oral and pelvic suckers in the genus *Sicyopterus*, and a different style among other gobiids called "powerbursting", in which rapid movements of the body and fins are interspersed with long periods of rest. As fish grow and increase in size, levels of performance and types of movements begin to converge across climbing styles, suggesting ontogenetic constrictions in functional diversity. Data from selection analyses on artificial waterfalls demonstrate that climbing performance can impose strong selection on juveniles for species using each of these behaviors, with patterns of correlational selection more prominent among powerburst climbers. Nonetheless, a range of performance can be seen in comparisons of both inching and powerburst species. Moreover, selection on predator evasion appears to counter selection on climbing performance, such that juveniles from populations of *S. stimpsoni* from the Island of Hawai'i, where climbing pressures are imposed early, are faster climbers than fish from Kaua'i, where predator exposure is prolonged. Thus, functional tradeoffs may promote functional diversity even within the constraints of environments requiring extreme performance. Similarities between oral movements during climbing and feeding (via algal scraping) in *S. stimpsoni* suggest that the incorporation of oral adhesion during inching climbing may have involved the coopting of motor patterns used during feeding. Thus, exaptation could be another mechanism that contributed to functional diversity among climbing gobies. The extent of functional diversity in the speciose gobiid lineage, as well as what anatomical and physiological factors contribute most to functional diversity, remain major areas of focus for future research.

Extremes at the micro-scale: flow velocity underpins microhabitat selection in gobies of the Australian Wet Tropics

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Water flow is a critical driver of aquatic ecosystem health and function and changing flow regimes could have serious implications for the future of freshwater biodiversity. Combining field observations of microhabitat-use with flow tank assessments of flow speed performance, we explored the functional link between flow velocity and microhabitat specialisation in a speciose group of freshwater gobioids (comprising up to 58% of total fish species richness) within insular streams of the Australian Wet Tropics. We aimed to determine: (i) What is the relative selectivity of species towards streambed composition and water flow velocity? and (ii) Can patterns of microhabitat occupation be explained by differences in intrinsic flow performance among species? Tropical freshwater gobies displayed strong specificity towards either slow (< 0.05 ms-1), moderate (0.05 - 0.5 ms-1) or fast (> 0.5 ms-1) flow velocities, while being relatively non-selective towards streambed composition. At opposite extremes of the spectrum, we found *Sicyopterus lagocephalus* occupying extremely high flow microhabitats up to 1.8 ms-1 while *Redigobius bikolanus* selected slower flow areas (< 0.05 ms-1). These patterns of microhabitat flow specificity were largely explained by the differential ability of species to swim and/or cling to the substratum under these different flow settings, with one species (*Schismatogobius* sp.) a notable exception. Our findings confirm previous suggestions that predictable base flows in tropical streams support habitat specialists, which in this group includes one species capable of occupying areas of extremely high flow (over 1.0 ms-1) that very few other fishes can withstand. With gobioid fishes found throughout tropical streams of the Indo-Pacific and Caribbean, this functional link between flow and microhabitat use may be a global phenomenon that could help inform flow management guidelines to maintain this substantial component of tropical freshwater biodiversity.

Mapping extremes in freshwater fish diversity across a range of climatic provinces: documenting unique examples of phenotypic and biological adaptations in Western Australia

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The western third of the Australian continent comprises three major drainage divisions that cover in excess of 2,500,000 km2 in the State of Western Australia with a coastline of over 12,000 km not including islands. The region is sparsely populated and experiences a range of climates across three drainages including: the Mediterranean and temperate areas of the South West Coastal Drainage Division, Mediterranean, subtropical and arid climates of the Pilbara (Indian Ocean Drainage Division), and the arid and tropical climates of the Kimberley which lie within the Timor Sea Drainage Division. Exposure to such environmental extremes has led to a unique array of fishes within each drainage division, with rates of endemism ranging from over 80% in the South West Coastal to approximately 40% of fishes in the Pilbara and Kimberley. The study presents two decades of surveys in many extreme environments that necessitated the use of many different techniques often in very remote and inhospitable environments. Examples of some of the unique fishes of the region and how they have adapted phenotypically and biologically to the extreme environmental conditions are given. Many of these species are now endangered and are vulnerable to future projected climatic changes. One example is the enigmatic Salamanderfish (*Lepidogalaxias salamandroides*), one of the few aestivating fishes on the Australian continent and one adapted to life in ephemeral, acidic pools. Other notable species in the state include Australia's only cave fishes, as well as the Pouched Lamprey (*Geotria australis*) and the critically endangered Trout Minnow (*Galaxias truttaceus*). Interestingly, the number of diadromous species utilising freshwaters increases from south to north, with the northern rivers offering refuge for endangered species such as the Freshwater Sawfish (*Pristis pristis*), a species morphologically and biologically adapted to survive within extreme environments from macro-tidal estuaries, offshore waters and intermittent rivers.

Salted fish: a review of fishes in extreme salinity and how anthropogenic changes in salinity have driven community shifts in Western Australia

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Osmoregulation to maintain homeostasis in fishes enables then to survive in an incredibly wide range of aquatic environments and community compositions can be strongly influenced by the prevailing salinity. Strategies to osmoregulate and excrete nitrogen allow euryhaline fishes to occupy environments of variable salinities and enable salinity extremophiles to occupy freshwater, estuarine and marine environments. This presentation reviews fishes in extreme salinities from different aquatic environments. Case studies from environments in Western Australia are then focussed upon to demonstrate how anthropogenic changes in salinity have caused community shifts to favour extremophile species. For example, much of south-western Australia's native vegetation has been cleared for agriculture that has resulted in rising water tables and subsequent mobilisation of salt stored in the soil causing severe secondary salinisation. This has dramatically altered the ecology of both lentic and lotic aquatic ecosystems. Major range contractions of stenohaline freshwater fishes have occurred in salinised systems to reaches that continue to receive fresh groundwater intrusion. Inland reaches of those systems are now dominated by halotolerant or euryhaline species that are typically associated with estuarine environments. The shift has also favoured the introduced euryhaline *Gambusia holbrooki* that currently occupies the entire range of aquatic environments in the region and has recently been recorded in salinities up to 73 ppt. A number of estuarine systems have also become hypersaline. Understanding osmoregulation and salinity tolerance of fishes can be crucial in explaining current and future community structures in many environments.

Flexibility and diversity of estuary-associated fishes under extreme salinity regimes

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A fundamental adaptation required by all fish species residing in estuaries is an ability to tolerate a wide range of salinity concentrations, which can vary from almost completely fresh during river flooding, to extreme hypersalinity during prolonged droughts associated with high evaporation. This presentation will demonstrate that many marine, estuarine and freshwater fish species occupying estuaries are capable of surviving in both oligohaline (0.5-4.9 PSU) and hyperhaline (+40 PSU) waters. Indeed, it could be argued that those species that can tolerate salinity extremes are able to get rid of a number of potential competitors and can therefore access food resources with minimal competition. The presentation will also focus on changes in the diversity of well-studied estuarine fish assemblages under different salinity regimes, as well as the responses of other estuarine biota to those same conditions. Emphasis will be placed on the changing food web structure under different salinity regimes, in addition to the susceptibility of the fish fauna to mass mortalities triggered by sudden declines in winter water temperatures.

Hybridisation - an evolutionary force for adaptation to extreme environments

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Hybridisation as an evolutionary force has oscillated between being considered a dead end and an important evolutionary force. Here I provide evidence for the evolutionary potential of interspecific hybridisation across a broad range of taxa, including fish. Specifically, evidence is given that high levels of adaptive introgression are possible when selection favours new variants in different, sometimes extreme environments. Three outstanding examples of hybridisation as a potent evolutionary force are provided, in this context. Firstly, the eukaryotic genome most likely emerged from the fusion of eubacterial and archaebacterial genomes with striking ramifications for biodiversity. Secondly, fungi and oomycetes (crucial in nutrient cycles) and their potential for interspecific hybridisation are considered together with the evolutionary ramifications thereof for adaptation to new niches. Finally, the possible role of hybridisation between closely related vertebrate species and the resulting capacity to use relatively extreme environments is considered. Hybridisation is hereby shown to be an important evolutionary force that has, is and may continue to contribute to adaptation of species to novel, sometimes extreme environments encountered in a changing world.

Peat swamp miniatures – Just how many are there?

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Peat swamp habitats are extensive in Southeast Asia historically, but are becoming more fragmented due to habitat modifications for silviculture, urbanization and bio-fuel mania. The dark acidic, nutrient poor waters harbor many stenotopic and endemic fish species, contrary to earlier works. From recent work, there are several groups of fish which are specialists in peat swamps (e.g. *Betta, Parosphromenus*, *Paedocypris* and *Sundadanio*). And many examples from these groups are miniatures, including the smallest vertebrate animal – *Paedocypris progenetica* described only in 2006. Hypotheses on the pathways of miniaturization, habitat segregation and field observations will be shared. The diversity of peat swamp miniatures will be covered and biogeographic implications discussed.

Diversity and adaptation of tropical ichthyofaunas in turbid and macrotidal environments

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The adaptation of species to a broad range of environmental conditions and the partitioning of resources by their individuals has led to the global utilization of the 'niche' from fresh through estuarine and marine habitats. These physiological and behavioral adaptations have combined, in part, to produce the remarkable faunal diversity encountered in these habitats. The tropical north-western Australian coast is a large but very remote and understudied region that contains one of the last true wilderness areas in Australia with the Kimberley being assessed as one of the least impacted coastal areas in the world. This coast is characterized by extreme environmental conditions from regular cyclonic storms, massive tidal ranges that exceed 10 m, strong tidal currents, highly turbid waters and contrasting extreme wet and dry seasons. Despite these conditions the Kimberley contains a diverse fish fauna and very well developed coral reef, mangrove, seagrass and filter feeding communities, with one small area containing 280 coral species. Such extreme conditions present strong selection pressures on marine species to converge in their physiology, morphology and behavior towards an optimal design for living in such conditions. Fish species have thus evolved specialized physiological traits to survive in these low visibility and high-flow environments such as acoustic and bioluminescent signaling to attract mates and to maintain species fidelity in an extreme environment. Large-scale studies have now begun to elucidate the environmental factors that structure the ichthyofaunal communities along this unique coast, being crucial for understanding the specialized attributes of species that characterise these environments and for developing strategies for protecting these important coastal ecosystems. As fauna must respond to changing conditions along environmental gradients, researchers must also respond and develop techniques and methodologies that allow them to sample these faunas adequately, particularly fauna encountered at the extreme ends of such gradients. The logistic challenges of sampling the ichthyofaunas in the extreme conditions of north-western Australia have resulted in a range of observation methods being employed in specialized ways in daily, lunar and seasonal cycles. From these observations we are now beginning to map the spatial and temporal diversity in this globally unique environment.

From physiology to physics: the strength of biotelemetry is its flexibility

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The remote measurement of data from free-ranging animals has been termed 'biotelemetry' and in recent years this relatively small set of tools has been instrumental in addressing remarkably-diverse questions - from 'why do sharks target seal colonies?' to 'why are whales big?'. While a single biotelemetry dataset can have the potential to test hypotheses spanning physiology, ecology, evolution and theoretical physics, explicit illustrations of this flexibility are scarce and this has probably contributed to the perception that biotelemetry is under-utilized. In this presentation, I will draw on examples from studies that have collected data on two parameters widespread in biotelemetry research (depth and acceleration), but that have interpreted their data in the context of diverse phenomena; from tests of biomechanical and diving-optimality models, to identification of feeding events and diel rhythms. With an emphasis on behavioral and physiological adaptations of aquatic animals living in extreme environments, our collection of examples suggests that data collected in the context of one physical, ecological, or physiological phenomenon may often be simultaneously relevant to another, and we argue for the multidisciplinary relevance of biotelemetry for aquatic animals.

Life history adaptations in fishes living in extreme environments: how farand how fast can fishes go?

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From the deep cold depths of the abyssal plains to hot mountainous acidic lakes, fishes have successfully colonised nearly every major extreme water body on the planet. But what actually constitutes an "extreme" environment and what drives extremism in fish habitat use in the first place? What adjustments have underpinned their successful colonisation of these extreme habitats? Are there common themes and life history strategies that enhance the potential for species to colonise extreme environments? And can we use these to provide insights on how fish communities might react to our rapidly changing world? More and more, we are seeing normal, usually stable environments shift towards more extreme ones through pollution, acidification, and habitat destruction. Set against a backdrop of theoretical, experimental and field studies, here I examine the shifts and extremes in life history traits and strategies that have enabled fishes to colonise extreme environments through their natural evolutionary history and ask whether we can use this life history information as an investigative tool to help us predict the response of fish communities to the extreme human-induced changes their environments are experiencing today.

Pushed to extremes: do fishes display the phenotypic diversity and flexibility to meet future environmental challenges?

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Examining how fish vary their phenotype with respect to specific environmental variables (e.g. temperature, flow) can yield powerful insights into the mechanisms underpinning the distribution of fish diversity across environmental gradients. Moreover, species living in extreme environments can indicate the potential response limits of fishes to current and future climatic variations. In this talk, I will review our current understanding of the distribution and expression of fish diversity across a range of physiochemical conditions to examine how current assessments of fish responses to environmental extremes compare with what climatic projections suggest may be imposed on fishes in the future. Drawing upon a survey of researchers working across a range of fields, I will also explore how much diversity we may yet uncover within extreme environments, what technology could be used to sample some of the more challenging places, and what should be the priority areas for future research.

Genetic architecture of habitat-related divergence in body shape in *Gnathopogon* (Teleostei: Cyprinidae)

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Advances in genomics technologies, especially the improving performance and accessibility of next-generation sequencers, have facilitated the genomic studies of non-model organisms. Although the genomic bases for the diversification of evolutionarily and ecologically significant traits of fishes are being revealed, the studies conducted are largely restricted to a few groups of fishes. Despite the enormous diversity of Cyprinidae, few studies have been conducted to elucidate the genetic background of the phenotypic diversification of cyprinid fishes. We conducted a genomic study to determine the genetic architecture of the lake–stream divergence of body shape – streamlined fish in lakes and robust fish in streams – in *Gnathopogon*, a phenomenon common among various taxa of fishes. First, we constructed a linkage map of *Gnathopogon* for quantitative trait locus (QTL) analysis of the diverged body shape and for comparative genomic analysis with the zebrafish *Danio rerio*, an important model organism. The genetic map was constructed using 198 F2 interspecific cross between two closely related *Gnathopogon* species of Japan: the riverine species *Gnathopogon elongatus* and the limnetic species *Gnathopogon caerulescens*. Based on the results of next generation-sequenced 1,622 restriction-site associated DNA (RAD) tag markers, a linkage map spanning 1,390.9 cM with 25 linkage groups and an average marker interval of 0.87 cM was constructed. In addition, we identified a region involving female-specific transmission ratio distortion (TRD). Synteny and collinearity were extensively conserved between *Gnathopogon* and zebrafish. Next, we studied the genetic architecture of the differentiated body shape of *Gnathopogon* between the riverine and limnetic species. Vertebral counts and geometric morphometrics were used to quantify body shape. QTL analysis of body shape-related traits was carried out for the above F2 interspecific cross by using RAD sequencing. We identified QTLs that exert moderate effect on the traits that have ecological significance in the variation of body shape. Most of the QTLs affected only one trait; however, we found several QTLs that affected multiple traits. The findings of our present study will contribute to understanding the genetic background of the diversification of cyprinid fishes.

Phylogeography of the Yellowfin Hind, *Cephalopholus hemistiktos*, reveals genetic discontinuity and cryptic speciation

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The Red Sea is a biodiversity hotspot containing many endemic marine taxa. The vast majority of these endemic taxa have been described using traditional morphological taxonomic techniques. Here we used mitochondrial DNA to assess the genetic variation and evolutionary connectivity of a fish species (the yellowfin hind, *Cephalopholus hemistiktos*) in which morphological differences (pectoral fin ray counts) have been reported across the species' range. Results show species-level molecular divergence congruent with the morphological difference observed across sampling sites, suggesting cryptic speciation among populations in the Red Sea and western Gulf of Aden versus the Arabian Gulf. This adds to a growing body of work suggesting endemism may be underreported in the Red Sea. These findings also highlight the importance of molecular techniques, not only in population and connectivity studies, but also as taxonomic tools.

Detecting snapper (*Pagrus auratus*) larval dispersal from a New Zealand marine reserve: preliminary results

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The benefits of marine reserves as a conservation tool are now widely recognised. However, whether they can substantially enhance surrounding fished populations through increased larval export and provide a buffer against overexploitation remains one of the major research gaps in marine reserve science. In New Zealand, Snapper (*Pagrus auratus*) support important commercial and recreational fisheries. A multi-disciplinary approach including 3D hydrodynamic modeling of larval dispersal and parentage analysis is being undertaken to quantify the extent of connectivity, dispersal, self-recruitment and local retention of snapper from a well-established marine reserve (Cape Rodney to Okakari Point marine reserve, Northeastern New Zealand). We present preliminary results from hydrodynamic modeling and DNA parentage analysis of over 3000 individual snapper using 17 hypervariable microsatellite loci, and discuss the importance of this reserve as a source of juveniles to fished populations.

Invasion genetics of Tilapiine species in Australia

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Recognizing the species and strain of invasive animals is the essential first step in their control. Genetics is a useful tool for this, particularly in lieu of morphological characters. Tilapiine fish species are popular and productive aquaculture species in many parts of the world, but are also archetypal invaders of freshwater ecosystems. They thrive in a wide range of environmental conditions and have a flexible reproductive strategy. Tilapias were introduced to Australia in the 1970's and have spread rapidly. Incursion by tilapias into the inland Murray-Darling Basin (the largest freshwater system in Australia) would be a significant threat to endemic fauna and fragile environments. Eight microsatellite loci and the control region of mtDNA were used to recognise the species and strain identities of tilapias collected from eleven locations in Queensland. Instead of being *Oreochromis mossambicus* as expected, all fish were interspecies hybrids involving *O. mossambicus, O. spirulus, O. urolepis* and *O. aureus* and there were three genetically distinct strains. Dates of first occurrence combined with genetic strain analysis across locations uncovered likely translocation pathways between catchments. Several recently established populations had zero nuclear heterozygosity, possible due to repeated bottlenecks or inbreeding in captivity. In one man-made freshwater lake, one strain replaced another over a twenty-year period. In nations where Tilapiines are a threat to native biodiversity, genetic analyses could trace translocations and incursions, help monitor the success of eradication trials, and predict invasiveness based on characteristics of the parental species.

Fish radiations in Sulawesi, with emphasis on sailfin silversides of the ancient Malili Lakes

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Fish species flocks restricted to isolated freshwater habitats are among the most popular model systems in speciation research, and research based on fish radiations has contributed significantly to our understanding of mechanisms and processes leading to species divergence. The Indonesian island Sulawesi is a biodiversity hotspot in the "Wallacea", and harbours radiations of several lineages of "secondary" freshwater fishes, including ricefishes (Adrianichthyidae) and halfbeaks (Zenarchopteridae). Most conspicuous are the endemic species flocks of the large ancient lakes of the island, including the ricefishes of Lake Poso and the sailfin silversides (Telmatherinidae) of the Malili Lakes. Most of the research on sailfin silversides has focused on those of the hydrological head of the lakes system, the extraordinarily deep Lake Matano, with two endemic lineages Telmatherina, distinguished by shapes of second dorsal and anal fins in "sharpfins" and "roundfins". Population structure, morphology, habitat use, trophic ecology and assortative mating suggest that adaptation to alternative modes of resource use, coupled with assortative mating, can explain intralacustrine divergence without geographic separation in roundfins. Substantial but not absolute restrictions in gene flow and indication for selection affecting only small parts of the genome suggest an early stage of ecological speciation in sympatry. Intersexual differences in feeding mechanics and correlated patterns in trophic resource use further enhance complexity of this small radiation. In contrast to morphospecies, male colour morphs appear not to be associated with population divergence. Lake Matano's sharpfins are more diverse than roundfins and highly introgressed by stream populations, but show likewise fine-scaled morphological and behavioural adaptation to alternative modes of resource use. Understanding individual fitness effects of adaptation as well as the role of hybridization in species-flock formation are among the prime research topics to be addressed using this system in future research.

Past demography and present day population genetic processes in coastal fishes of the Arabian Seas region

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Coastal seas around the Arabian Peninsula range from ecologically diverse systems such as the open Indian Ocean coasts of the Arabian Sea to the shallow coastal waters of the Arabian Gulf and the comparatively disconnected Red Sea. While featuring high levels of endemism, the Red Sea is also home to a high proportion of fishes with distribution ranges extending into the Indo-Pacific. However, many of these widely distributed species may show signatures of deep geographic population structure. The evolution of new species seems largely coupled to a progenitor's dispersal capacity and resulting population connectivity. Patterns of present day population genetic differentiation may thus reflect signatures of ongoing speciation and, in some instances, can be used as a proxy for variables that governed past speciation processes. To identify such variables, we studied three species of reef fish with distinct life history traits that may be differentially affected by specific barriers to gene flow. In particular, we assessed the degree of genetic differentiation among populations of three coastal species, which all occur around the Arabian Peninsula, but differ in their larval dispersal characteristics and distributional range: the brooding damselfish *Dascyllus marginatus* with a comparatively short larval duration and a distribution restricted to the Arabian Seas region, and two broadcast-spawners, *Acanthurus sohal*, a surgeonfish endemic to the Arabian Seas region, and *Thalassoma lunare*, a labrid distributed across the Indo-Pacific. Population genetic differentiation of these species was investigated along the coast of the Arabian Peninsula, covering five biogeographic sub-regions and spanning the putative phylogeographic breaks between them. The relative strength of the alleged connectivity barriers and the migration rate among separated populations is estimated and discussed in the context of ongoing population differentiation and past speciation processes. Additionally, we studied the past demography of populations from systems with distinct environmental histories by coalescent-based analyses. These results are discussed in the context of the temporal course of population size change (i.e. decline or expansion) in relation to regional oceanographic and ecological characteristics and past environmental change.

Habitat availability and heterogeneity and the Indo-Pacific warm pool as predictors of marine species richness in the tropical Indo-Pacific

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Range overlap patterns were observed in a dataset of 10,446 expert-derived marine species distribution maps, including 8,295 coastal fishes, 1,212 invertebrates (crustaceans and molluscs), 820 reef-building corals, 50 seagrasses, and 69 mangroves. Distributions of tropical Indo-Pacific shore fishes revealed a concentration of species richness in the northern apex and central region of the Coral Triangle epicenter of marine biodiversity. This pattern was supported by distributions of invertebrates and habitat-forming primary producers. Habitat availability, heterogeneity, and sea surface temperatures were highly correlated with species richness across spatial grains ranging from 23,000 to 5,100,000 km2 with and without correction for autocorrelation. The consistent retention of habitat variables in our predictive models supports the area of refuge hypothesis which posits reduced extinction rates in the Coral Triangle. This does not preclude support for a center of origin hypothesis that suggests increased speciation in the region may contribute to species richness. In addition, consistent retention of sea surface temperatures in models suggests that available kinetic energy may also be an important factor in shaping patterns of marine species richness. Kinetic energy may hasten rates of both extinction and speciation. The position of the Indo-Pacific Warm Pool to the east of the Coral Triangle in central Oceania and a pattern of increasing species richness from this region into the central and northern parts of the Coral Triangle suggests peripheral speciation with enhanced survival in the cooler parts of the Coral Triangle that also have highly concentrated available habitat. These results indicate that conservation of habitat availability and heterogeneity is important to reduce extinction of marine species and that changes in sea surface temperatures may influence the evolutionary potential of the region.

The Caribbean sandwich: biogeographical revelations from shore-fishes

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Traditionally, zoogeographic pies have been sliced up using arbitrary levels of endemism to separate sections. The reef-fish fauna of the Greater Caribbean (the Caribbean plus adjacent tropical areas to the north) has a significant level of regional endemism (~35%), as well as strong connections to the reef-fish fauna of Brazil. Many of the Greater Caribbean endemic reef-fishes are broadly distributed throughout much of that area, and the resultant low rates of local endemism in different parts of that area have led to its being considered a rather homogeneous region. We used the distributions of the entire shallow-water Caribbean shore-fish fauna to quantitatively determine the biogeographic configuration of the Greater Caribbean. We assessed similarities in the distributions of 1559 species belonging to various ecotypes (including 796 reef-fishes) across 45 areas that included all the islands and continental shore of this geographically complex area. Our analysis revealed that, biogeographically the Greater Caribbean is subdivided like a sandwich. It has a central filling comprised of the western continental shore and islands of the Caribbean plus the Bahamas and Bermuda, a thin lower crust of the entire north coast of South America, and a thick upper crust made up of the entire Gulf of Mexico and Florida peninsula. This whole-fauna pattern generally holds for different ecotypes of fishes, indicating a fauna-level response to region-wide geographical conditions. Those include large scale environmental differences in the distributions of freshwater input, the abundance of reef vs soft-bottom coastlines, latitudinal variation in temperature, and local upwellings. Whether ongoing taxonomic reassessments that indicate much greater local endemism than previously thought in the region may eventually change this large-scale pattern is unclear. The sandwich configuration also raises the issue of whether continental Colombia and Venezuela, are, from a shorefish perspective, really parts of Brazil.

Genetic diversity and the effects of climate change on the distribution of three shared fishery species in the subtropical Western Indian Ocean

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The most obvious changes associated with increased sea surface temperatures around the Western Indian Ocean will be shifts in the distribution and abundance of individual species or species assemblages according to their thermal tolerance and ability to adapt. Although marine species generally face fewer constraints to their movement than terrestrial species climate change may pose a greater threat to species when their dispersal capabilities are limited or suitable habitat is unavailable. This study estimated the genetic diversity and stock structure of three commercially important shared fisheries species endemic to the subtropical WIO. A climatic envelope method was also used to explore the extent to which the range of the selected species might shift in response to changes in the surrounding environment with climate change. Comparative analysis between three southern African endemic species (*Chrysoblephus puniceus, Polysteganus praeorbitalis* and *Epinephelus andersoni*), with different life history strategies but similar range limits will help to determine which aspects of life history are most important in generating past and present population genetic structures and subsequent adaptation to the subtropical region. Results from the genetic analyses will then be used to interpret the climatic envelope model and an overall 'model' developed for each species. These results will provide important information for the management of shared endemic fisheries species in South Africa and Mozambique.

Mitochondrial phylogenomics to resolve the cypriniform tree of life: Higher-level and detailed relationships inferred from over 500 sequences

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Fishes of the order Cypriniformes are almost completely restricted to freshwaters and comprise over 3900 species placed in six to 13 families. Monophyly, interrelationships and definition of these families or subfamilies/tribes have been poorly resolved. After publication of our previous mitochondrial phylogenomic study (Saitoh et al 2011) based on the 60 sequences, we newly determined over 400 whole mitogenome sequences for cypriniforms and make a step forward to resolve the higher-level and detailed relationships of the world's largest freshwater-fish clade based on more extensive taxon sampling from over 500 cypriniform species (including phylogenetically enigmatic *Psilorhynchus*, *Ellopostoma* and *Paedocypris*, etc). Unambiguously aligned, concatenated mitogenome sequences from 13 protein coding (11,373 bp), two rRNA (2,177 bp) and 22 tRNA (1,474 bp) genes were divided into five partitions (1st, 2nd, and 3rd codon positions, rRNA and tRNA). Maximum likelihood phylogenetic analyses based on the partitioned dataset gave phylogenetic reletionships that are largely congruent with the previous findings (Saitoh et al 2011), although the addition of over 400 species provides a much more detailed picture of cypriniform relationships. As for the unusual taxa, *Psilorhynchus* is the sister group of the subfamily Cyprininae (sensu lato); *Ellopostoma* is closely related to the subfamily Balitorinae (not Nemacheilinae as previously thought). Although our present study comprises the most extensive taxon and nucleotide site sampling, several branching nodes have not well resolved; the placement of *Paedocypris*, *Tinca*, etc.

Molecular phylogenetic and phylogeographic evidence of unrecognized diversity within nominal species of *Labeobarbus* from Indian Ocean drainages and endorheic rivers of the Great Rift Valley of Kenya

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Studies of molecular phylogenetics and phylogeography of freshwater fishes from major river drainages of the Indian Ocean and endorheic basins of the Great Rift Valley of central, western and southern Kenya have revealed deep genetic divergences within several nominal species. The present study focuses on phylogeography of Kenyan populations of putative hexaploid cyprinid fishes, originally described as species of *Barbus* or *Labeobarbus*, and now regarded as species of *Labeobarbus* Rüppell. The nominal species under study here are the Ripon Barbel, *Barbus altianalis* Boulenger, the Pangani Barb, *Barbus oxyrhynchus* Pfeffer, and *Labeobarbus intermedius* Rüppell. All of the studied species and populations are recovered as a monophyletic group with strong bootstrap support. The most basal lineage is a population from the Yala River (Lake Victoria Basin), which is sister to a lineage comprising all other nominal species. *Barbus altianalis* and *Labeobarbus intermedius* for a group sister to *Barbus oxyrhynchus*, which itself comprises several divergent lineages. The phylogeny provides evidence that *L. intermedius* and *B. altianalis* are co-distributed in the Lake Victoria Basin. We present preliminary morphological evidence in an attempt to diagnose species.

Evolutionary relationships of the enigmatic anglerfishes (Order Lophiiformes): Preliminary evidence from nuclear loci

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Anglerfishes, Order Lophiiformes, are a morphologically diverse group of teleost fishes found world-wide from tropical near-shore habitats to the deep ocean. Previous studies examining evolutionary relationships within the Lophiiformes using morphological and mitochondrial data are incongruent, especially within the deep-sea ceratioid anglerfishes. In this study, I use mitochondrial sequences from a previous study and five newly added nuclear loci to examine evolutionary relationships. The use of Bayesian and maximum likelihood phylogenetic analyses of concatenated datasets is examined and compared to a species tree approach that accounts for heterogeneity among gene trees. Preliminary evidence suggests that the genus *Lasiognathus* belongs within the family Oneirodidae rather than the Thaumatichthyidae, and that the Melanocetidae and Diceratiidae are sisters, with the Himantolophidae as sister to them, as reported in the mitochondrial study. Interestingly, phylogenetic analyses of the nuclear loci sequenced thus far indicate that the handfishes, family Brachionichthyidae, are deeply nested within the frogfish family Antennariidae. Within the Antennariidae, the subfamily Histiophryninae appears to be more closely related to the handfishes than to the remaining genera belonging to the subfamily Antennariinae. Both the family Brachionichthyidae and the genera within the subfamily Histiophryninae are confined to the Indo-Pacific archipelago and have similar life history traits, while the remaining genera within the Antennariinae are widely distributed and have different life history characteristics. Reproductive modes, including male parasitism within deep-sea ceratioids, ovarian morphology, and life history, are mapped onto the phylogeny resulting from the nuclear loci analyzed using a coalescent-based approach.

Phylogenetic analysis and molecular evolution of copulatory behavior in two cottid genera

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Copulation is defined as a reproductive mode in which males ejaculate spermatozoa into a female reproductive tract. This reproductive mode is employed by many families of fish. The copulatory species in fish are believed to have evolved from non-copulatory species because copulation can increase reproductive success of males. It is important to find appropriate model fish phylogenies to trace the evolutionary process of copulation. Cottid fish is a common name of the Cottidae in order Scorpaeniformes, suborder Cottoidei (sculpins). It is a diverse demersal fish family containing about 300 species classified into more than 70 genera. Cottid fish is widely distributed in marine habitats along the Northern Pacific coastline and freshwater habitats of the Northern Hemisphere, and some additional species in the Arctic. The characters of this group are not only species diversity but also reproductive mode including copulation behaviors. Copulating fishes are widely distributed in several genera of Cottidae and the reproductive behaviors are different among species even in a genus. At least three genera include both the copulating species and non-copulating ones. This suggests that copulatory behavior has evolved parallel within the family. Cottid species offer us an ideal group to study the evolution of copulatory behavior in fish. In this study, multiple molecular markers including mitochondrial sequences and nuclear genes have been used in phylogenetic reconstruction and evolutionary history analysis of two cottid genera (*Icelus* and *Enophrys*) which have diversified reproductive mode. The result of phylogenetic analysis is consistent with previous morphological classification and further confirms that copulation has evolved polyphyletically among the family Cottidea. The complete mitogenome sequences of *Enophrys diceraus* species complex were obtained and the cryptic diversity and speciation of them was discussed by analyzing both mitogenome and several nuclear genes. Results of the comparative analysis show obvious separation between the two groups of *Enophrys diceraus* species complex. A distinct phylogenetic species was identified in this study.

The evolutionary history of the coral groupers (Epinephelidae: *Plectropomus*)

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The genus *Plectropomus* comprises of eight species of serranids inhabiting the shallow waters of the Indo-Pacific. In contrast to the concealed ambush feeding mode displayed by most groupers, *Plectropomus* forage above the reef substratum and may achieve large size and high abundances at many localities. These features plus the formation of readily detected spawning aggregations render them heavily targeted species in the Indo-Pacific. Although a previous phylogenetic analysis has identified *Plectropomus* as a basal taxon in the Epinephelidae, their evolutionary history and taxonomic status of the species requires clarification. This study presents the first species tree and divergence time estimation of the all *Plectropomus* species, using a multilocus (two mitochondrial (COI, 16S) and three nuclear markers (S7 intron, ETS2 intron and an exon-primed-intron-corssing locus 36298E1)) sequence dataset. The phylogenetic analysis confirmed the monotypic genus *Saloptia*, which inhabits deep reef in the western and southwestern Pacific, as the sister taxon of *Plectropomus* diverging in the upper Miocene. The diversification within the genus commenced in the mid Pliocene with further diversification confined to the late Pliocene/Pleistocene. The clades contain mixtures of widespread and endemic species with strong signals of vicariance speciation in at least two instances. Ancestral areas reconstruction using RASP suggested that Plectropomus originated in the western Pacific and colonized the Indian Ocean multiple times, with *P.areolatus* and *P. pessuliferus marisburi* also colonized the Red Sea. Divergence events in the western Pacific were associated with differentiation of habitat preferences leading to the conclusion that both geography and ecology may have played significant roles in the evolutionary history of Plectropomus. Our phylogeny calls for taxonomic revision as *P. pessuliferus* was found to be polyphyletic. The genus represents a further example of recent diversification and very rapid colonization of the Indo-Pacific and Red Sea biogeographic areas by coral reef fishes.

Inter-annual changes in genetic structures of hybrid populations of two largemouth bass subspecies in Japan based on SNPs analysis

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The largemouth bass *Micropterus salmoides*, one of the most intensively managed sport fish species in the United States, has been introduced into freshwater habitats around the world. In Japan, the northern subspecies, *M. s. salmoides*, was first introduced into a lake in 1925 (Lake Nishino). This subspecies has subsequently expanded its distribution to the whole of Japan, and this has had serious consequences for the native aquatic biodiversity. In 1988, another Florida subspecies, *M. s. floridanus*, was also introduced into a lake in central Japan (Ikehara Reservoir). Although it had been considered unlikely that the Florida subspecies would establish in this lake because of the low water temperature of the lake and the existing presence of the northern subspecies, its establishment and interbreeding with the northern subspecies were subsequently confirmed by genetic studies in 1996. Since the 2000s, the Florida subspecies or hybrid progeny have been detected in other lakes and ponds in central Japan, including Lake Biwa which is inhabited by many endemic species. Secondary introductions of the Florida subspecies into water bodies already inhabited by established populations of the northern subspecies may result in fish of larger size, and with altered ecological traits, thereby potentially enhancing damages to the biodiversity. In this study, in order to reveal the genetic impacts of secondary introductions of Florida largemouth bass, inter-annual changes in the genetic structure of largemouth bass populations where both subspecies co-exist were analyzed using seven new nuclear single-nucleotide polymorphism markers. A total of 381 fish were collected from three lakes (Ikehara Reservoir, Nanairo Reservoir, and Lake Biwa) in central Japan during the period from 1996 to 2010. Population structure analyses of populations from the three lakes revealed that both subspecies had mated randomly with each other and that for most gene frequencies of the Florida subspecies alleles had been constantly increasing. These results strongly suggest that when a northern subspecies population is secondarily invaded by the Florida subspecies, it is genetically replaced by the Florida subspecies through interbreeding. Accordingly, positive selective advantages may exist for certain ecological traits of the Florida subspecies in Japanese freshwater habitats.

Phylogenetic revamp of phonetic clingfish classification

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The roughly 150 species and 45 genera of clingfishes (family Gobiesocidae) are currently divided between nine subfamilies in a "phenetic" classification scheme proposed over 50 years ago. Though heavily criticized, this classification is still widely utilized and reflects the paucity of phylogenetic studies conducted on these small and cryptic marine fishes. Using a combination of mitochondrial (CO1 & 12S) and nuclear (RAG1) sequence data we investigated the phylogenetic relationships of 40 clingfishes, representing 18 genera and 7 subfamilies of the Gobiesocidae. Preliminary topologies derived from Parsimony and Maximum Likelihood analyses of individual and concatenated data matrices depict relationships that are largely congruent with current clingfish subfamilial groupings (including a monophyletic Gobiesocinae and Diademichthyinae) but are not entirely free of conflict (e.g., Lepadogastrinae and Aspasminae as currently recognized are paraphyletic). Our preliminary findings also support the placement of the Australian shore eels (genus *Alabes*) within the Gobiesocidae, supporting previous hypotheses based on morphological synapomorphies. In closing, we compare topologies derived from preliminary molecular phylogenetic analyses with those obtained from ongoing morphological investigations, highlight areas of conflict between the two, and tentatively propose changes to the current clingfish classification to recognize monophyletic groups recovered in both molecular and morphological phylogenetic analyses.

A multi-locus timetree of surgeonfishes (Acanthuridae, Percomorpha)

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The evolutionary relationships among surgeonfish and allies (Family: Acanthuridae) have been the subject of numerous morphological and molecular studies, but they have primarily focused on higher-level relationships, or were limited to acanthurid subclades. Only one study has attempted to address the timing of evolution of acanthurids using a species-level phylogeny, but it was limited to the genus *Naso*. Therefore, we generated the first comprehensive time-calibrated, species-level hypothesis of the tempo of Acanthuridae evolution, including 75% of the extant diversity. We generated sequence data for two mitochondrial (*coxI*, *Cytb*) and six nuclear genes (*ENC1*, *myh6*, *plagl2*, *Rag1*, *Rh*, *zic1*), and combined it with available data for the nuclear locus *ETS2* from GenBank. Our dataset underwent maximum likelihood and Bayesian phylogenetic analysis, and we used two fossil calibration points to time-calibrate the phylogeny using BEAST 1.7.4. We recovered two major acanthurid clades, Nasinae and Acanthurinae, with the Nasinae (*Naso*) representing a recent radiation that diversified throughout the Late Miocene. The Acanthurinae represent an older group that originated ~ 45 Ma, with most diversification occurring since the Late Oligocene (beginning ~ 25 Ma). Our results suggest a paraphyletic *Acanthurus*, which has been suggested by previous morphological and molecular data. We also recover strong support for a paraphyletic *Ctenochaetus*, suggesting further taxonomic investigation into the validity of this genus.

Testing macroevolutionary scenarios in marine fishes by combining phylogenomic and paleobiological data

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In this talk we will present the results of our study of several major groups of marine teleosts, such as tetraodontiforms (puffers, triggerfishes and allies), acanthuroids (surgeonfishes, luvar), and sparids (seabreams, porgies and allies). All of these groups possess a rich fossil record, which to date has rarely been used in evolutionary studies. For each group we assembled both a molecular and a morphological dataset, containing both extant and fossil taxa (tetraodontiforms: 256 extant and 42 fossil taxa, 9 genes and 229 morphological characters; acanthurids: 65 extant and 22 fossil taxa, 8 genes and 75 morphological characters; sparids: 96 extant and 6 fossil taxa, 5 genes and 87 morphological characters). We produced time-calibrated phylogenies using relaxed Bayesian clock methods and both node-dating and total-evidence (i.e., tip-dating) approaches, and used the resulting timetrees to investigate the tempo and mode of evolution within these clades. Our results show how failing to include the extinct diversity can severely alter the macroevolutionary signal of adaptive radiation that we recover in these clades. Furthermore, incorporating fossils in total-evidence dating approaches greatly increases the estimated ages of these groups, challenging the current understanding of the timing of major events in teleost evolution (e.g., post-K/Pg acanthomorph radiation, Late-Oligocene reef-fish radiation). Our results illustrate the need to integrate paleobiological and phylogenomic datasets, and suggest new and exciting ways to foster collaborations between comparative fish morphologists and molecular phylogeneticists.

Behaviour shapes evolutionary outcomes of hybridisation in a coral reef fish

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Evolutionary outcomes for species are inherently linked with reproductive traits and mating systems, where behaviour and ecology can be significant in shaping diverse communities in nature, and may act to isolate taxa from one another. Within the context of hybridisation, species-specific behaviours directly influence gene exchange between species, and as such, the outcomes associated with hybridisation events. Anemonefish behaviour provides an acute example of this, with strong territorial inheritance within a size-based dominance hierarchy. Here, the putative hybrid anemonefish *Amphiprion leucokranos* was examined using ecological, morphological and genetic approaches to test a hypothesis of behavioural isolation within a size-based hierarchal group. In Kimbe Bay (PNG), located within the known narrow hybrid zone, strong evidence confirms that *A. leucokranos* is a hybrid of smaller *A. sandaracinos* and larger *A. chrysopterus*, where the larger species is exclusively the mother to each hybrid produced. The parent species and *A. leucokranos* overlapped in habitat, depth range and host anemone use, where the hybrid often had intermediate characteristics. Putative parents and hybrids commonly co-inhabited anemones with over 25% of anemones shared by *A. leucokranos* and either parent. Moreover, *A. leucokranos* was intermediate to parent species in body size. Most *A. leucokranos (*55%) were morphologically identified as first generation (F1) hybrids with intermediate colour and pattern relative to parents; with the remainder more similar to *A. sandaracinos* in colour and pattern. mtDNA indicated unidirectional hybridization and introgression of *A. chrysopterus* mtDNA into *A. sandaracinos* via hybrid backcrosses in Kimbe Bay, always with larger hybrids as mothers. nDNA introgression was also detected, with distinct intermediate *A. leucokranos* genotypes flowing into both parent species; where the hybrid is always the female in crosses with smaller *A. sandaracinos.* These findings validate the hypothesis of "asymmetrical behavioural isolation" as a result of known anemonefish social structure, indicating how behaviour can shape the evolutionary outcomes of hybridisation, where hybrids persist as a distinct population. Importantly, this hybridisation event increased the genetic diversity of a vulnerable species, *A. sandaracinos,* in Kimbe Bay, reducing local extinction risk due to inbreeding depression within a small population.

Molecular characterization and phylogenetic analysis of four Indian cyprinid genera using mitochondrial *CO1*gene

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Increasing worldwide destruction and disturbance of natural ecosystems are precipitating the catastrophic extinctions of species. There are over one million of known species on earth including fishes and probably several million more not yet identified. Good systematics and taxonomy are desirable for understanding the bio-geographical patterns of species diversity and designing the conservation programmes. Taxonomy seeks to discover the order hidden in the apparently bewildering diversity of living beings. Traditional morphology-based taxonomic which may sometimes be misidentifying the species, particularly in the early stages of development when only a few morphological characters are observable. Same species which live in different habitat type may have different body shape and size because ecology predicts the morphological structure. Therefore a multidisciplinary approach to taxonomy that includes morphological, molecular, and distributional data is essential for correct identification of the species. It has shown that the analysis of short, standardized genomic regions (DNA barcodes) can discriminate morphologically recognized animal species. In particular, the mitochondrial *cytochrome c oxidase I* (COI) gene can serve as a uniform target gene for a bio-identification system. Molecular taxonomy also provides the opportunity to survey deeply and accurately the history and the relationships between different evolutionary lineages by using the traditional field of systematics and the growing field of bioinformatics. *Hypselobarbus, Puntius, Neolissochilus* and *Tor* are the four economically and ecologically important fresh water Cyprinids from Southern Western Ghats, India were analysed in the present study.These four Cyprinid genus is having more taxonomic ambiguities, which is not able to solve by using traditional taxonomic methods. Most of these fishes are endemic to Western Ghats is in endangered status in the IUCN list. The genetic relatedness of the present study supports the morphological concept of relationship among the taxa. The phylogenetic tree constructed has given a clear systematic position of these four genera at species level and generic level. Our result revealed that the mitochondrial *CO1* gene is a highly effective molecular marker for the identification and the evaluation the phylogenetic relationship among the taxa.

The evolution of basal actinopterygians revealed by gene capture and next-generation sequencing

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Basal actinopterygians are relict basal ray-finned fishes, including species such as bichirs, sturgeons, gars and bowfin. Although only a small number of extant species compared to their fossil relatives, basal actinopterygians are important evolution offshoots after the divergence of ray-finned fish from their lobe-fined sister group. Basal actinopterygians have many interesting traits that are distinct from the derived teleosts (e.g., cartilaginous skeleton, heterocercal tail and ganoid scales in some species, and lack of genome duplication events found in teleosts). In this study, we used gene capture and next-generation sequencing methods to reconstruct the interrelationships among basal actinopterygians and basal teleosts. Our result could help us to study the evolution of the traits distinguishing the basal actinopterygians from the derived teleosts, and it would also help us to understand the changes that led to the diversification of the largest vertebrate group – teleosts.

Molecular phylogeny of grunts and sweetlips (Perciformes, Haemulidae)

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The fish family Haemulidae is divided in two subfamilies; grunts (Haemulinae) and sweetlips (Plectorhynchinae), together they include approximately 145 species allocated in 17 genera. Most of the diversity is restricted to marine waters with some species inhabiting brackish and freshwater. This family embraces a wide geographical distribution inluding contrasting ecological habitats resulting in a unique potential to test evolutionary hypotheses. We present a robust molecular phylogeny of Haemulidae based on the combined data of three mitochondrial and four nuclear genes gathered from 102 recognized species including 99% of the New World diversity. Our results support the monophyly of both sub-families, however only few monophyletic genera were recovered which underscores the need for major taxonomic reassessment of the family. Data also show that differential use of habitat might have played an important role in the speciation dynamics of this group of fishes, in particular among New World species where extensive sample coverage was available.

Drivers of temporal and spatial movement patterns in luderick *Girella tricuspidata* in NSW, Australia

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Girella tricuspidata (Kyphosidae), known as luderick and parore, is a common teleost found in estuaries and near-shore waters of eastern and southern Australia as well as around the northern Island of New Zealand. Luderick is heavily commercially exploited in estuaries and targeted by recreational fishermen. The species is primarily herbivorous and is often associated with vegetated habitats including seagrasses and shallow rocky reefs. This study aims at determining the movement patterns of luderick (i) within estuaries in relation to environmental factors and (ii) exchanges between estuaries and migratory pathways along the New South Wales (NSW) coast. Forty-five adults (mean *LF* ± S.E.: 301 ± 5 mm) were acoustically tagged in three estuaries along a 200 km stretch of the NSW coast. Each estuary is monitored with an array of acoustic receivers (38 to 42) distributed every 1.3 km on average to completely cover the brackish extend of the estuaries. These estuarine arrays are complemented by an extensive coastal network of receivers with over 500 receivers spread along the NSW coast. Fish were captured, tagged and released at different locations from the mouth of each estuary to 24 km upstream. Environmental parameters of the water column were regularly monitored at each receiver location. Within estuary, movements of luderick were greatly influenced by changes in salinity structure. The decrease of salinity resulting from large amounts of freshwater inputs via rainfall drives the major movements in downstream direction (over 10's kms). Where individuals that have left the estuary and been detected outside the system (20% of the individuals), the departure from the system occurred in conjunction of heavy rainfall events. The movements observed in coastal waters were in a northward direction after the fish had left the estuary. Individuals were detected up to 300 km away from their tagging site and such distance has been covered in 7 days. The departure of luderick from estuaries occurred outside documented spawning periods, suggesting that such large scale movements may not be related to reproduction.

The fishery biology of the Lethrinidae species in the Arabian Gulf

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The fisheries of the Arabian Gulf depend mainly on demersal fin-fish species. Members of the family Lethrinidae genus *Lethrinus* (emperor) *Lethrinus nebulosus*, *L. harak*. *L. miniatus* and *L. lentjan* were generally the most abundant species in the commercial trap fishery along the UAE coast. Gonadosomatic index (GSI) of all sampled species showed an extended spawning season from March-October with a peak in April and decline from May. Length-weight relationship were used to estimate the values of a and b for the four species using the equation W=aLb. Age determination using classified tissues showed better result on Otolith compared with vertebra. Preliminary results show that lethrinidae species had a strong association with artificial reef. Coastal development, desalination and absent of any time and habitat closures could be the main limiting factors for the sustainability of this economically important resource.

Movement and spawning dynamics of emperorfishes in a marine reserve, based on acoustic telemetry

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A critical feature of an effective marine protected area (MPA) is that it is large enough to encompass the home range of target species, thereby allowing a significant portion of the population to persist without the threat of exploitation. In the present study, patterns of movement and home range for *Lethrinus harak* and *Lethrinus obsoletus* were quantified using an array of 33 acoustic receivers which covered approximately three quarters of Piti Marine Reserve in the US Pacific Island territory of Guam. This array was designed to ensure complete overlap of receiver ranges throughout the study area. Ultrasonic transmitters were surgically implanted in 18 individuals (12 *L. harak*; 6 *L. obsoletus*) who were released and passively tracked for four months. Both species displayed extremely high site fidelity and relatively small home ranges while the size of individual home ranges increased with body size. Short monthly migrations were observed for *L. harak*, most likely for spawning. These migrations occurred nightly between full moon and last quarter moon each month for at least eleven lunar cycles of the year and coincided with a strong ebbing tide. Results indicate that the protected area sufficiently encompasses the home range of these emperors and, in addition, protects a significant spawning site for *L. harak*. These species are heavily targeted in Guam and previous studies have identified major demographic differences between fished and protected sites. Hence, the present study further highlights the role of protected area management in sustaining reproductive viability of populations.

Systematics and evolution of moray eel leptocephali

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The Muraenidae, or moray eels, is one of the most diverse families of anguilliform fishes and consists of two subfamilies, 16 genera and 200 species. Moray eels have remarkably few specific characters because they have very simplified morphologies that include a lack of pectoral and pelvic fins, a confluence of the dorsal, caudal and anal fins, and either the fusion or deletion of many bones. Therefore, their lack of specific morphological characters has made them most perplexing to classify; the state of muraenid taxonomy, particularly at the generic level, remains incomplete. In order to resolve this problem, we examined leptocephalus morphologies as a means of determining species identification. We were able to clarify the leptocephalus morphologies of Indo-Pacific moray eels from two subfamilies, 10 genera, 33 species and 43 types. The results were compared with those from a molecular phylogenetic tree constructed from leptocephali and adults. This comparison indicated that the leptocephalus morphologies were congruent with topology of the tree. Therefore, leptocephalus morphologies were shown to be useful for taxonomic identification of moray eels. We also mapped suitable habitat use of adult morays and these traits were well accorded with both the topology of the tree and with leptocephalus morphology. Thus, from an evolutionary perspective leptocephalus characters are related closely to suitable habitat use of adult morays. Based upon this result, we discuss how leptocephalus morphology evolved adaptively.

Danionella dracula, an escape from the cypriniform bauplan via developmental truncation?

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During the last decade a number of tiny cypriniforms measuring less than 20 mm length have been described. Several of these are highly developmentally truncated and exhibit a number of remarkable evolutionary novelties indicating a link between truncation and novelty. Probably the most interesting and bizarre novelties among these miniature cyprinids are the radical and sexually dimorphic jaw modifications of the Dracula minnow, *Danionella dracula*, from freshwater streams in northern Myanmar. Uniquely among the almost 4000 species of cypriniforms, male *D. dracula* show a series of conspicuous odontoid processes on both jaws, which resemble teeth very closely, structures lost in the lineage leading to cypriniforms at least 50 Mya. Here we show that in addition to its unique odontoid processes, the miniature and developmentally truncated *D. dracula* provides an astonishing example of a major deviation from the cypriniform bauplan. Unlike any other member of its order *Danionella dracula* has lost six out of the eight unique synapomorphies of cypriniforms including the kinethmoid. This bone is essential for the protrusion of the upper jaw and represents one of the key innovations of cypriniforms hypothesized to be responsible for the evolutionary success of the order.

Development of the upper jaw in squirrelfishes and soldierfishes (Beryciformes: Holocentridae): A unique ontogenetic trajectory

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The Holocentridae are nocturnal fishes inhabiting shallow to deep water coral and rocky reefs in tropical parts of the Indian, Pacific and Atlantic Oceans. Two subfamilies can be distinguished, the squirrelfishes (Holocentrinae) and the soldierfishes (Miripristinae). Unlike the adults, holocentrid larvae are pelagic and are characterized by elaborate head spination, including prominent rostral, supraoccipital and preopercular spines. The rostral spine, formed by ephemeral fusion of the paired nasals, can project far anterior to the mouth. The spine-bearing bones, the lower jaw bones and one set of upper jaw bones (maxillae) are the first to ossify (at SL: 1.4 mm) during early life history. In several cleared and double stained ontogenetic series of Holocentridae (SL: 1.4 mm - 35 mm) we found a unique ontogenetic trajectory of the other set of upper jaw bones (premaxillae). The premaxillae develop late, well after the other jaw bones and head spines are developed and most of the remaining skeleton is ossified (between 5.9 mm and 6.6 mm). Usually in larval fishes both sets of upper jaw bones as well as the lower jaw, the caudal fin and pectoral girdle are the first elements to ossify in order to ensure feeding and swimming mechanics. The unusual ontogenetic trajectory of holocentrids gives rise to numerous questions, such as whether the rostral spine has a role in feeding in the absence of premaxillae, how early feeding is managed in their absence, and whether feeding changes during early life history. We also compare our results with jaw and rostrum development in the only other fish larvae known to have a rostral spine formed from ephemeral fusion of the nasal bones, those of the tilefishes (Malacanthidae).

Larvae of two Indo-West Pacific anthiine fishes, *Giganthias immaculatus* and *Serranocirrhitus latus* (Perciformes: Serranidae)

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The serranid Anthiinae is very diverse in the Indo-Pacific region, but their larvae are very little known mainly due to indistinctive meristic characters except some genera. This paper describes larval characters of two anthiine fishes based on two specimens of *Giganthias immaculatus* and a single specimen of *Serranocirrhitus latus* collected in the East China Sea. Identification of the larvae was made by specific numbers of dorsal-fin spines and myomeres for *G. immaculatus* (D IX, 13; V 25) and a combination of fin-ray counts for *S. latus* (D X, 19; A III, 7; P1 13) with the general larval characteristics such as early forming dorsal- and pelvic-fin spines, and head spines. A 4.2-mm NL flexion and 5.4-mm BL postflexion larvae of *G. immaculatus* have a kite-shaped, remarkably deep, laterally compressed body which is unique in the subfamily. The head is triangular and large. The body is the deepest between the pelvic-fin base and origin of the dorsal fin. Anus position is beyond the half body. Head spination is moderately developed. A supraoccipital spine is in low, widely-based triangular shape being unique. Preopercular spine at angle is long and about 4 times longer than the interopercular spine. Both spines, and anterior dorsal- and pelvic-fin spines are smooth. Pigment is distinct at the tip of the lower jaw, the symphysis of the shoulder girdle and over the brain. A 6.8-mm BL postflexion larva of *S. latus* is deep-bodied and compressed with the taper tail. The head is large occupying 52% BL. The pelvic-fin base is inserted in the isthmus and the first soft ray reaches to at least the posterior anal fin. The anus is situated slightly beyond the half body. Head spines are moderately developed. There is no supraoccipital spine. Preopercular spine at angle is slightly longer than the interopercular ones. No serration appears on head spines, and dorsal- and pelvic-fin spines. Pigment is present at the tip of the upper jaw, the dorsolateral trunk and tail and over the brain, but overall poor. The presentation will make a comparison between the selected characters of the present larvae and others.

Ontogenetic development of hapuku, *Polyprion oxygeneios* (Polyprionidae), and possible relationships based on larval characters

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The placement of *Polyprion* has had a history of instability, at times placed in catch-all families Acropomatidae and Percichthyidae, and as a separate family. There remains uncertainty about relationships of *Polyprion* to other percoid families based solely on morphological characters of adults. The rearing of *Polyprion oxygeneios* in an aquaculture facility has provided, for the first time, a full ontogenetic series and the opportunity for description of its larval and early juvenile morphological development. Larvae have precocious development of head spines, in particular on the supraoccipital, supraorbital, preopercle, pterotic and supracleithral. Scales develop ornamentation at an early stage of development. Using larval characters, morphologically similar larvae were analysed to propose closely-related families.

Evidence for the presence of spines in scales of the Apogonidae (Pisces, Perciformes) and its ontogenetic and phylogenetic significance

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Over the years, the application of the term 'ctenoid' to fish scales with spines or projections on the posterior field and/or its margin has overlooked, indeed sometimes disregarded, both the immense diversity of spiny scales in teleost fishes and the phylogenetic information hidden in them. In his extensive review of fish scale morphology, Roberts (1993) recognized three major types of 'ctenoid' or spiny scales: crenate, spinoid and ctenoid. The majority of taxa in the cardinalfish family Apogonidae have ctenoid scales while a small number of species have cycloid ones. Spinoid scales were discovered recently in the genus *Siphamia*, resulting in the unusual situation of three major scale types, i.e. cycloid, spinoid and ctenoid, being present in a single fish family as well as in a single genus within this family. Furthermore, the two *Siphamia* species with ctenoid scales actually had both true spines and true (transforming) ctenii on their scales. This presentation reports on the results of a survey of the Apogonidae and several other percomorph families for the presence of spines (as opposed to ctenii) in their scales. Scales were taken from adult and, when available, juvenile specimens and mounted on scanning electron microscope stubs, coated with gold dust and observed at the Electron Microscopy Unit of Rhodes University, South Africa. The results show the presence of spines (and ctenii) on the scales of many apogonid species. The position of the spines on the scales of juveniles and adults indicates that spines precede ctenii in the ontogeny of these species and, by extension, that spinoid scales are indeed ancestral to ctenoid ones. It also implies that cycloid scales in the Apogonidae are derived, and lends support to Robert's (1993) similar conclusion for the percomorph group as a whole.

Temporally and spatially overlapping distribution of larvae of the closely related two pagrines (*Evynnis japonica* and *Pagrus major*) in coastal Tosa Bay, southern Japan

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Japanese sparid fishes have 13 species from seven genus, of which *Evynnis japonica and Pagrus major, belongingto Pagrinae,* closely resemble in morphology and coloration (beautiful pink), but have seasonally opposite spawning, i.e. the former in the autumn v.s. the latter in the spring. Through their ontogeny, two species can be classified by the pigmentation along the dorsal caudal peduncle in late larval and juvenile stages, but was hardly distinguishable during larvae earlier than flexion stage. Recently, early juveniles of the two species were caught by a *shirasu* (for chiefly anchovy juveniles) trawling along the shallow coastal waters of Tosa Bayin the winter. This suggests that the two pagrine species spawn simultaneously, furthermore a risk for hybridization between the two species. To examine this phenomenon, vertical distribution in planktonic period was clarified, and compared between the two species. Discrete horizontal tows with a larva net (mouth diameter = 1.3 m; aperture size = 0.5 mm) were performed at five layers (surface, 10, 20, 30 and 40 m) of 45 m depth station off the mouth of Niyodo Riverin Tosa Bay monthly from September 2011 to May 2012. Even in pelagic period, both two pagrine larvae occurred in the winter of January to March, and there was little differentiation in the vertical distribution pattern between *E. japonica* in November to January and *P. major* in March to May, i.e. the earlier larvae than postflexion tended to be dispersed in middle layers, and the late larvae and early juveniles started to migrate near bottom layer. Their sagitta and/or lapillus increments were examined to compare spawning seasons between two species, so that their hatchings had been overlapped for December to February. It is like that the significant incidence was attributed to accelerating to start spawning in P. major by a global warming.

Study of the diagnostic character of Scaridae larvae

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Parrotfishes (family: Scaridae) are widely distributed in tropical and subtropical waters. Although they are important fisheries resource for food, little is known about its early life history because of difficulty in larval identification. In this study, we tried to find out diagnostic characters of Scaridae larvae using genetic identification and morphologic analysis. Larvae were collected at coastal waters of northern Okinawa Island using an aquatic lamp (78 specimens). Development stage of all larvae was postflexion closing juvenile. Total DNA was extracted from right eye to keep form of left side of the body, and part of mitochondrial DNA 16s region (499 bp) and cytcrome b region (471 bp) were sequenced. Sequences of larvae were cross-checked with adult fish distributed in Japanese water (32 species). As a result, 9 species of larvae (*Bolbometopon muricatum*, *Calotomus spinidens*, *Chlorurus microrhinos*, *Ch. sordidus*, *Leptoscarus vaigiensis*, *Scarus ghobban*, *S. psittacus*, *S. rivulatus* and *Scarus* sp.) were identified. We studied morphologic characters of larvae based on the result of genetic identification, and some morphological features were found. 2 species of subfamily Sparisomatinae, *Ca. spinidens* and *L. vaigiensis*, had large elongate body (10.4–15.0 mm SL) compared to Scarinae (6.9–8.2 mm SL). They were identified by pigment patterns on the anal fin base. 4 species of genus *Scarus* shared discriminative pigment pattern on the posterior abdominal cavity. Above all, *S. ghobban* and *S. psittacus* had an unique pigment pattern which might be useful in species identification. However, morphological difference between *S. psittacus* and *Scarus* sp. Were not found. Similarly, *B. muricatum, Ch. microrhinos* and *Ch. sordidus* could not be identified using morphologic characters.

Evolution of larval and juvenile pigment patterns in *Gymnogobius* fishes (Gobionellinae, Gobiidae)

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Pigment patterns in larval and juvenile fishes are the consequences of phylogenetic constraints and adaptations. Although Mabee (1995) suggested its utility in a phylogenetic study of centrarchid fishes, pigmentation is often disregarded as a source of characters containing historical information because of its high pattern variability within individuals and species. Here we show the diversity of external and internal pigment pattern developments in *Gymnogobius* larvae and juveniles, and discuss their evolution using a molecular phylogenetic tree. Taxonomy of *Gymnogobius* is in a state of transition, but this genus, as currently recognized, contains about 13 species (Stevenson, 2002) distributed in the Western North Pacific and has various life histories, marine, brackish, freshwater amphidromy, lacustrine and fluvial. We investigated four kinds of pigment patterns: (1) external larval melanophores (ELM), (2) internal larval melanophores on the roof of a mouth and the dorsolateral part of an abdominal cavity (ILM), (3) external metamorphic melanophores from larval to juvenile stage (EMM), (4) internal metamorphic melanophores along vertebra from larval to juvenile stage (IMM), using larvae and juveniles of 12 *Gymnogobius* and 2 *Chaenogobius* (outgroup) species collected by field sampling in Japan. The distribution patterns of ELM could be divided into 4 types: heavy (expanded melanophores intermittently distribute along dorsal and ventral midline), moderate1, moderate2 and sparse (small melanophores mainly distribute ventrally), and changes from heavy to moderate and sparse happened at least 4 times independently by the most-parsimonious reconstruction. We speculate that the ancestor evolved the heavy ELM type, breaking up the body shape, as camouflage in the shallow rocky shore environment and later melanophore reductions occurred in some *Gymnogobius* species as early life histories changed. The distribution patterns of ILM were closely related to those of ELM, and both kinds of pigmentations relatively represent the adaptational aspect. On the other hand, the phylogenetic aspect was relatively observed in EMM and IMM since higher similarity was observed in each smaller monophyletic group.

Ontogenetic close resemblance between two endemic gobies to Ariake Bay, western Japan, *Boleophthalmus* and *Odontamblyopus* belonging to different subfamilies

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Boleophthalmus pectinirostris (Oxudercinae) romping about over the tidal madflat and *Odontamblyopus lacepedii* (Amblyopinae) with vestigial, both being endemic to Ariake Bay within Japan, are associated with shallow, muddy bottom of estuaries. Larval distribution of the two gobies was examined around inner part estuary of the bay, which consists of a heavily turbid, vertically mixed, strong tidal current environment. Horizontally, the both pelagic larvae were distributed chiefly around the river mouth with few occurring in the open sea outside the river mouth. Although two species are from different subfamily, their ontogeny are closely resemble, i.e. body is increasingly elongate and compressed. The gut is short, and the tail is much long. The snout is slightly convex, and the head is oriented slightly downward relative to the body axis. The eye is both small, and narrow in *O. lacepedii*, but rounded in *B. pectinirostris*. When osteological development was compared between the two gobies, ossification sequence was advanced in smaller size in the former than in the latter. Hence, in larval morphology, there was little differentiation between *O. lacepedii* and *B. pectinirostris*, which was rather than dissimilar from the other mud-skippers, Periophthalmus belonging to the same subfamily: Oxudercinae. The present ontogenetic fact could be supported by recent molecular phylogenetic studies about gobies.

Larval study to find crypto-benthic gobies

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Crypto-benthic fishes are difficult to find because they usually cannot be located without extensively excavating the substrate. However, their pelagic larvae can sometimes be collected easily. Here we provide two typical examples from a larval study performed in marine and freshwater habitats on Okinawa Island, Japan. Fish of the genus *Luciogobius* are usually found in interstitial habitats in gravel bottoms of coasts, estuaries, freshwater streams, and subterranean waters. *Luciogobius ryukyuensis* is the only nominal species known from Okinawa Island, but we have found that larval samples collected from Okinawa Island actually include 11 species, clearly distinguished by the number of fin rays and vertebrae, body length, proportions, and pigment arrangements. Most of these species exhibited different characteristics from all *Luciogobius* species described so far. Thorough searches for adults near larval sampling sites have located adults belonging to six of the 11 species, but adults of the other five have continued to elude collection. The second example is of amblyopine goby from Okinawa Island which inhabit burrows in mudflats or muddy bottoms of inner bays. We collected larvae of two *Taenioides* species, two *Trypauchenopsis* species, and *Caragobius urolepis*. One of the *Taenioides* species has a much larger number of fin rays than other one collected previously from this region. Only recently was the first adult specimen of the former species, with the high fin ray count, finally captured. Although the genus *Trypauchenopsis* has been considered to contain only one species, there is no doubt that our *Trypauchenopsis* larvae represent two species. They were clearly distinguished by pigment arrangements and meristic characters. It is concluded that larval gobies are sometimes easier to collect and more readily identifiable than adults. It is emphasized that larval collection is often useful to understand fish taxonomy and diversity.

The reality of coral reef monitoring in remote field sites: a case study from the Birds Head Seascape, Indonesia

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The Bird's Head Seascape (BHS), located within the heart of the Coral Triangle, has the highest coral and reef fish diversity documented in the world's oceans for an area of its size. Through extensive conservation efforts, a resilient network of marine protected areas (MPAs) covering over 13,000 square miles has been created within the BHS. Ecological monitoring is needed to determine the effectiveness of conservation interventions. Collaboration is in place between three NGOs for continued monitoring within MPAs using standardized reef health monitoring protocol. Yet, the remoteness and large area of the BHS, compounded with limited resources and the dynamic nature of ecosystems present challenges to ecological monitoring and data analyses. These include variability in the skills of the monitors, different interpretation of monitoring protocols, and the natural fluctuations that occur temporally with fish populations with tidal, diurnal, and seasonal changes. We will discuss our approach to addressing these challenges in order to optimize the utility of the current data, and improving on current monitoring strategies in the BHS and elsewhere in Indonesia. Site selection is also critical for evaluating MPA effectiveness, and ideally, includes sites within and outside (control) of MPAs. Subsequently, we will also discuss our criteria for identifying control sites for impact evaluation in the BHS.

Experimental removal of the introduced predator *Cephalipholis argus* in Puako, Hawaii; a community-based approach to coral reef ecosystem restoration

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Introduced predators can reduce biodiversity and abundance of native species by direct predation or indirectly through competition for resources. This research focused on the effects of an introduced grouper (roi, *Cephalopholis argus*) on native reef-fish populations. Our objectives were to 1) engage the local-community in testing the effects of roi on fish assemblages using a predator removal experiment and 2) assess the feasibility of roi removal as a management tool. Native fish abundance increased at all study sites 18-months following roi removal. This increase was significantly greater at the treatment site; however fish biomass was similar among locations. Fish biomass increase as a result of predation release is expected to take > 18-months to detect. Therefore bi-annual monitoring will continue for three years to determine the long-term effects of roi removal. Short-term analysis of small (5cm≤15cm) prey species abundance increased significantly at the treatment site compared to control locations. The spatial distributions of roi were monitored with a mark and re-capture program. Tagged roi were found to travel distances ~50150m from the periphery of the removal area toward its center at a rate of ~1 every 1-2 months, demonstrating the feasibility of roi removal as a management tool in Hawaii.

Demography and reproductive biology of the white-streaked grouper *Epinephelus ongus*: estimation of the effect of restoring stock by conservation of spawning aggregation associated with consistent lunar cycle in the Yaeyama Islands, Okinawa

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The white-streaked grouper, *Epinephelus ongus* (Epinephelidae), which forms spawning aggregations at specific times and sites has been a traditional target by local fishers in the Yaeyama Islands, Okinawa. To examine population status and fisheries management procedure of the species in the Yaeyama Islands, demography and reproductive biology were studied. Firstly, gonadal histology and otolith assessment revealed the sexual pattern (monandric protogynous hermaphrodite), growth, maturity, and spawning season from April to June. Secondly, combination of analysis of gonadal histology and daily catch data over 20 years demonstrated that spawning and spawning aggregation formation showed consistent lunar periodicity and that spawning concentrated within a few days after the last quarter moon. Analysis of oocyte size distribution indicated that individual female spawned more than once, but would be determinant spawner during the course of a single aggregation. Furthermore, three typical patterns of annual spawning aggregation formation, which formed once or twice from the third month to the fifth month in the lunar calendar, could be explained by the mean water temperature before the first spawning in each year. Thirdly, catch data over 20 years showed that concentrated catch in the spawning periods was account for ~40% of annual catches and that annual catches have decreased by 40% from the level of 20 years ago. These findings highlight the importance of protection of the spawning aggregations as one of the few occasions for their reproduction. Based on these findings and empirical information of local fishers, temporal closure of the main spawning ground for 5 days around the peak of spawning aggregation at the last quarter moon has been established since 2010. It was estimated that this 5 days closure would achieve from 5 to 10% decline in annual catches, based on the consistent catch patterns associated with the lunar cycle. Estimation using the virtual population analysis based on catch data and age structure of the landings from 2003 to 2011 showed that the short time closure could gradually restore the local population of *E. ongus* in the Yaeyama Islands.

Behavioral patterns in corallivorous butterflyfish vary according to dietary specificity and environmental Context

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Allocation of time towards essential daily tasks through which coral reef fishes obtain and expend energy is thought to be shaped by the demands of finding their preferred food within a complex reef environment while avoiding agnostic interactions. We explored the relative roles of dietary specificity (targeting specific corals versus more generalist preferences) and environmental context (front reef versus back reef) in shaping the time allocated towards different behaviors (e.g. travelling, searching, feeding, aggressive interaction, refuging) in four obligate corallivorous butterflyfish species from the Great Barrier Reef. Based on 3-minute video recordings of the routine behavior of these fishes at each site, we found specialist species (*Chaetodon trifascialis*, *C. plebius*) that predominantly fed upon corals of one genus tended to display disproportionately longer time on traveling than searching or feeding; more generalist species (*C. baronessa*, *C. lunulatus*) feeding on a wider range of corals tended to allocate equal time to travelling, searching and feeding. While subtle differences in behavioral partitioning by species were evident across front and back reef sites (where preferred coral availability is known to differ), the general interspecific pattern held true across a range of environmental contexts. Suggesting that dietary specialization has an overarching influence on the routine behavioral patterns displayed by these species, we explore how this advances our understanding of foraging patterns in coral reef fishes, and how various behavioral metrics influence our appreciation of how species invest in different daily tasks and resources.

A ligament influences the diversification of damselfishes (Pomacentridae)

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The Pomacentridae (damselfishes) is one of the most successful families of reef-associated fishes (386 species). In 1981, Stiassny described a synapomorphic trait of the Pomacentridae: the cerato-mandibular ligament (CML) joining the hyoid bar (ceratohyal) to the internal part of the mandible (coronoid process of the articulo-angular). Here, we highlight that this ligament is lacking in at least 18 damselfish species from different subclades (i.e. Chrominae, Abudefdufinae and Pomacentrinae) and we explore the impact of its disappearance on lineage, morphological and ecological diversification through their evolutionary history. Using a time-calibrated phylogeny including 208 species, we found no support for different rates of lineage diversification between species that lack the CML and the others. Yet, the CML clearly governs a part of the morphological diversity in damselfishes. Indeed, the body and mandible shapes differ significantly between species without CML and the others. Evolutionary modeling of some phenotypic traits (i.e. body and mandible shape) mainly supports models with two rates of morphological diversification across the time-tree with the species without CML having a higher rate of morphological diversification than the others. Mapping the diet of all studied species illustrates that damselfishes lacking CML are highly zooplanktivorous species. Their shapes suggest they feed on planktonic copepods with a higher contribution of ram-feeding (i.e. predator movement towards prey) in comparison with the other planktivorous damselfishes. Finally, the CML could have promoted easy shifts among the three main trophic guilds in damselfishes (i.e. grazers, zooplanktivorous and omnivorous) during evolution but the disappearance of the CML allowed a functional specialization linked to prey-capture strategies. These results support the primary role of the CML in the evolution and diversification of pomacentrids.

Common surgeonfish remove macroalgal recruits within the epilithic algal matrix of coral reefs

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Coral reef deterioration is often associated with blooms of benthic algae that lead to a phase-shift from a coral-dominated to an algal-dominated ecosystem state. Herbivorous reef fishes exert top-down control on algal biomass, productivity, and succession; thereby reducing the establishment and growth of algal communities that compete with corals for space and inhibit coral recruitment. Therefore, herbivory is widely acknowledged as a key ecological process that structures reef benthic communities and is important for the resilience of coral reefs. *Acanthurus nigrofuscus* is a widespread, abundant surgeonfish throughout Indo-Pacific coral reefs, and functionally classified as a 'grazer' that feeds upon algal turfs, tearing epilithic microalgal turf filaments from the substratum. Despite the prevalence of these diminutive surgeonfish on most Indo-Pacific reefs, little is known of their overall grazing impact on algal communities. Blooms of macroalgae require the establishment of new recruits, and it is a long-held, but untested, assumption that algal turf grazers remove macroalgal recruits from within the epilithic algal matrix. However, most studies have focused on the top-down control of adult plants. This is the first study to empirically evaluate the impact of a grazing reef fish on macroalgal recruits. Through aquaria experiments, we show that *A. nigrofuscus* remove macroalgal recruits (< 2mm, *Sargassum* spp.) from within the epilithic algal matrix in significant quantities. Therefore, it is possible that these surgeonfish contribute to reducing overall macroalgal cover and provide an important mitigation service against algal blooms on coral reefs. We also investigate the relationship between the initial recruit density and type of substrate attachment for the overall survivorship of macroalgal recruits when subjected to grazing. It is important to determine the nature of the top-down control of grazers upon algal recruits as part of a complete analysis of all the drivers that might promote or mitigate an algal bloom on reefs. Additionally, investigating the specific ecological role of key herbivorous fish species is essential for understanding reef resilience.

Diver surveys affect counts and behavioural response of fish across MPA boundaries

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Diving surveys are frequently used to count differences in reef fish abundance and size across boundaries of marine protected areas (MPAs). Fish behaviour is also observed to differ inside and outside MPAs as fish are often accustomed to divers within frequently dived MPAs and shy of divers and spearfishermen outside these boundaries. Nonetheless, fish behaviour towards divers is largely ignored when assessing the effectiveness of MPAs, with conclusions often attributed solely to absolute differences in abundance. To test how fish behaviour towards divers may affect conclusions about MPA efficiency, we compared three fish survey methods across two MPAs on the coral reefs of Guam, Micronesia. The three methods were: 1) Stereo video diver transects using conventional open circuit SCUBA diving, 2) Transects using closed circuit rebreather (CCR) diving, and 3) Baited remote underwater stereo video stations (stereo-BRUVS), a diver independent method. We observed differences in the counts of certain fish species and family groups between survey methods. While the use of a CCR unit which does not produce bubbles allowed the diver to approach closer to fish than when using an open circuit SCUBA diving system. We highlight that fish behaviour towards divers is expected to influence the counts of fish when comparing areas with different levels of dive tourism and fishing pressure and this should be acknowledged and minimised where possible.

The effects of sealevel rise on reefflat food webs

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The effects of sealevel rise on fishes are typically considered in coastal nursery habitat types, such as seagrass beds and mangroves. However, extensive Pacific reef flats are also particularly susceptible to changing sea level because they are adapted to functioning in very shallow water. Tidal fluctuations on reef flats of the Great Barrier Reef lead to water depths varying from >2m to <50 cm, driving profound changes in reef fish assemblages. For example, many larger species that are present at high tide migrate into deeper habitats during periods of very shallow water. Here we investigate the functioning of reefflat food webs over a tidal cycle by parameterising Ecopath models at three tidal states with sitespecific data from multiple locations across reef flats at Heron Island and Lizard Island (Great Barrier Reef). We quantify changes in fish assemblages using a combination of visual and video surveys stratified across tidal states, and use these data to build food web models for lowtide, midtide, and hightide scenarios. By focusing the models on changes in fish assemblages with natural fluctuations in water depth, we firstly demonstrate the significant spatial and temporal changes in fish food web dynamics over tidal cycles and with position in the reefflat seascape. Future sealevel rise will potentially lead to greater water depths at low tide, fewer changes in fish assemblages with tidal state, and less temporal variation in food webs. Consequently, we use the food web models to provide the first insights into the implications of this 'permanent high tide' on the food webs and fishing of reef flats. We demonstrate that the loss of a refuge from predation at low tide has the potential to unbalance the food web models for some taxa at some locations. For example, invertivores at the inshore site at Heron Island have the potential to be exposed to unsustainable predation if piscivores are able to remain on the reef flat throughout tidal cycles. These findings expand our ability to predict the effects of sealevel rise on reefs, and provide a novel example of how sealevel rise will affect reef fishes.

Effects of depth on the distribution, habitat use and specialisation of coral reef fishes

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Organisms exhibit distinctive patterns of distribution in response to a range of environmental gradients. A major goal in ecology is to explain these patterns in distribution along environmental gradients. For example coral reef fish communities are known to vary along gradients of depth and exposure. Depth is often a major source of variation in fish communities and has been shown to influence both diversity and composition. We examined the effects of depth on the distribution, habitat use and specialisation of coral reef fish communities. Depth explained considerable variation in reef fish assemblages. The depth ranges of species of Pomacentrids and Labrids were greatest for species with a mean depth of occurrence around the middle of the depth gradient surveyed and depth ranges became more restricted towards the extremes of the depth gradient. Niche breath decreased overall with increasing mean depth of occurrence, suggesting that deeper species were more specialised. When looking at taxonomic diversity and distinctness there was a decline with depth. Habitat use tended to match habitat availability apart from when looking at branching coral suggesting habitat availability may be an important driving factor in depth related patterns. This research suggests that depth can influence both the fish and benthic habitat present on reefs. Furthermore fish that occur at shallow depths as well as those at the deepest parts of the reef may be the most restricted in terms of their depth distribution, perhaps making them more vulnerable to impacts on the habitats within their favoured depth range. This could have important implications for their ability to seek a 'depth refuge' from increasing impacts and habitat degradation in shallow reef habitats.

13 years of expatriating tropical fish surveys: long enough???

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Major hotspots for climate-change effects on coastal seas are poleward extensions of western boundary currents. Rises in sea surface temperatures and extension of surface current influences can be linked to shifts in tropical species ranges. However, most research has involved modelling distribution changes of marine organisms such as fishes based on known physiological tolerances mapped against predicted environmental changes. Here we present results of a 13-year (and counting!) study of expatriating tropical fishes along the SE coastline of Australia. Many temporal and spatial patterns emerged, but although some examples of recruitment events of taxa such as chaetodons were directly linked with onshore movement of the East Australian Current (EAC), pulses of recruitment generally were not closely related to EAC strength, onshore wind strength etc. Also, while some species were consistent recruiters, each year had its unique suite of "one-off" species. Persistence of species varied, with most disappearing from southern sites around June-July. Some species were more likely to overwinter, some of which persisted through a number of winters. In particular, sites in Sydney (Latitude 34S) were of interest in monitoring overwinter success, given we have previously shown that an "overwintering threshold" of 18C exists, and Sydney winters fluctuate around this minimum. Overall, while recruitment of species has been less predictable against physical factors such as EAC strength and SST, overwintering appears somewhat more deterministically-related to winter SST, so may be a better predictor of future range shifts.

Review of the apogonid fishes (Teleostei: Perciformes) in Japanese waters

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Apogonidae is the fourth most speciose family among the Indo-Pacific reef fishes. During this study, 102 species of apogonids, including two undescribed species, are confirmed to occur in Japanese waters. Sixty-nine species are restricted to south of the Amami Islands, and 67% of all include Japanese species. *Apogon susanae* Greenfield and *Pseudamia rubra* Randall and Ida have been collected only from the Ogasawara Islands. *Apogon evermanni* Jordan and Snyder and *A.dispar* Fraser and Randall are known only from the Miyako Islands in the Ryukyu Islands. *A. franssedai* Allen et al., *A. hyalosoma* Bleeker, *A. lateralis* Valenciennes, *A. rhodopterus* Bleeker, *Archamia biguttata* Lachiner, *Pseudamia amblyuroptera* (Bleeker), and *P. zonata* Randall et al. occur only in the Yaeyama Islands in the Ryukyu Islands. The distribution of *Apogon lineatus* Temminck and Schlegel is extended north to Hokkaido, northern Japan. *Apogon fleurieu* (Lacepède), *A. chrysotaenia* Bleeker, and *A. hartzfeldii* Bleeker are recorded in Japanese waters for the first time; although the records of the latter two species are based only on underwater photographs. Two undescribed species of *Apogon* are found in Japan. A total of 133 specimens of *Apogon* sp. 1 were collected from the Pacific coast of Japan from Shizuoka to Kagoshima Prefectures. *Apogon* sp. 1 is most similar to *A. gularis* Fraser and Lachner in lacking stripes or spots on the body, but differs from *A. gularis* in having 7 (vs. 6 in the latter) 1st dorsal-fin spines, 20–24 (vs. 25–26) developed gill rakers, and 15 (vs. usually 14) pectoral-fin rays. *Apogon* sp. 2, previously mis-identified as *A. taeniophorus* Regan, is distinguished from *A. taeniophorus* in having the third body stripe curved upward posteriorly and joining the second stripe below the first dorsal fin (vs. third stripe not joining the second stripe in the latter) and the fourth body stripe extending beyond the caudal-fin base and reaching the caudal-fin margin (vs. fourth stripe ending at the caudal-fin base and forming a poorly defined large black spot). *Apogon* sp. 2 is known only from Shikoku and the Ryukyu Islands.

Ponyfish species survey from Peninsular Malaysian waters

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The ponyfish resources in the waters off the east and west coast of Peninsular Malaysia were conducted by several series of trawl surveys using commercial trawlers. The update of ponyfish species present in Malaysian waters is probably needed because the taxonomy of ponyfishes has changed dramatically in recent years. Specimens were examined for their morphological, light organ system and osteological features differences. The results showed that 20 species of ponyfishes were caught throughout the study. The number of fish species occurred in the east coast was 16 and west coast was 14. Furthermore, ten species were ubiquitous in the waters off Peninsular Malaysia. *Aurigequula fasciata*, *Aurigequula longispinis*, *Equulites elongatus*, *Equulites laterofenestra*, *Karalla daura* and *Secutor indicius* were found only in east coast. While *Gazza rhombea*, *Leiognathus robustus*, *Nuchequula blochii* and *Secutor ruconius* were existed only in west coast. The results showed that Malaysia harbours one of the richest assemblages of ponyfish species in the world, regardless of the East Malaysian waters.

Chrysophrys Quoy and Gaimard 1824, a valid generic name for Pacific species formerly used as *Pagrus* Cuvier 1816 and taxonomical review of the genus *Chrysophrys* (Perciformes: Sparidae)

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Fishes of the genus *Pagrus* are distributed in the Atlantic and Western Pacific Oceans (eg., *Pagrus pagrus* and *P. major*, respectively) and are also important commercial species in fisheries and aquaculture and are of significant sports fishing interest. These disjunctly distributed sparid species have long been considered as belonging to the same genus *Pagrus,* but recent genetic results strongly suggest non-monophyletic groups within the family Sparidae. Clear differences of cranium characteristics also suggest polyphyletic Atlantic and Pacific groups. The valid generic name for Pacific species is *Chrysophrys* (Quoy and Gaimard 1824: *C. unicolor*; type locality: Shark Bay, Western Australia). The Pacific *Pagrus* species have been variously recognized as a single species, *P. auratus* (Foster 1801), or as two species: *P. major* (Temminck and Schlegel 1843) for Red Sea Bream of the northern hemisphere, and *P. auratus* for Silver Sea Bream (snapper) of the southern hemisphere. A comprehensive geographic investigation of the generally disjunct antitropical populations (East Asia, Australia, and New Zealand) reveals variation in morphological characters and genetic differences. These three populations can be diagnosed by several meristic differences. Furthermore, different conditions of ontogenic hyperostification of the cranium were clearly observed among the three populations. The mtDNA (16S ribosomal RNA) clearly showed different haplotypes among three populations. Other mtDNA regions (cytochrome *b* [Cyt-*b*] and cytochrome oxidase I [COI]) also show mostly different haplotypes. We conclude that the northern and southern hemisphere entities should be recognized as separate species while the two populations in Australia and New Zealand should be recognized as subspecies. These are defined as *Chrysophrys auratus auratus* (Foster in Bloch and Schneider 1801) from New Zealand, *C. auratus unicolor* Quoy and Gaimard 1824 from Australia, and *C. major* (Temminck and Schlegel 1843) from East Asia.

Generic status of the genus *Dentex* (Perciformes: Sparidae) on the bases of morphological characters and genetic analysis

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We examined generic status of the sparid genus *Dentex* (type species: *Sparus dentex* Linnaeus 1758) on osteological and external morphology, as well as genetic analysis of all known species of *Dentex* and other six related genera (*Argyrozona, Cheimerius*, *Petrus*, *Polysteganus*, *Sparidentex,* and *Virididentex*) of the subfamily Denticinae. The genus *Dentex* comprises eight eastern Atlantic species (*D. angolensis*, *D. barnardi*, *D. canariensis*, *D. congoensis*, *D. dentex*, *D. gibbosus*, *D. macrophthalmus*, and *D. maroccanus*) and four western Pacific species (*D. abei*, *D. fourmanoiri*, *D. hypselosomus*, and *D. spariformis*). The species of the genus *Dentex* are characterized by four and six canine teeth at front of upper and lower jaws, respectively (10 in both jaws only for *D. macrophthalmus*), and one additional inner row of conical teeth on each side of both jaws. The genus *Dentex* was classified into three genera by the following morphological characters: squamation on preopercular flange and interorbital-bone region, conditions of dorsal-fin spines and lateral teeth, shape of posterior nostrils, hypersterophied circumstance of anterior frontal bone, configuration of dorsal ethmoid, abdominal part of parasphenoid, convex region of prootic, basioccipital, and exoccipital bones as followings: 1) *D. angolensis*, *D. congoensis*, *D. macrophthalmus*, and *D. maroccanus* from eastern Atlantic; 2) *D. abei*, *D. fourmanoiri*, *D. hypselosomus*, and *D. spariformis* from western Pacific; 3)*, Dentex. barnardi*, *D. canariensis*, *D. dentex* and *D. gibbosus* from eastern Atlantic. Phylogeny of mitochondrial cytochrome *b* gene strongly suggested that *Dentex* was a non-monophyletic group. Furthermore, the genetic fact of *Spicara alta* (Osório 1917)(the family Centracanthidae) is connected with 1)'s clade (ex. *D. macrophthalmus*). Only *Chemerius nufar* (Valenciennes 1830) should be presumably included in 3)'s group because *C. nufar* is contained within 3)'s clade, such strongly suggesting to need further study. Accordingly, the genus *Dentex* is divided into three following valid genera: 1) *Opsodentex* Fowler 1925 (type species: *Sparus macrophthalmus* Bloch 1791[=*D. macrophthalmus*]); 2) *Taius* Thompson 1912 (type species: *Chrysoprys tumifrons* Temminck and Schlegel 1843[=*D. hypselosomus*]); 3) *Dentex* Cuvier 1814 (type species: *Sparus dentex* Linnaeus, 1758[=*D. dentex*]).

Applying otolith morphology on sciaenid systematics

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Sciaenidae is characterized by having a pair of distinctly large and often thick otolith. Otolith morphology, especially the shape, thickness and sulcus mark on the inner surface of sciaenids are characteristic at genus or species levels, which are widely applied in systematics, fishery biology, trophic ecology, paleontology and archeology studies. However, the sciaenid otolith morphologies have not been systematically listed except in some otolith atlases. In total, 432 records attributed to 64 genera and 195 species of the sciaenids were documented; covering 97.0% of valid species (286) and 68.7% genera (66) world wide. Otoliths of 43 genera and 118 species are currently archived in the NMMBA for the Global Sciaenidae Conservation Network (GSCN). There are unique morphological patterns and characteristics to preliminarily group the sciaenids. Three genera found in the New World, *Cynoscion, Aplidinotus, Menticirrhus*, have thinner sagittal otoliths and the last genus which lost gas bladder in adults have thinner and smaller sagitta than the other two. The genera *Johnius* (Indo-Pacific) and *Stelliferini* (New World) have reduced sagitta and enlarged lapillus. Except for the species-specific characters, the sciaenid otoliths may also change ontogenetically. In order to quantify our observed patterns, the otolith dimension characteristics (ODC) and Fourier shape descriptors (FSD) are measured and analyzed with the photographed sciaenid otoliths archived at NMMBA, and the rest non-collected species will be supplemented from the existing atlases. The multivariate analysis will be applied for comparing the differences of ODC and FSD among genera and species to build up sciaenid systematization using their otoliths. The diagnostic keys using their otolith morphologies will also be established.

A review of the genus *Pempheris* (Pempherididae) from the Indo-Pacific Ocean

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The fishes of the Family Pempheridae are distributed on rocky and coral reefs of the tropical to temperate Indo-Pacific and western Atlantic. There exist two genera: *Parapriacanthus* and *Pempheris*, the latter currently reported with 37 nominal species, with 31 of them from the Indo-Pacific region. The genus *Pempheris* contains one of the most abundant nocturnal fish group in shallow waters, but its taxonomy was seriously confused. Totally 2,231 specimens including the types of 30 species were examined in 24 museums worldwide, and the base sequences of 16S ribosomal DNA were determined to reveal the phylogenetic relationships among the species. Five undescribed species were found from Daito Islands and Ogasawara Islands, Andaman Sea, Indian Ocean, and south western Indian Ocean. These species can be distinguished from other known species by differences in colorations, count characters, and measured characters. Six species were concluded to be invalid species within the 31 nominal species. The remaining valid 25 species could be separated into two groups by the definite scale characters. Six species belonging to the first group had strongly ctenoid, adherent, and divided into basal and distal halves scales. This group mostly consisted by endemic species from temperate Australia, except one species which was reported from the Northern Hemisphere (*P. japonica* Döderlein, 1883). Within the second group, 19 known species and five undescribed species had weak ctenoid, deciduous and semicircular scales. Most of them are distributed in tropical to temperate areas from the Indo-Pacific region. However in molecular analysis, the two endemic Australian species, *P. affinis* McCulloch, 1911 and *P. multiradiata* Klunzinger, 1879, which had scale characters of the second group, formed a monophyletic clade with the species of first group. Additionally, the sequences of the first group species were closer to the sequences of the species belonging to the genus *Parapriacanthus* than to the second group of genus *Pempheris*. The present results demonstrated the inherent necessity to separate the genus *Pempheris* into two genera: the first group should inherit the genus *Pempheris*, while a new genus name for the second group is needed.

A review of symphurine tonguefishes (Cynoglossidae: *Symphurus*) from Taiwanese waters

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Symphurine tonguefishes (Genus *Symphurus*) represent approximately 80 valid species of small-sized, left-sided flatfishes. *Symphurus* is the most speciose and widely distributed genus in the Cynoglossidae, which at present comprises three genera and about 130 species. Although the genus *Symphurus* has such great diversity, previous studies of symphurine species occurring in Taiwanese waters have been insufficient and have significantly underestimated the diversity of species occurring in this region. The brevity of research on *Symphurus* from this region likely results from a couple of factors. These species usually inhabit deep waters rendering it difficult to collect them in sufficient numbers to make definitive conclusions regarding their identity and taxonomic status. Lack of adequate information on these species may also be due to the inherent difficulties in species-level taxonomy of symphurine tonguefishes, especially in recognizing and determining boundaries between morphologically similar species. To help resolve taxonomic problems of *Symphurus* from Taiwanese waters, our study included numerous specimens curated in fish collections and also a number of specimens collected more recently during investigations conducted in Taiwanese waters by research vessels and commercial deep-sea trawlers. In addition to morphological information, also utilized molecular data to better understand the taxonomy and relationships of these species. Molecular tools, including comparisons of sequence differences between similar morphological nominal species, have been particularly helpful in resolving the taxonomy of some of these species, especially those represented by only a small number of specimens. To date, our results indicate that at least 11 species of *Symphurus*, including three possible undescribed species, occur in waters around Taiwan. This assemblage comprises three species featuring 12 caudal-fin rays (*S. orientalis*, an undescribed member of the *S. microrhynchus* species complex, and undescribed *Symphurus* sp.1), and eight species that possess 14 caudal-fin rays (*S. bathyspilus*, *S. hondoensis*, *S. megasomus*, *S. multimaculatus*, *S. strictus*, *S. undatus*, and two undescribed species: *Symphurus* sp.2 and *Symphurus* sp.3). Herein, we present diagnostic information for each nominal species, and discuss other long-term taxonomic problems involving nominal species of *Symphurus* form Indo-Pacific region.

New southern pacific species of bothid flatfishes (Pleuronectiformes: Bothidae:*Lophonectes*)

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On-going studies of marine fishes inhabiting waters around New Zealand have discovered numerous undescribed species, including several flatfishes new to science. Among flatfishes inhabiting these waters are several species previously poorly-known, but now represented by larger series of specimens, as well as several other nominal species currently residing in synonymy that should now be recognized as valid based on newly available data. Included in this latter category are members of the bothid genus *Lophonectes* Günther, 1880, originally created for *L. gallus*, based on specimens collected off southern Australia. *Lophonectes* is distinguished from other bothid flatfishes by the presence in mature males of several, elongate, anterior dorsal-fin rays and well-developed cephalic tubercles. Female *L. gallus* also have elongate anterior dorsal-fin rays, but these are shorter and fewer in number than those occurring in males, and females also differ in lacking cephalic tubercles that feature so prominently in mature males. *Arnoglossus mongonuiensis* Regan 1914, described from a small syntype series collected off the North Island of New Zealand, was later transferred to *Lophonectes*, and following that decision was later considered as a junior subjective synonym of *L. gallus* by most authors working with this species. Comparisons of 250+ specimens from off the main islands of New Zealand and southern Australia reveal that both nominal species are valid. Two other allopatric populations of specimens of *Lophonectes*, separated by 7001000 km from specimens of *L. mongonuiensis* occurring in coastal seas of the main islands of New Zealand, inhabit Wanganella Bank off northwest New Zealand and Raoul Island in the Kermadec Islands to the north of the North Island of New Zealand. Both of these populations are known from relatively few specimens. Comparisons of meristic and morphometric data indicate that all four allopatric populations of *Lophonectes* represent distinct species. In this review, redescriptions of *L. gallus* and *L. mongonuiensis* are provided, along with descriptions of two undescribed species. Additional information is provided on size and maturity, sexual dimorphism, and bathymetric and geographic distributions for all four species.

A new pufferfish of the genus *Torquigener* building "mystery circles" on a sandy bottom in the Ryukyu Islands with comments on other species of *Torquigener* (Tetraodontiformes, Tetraodontidae)

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Strange circles have been found on a sandy bottom at depths around 10 to 25 m in Amami-oshima Island of the Ryukyu Islands over the past 15 years. These "mystery circles" on the sea floor are relatively large, being about 2 m in diameter, and characterized by having double rounded edges and radiating troughs giving a spoke-like appearance. It has long been a mystery for local SCUBA divers; how are these mystery circles constructed and who builds them. Recently an underwater photographer had a chance to observe a pufferfish of the genus *Torquigener* building the circles. Following his observation, a team comprising TV staff and ichthyologists (including me) recorded the behavior of this pufferfish for about 4 weeks in July 2012. Although specimens have not been collected yet, beautiful underwater photographs of the pufferfish revealed that it is a new species clearly distinguished from other species of *Torquigener* by color pattern. The underwater observations have shown that circles are constructed by a single male of the new *Torquigener*. It usually takes about a week for the male to finish constructing the circle. A few days before the full moon or new moon, a female visits a circle to court with the male, and then spawns her eggs around the center of the circle. I hope to collect specimens of the new pufferfish soon so that it can be described. During the course of my study on this new pufferfish, taxonomic problems have been found in several species including *Torquigener balteatus* (Hardy, 1989). These taxonomic issues will be discussed.

Virtual access to the Australian fish fauna

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By world standards, the Australian fish fauna, with more than 5000 species, is large and diverse. A number of online projects developed in recent years now provide information on Australian fishes to a range of user groups – including scientists, students and teachers, divers and anglers, and the general public. The three volume Zoological Catalogue of Australia, Fishes, now online as The Australian Faunal Directory (AFD), represents the accepted classification of species names for Australian fishes. OZCAM, the Online Zoological Collections of Australian Museums, allows virtual access to the combined faunal collections of Australia's museums. The Atlas of Living Australia (ALA) aggregates and shares biodiversity information on Australian fishes from a wide range of data providers. Finally, Fishes of Australia, an initiative of many Australian fish taxonomists, is being developed as a one-stop shop for information, images, videos, maps and identification guides to the vast array of species inhabiting Australia's marine and freshwaters.

Species composition of fish eggs in the northwest Pacific

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In order to study on the spawning ecology of fish in the northwest Pacific, we collected fish eggs from 326 stations in June, 2012. And also we simultaneously measured temperature and salinity at the 3m depth. The range of temperature and salinity were 20.4~30.4°C and 31.53~34.69 psu, respectively. The 16SrDNA sequences were obtained from 444 single specimens out of 548 specimens collected. Based on the 16SrDNA sequences, the specimens were identified into 38 species including four unidentified species in fish, two species in squid, and three species in euphausiid. The temperature and salinity were more than 20.8°C and 32.25 psu in the sea area where fish eggs appeared. In major species including dominant species, *Encrasicholina punctifer*, the environmental feature was different according to the species in the sea area where they distributed. *E. punctifer* and *Acanthocybium solandri* were sampled in the places temperature and salinity were higher (> 29.1°C and > 34.06 psu), of which both variations were very narrow. Four species such as *Katsuwonus pelamis*, *Thunnus* sp., and two unidentified species were found in the range of salinity (34.06~34.69 psu) in contrast to wide range of temperature (24.3~30.4°C). Two species, *Auxis rochei* and *Coryphaena hippurus,* were distributed in the wide range of temperature (20.8~29.7°C) and salinity (32.25~34.56 psu). *Engraulis japonicus* was collected in the lowest temperature (20.8~20.9°C) and salinity (33.09~33.60 psu). This species-specific distribution pattern of fish eggs suggested that is to be a biological indicator to inform the marine environmental feature.

Biodiversity and DNA barcoding of cyprinid fishes in China

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There are about 800 freshwater fish species exist in China, most of which are members of Cypriniformes. Cyprinidae is the largest representative group of the Order Cypriniformes with 2000 species included in 12 subfamilies in the world, and among which about 530 species occur in China. These cyprinids include some of the most economically important freshwater fishes in terms of aquaculture, such as silver carp (*Hypophthalmichthys molitrix*), bighead carp (*Hypophthalmichthys nobilis*), grass carp (*Ctenopharyngodon idella*) and black carp (*Mylopharyngodon piceus*). For such a primary group in the fish fauna in China, we want to use the DNA barcoding to determine taxonomic identifications, explore biodiversity and establish phylogenetic relationships of the cyprinids. We choose all the available species of cyprinids to carry out the DNA barcoding research and construction of the phylogenetic trees. At present, two thousands and three hundred individuals from the four main river drainages in China have been sequenced (barcoded) for a 630 bp region of the mitochondrial cytochrome oxidase subunit I (COI) gene. These individuals represent 83 species in 63 genera. The average content of T, C, A, and G in these species and average Kimura two parameter (K2P) distances within-species, genus were analyzed to examine using of COI sequence to identify the cyprinid species. The phylogeny of cyprinids and identification of populations were also analyzed using the COI sequences. The present study is important for the conservation of aquatic diversity in China.

DNA barcoding of Western Indian Ocean fish species

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The International Barcode of Life programme (iBOL) is a multinational effort to assemble a standardized database of DNA sequences from known organisms to facilitate reliable species diagnostics and rapid assessments of biodiversity. The sequence of choice in vertebrate barcoding has been a 650-base pair segment of the mitochondrial cytochrome oxidase I (COI) gene. Previous studies with barcode data strongly support the contention that COI sequences are useful for the identification of fish species. The conservation of biodiversity and management of fisheries rely on accurate species identification to understand the diversity, dispersal and connectivity of fish populations. Here, we present recent results demonstrating the feasibility of DNA barcoding as a technique for identifying marine fish species in the Western Indian Ocean (WIO). We have assembled a database of over 2000 individual barcodes from several locations spanning the WIO region, most of them linked to vouchered specimens. The results show significant differentiation among genera and species. The genetic distances between conspecifics were on average markedly smaller than those between congenerics, allowing for the samples to be assigned to a particular species based on DNA distances. In an overwhelming majority of cases, the expert identification of the fish matched the barcode designation, suggesting that barcoding is indeed a reliable tool for identifying fish species in the region. We will discuss how barcoding can be used to resolve problematic taxonomic cases in combination with morphological analyses. We will also examine the utility of barcoding in resolving phylogeographic patterns in the region.

The new and improved Fishnet2

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FishNet2 (http://www.fishnet2.net) is an enhanced, cache-based version of the former distributed-database-query network. The enhanced platform gives researchers rapid access to data on specimen holdings in an expanding number of fish collections around the world. Over the past two years a number of additional improvements have been made to the underlying architecture, including geospatial query capabilities, improved result summaries, significant improvements to the UI, and an API that supports third-party integration. The data harvesting architecture for FishNet2 has been generalized as the Biological Object Search Service (BOSS) permitting the establishment of cache-based instances of two other popular vertebrate database networks (HerpNet2 and ORNIS2). A new project is allowing US institutions to collaboratively georeference global fish occurrence records within Fishnet2, using the collaborative georeferencing cyberinfrastructure of the GEOLocate Project. In this presentation, we describe and demonstrate all of the recent enhancements to Fishnet2, GEOLocate's collaborative georeferencing infrastructure and the ongoing collaborative georeferencing project, Fishnet2's new search capabilities, and the new kinds of research the network now supports.

Morphological Diversity and Function of Spiracular Organs in Elasmobranch Fishes

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Spiracle and its associated organs (termed here as "spiracular organs") of 24 elasmobranch species in eight orders, 18 families and 21 genera were examined from the point of comparative anatomy. Spiracular organs fundamentally consist of four elements, i.e. "external aperture" which is an opening on external surface of the head, "internal aperture (new term)" an opening inside the mouth, "spiracular tube (new term)" that connects external and internal apertures, and "spiracular caecum" a blind tube diverging from the spiracular tube toward the neurocranium. All species examined hade an internal aperture, and they were divided into the following three morphotypes, based on other three elements: 1) Simple type (with external aperture, internal aperture, and spiracular tube): *Heptranchias perlo*, *Squalus suckleyi*, *Isistius brasiliensis*, *Pristiophorus japonicus*, *Nebrius ferrugineus*, *Stegostoma fasciatum*, *Megachasma pelagios*, *Cetorhinus maximus*, *Isurus oxyrinchus, Rhynchobatus djiddensis*, *Gymnura japonica*; 2) Caecum type (with external aperture, internal aperture, spiracular tube, and caecum): *Heterodontus japonicus*, *Orectolobus japonicus*, *Cephaloscyllium umbratile*, *Proscyllium venustum*, *Mustelus griseus*, *M. manazo*, *Galeocerdo cuvier*; 3) Closed type (with internal aperture): *Carcharhinus brachyurus, C. limbatus, C. obscurus, Prionace glauca, Triaenodon obesus, Sphyrna zygaena*. Although spiracle has generally been considered to be related to the respiration, spiracular organs examined here might be related to the hearing, especially in the caecum type. Most of the morphological characteristics and functions of the spiracular organs have not been clarified, and further comprehensive studies need to be conducted.

A comparative study on osteological and morphological variations of three Indian cyprinids of genus *Puntius*

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The evolutionary relationship of the species of *Puntius* and the phylogenetic placement of the genus within the family cyprinidae and sub – family cyprininae provide pertinent fundamental systematics to meet the modern comparative research. The genus Puntius Hamilton (1822) is classified under the Cyprinid family which represented by a large number of species in the Asian tropics. Daniel stated that hill-stream fishes are indeed sensitive to certain environmental factors such as the levels of dissolved oxygen, temperature and velocity of the water. It has been observed that there are very minimal morphological variations between *Puntius filamentosus, Puntius faciatus* and *Puntius melanampyx* and it leads to taxonomic ambiguities. Hence a study has been conducted to resolve the taxonomic ambiguities between *Puntius filamentosus, Puntius faciatus* and *Puntius melanampyx* through morphology and osteological characters. Ten individuals from each species were collected from different locality and habitat type for morphology and osteological characterization. Principle Component Analysis (PCA) and Cluster analysis were performed using SPSS. total of 56 characters were considered for the Morphometry analysis, which included 30 characters related to body parameters and 26 characters related to meristic characters. The principal component analysis (PCA) and Cluster Analysis has been performed for grouping the species based on the morphological character. The PCA clustering of group shows that phenotypically very less variations between the species. The cluster analysis dendogram separates three groups clear like *Puntius filamentosus, Puntius faciatus* and *Puntius melanampyx* with 60.35% variance between species. In *Puntius filamentous* only maxillary barbels is present and in *Puntius faciatus* both Maxillary and rostral barbels are present. *Puntius filamentous* the lateral line count *is* 19 – 20 and in *Puntius faciatus* it is only 15 - 16. The Osteological analysis most of the characters show maximum similarity between this three species except Vertebral counts, Distance rudimentary arch & Epural and Hypural count. The vertebrate count in *Puntius filamentosus is 31,* in *Puntius melanampyx 30* and *Puntius faciatus* is *32;* the Distance between rudimentary arch & Epural in *Puntius filamentosus* is *3.4,*in *Puntius melanampyx* is *3.3 and* in *Puntius faciatus* is 2.9*;* Hypural count in *Puntius filamentous is* 6*,* in *Puntius melanampyx* is 7 and in *Puntius faciatus* is 6. The anal fin ray count various between these there species like *Puntius filamentous* is 5 *Puntius faciatus* is 6 and *Puntius melanampyx* 6*.* varies with the count in the anal fin (5, 6). Pelvic fin rays count of *Puntius filamentous* 8*, Puntius faciatus* is 9 and *Puntius melanampyx* is 7. There is a clear difference in the caudal skeleton between these three species. The *Puntius filamentous* is 15*, Puntius faciatus* is 13 and in *Puntius melanampyx* is 11. All the Osteological characters clearly exhibit the variations between the species and it helps to solve the taxonomic ambiguities between these species.

Phylogenetic relationships of lizardfishes (Synodontidae, Aulopiformes)

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The family Synodontidae, including 4 genera and ca. 57 species, are mostly known from sea bottoms of temperate and tropical regions in the Atlantic, Indian, and Pacific Oceans (Nelson, 2006). Phylogenetic relationships of the family were previously proposed by a few studies, which focused on relationships of the order Aulopiformes and included only a small number of synodontids. In this study, 13 representative species of Synodontidae and 3 species of Aulopidae, as an outgroup, were examined and osteological and myological characters in 74 transformation series were used in analyzing the phylogenetic relationships. A single most parsimonious tree was obtained (consistency index = 0.58, retention index = 0.69). The results confirm that the Synodontidae is monophyletic, supported by 12 synapomorphies, including 4 that have not been previously reported: the presence of vertebrae without the epiplurals, plural ribs or elongation of haemal spines; the basal portion of the first proximal pterygiophore of the anal fin slender; the infraorbital length shorter than the upper jaw length; and the origin of the adductor profundus on the actinost. Within the family, members of the genera *Saurida* and *Harpadon* were inferred to be unambiguously monophyletic with 4 and 9 unambiguous synapomorphies, respectively. In contrast, monotypic *Trachinocephalus* is deeply nested within members of *Synodus*, and thus, the latter is paraphyletic if *Trachinocephalus* is retained. Previous authors have not recognized the paraphyly of *Synodus*. Based on the reconstructed relationships, a new classification of the Synodontidae is proposed.

Morphological characters of *Hypopleuron caninum* (Ophidiiformes: Ophidiidae)

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The monotypic ophidiid *Hypopleuron caninum* is a rare Indo-West Pacific species that has been reported only on a few occasions since the original description by Smith and Radcliffe (1913). Without justification, Cohen and Nielsen (1978) referred *H. caninum* to the Neobythitinae, a morphologically variable subfamily that includes 40 genera and has no clear diagnosis. *Hypopleuron caninum* has extremely unique characters, including a canine tooth at the front of each upper jaw, and broad, inflated parapophyses inclosing the swimbladder. Especially, the latter character is unique within the Ophidiiformes. However, a detailed morphological description has not been published and relationships with other groups have not been constructed. The purposes of this study are to present the morphological characters of *H. caninum* in detail and to compare them with other ophidiids and ophidiiforms. As a result of the detailed observation, several other remarkable characters were recognized (e.g., slightly compressed basihyal, specialized shape of the urohyal, fused pelvic bones on both side, pelvic fins on both sides connected by membrane). These characters have not been reported in other ophidiids, but several characters (a canine tooth of upper jaw, shape of basihyal and urohyal, and connection of pelvic fins) are similar to those of *Pyramodon*, regarded as the most primitive genus in the Carapidae. This study compares morphological characters of *H. caninum* with those in carapid *Pyramodon* and other ophidiiform taxa in detail, and discusses its phylogenetic position in the Ophidiiformes.

Feeding apparatus comparison between *Chromis notata* and *Chromis fumea* from Jeju, Korea

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Damselfishes are widely distributed in tropic and subtropic waters, and this family is very diverse and largest group in coral ecosystem. Many researchers are consequently investigating about damselfishes in the various fields and recently trying to reverse-estimate their evolution history and phylogenetic relationship by using many studies, such as feeding strategy, trophic morphology and feeding ecology. *Chromis notata* distributed in mainly middle layer of all coasts including Dokdo in Korea whereas *C. fumea* only distributed in mainly benthic layer of coast in Jeju Island, Korea. Therefore, we established two hypotheses: (1) *C. notata* and *C. fumea* may be different feeding apparatus and (2) different dietary. In order to verify the hypotheses, we investigated the stomach contents and the jaw bones of the two species. In addition, stomach contents of *C. notata* between the two regions (Jeju Island and Dokdo) were compared. *C. notata* from two regions and *C. fumea* collected from Jeju Island in Korea were used. The shape of jaw bones (premxilla, dentary, articular and angular) varies considerably between two species. Also, *C. notata* eats randomly various prey whereas *C. fumea* seems to prefer benthic prey.

The use of otolith morphology in ichthyology

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Otoliths have been a standard tool for paleontological systematics since 1884. In neontological ichthyological work they have been used rather scarcely. The presentation gives a brief introduction of the general features and morphological terms of sagittal otoliths, main patterns and principle observations on functional morphology. A set of examples are shown highlighting both the additional value that can be gained from research of otolith morphology as well as potential pitfalls and limitations of their usage. Examples are: 1. Acropomatidae, showing two distinctly different otolith patterns; 2. a selection of otoliths from ophidiiform genera (*Diancistrus, Ogilbichthys* and *Porogadus*), exhibiting a combination of diverse and extremely similar sets of morphologies and potential pitfalls therewith; 3. a discussion on similarity and dissimilarity of otoliths of the genera *Polyipnus* and *Ichthyococcus*, as well as of *Hoplichthys* and the Gobioidei; 4. diversification of the otolith morphology observed in the genus *Diaphus* (Myctophidae); 5. observations on phylogenetic polarity observed in otoliths of the genus *Hymenocephalus* (Macrouridae). Otoliths are negatively effected by lengthy exposure to formalin. Therefore, it is advocated to extract otoliths from the right side of fishes early, before destruction by formalin, in order to secure a useful character for further research.

Muscular system in *Gasterochisma melampus* (Scombridae)

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The muscular system in the scombrid *Gasterochisma melampus* was studied in detail. Eighty-five elements, including subdivisions of components, are identified. This number is slightly less than those in a basal perciform (i.e., acropomatid *Malakichthys wakiyae*, 88 elements) and two other scombrids [*Scomber japonicus* (97); *Scomberomorus niphonius* (89)]. On the other hand, this number is more than that in *Thunnus orientalis* (82). Within Scombridae, *G. melampus* is unique in absence of the adductor hyomandibulae known thus far. Although it resembles *Scomber japonicus* in having the separated abductor profundus pelvicus, the flexor ventralis inferior and a subsection of the flexor ventralis, it differs from the latter in the followings: presence of the levator posterior; absence of the transversus dorsalis 1, recti dorsales 2-3, gill filament muscles 1-2, a subsection of the sternohyoideus, recti ventrales 1'-3' and spinalis. Other elements of the muscular system in *G. melampus* are also compared with those in other scombrids and their characteristics are discussed.

Importance of environmental and biological drivers in the presence and space use of a reef-associated shark

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As coral reef ecosystems come under increasing pressure from fisheries and climate change understanding how species that rely on these habitats respond to changes within their environment is increasingly important. The presence and movement of 28 grey reef sharks (*Carcharhinus amblyrhynchos*) were monitored for 15 months in the southern Great Barrier Reef to determine if presence and movement were related to environmental conditions. Testing of 28 models integrating activity space use, water temperature, atmospheric pressure, wind speed and rainfall and time (week or month) indicated no relationship between shark activity space and environmental parameters. Week was a significant factor in the top performing models with males showing increased activity space during weeks in September. These results suggest changes in movement were biologically driven, specifically related to mating, rather than environmental. Model results for presence of individuals in relation to environmental conditions also failed to indicate any patterns related to environmental conditions or time. These results indicate that *C. amblyrhynchos* are adapted to a wide range of conditions in coral reef habitats and that movement between or away from reef platforms is likely related to biological factors such as prey density, reproduction or dispersal, rather than environmental or seasonal changes.

Accelerometry estimates in a free-living, benthic elasmobranch, the Common Stingaree (*Trygonoptera testacea*)

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Estimating the metabolic rate is key to understanding physiological and behavioural ecology of animals. Quantification of energetics in elasmobranchs will provide information that can assist in addressing large-scale ecological questions (e.g. trophic relationships and production), as well as species-related ecological questions (e.g. physiological responses and behavioural modification relevant to environmental conditions). Recently, accelerometry has emerged as a means to estimate the energetic expenditure of animals in captivity, and in the wild. We coupled estimates of metabolic rate, determined in laboratory conditions, with field accelerometry data to estimate patterns of energy expenditure in free-living common stingarees (Trygonoptera testacea). By combining field accelerometry data with laboratory metabolic rate estimates, we may begin to grasp the underlying physiological causes of day-to-day, seasonal and annual behaviours in these animals.

Age, growth, and reproduction of the fanray, *Platyrhina tangi* in the northeastern waters off Taiwan

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Age, growth, and reproduction of the yellow-spotted fanray, *Platyrhina tangi*, were described from 681 specimens (465 females and 216 males, including 37 neonates) collected from Sep. 2009 to Nov. 2010 in waters off northeastern Taiwan. Annuli in ventral vertebrae form once a year and were counted up to 20 and 11 for females and males, respectively. The von Bertalanffy growth parameters estimated based on observed length at age data were as follows: asymptotic length ($L\infty$) = 59.3 cm total length (TL), growth coefficient (k) = 0.12/yr, theoretical age at 0 length ($t0$) = -1.83 yr for females; and $L\infty$=49.6 cm TL, k = 0.185/yr, $t0$ = -1.68 yr for males. The lengths at 50% sexual maturity were estimated to be 33.8 and 32.6 cm TL for females and males, which corresponded to 4.1-year-old. Mating and breeding season occurred from Nov. to Dec. and Oct. to Dec., respectively. Gestation period was estimated to be 12 months, but a six to eight months phase of embryonic diapause was taken into account. The reproductive cycle was also estimated to be once a year. Uterus fecundity ranged from 2 to 23 embryos (median = 8), and fecundity increased with the size of the mother ($N = -23.83 + 0.73TL$). Mean TL at birth of 37 neonates was 11.9 cm, and the sex ratio was not significantly different from 1:1 for embryos and neonates.

Analyses of stomach contents of four large shark species in the northeastern waters off Taiwan

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This study analyzed stomach contents of four shark species, the shortfin mako (*Isurus oxyrinchus*), pelagic thresher (*Alopias pelagicus*), bigeye thresher (*A. superciliosus*), and scalloped hammerhead shark (*Sphyrna lewini*) caught by long-liners from northeastern Taiwan waters and landed at Nan Fan Ao fish market between September 2009 and January 2011. Their dietary compositions were analyzed and compared in relation to the body sizes, sexes, mature stages and seasons. Total of 18 prey taxa were identified and indicated that the dolphin fish (*Coryphaena hippurus*) was the most important food item (IRI%=59.4%) of the shortfin mako (55.4% stomachs empty), and the followings were mackerels (*Scomber spp.*) and hair-tail fish (*Trichiurus spp.*). For the pelagic thresher, there were 49.3% stomachs empty, and a total of 26 prey taxa were identified and indicated that hair-tail fish was the most important food item (IRI%=91.71%). The next items were mackerels and Pacific pomfret (*Brama japonica*). There were 27 prey taxa identified and indicated that hair-tail fish was the most important food item (IRI%=59.4%) of the bigeye thresher (54.6% of stomachs empty), and the next items were oilfish (*Lepidocybium flavobrunneum*) and Pacific pomfret. For the hammerhead shark, there were 73.2% empty stomach, and a total of 16 prey taxa were identified and indicated that cephalopods were the most important food item (IRI%=29.72%). The next items were unidentified teleosts and mackerels. The Pair-wise comparison was applied for different size classes, and dietary shift along with growth was detected. The dietary compositions were not significantly different between sexes for all four species. The dietary compositions were significantly different between immature and mature stages for all four species. And the dietary compositions were significantly different among seasons for *I. oxyrinchus* (summer/other seasons), *A. pelagicus* (spring/summer), *A. superciliosus* (winter/spring and summer), *S. lewini* (spring/autumn). Nevertheless, our study shows that the distinction of dietary compositions in different species also by fishing ground.

Stable isotope and signature fatty acid analyses show reef manta rays snack on surface zooplankton and feast on demersal zooplankton

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Assessing the trophic role and interaction of an animal is key to understanding its general ecology and the dynamics of its community. Conventional techniques, such as stomach content analysis, used to elucidate diet are not suitable for large threatened marine species. Non-lethal biochemical methods provide a practical alternative for investigating the feeding ecology of these species. Based on daytime field observations, reef manta rays (*Manta alfredi*) have been widely assumed to feed on near-surface zooplankton during productive events in coastal areas. This has been assumed to be their primary food source. Stable isotope and signature fatty acid analyses of muscle tissue were used for the first time to examine the assimilated diet of the reef manta ray, and were compared with different zooplankton functional groups (i.e. near-surface zooplankton collected during manta ray feeding and not-feeding events, epipelagic zooplankton, emergent zooplankton and several different zooplankton taxa). Stable isotope $\delta^{15}N$ values and the occurrence of elevated levels of the fatty acid trophic marker for carnivory (18:1ω9) confirmed that the reef manta ray is a secondary consumer. Near-surface and epipelagic zooplankton fatty acid composition indicate they had a dominant flagellate-based food source with high levels of docosahexaenoic acid. The reef manta ray had relatively high levels of docosahexaenoic acid also indicating a flagellate-based food source in the diet. However, high levels of ω6 fatty acids and slightly enriched $\delta^{13}C$ values in reef manta ray tissue suggest that the species do not predominantly feed on near-surface pelagic zooplankton, but rather obtain a major part of their diet from another origin. The closest match is with demersal zooplankton, suggesting it is an important part of the reef manta ray diet. The ability to feed on demersal zooplankton is likely linked to the horizontal and vertical movement patterns of the reef manta ray. These new insights into the habitat use and feeding ecology of the reef manta ray will assist in the effective evaluation of its conservation status.

Long-term observation of the clasper development and the serum concentration of testosterone in captive male whale shark at maturity

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The clasper development and the serum concentration of testosterone of a captive male individual of whale shark were observed to obtain maturity and reproductive information. Material examined for this research was a male kept in 7500m3 tank in Okinawa Churaumi Aquarium for over 17 years. We have monitored the clasper elongation by examining the ratio of the clasper outer length (COL) to the pelvic inner margin (P2I) since March 2005. The ration of COL/P2I began to increase slowly at 8.5 m TL (1.09 in August 2011), and rapidly increased to 1.60 within 11 months (July 2012). However, there was no further clasper elongation since July 2012. In addition, the morphological transformation of the clasper was observed. Those facts indicate that the clasper elongation and development were occurred at about 8.5 m TL, and in consequence, the individual has attained maturation at this size. The serum concentration of testosterone by the time-resolved fluorescent antibody technique (TR-FIA) reveal that the increase of the testosterone was recognized in June 2011 (11.45 ng/ml), and it was maintained in higher level of its concentration for one year to June 2012 (21.49 ng/ml). However, it was reduced to lower level after July 2012 (8.42 ng/ml). These hormonal trends corresponded approximately to duration of rapidly clasper elongation. Additionally, we observed behavioral change that the whale shark rotated laterally its entire body with crossing both claspers from April 2012. We estimate that this whale shark has also reached behavioral maturity. In this aquarium, we will promote the reproduction success in this species in captivity and aim to clarify its shadowy reproduction.

Difference between philosophy of conservation of organisms between Japan and other countries

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I have been appointed as the Regional Vice-Chairman of Shark Specialist Group, IUCN since 1994 and have been studying how we conserve biodiversity of nature. In the meantime, am aware that philosophy how we conserve nature is different between Japan and other countries. Philosophy of majority of Japanese people for conserving nature might be almost equal to international trends, but that of Japanese public institutions is not the same, which has lead the history of argument between foreign countries and mainly Fisheries Agency of Japan. The author will clarify the history of argument and discuss how we solve this problem.

Hook vs Net : The influence of gear type on shark population surveys

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A major challenge in undertaking marine faunal surveys is to capture a true representation of the target communities. For marine fishes, the associated bias of sampling gear compounds this issue. In this study, following a faunal survey of sharks and rays within subtropical Hervey Bay, Queensland, Australia, the composition of species sampled when using a set line was compared to the species composition sampled when using a gill net. The set line and gill net captured significantly different assemblages of species (ANOSIM, $P < 0.05$), with the set line capturing significantly larger animals and an overall higher species diversity. In comparison to a theoretical assemblage of species, based off species likely to inhabit Hervey Bay, the gill net captured an underrepresentation of the theoretical assemblage of sharks and rays (TAXDIST, $P < 0.05$). The species captured by the set line and by both gears combined, provided a non-bias representation of the species that were likely to inhabit Hervey. Additionally by deploying both gears simultaneously, a higher diversity of sharks and rays was captured. Given the different suite of species and size classes that were captured by both gears, future studies should give considerations to the key questions driving specific faunal surveys. These include the target species or groups, the size-class of target animals and the timeframe for the assessment.

Latitudinal variation in mating competitiveness and mate chooosiness in the Japanese medaka

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Latitudinal clines in sexual dimorphism have been reported in some taxa. Although it has been hypothesized that these clines reflect latitudinal clines in the strength of sexual selection pressure, there is no research on latitudinal variation in mating behaviors that supports this view. In the Japanese medaka (*Oryzias sakaizumii* and *O. latipes*), lower-latitude populations are more sexually dimorphic than higher-latitude populations, suggesting stronger sexual selection pressure at lower latitudes. In this study, male mating competitiveness and females mate choosiness were compared among three latitudinal populations (Aomori, Tsuruga, and Okinawa). Laboratory mating experiments revealed that males from lower-latitude populations show more frequent fighting and courtship behaviors than males from higher-latitude populations. On the other hand, females from lower-latitude populations refused male courtship more frequently and spent a longer time on accepting a male than females from higher-latitudes. These results suggest that lower-latitude males and females are more competitive and choosy, respectively, supporting the view that sexual selection pressure is stronger at lower latitudes. Furthermore, phenotypic and genetic correlations among the behavioral and sexually-dimorphic traits were examined to discuss if behaviors and morphology can independently evolve in response to the latitudinal difference in sexual selection pressure.

Temporal sharing of spawning area between two species of the family Lutjanidae, Symphorichthys spilurus and Lutjanus bohar in southern Palau

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Symphorichthys spilurus(Ss) is a species of the family Lutjanidae, widely distributed in tropical to subtropical western Pacific. *Lutjanus bohar(Lb)* belongs to the same family of *Ss*, distributed widely in Indo-Pacific regions. We reported on the huge aggregation of *Ss* for spawning, at a point of southern reef of Peliliu Island, Palau. We have observed *Lb*'s spawning behavior in the same area for 4 years, from 2009 to 2012. *Lb* showed similar spawning behavior with *Ss* and they share the same site area for spawning. However, we found some differences in the mode of spawning between the two species. Firstly, *Ss* aggregated twice a year, in February to May and September to November, but *Lb* aggregated every month. Secondly, in the aggregation of *Ss*, there are more than one hundred-thousand individuals while that of *Lb* are less than ten thousands in their aggregation. Thirdly, *Ss* spawns at half moon to before new moon, *Lb* spawn at before full moon. Fourthly, the distance between the spawning area and the resting area. Both species rest in the area with weak current between first and second or the following spawning. *Ss* rest in eastern reef which is far(ca. 1500m) from the spawning area, on the contrary, *Lb* rest in western reef which is close(ca. 500m) to the spawning area. We are surveying difference in early life history between two species to clarify the mechanism of temporal sharing of spawning area.

Indirect effects of the cleaner fish *Labroides dimidiatus* on the coral reef benthos

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A recent experimental manipulation of the cleaner fish *Labroides dimidiatus* at Lizard Island, Great Barrier Reef, showed that the abundance and species richness of resident and visitor fish, and abundance of visitor herbivore fish (Acanthuridae) is reduced on patch reefs maintained free of cleaner fish for 8.5 y (removals) compared with controls. To determine whether cleaner fish presence subsequently indirectly affects the benthos, we examined fouling material on settlement tiles over 3.5 months, estimated the composition of the benthos, and recorded the foraging bites of visiting herbivores. Organic weight (log10) of fouling material on settlement tiles differed according to an interaction between cleaner presence, site, and the covariate dry weight (log10) ($P<0.05$); this was due to a difference in the slopes between organic and dry weight at the Lagoon site: with more organic weight on removal compared with control reefs, but only on tiles with low levels of dry weight of fouling material. This suggests cleaner presence may indirectly affect fouling material on settlement tiles at one site. The percent cover of dead coral was higher on removal reefs ($P<0.05$), whereas there was no effect of cleaner presence on live coral or algae (both $P>0.05$); however, live coral cover was higher on reefs at the Casuarina Beach compared with Lagoon site, whereas algal cover was higher at the Lagoon site (both $P<0.05$). Individual foraging rate among visitor herbivore species (*Acanthurus* spp., *Ctenochaetus striatus, Scarus globiceps, Scarus rivulatus, Siganus doliatus*) did not differ with cleaner presence nor between sites (both $P>0.05$), but did differ among species and with fish size (both $P<0.05$). On control reefs, foraging was not correlated with cleaning time within the two species with the largest sample sizes (*Acanthurus* spp., *Ctenochaetus striatus*) ($P>0.05$). These data suggest that individual foraging behavior is not affected by cleaner presence. This study demonstrates the potential for subsequent indirect ecosystem-wide effects of cleaner fish, on coral reefs systems.

Reproductive behavior and habitat modifications of a temperate reef fish *Chromis crusma* (Pisces: Pomacentridae)

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Structures built by animals provide useful information of processes that occur at population level. Variation in behavioral traits may be observed as phenotypic traits that are shaped by sexual and natural selection. Using standardized ecological sampling of benthic substrata and underwater video recordings, we assessed the habitat modifications, nest formation, and parental care performed by an abundant temperate reef fish, *Chromis crusma*. As in many pomacentrids nests are generated by males, which subsequently provide care to developing young. The nest had the lowest number of benthic species. The number of species in the benthic substrata determined the quality of the nest. In turn, nest with filamentous green or red algae had the highest percent cover of eggs. Using video recordings, we provided evidence of parental care. Male individuals spent most of the time inside the nest, aerating the eggs with the fins and the mouth, removing unwanted materials and defending the nest against conspecific, heterospecific, and other predators. One-oil globule and adhesive filaments characterize the collected eggs that hatched after 7-8 days in the laboratory. Larval growth rate is slow which characterized many temperate reef fishes of the region. The reproductive behavior of *Chromis crusma* had many similarities with other species that inhabit in other temperate regions. The importance of this behavior (nest builder, parental career) in the region is discussed.

Wrasse mating sites and systems in relation to fish feeding stations

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A number of species of wrasses (Labridae) utilize specific sites for courtship and spawning, either in an haremic mating system or in temporary resident spawning aggregations. These sites are usually distributed in discrete locations. At Apra Harbor, Guam, haremic mating sites are distributed along the edge of a reef slope at discrete intervals, are defended by terminal-phase males, and mating groups consist typically of 2-6 females for most species. At Finger Reef, a protrusion into the harbor at the western end of the reef slope, a spawning aggregation site exists for thirteen species of wrasses. Some species, such as *Cheilinus trilobatus, Cheilio inermis*, *Epibulus insidiator, Hemigymnus melapterus*, *Novaculichthys taeniourus*, *Oxycheilinus unifasciatus*, and *Thalassoma trilobatum*, court and spawn in relatively low numbers, either as pairs or small haremic groups within the spawning aggregation site. This site is also popular with groups of scuba divers that frequently feed fishes at this site. Our data indicate that the numbers of terminal-phase males, and initial-phase males and females of a number of species, but especially *Thalassoma hardwicke* and *Gomphosus varius*, are significantly higher than in non-feeding areas of the reef. In addition, there is a marked increase in both male-male territorial interactions in a lek-like system and also in sneaking during spawning events. The increased abundance of fishes and corresponding behavioral interactions are likely the result of fish-feeding at this spawning aggregation site. The shift in mating system as a consequence of this increased abundance, and hence density, confirms previous predictions about the choice of mating system used relative to local population density. In addition, egg predation rates by planktivorous fishes are greater at the fish feeding site and this affects spawning success of courting wrasses.

Reproductive behaviour and site-fidelity in a coral reef fish (f. Apogonidae)

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For many terrestrial and avian species a strong link between reproductive parameters, such as reproductive behaviour and output, and habitat use in the form of habitat selection, site fidelity and movement rate has been established. In marine systems however there have been few studies addressing this topic, despite the fact that in ecosystems such as coral reefs there is a known, intimate relationship between fish and their habitat. Cardinalfish (family Apogonidae) are one of the most abundant and speciose fish families on coral reefs and play an important ecological role. Studies conducted in temperate regions or rocky reef areas indicate that their reproductive behaviour shows great diversity and is particularly interesting in terms of parental care and gender allocation. They are paternal mouthbrooders in which females have a higher potential reproductive output which may lead to a biased operational sex ratio (OSR) and reversed gender roles. This paper explores the relationship between the reproductive behaviour of a common cardinalfish species from tropical coral reefs and the fishes habitat use, particularly in relation to the its site fidelity. 105 Ostorhinchus cyanosoma on the central Great Barrier Reef were tagged and observed over 5 weeks during which displacement and mate removal experiments were conducted. Control fish typically formed monogamous, lasting pairs throughout the study period. Although the OSR was not female biased, females were larger and more aggressive indicating that males are the choosier sex and a reversed gender role operates in this species. However, in general, gender had very little effect on mating behaviour and habitat use. Site fidelity and homing success differed with a fish's social status. Paired individuals showed three times higher site fidelity than single ones and when mates were removed, movement of the isolated individuals increased two fold. Mate availability at the study location appears to limit reproductive potential of the local population. Differences in site fidelity and mating frequency among genders remain likely for other coral reef cardinalfish species. Greater flexibility in site during use by individuals that are searching for a mate may enhance their adaptive capacity to respond to loss of breeding and resting sites.

Coral trout choose the most effective moray collaborators

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Recent groundbreaking research found that chimpanzees choose appropriately when and with whom to collaborate. This finding was taken to indicate that these two cognitive abilities that are key to human cooperation were present in our common ancestor with chimpanzees. However, an evolutionary view of cognition predicts that such abilities may have evolved in wide variety of taxa with an ecological need for them. One such taxon is fish of the genus *Plectropomus,* which hunt collaboratively with moray eels on coral reefs in the Red Sea and Great Barrier Reef. Plectropomids uses a characteristic shimmy signal to initiate a joint hunt and complement the eel's ability to access prey hidden in crevices with their speed in the open. We used aquaria experiments to determine whether the coral trout *Plectropomus leopardus* can choose appropriately: 1) when a situation requires collaboration, and 2) which individual morays are most skillful at helping it hunt. In experiment 1, coral trout were presented with two situations: one where a prey fish could apparently be reached alone (solo condition) and another where the prey was hidden in a crevice (collaborative condition). Coral trout recruited a model moray eel more often in the collaborative than solo condition. In Experiment 2, coral trout could choose between two model morays to help them flush out hidden prey. One moray was designated the skilled collaborator, and would move directly to the prey if recruited by the coral trout, whereas the moray designated as unskilled would move away from the prey if recruited. Coral trout quickly developed a preference for recruiting the skilled collaborator. Our findings demonstrate that fish can choose appropriately when and with whom to collaborate: skills that are evolutionarily convergent with those of great apes. This cautions against interpretations of shared evolutionary ancestry based on behavior alone.

Spawning migration and homing pattern of white-streaked grouper *Epinephelus ongus* determined by acoustic telemetry

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White-streaked grouper (*Epinephelus ongus*) is an important fisheries target and forms spawning aggregations at particular spawning grounds in the Okinawan region, Japan. The aims of the present study were to investigate the reproductive movement to spawning aggregations such as departure timing from the home ground, the duration of remaining in the spawning ground and the homing pattern just after the spawning events by using acoustic telemetry. Among the 30 individuals, three types of movement pattern were observed: type 1) high site fidelity to the release area was observed before the spawning migration, migration to the spawning ground and remaining there during the spawning period and then returned to the release area (home ground) just after the spawning period (17 individuals); type 2) high site fidelity to the release area was observed, disappearance from the area during the spawning period but was not detected at the spawning ground and then returned to the release area (8 individuals); type 3) high site fidelity to the release area was observed before, during and after the spawning period (5 individuals). For the 17 individuals that were categorized into type 1, the dates of departure from their respective home grounds and the dates of return to the release area of males were significantly earlier and later than those of females, respectively. As a result, the duration between the departure date and the return date (duration away) of males was significantly longer than that of females. Although it was not significant, the "duration away" tended to be positively related with condition factor [(weight, g) / (total length, cm)^3 ×100] for males. The results of the present study firstly showed the reproductive movement and homing ability of white-streaked grouper by using acoustic telemetry. It is suggested that the duration of protection of the spawning ground should be considered based on the migration activity of males. Since *E. ongus* showed a strong homing ability, intense commercial fishing of the spawning aggregation would cause the population size to decrease in their home ground areas.

A biomechanics approach to feeding ecology of fish in the wild: an animal-attached gyroscope/accelerometer for detecting the different feeding behaviors of white-streaked grouper *Epinephelus ongus*

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Generalist predators are assumed to have evolved to feed on different prey items, depending on the prey compositions and environmental constraints, in a way that maximizes their fitness. Many predatory fishes forage on more than two types of preys (i.e. crustacean and fishes); therefore, they are assumed to switch prey items depending on the context. However, due to the lack of the monitoring method for detecting feeding events, there is little knowledge on when and how the predatory fishes switch prey items. In this study, we have tested the applicability of an animal-attached inertial sensor (gyroscope and accelerometer) for detecting the feeding events of a generalist predator, white-streaked grouper, on different prey items (crab and fish). The seven groupers tagged with inertial sensors were kept in an aquarium tank, and fed with crab and fish. In order to test whether the method can accurately classify the behaviors, we also recorded an escape response which is, at a glance, similar to the feeding behavior. In total, we have obtained 54, 38 and 33 events on crab feeding, fish feeding and escaping. The movement patterns were apparently different among the two feeding behaviors, escape and routine activity. During the feeding on a crab, the grouper inclined and picked the prey at a low speed; during the feeding on fish, the grouper attacked at a high speed in a linear manner; during the escape, the grouper bended in a C-shape at a high speed and then moved forward by a return tail flip. These different movement patterns were clearly reflected in the obtained data: there were significant differences in the derived parameters such as ranges of acceleration and angular velocity between the behaviors (ANOVA, $P < 0.01$). In the presentation, we will discuss the accuracy of the classification using a combination of different parameters.

Behavioral study of a facultative air-breathing fish, *Praealticus tanegashimae* (Blenniidae) on tide-pools of Kuchierabu-jima Island, southern Japan

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Air-breathing fishes provide valuable data discerning the evolutional background of adaptation to terrestrial environment of aquatic animals. However, biological reports on the air-breathing fishes based on field study still have been limited. The rock skipper blenny *Praealticus tanegashimae* are commonly found on tide pools in subtropical water areas, including Kuchierabu-jima Island. In the process of the field observation of *P. tanegashimae* on rocky pools of the island, we found that the blenny often crept up from the water. To investigate how *P. tanegashimae* goes out of water, we conducted field observation in June - October 2012. We found that *P. tanegashimae* frequently showed an inspection-like behavior as making the head-part leaning out of the water. Some individuals of *P. tanegashimae* went their whole bodies out of water, and sometimes jumped into adjacent pools subsequently. Mean duration of each landing event of the blenny was 129 sec (n = 32; max over 10 min). The blenny maintained mating nests on rocky substrates underwater, and it showed feeding behaviors at the bottom of pools. Therefore the ecological habits of *P. tanegashimae* seem to be basically close to underwater blenniid species, but it occasionally goes out of water. We discuss why *P. tanegashimae* use space out of water, with showing data of the ecological conditions of the tide-pool habitats.

Homing behaviour in intertidal gobies: Linking brains, behaviour and ecology

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The ecological cognition hypothesis postulates that the brains and behaviour of animals is shaped by the challenges they face in their every-day lives. Here we examined the site fidelity, homing behaviour and brains of five species of intertidal fishes in Sydney. Three of the species we examined are intertidal residents spending their entire lives in rockpools, while the other two species temporarily inhabit rockpools during early ontogeny before shifting to alternative habitats. Our data revealed that rockpool residents show very high site fidelity compared to non-residents, with most resident individuals still present in their home pool 42 days after tagging. Fish were subsequently displaced distances up to 30m from their home pool and we monitored homing behaviour. Resident fish show very high rates of homing behaviour with the majority of displaced fish returning to the home pool. Nonresidents, however, showed much poorer homing abilities. Examination of the brains using a range of imaging techniques revealed that resident species had relatively larger telencephalons compared with non-resident species. This brain region is known to be involved in spatial learning in fishes. Evolution has clearly favoured enhanced spatial learning in intertidal rockpool species and this ability is underlined by the appropriate cognitive hardware.

Habitat utilization pattern in the Picasso triggerfish (Tetraodontiformes*:* Balistidae) from Sesoko Island, Japan

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The colorful Picasso triggerfish (*Rhinecanthus aculeatus*) is widely distributed throughout the tropical and subtropical seas of the Indo-Pacific. This species has no commercial importance as a food resource but is locally harvested for ornamental reasons. Triggerfishes (Balistidae) are notable for their specialized mating systems and parental care (e.g. aggressive behavior). Adult Picasso triggerfish are polygynous and establish long-term territories in flat reef areas and shallow lagoons. There have been no studies about specific habitat preferences and utilization during their development. In order to understand behavioral responses at different life stages, explicit patterns of distribution and size-specific microhabitat requirements were investigated in a triggerfish population on a fringing reef at Sesoko Island, Okinawa. The population in the established study area was monitored from November 2012 and comprised of individuals at various sizes and different life stages. Movements and behaviors of individuals were directly measured by following marked fish (using polyethylene streamer tags). On Okinawa Island, spawning of the Picasso triggerfish occurs within individual territories between May and September. Generally, newly arrived settlers are most numerous from August to September and can be found in shallow coastal areas around the island. After settlement, metamorphosed juveniles subsequently grow over the summer and autumns months and reduce their growth during the colder season. In the study area, the last settler arrived in November 2012. Both settlers and juveniles showed strong site fidelities, had small home ranges and were strongly associated with shelters and refuges in the near shore rocky area. With increasing size, juveniles shifted to adjacent sandy habitats interspersed with live corals and were thereafter called recruits. Typically, these recruits were non-territorial, varied greatly in size and tended to aggregate at two specific sites. Adult males and females were found in the more distant flat reef area within their well-defined territories. Recruits are thought to be spatially restricted to habitats unoccupied by territorial adults. It is suggested that the Picasso triggerfish population is strongly influenced by size-dependent processes and corresponding habitat preferences. The observed zonation in habitat utilization might be related to ontogenetic habitat shifts and subsequent maturation.

Spawning behavior and paternal egg care in a circular structure constructed by a puffer, *Torquigener* sp. (Tetraodontidae)

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We have reported that a small male puffer *Torquigener* sp. constructed a huge geometric circular structure, a nest site surrounded by radially aligned peaks and valleys, for reproduction on the seabed. Here, we report spawning behavior, parental egg care and periodicity of reproduction of the puffer based on underwater observations carried out off southern Amami-Oshima, Japan from April 2011 to September 2012. When the circular structure was completed, females visited the structure to inspect the nest site. The male bit the female on the side of her body, and subsequently the male and female touched their abdomens on the bottom and vibrated their bodies. The female left the nest site, but soon came back again. This behavior was repeated several times. The male stayed at the nest site and cared for the eggs deposited on the bottom. He cared for the eggs by flapping his fins, thereby stirring the sand (and attached eggs), removing garbage that had washed into the nest, and driving away fishes that intruded into the nest. The paternal egg-care continued for 6–7 days until hatching, which occurred after sunset. Spawning and hatching occurred around neap and spring tides respectively, indicating that spawning cycles in the puffer are semi-lunar.

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The historical biogeography of coral reef fishes: global patterns of origination and dispersal

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The world's largest marine biodiversity hotspot is centred in the Indo-Australian Archipelago (IAA). To date, much of the study on this hotspot has concentrated on processes that maintain species richness within the hotspot. Less emphasis has been placed on the origin of biodiversity and evolution of taxa that form the hotspot. Ancestral range reconstruction of the coral reef fish families Labridae, Pomacentridae and Chaetodontidae reveal marked temporal congruence in inferred origination and dispersal of lineages between the East Pacific, Atlantic, Indian Ocean, the IAA hotspot and Central Pacific regions. The East Pacific and Atlantic have a history of isolation, developing from broader connectivity with the Indo-Pacific from the early Eocene. The IAA has a history of connectivity with adjacent regions. It has sequentially and then simultaneously acted as a centre of accumulation (Palaeocene/Eocene onwards), survival (Eocene/Oligocene), origin (Miocene onwards), and export (Pliocene/Recent) for reef fishes. While association with coral reefs may provide a mechanism for the cladogenesis of several reef fish lineages in the Miocene, it appears to be the unique attribute of expanding reef habitat in the mosaic of island archipelagos in the IAA hotspot that has allowed the survival, proliferation and expansion of coral reef fish lineages to form the hotspot that we see today.

A phylogeographic approach to cataloguing marine biodiversity in the Red Sea

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The Red Sea is one of the most understudied areas in the world in terms of marine biodiversity, and yet the high level of endemism indicates that additional evolutionary partitions await discovery. Here we present preliminary data from the first stages of a broad-scale survey of reef organisms employing modern (molecular) taxonomic and phylogeographic approaches at multiple sites along 2000 km of Saudi Arabia's Red Sea coastline. This coast is unique in that it consists of extreme latitudinal gradients in water temperature, salinity, and nutrient load that may act as an ecological barrier to larval dispersal and the eventual settlement of marine fauna. For fish, the distribution and abundance of species from more than 30 families based on visual censuses indicate that there are apparent partitions representing ecological barriers that may arise from these gradients. We have also identified several new reef fish species as being genetically distinct from their Indian-Ocean counterparts or highly differentiated between the Northern/Central Red Sea and Southern Red Sea regions. We will present a few case studies of these fishes as well as other reef-associated organisms. We highlight how this collaborative project will provide a scientific foundation for establishing MPA networks, maintain representative examples of biodiversity in each region, and preserve source populations that may act to replenish coastal stocks, information currently unavailable in Saudi Arabia and much of the Red Sea in general.

After continents divide: Comparative phylogeography of reef fishes from the Red Sea and Indian Ocean

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The Red Sea is a biodiversity hotspot characterized by unique marine fauna and high endemism. This sea began forming approximately 24 million years ago with the separation of the African and Arabian plates, and has been characterized by periods of desiccation, hypersalinity and intermittent connection to the Indian Ocean. We evaluated the impact of more recent pleistocene glaciation events on the genetic architecture of the Red Sea reef fish fauna by surveying seven reef fish species from the Red Sea and adjacent Indian Ocean using mitochondrial DNA cytochrome-c oxidase subunit I and cytochrome *b* sequences. We assessed genetic variation and evolutionary connectivity within and between these regions, reconstructed phylogenetic relationships among haplotypes, and estimated gene flow and time of population separation using Bayesian coalescent-based methodology. Our analyses revealed a range of scenarios from shallow population structure to diagnostic differences that indicate evolutionary partitions, time frames for divergence ranging from 830,000 years to contemporary exchange or recent range expansion, and bi-directional colonization routes. We conclude that: (1) at least some Red Sea reef fauna survived multiple salinity crises; (2) endemism is higher in the Red Sea than previously reported; and (3) the Red Sea is an evolutionary incubator, occasionally contributing species to the adjacent Indian Ocean. Our results are discussed in the broader context of an ongoing, multi-disciplinary research project that uses traditional and next-generation sequencing technology to characterize all levels of marine biodiversity within the Red Sea.

Reproductive strategies of reef fishes predict both within-species genetic differentiation and within-family species richness

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Reductions or interruptions in gene flow are central to the divergence of populations and species. Yet, no single biological trait affecting gene flow has been demonstrated to affect both micro and macroevolutionary patterns of diversity. A simple dichotomy of dispersal-related traits is found in reef fishes, where some fishes guard negatively buoyant eggs and others release small pelagic eggs directly into the water column. Here, we show that benthic guarding species have significantly greater population genetic structure than pelagic spawning species. Similarly, species richness is greater in benthic guarding families as compared to pelagic spawning families, with clade age as an additional independent predictor of species richness. These results remain valid taking phylogenetic correlations among species and families into consideration. Our findings illustrate that long range dispersal is likely to be more common in pelagic spawning fishes and that dispersal related traits also shape macroevolutionary patterns of reef fish diversity.

Phylogeography of the black surfperch *Embiotoca jacksoni*: evolutionary consequences of an apelagic lifestyle

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Surfperches (Teleostei: Embiotocidae) are temperate fishes that include about 23 species that are found in the northern Pacific from Japan (3 species) to Baja California, Mexico. They are livebearers that lack a pelagic larval stage (apelagic) and with broods typically including 15 to 30 young. Dispersal is very limited, mostly occurring during the adult stage, resulting in reduced levels of gene flow. This system allows for testing several evolutionary and ecological questions including dispersal, phylogeography, sexual selection, and local adaptation. Using mitochondrial sequences, microsatellites, and RAD sequencing, we were able to show that black surfperches are an ideal system to approach these questions.

Progress towards a global molecular phylogeny for the cardinalfishes (family Apogonidae)

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The cardinalfishes (Family Apogonidae) are small, carnivorous and predominantly reef-associated fishes occurring in tropical, subtropical and warm-temperate waters. The family is among the most diverse within the Perciformes and contains in excess of 330 species in about 23 genera. The taxonomy of the Apogonidae has been problematic. Two subfamilies have been recognised, but familial boundaries have not been clear. Additionally, numerous subgenera have been proposed (principally on the basis of osteology) within several genera, including *Apogon*, the most speciose genus of the family. Some of these have been recognised, but not universally accepted, at the generic level. Various phylogenetic hypotheses have also been proposed for the family. At the 8th IPFC (Australia, 2009), the first two authors presented a preliminary molecular phylogeny, testing the monophyly and the current arrangement of subfamilies, genera and subgenera. This was derived from the analysis of sequence data from the mitochondrial 16S rRNA gene, and included representatives of *Apogon* and 15 other genera. Although limited, this data confirmed several taxonomic inconsistencies. Subsequently, this data set has been expanded and several key gaps in the taxonomic coverage have been closed. Representatives of more than 100 taxa and of most genera have now been included. Further, data from two additional gene fragments have been generated for the data set. This includes fragments of the mitochondrial cytochrome *b* and nuclear RAG-1 genes. Independent and combined analyses of these data sets, using parsimony, likelihood and Bayesian approaches, have provided the means to test the earlier single-gene hypothesis and have provided robust hypotheses against which earlier taxonomic arrangements and phylogenies, and those proposed subsequent to that presentation – such as that by Thacker and Roje (2009) – can be evaluated. These hypotheses have also provided a useful framework to consider the relationships within taxonomic groups that have recently been revised (e.g., *Siphamia*), the importance and evolution of certain morphological characters (e.g., scale type, bioluminescence), and the evolution and biogeography of the family.

Evolution of the pygmy angelfishes: recent divergence, introgression, and the usefulness of color in fish taxonomy

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CentropygeCentropyge is part of a ubiquitous coral reef fish family, the Angelfishes. Since members of the genus are typically small in size they are commonly referred to as Pygmy Angelfishes. There are 33 valid species, 30 distributed in the Indo-Pacific and three in the Atlantic. The genus is further divided into subgenera and species complexes, and color is one of the main characters used to differentiate among closely related species. This group is known for extensive natural hybridization. Aiming to resolve the relationships among species in this genus, we sequenced two mitochondrial (cytochrome oxidase I and cytochrome b) and three nuclear (TMO 4c4, recombination activating gene 2 and S7 ribosomal protein intron 1) DNA markers for 27 of the 33 valid species of the genus plus outgroups of all other Angelfish genera. Our results indicate that the genera *Genicanthus* and *Apolemichthys* nest within the paraphyletic "*Centropyge*". The subgeneric classification based on morphology, which divides the genus into the subgenera *Centropyge*, *Xiphypops* and *Paracentropyge* is supported, with the exception of the subgenus *Centropyge*, which is not monophyletic. Some species, such as those in the *C. flavissima* complex, hybridize, and introgression is leaving clear signals in some parts of the phylogeny. Even though color is used extensively to differentiate species in this genus, it does not seem to support phylogenetic relationships reconstructed using traditional Sanger sequencing. For some poorly resolved lineages we have employed next-generation sequencing to help delineate species boundaries and provide support for our hypothesis of recent divergence among species of the genus.

The convoluted evolutionary relationships among species of the Orangeband Surgeonfish complex: Using next-generation sequencing to resolve species' histories

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In the tropical oceans, many coral reef fishes possess vibrant color patterns that are sometimes the primary character used to delineate species. However, accumulating evidence indicates that color is not a reliable taxonomic character. Unique color patterns are expected to evolve slowly in isolated populations if the genes controlling color are primarily under the influence of genetic drift. On the other hand, changes in color can evolve rapidly if this character is involved in mate recognition or driven by strong selective pressures. Here we explore the relationship between color and genetic partitions in three species of closely related surgeonfishes (Acanthuridae): the Orangeband Surgeonfish, *Acanthurus olivaceus*; the Marquesan Surgeonfish, *A. reversus*; and the Doubleband Surgeonfish, *A. tennentii*. Their geographic ranges vary greatly in size and are largely allopatric. *A. olivaceus* is found across the Pacific from Hawai'i to the eastern Indian Ocean, *A. tennentii* is restricted to the Indian Ocean from Africa to western Indonesia but overlaps with *A. olivaceus* in the eastern Indian Ocean, and *A. reversus* is endemic to the Marquesas Islands of French Polynesia. These three species are distinguished largely by color, as only slight meristic differences are evident between the three groups. Phylogenetic reconstructions based on mtDNA reveal two well supported lineages (d = 11.5%): an Indian Ocean lineage (*A. tennenti*) and a Pacific Ocean lineage (*A. olivaceus* and *A. reversus*). The time to the most recent common ancestor for these two lineages is estimated at 3.2 mya, a period of time when dispersal pathways between ocean basins were restricted due to Miocene tectonic rearrangements as well as sea level fluctuations that date to at least the Pliocene. However, the nuclear dataset reveals a contrasting pattern of gene flow with introgression between the two lineages. In this case, next-generation sequencing was employed to resolve the evolutionary relationships between these three species and offers support for our findings of divergence, gene flow, and asymmetrical introgression.

Speciation with gene flow in coral reef fishes? Lessons from massively parallel sequencing of grunts (genus: *Haemulon*)

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Marine environments are characterized by a paucity of the strong physical barriers required for allopatric speciation. In addition, dispersal during the pelagic larval stages of most marine organisms can facilitate connectivity even between distantly located biogeographic provinces. This poises an interesting dichotomy, as coral reefs harbor levels of diversity that are comparable to tropical rainforests. Ecological speciation in the absence of complete reproductive isolation has recently been suggested as an alternative to allopatric speciation. Reef fishes of the genus *Haemulon* offer great potential to study such mechanisms. Previous studies on this highly dispersive group demonstrate most sister species have overlapping distributions. For example, *H. flaviguttatum* and *H. maculicauda* from the Tropical Eastern Pacific overlap from Baja California to Panama, forming large hetero-specific groups. In this particular case preliminary data shows discordance between mitochondrial and nuclear markers with estimates of time of divergence using mitochondrial makers at approximately 0.2Mya, while nuclear markers suggest 6Mya. Similar patterns have been ascribed to recent hybridization and introgression of the mitochondrial genome. Here we employ single nucleotide polymorphisms via Restriction Site Associated DNA (RADtags) to test for introgression between the sister species *H. maculicauda* and *H. flaviguttatum*. We compare these results with analyses of allopatric populations of *H. steindachneri* on both sites of the Isthmus of Panama, in an effort to identify genomic fingerprints that can distinguish patterns of divergence between ecological and allopatric speciation.

Biogeography and the structure of coral reef fish communities at isolated islands on the Indo-Pacific biogeographic border

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Theory predicts that isolation and biogeographic position are key determinants of community structure. Isolated islands distributed across biogeographic borders provide the opportunity to determine how isolation and biogeographic position affect marine communities. The Indo-Pacific biogeographic border is situated in the tropical eastern Indian Ocean and represents the junction of Indian and Pacific Ocean regional biotas. Situated on this border are two isolated locations: Christmas Island and the Cocos Islands. In this study we examine coral reef fishes at these oceanic islands to determine how biogeography, isolation and species geographic range size influence patterns of species richness, endemism, species composition and abundance. The reef fish communities at these two isolated locations were found to be species-poor and contained a distinct taxonomic composition with an overrepresentation of species with high dispersal potential. Despite low species richness, we found no evidence of density compensation, with population densities on the islands similar to those of species-rich mainland assemblages. The mix of Indian and Pacific Ocean species and the proportional representations of the various regional faunas in the assemblages were not influenced by the relative proximity of the islands to different biogeographical provinces. Species at the edge of their geographic range did not have a lower abundance than species at the centre of their range, and endemic species had substantially higher abundances than widespread species. At both locations, endemism was low (less than 1.2% of the community); this may be because the locations are not sufficiently isolated or old enough to promote the evolution of endemic species. Overall, the patterns of community structure conformed to biogeographical theory. However, species abundances differed from expectations based on terrestrial island communities, and this may be because of the life history of reef fishes and the processes maintaining isolated populations in marine ecosytems.

Taking an artisanal fishery into the Next Generation: Applying advanced genomics tools to a spatially explicit stock assessment of the Indo-Pacific fusilier *Caesio cuning*

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As anthropogenic pressure on coastal reef resources continues to rise in the Coral Triangle, informed management of coral reef ecosystems is increasingly becoming a priority for the conservation and sustainability of these resources in the coming decades. Genetic tools have been used to delimit the spatial distribution of fishery stocks and to inform conservation planning in marine ecosystems. A recent analysis of gene flow using mitochondrial DNA in a significant artisanal fishery in this region, the redbelly yellowtail fusilier *Caesio cuning,* indicates the presence of two distinct clades across its range and evidence for within-clade hierarchical structure. However, mitchondrial markers sort at evolutionary times scales and rarely provide the resolution of population structure needed to inform management of coral reef fishes such as *C. cuning* at the national level. Emerging next-generation sequencing tools provide scientists with the means to easily sample multiple independent genetic markers from any species and to deploy markers that have the power to sort at the fine-scale. With the goal of developing markers that sort at this level, we built a reduced representation genomic library from an ascertainment panel of three *C. cuning* from disparate locations in Philippines. We pyrosequenced the library on 3/8 PTP using the Roche 454 platform which returned 250k genomic fragments. From the de novo assembly, we are preferentially selecting amplicons of 120bp or less with 3+ single nucleotide polymorphisms in order to develop a panel of at least 100 anonymous nuclear markers from throughout the genome. These data will be used in coalescent models evaluating explicit hypotheses of *C. cuning* stock structure and directional gene flow (1) east and west of the Sulu Sea Throughflow in the Philippines and (2) along the flow path of the Kuroshio Current to the limit of the species' range in the Ryukyu Islands. A better understanding of the spatial dynamics of populations in the Philippines can be used to inform the optimal placement of marine preserves and guide management decisions within a single country, as well as to ascertain the process by which populations are sustained at the very edge of *C. cuning*'s distribution.

Australian mackerel found with mitochondrial genomes from two species

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This study explores the unusual mitochondrial genomes of three Australian fish (mackerel of the genus *Scomberomorus*). Complete mitochondrial genome sequencing plus nuclear microsatellite typing of the fish suggested affinities primarily to spotted mackerel (*S. munroi*), but two of the fish carried a complete, and one fish carried a partial, mitochondrial genome of grey mackerel (*S. semifasciatus*). The *S. semifasciatus* genomes had been linearized but otherwise were identical to extant *S. semifasciatus* mitochondrial DNA. Hybridization between related fish species is not uncommon as fish eggs are broadcast into the water column and fertilization is external. Normally only the mothers mitochondrial DNA is inherited, even in hybrid fish. Paternal leakage of mitochondrial DNA is rare. The presence of two complete genomes suggests recent hybridization between *S. semifasciatus* and *S. munroi* mackerel followed by paternal leakage of mitochondrial DNA. The waters off Port Douglas in northern Australia may have provided suitable habitat and environmental conditions for hybridisation between the two species. It is unclear if the linearised *S. semifasciatus* mitochondrial DNA has remained in the mitochondria, or if it has been translocated to the nucleus. If it remains in the mitochondria this is the first report of a linear mitochondrial genome in a vertebrate. If it has translocated to the nuclear genome then this is the first report of a complete mitochondrial genome translocation (numt) in eukaryotes. Mitochondrial genomes are indispensible genetic markers for species identification and for population level studies. Contraventions of common assumptions (such as its circular nature, exclusive presence inside the mitochondria, absence of paternal inheritance and the absence of recombination) may have significant implications for genetic studies. This study provides a possible explanation for mtDNA outliers in animal population studies.

Species detection from the netted sample with multi-species using the DNA barcode

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Evaluation of species occurrence and distribution is a first step toward biodiversity assessment and is a necessary procedure in the studies of biogeography, conservation biology and ecology. Identification of fish eggs becomes more important for detection of spawning periods and grounds in establishment of their proper management and conservation plans. However, the eggs of most species in Korean waters have trouble in identification of their species. The morphological characters of the eggs are similar in many cases and even overlap among the species. In this study, we developed the species-specific probes and primers from the mitochondrial DNA COI sequences so called the DNA barcode which enabled us to identify the eggs of some fish species in the net samples. Using the probes and primers, we verified the presence of some species in multi-species mixed samples via the process of realtime-PCR which was indicated by the result of next generation sequencing of the samples.

Sequencing formalin-fixed samples

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Museums collections represent an archive of material to study taxonomy, often via morphological characters. For preservation purpose, a large portion of these collections has been fixed in formalin-containing solutions. Formalin treatment could result in cross-linking among biomolecules and sometime the DNA might also be modified. Cross-linking not only could complicate isolation of nucleic acid from the fixed tissue but also may introduce polymerase blocks during PCR. DNA modification can lead to sequencing error as well. Therefore, formalin-fixed samples cannot be directly applied to genetic study. Previous efforts mainly focused on optimizing conditions for isolation DNA from the fixed samples. Other studies attempted to use next-generation sequencing to attain longer assemblies of the target genes. But none of these methods could obtain correct sequence of the full target genes. In this study, we treat fresh tissue samples of paddlefish (*Polydon spathula*) with 10% formalin for different period of time (1hr, 3hrs, 1day, 1 week and 1 month). Then we tried different approaches to retrieve the correct mitochondrial genome sequence from those samples, including using enzymes to break down the modified nucleotides or applying double-stranded sequencing method to resolve the errors due to the DNA modifications. Our study showed potential solutions to the long perplexing issue of using formalin fixed samples as genetic material.

On age and growth, feeding habits of *Semicossyphus reticulatus* (Labridae) in the western–central waters of the Seto Inland Sea

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The Asian sheephead wrasse *Semicossyphus reticulates* is a labrid species occurring exclusively in temperate waters of western Pacific and is well known for its giant body size often reaching up to 1 m and its unique feature. Regardless of the popularity in general, biological and/or ecological studies have hardly conducted on the wrasse. Without scientific data, it is suggested that the wrasse drastically changes its body forms and body colors with growth and that it has a sexuality of the protogynous hermaphrodite. The purpose of the present study is to reveal the ecological information of the fish, especially the age and growth and feeding habits, which still remains unclear. A total of 250 individuals were sampled in western Seto Inland Sea from 2005 to 2012. Their ages were determined by the annuli of scales. We analyzed gut contents of the wrasse regarding to seasonal patterns and intraspecific variation relating with growth. By adopting the von Bertalanffy growth equation, we found that it took 5 years to reach 300 mm (sexual maturation 250-300mm) and 15 years to 500 mm (minimum male body size 460mm) in standard length, respectively, indicating the long life span and slow growth of the wrasse. In accordance with the morphological change gradually developing humps at forehead and lower jaw, the wrasse changed trophi (tooth and pharyngeal tooth). We found that development of the trophi enables the wrasse to feed on animals having hard shells (e.g., bivalves like oysters, barnacles, sea urchins) that difficult to use other smaller fishes. We observed feeding behavior of the wrasse in tanks and field. The wrasse sucked in whole of prey, and then crushed the shells by using their pharyngeal tooth. Development of the trophi may enable the wrasse to have distinctive survival strategy in temperate waters, where it occupies dominant niche on the coastal area

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Fish production of the oil platforms off the coast of California, USA

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To investigate the conservation and fisheries value of active and decommissioned oil platforms, standing stock biomass and production of fishes on oil platforms (and natural rocky reefs for comparison) off of southern California, USA were modeled using fisheries independent empirically-collected submersible and scuba survey data. All platforms and natural reefs included in the study were surveyed for at least 5 years. Standing stock biomass estimates incorporated depth-specific fish density and size structure with published weight-length relationships. Production of these fishes was then modeled over one year using von Bertalanffy growth function parameters and size-based species-specific estimates of natural mortality. Reproductive potential was also evaluated between platforms and natural reefs for species with published size-fecundity relationships (or other size-based measures of reproductive potential). Fish production estimates for oil platforms were high, often one to two orders of magnitude greater than rocky-reefs in the region. Per unit area of seafloor, oil platform fish populations also have significantly greater reproductive potential relative to those on rocky reefs. These results indicate that the potential contribution of oil platform habitat to biological resources in this region is substantial.

Do unreachable area act as natural refugia? Ecology of tropical sea cucumbers and effects of fishing pressure

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Sea cucumbers have been a popular delicacy in many parts of southeastern Asia for many years and . are an important source of foreign currency for a number of the developing nations in the Pacific Islands. However, recent increases in demand from China and elsewhere, coupled with the ease of harvesting, has led many local stocks to collapse and become commercially extinct. When shallower population becomes depleted, fishers tend to search deeper using SCUBA and hooka gear. Since there is a limit on the depth of fishing activity due to the risks of decompression sickness, these "unreachable areas" may act as natural refugia for these populations from harvest pressure. We examined five species of commercially targeted species (*Holothuria nobilis*, *H. fuscogilva*, *H. scabra*, *Thelenota ananas*, and Pentard) in Seychelles and looked at their habitat preference, size distribution, and response to fishing pressure. Ordination analysis showed *H. nobilis* and *T. ananas* preferred shallower coral habitat, while *H. scabra* preferred sandy habitat with no strong correlation with depth. Pentard were mostly found in intermediate depth sites (20m-40m) whereas *H. fuscogilva* showed only slight preference toward deeper sites but showed no correlation with habitat. Despite high exploitation, none of the species examined had higher density or larger size in deep habitats (>40m), contrary to the general perception of adults migrating to the deep, and depth acting as a refuge from fishing. The habitat analysis showed that deep habitats hardly have any biological cover, which leads to reduced energy source for sea cucumbers, and could thus lead to smaller size and low density. Structural equation modeling (SEM) showed that fishing pressure is a key factor for the distribution of commercially targeted Holothurians. This study demonstrated the importance of incorporating ecological information into fishery management by showing the different density at different habitats. The study will be incorporated into habitat based fishery stock assessment model in the future.

Habitat use by an annual algal-grazing fish *Plecoglossus altivelis ryukyuensis* (Ryukyu-ayu) in a subtropical stream

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Plecoglossus altivelis ryukyuensis (Ryukyu-ayu) is a critically endangered fish found only in Amami-Oshima Island and Okinawa Island in southern Japan. Ryukyu-ayu is an amphidromous fish having an annual life history. Sexually mature fish spawn in the lower reach of streams in autumn, with the newly hatched larvae drifting into the sea. Young fish migrate upstream in spring, after which they grow and mature in the middle reach of streams. They die after spawning. Since Ryukyu-ayu predominantly forages on benthic algae in summer, its habitat use should be affected by the proportion of riparian canopy over streams, which negatively correlates algal productivity in general. We studied seasonal changes in distribution of Ryukyu-ayu and determinants of their habitat use in a subtropical stream of Amami-Oshima Island. We counted Ryukyu-ayu by snorkeling within 21, 12 and 10 areas established in upper, middle and lower reaches, respectively and measured physical environment in each area. In summer, Ryukyu-ayu mainly utilized upper and middle reaches of streams; especially fish having feeding territory (territorial fish) more frequently appeared in the middle reach. In both upper and middle reaches, densities of Ryukyu-ayu were negatively correlated with the proportion of forest canopy cover over streams. Considering behavioral modes of Ryukyu-ayu, however, in the upper reach, territorial fish more frequently appeared in sunny rapids, whereas schooling fish, which frequently consumed drifting materials, more frequently occurred in deeper pools. Abundances of potential food competitors of Ryukyu-ayu such as the grazing goby *Sicyopterus japonicas* and the grazing snail *Clithon retropictus* did not affect habitat use of Ryukyu-ayu. In autumn, the distribution of Ryukyu-ayu shifted to middle and lower reaches. Additionally, a higher proportion of Ryukyu-ayu formed schools and territorial behavior was not observed in this season. Different from the habitat use in summer, densities of Ryukyu-ayu were positively correlated with the proportion of canopy cover. These results suggest that distribution and behavioral modes of Ryukyu-ayu change seasonally, depending on foraging and reproductive season. Furthermore, algal food availability is an important factor for the habitat use of Ryukyu-ayu in summer, whereas differences in behavioral modes are also related to their habitat use.

Life history variation in non-migratory galaxiids: Implications for endangered species management

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Species' life history traits such as egg size, fecundity and age at sexual maturity are optimised to maximise survival and reproduction. As no single strategy is optimum for all environments, traits are 'fine-tuned' according to evolutionary pressures faced. Optimisation of one trait occurs to the detriment of others, leading to life history trade-offs. The 'vulgaris' complex is a suite of at least 10 non-migratory galaxiid lineages present on the South Island of New Zealand. Distributions range from species only found in isolated populations in low productivity headwater creeks to relatively widespread species which are predominantly found in comparatively productive, higher order streams. In their evolution from a common amphidromous ancestor, there is likely to have been substantial interspecific life history divergence as species specialised to their own particular environment. This study aims to examine interspecific differences in life history traits within the 'vulgaris' complex and explore implications for species management. Collections of gravid females of four species (five populations per species) were performed immediately before predicted spawning time. Measurements of oocyte size, fecundity and reproductive investment were made. Electrofishing surveys were also made to assess population structure of sexually mature fish. Results indicate substantial differences in dominant life history characteristics between species. Species which predominantly inhabit low productivity headwater streams are characterised by a large egg, low fecundity and mature relatively late. Lower catchment species exhibit smaller egg size, lower fecundity and early maturation. Implications for species management, particularly concerning pressures from invasive salmonids, are discussed.

Otolith chemistry of flathead mullet *Mugil cephalus* L. in the waters of Taiwan reveals variable patterns of habitat use

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The migratory history of flathead mullet *Mugil cephalus* in the coastal waters of Taiwan was evaluated by examining the elemental composition in otoliths collected from 3 habitats of different salinity by laser-ablation inductively coupled plasma mass spectrometry. The mean (±SD) Sr/Ca ratio in the otolith edge differed significantly among 3 habitats of varying ambient salinity. The otolith mean Sr/Ca ratio from fish offshore was $6.7 \pm 2.0 \times 10^{-3}$ and $4.2 \pm 1.5 \times 10^{-3}$ in the estuary, which were significantly larger than that for freshwater ($2.8 \pm 1.1 \times 10^{-3}$). In contrast, the mean Ba/Ca ratio in the otolith edge of fish from offshore was $87.1 \pm 113.0 \times 10^{-6}$ and $52.1 \pm 22.3 \times 10^{-6}$ in the estuary, which was significantly lower than that for freshwater habitat ($144.5 \pm 54.8 \times 10^{-6}$). Thus, the Ba/Ca ratio was an alternative to the Sr/Ca ratio to evaluate the migration of *M. cephalus* between freshwater and saline water. Accordingly Sr/Ca and Ba/Ca ratios in otolith can be used to reconstruct the past salinity history of *M. cephalus*. Variation of Sr/Ca and Ba/Ca across life history profiles suggested seasonal migratory behaviour in relation to salinity, and importantly, that the use of marine, estuarine and freshwater habitats at different life history stages is not necessarily obligatory in *M. cephalus*. These results have implications for developing more extensive studies to resolve the relative importance of marine estuarine and freshwater habitats for sustaining production of *M. cephalus* fisheries.

Age and gowth of two lionfishes, *Dendrochirus zebra* and *Pterois volitans*, around Okinawa-jima Island

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The zebra lionfish *Dendrochirus zebra* and the red lionfish *Pterois volitans* are belonging to the same subfamily of Pteroinae (Scorpionfishes), and are widely found in coral reefs and rocky habitats of the Indo-Pacific Ocean. The red lionfish is known as one of the most successful invasive marine predator in the tropical western Atlantic, where it was introduced during the 1980s. Since then, its spread gave considerable damage on reef ecosystems and coastal areas. Recent surveys focused on the invasive aspect, but only a handful studies are known from the origin. The present study revealed the age and growth of both lionfishes using sectioned otoliths. Totally, 180 zebra lionfish (23.9–151.2 mm SL) and 84 red lionfish (29.8–319.0 mm SL) were collected in Okinawa Island. Opaque rings in otoliths were counted for age determination. Observed age at SL was applied to the von Bertalanffy growth curve. Additionally, stomachs were obtained to briefly determine the gut content. Maximum age differed for females and males in both species (zebra lionfish: 6 vs. 5 years old; red lionfish: 9 vs. 5 years old; for females and males, respectively). The growth of male is faster than female in the zebra lionfish (male: k=0.9; female: k=0.6), and the growths of both species were generally fast until their lifecycle (zebra lionfish: k=0.8; red lionfish: k=0.4). However, the lengths at each age class were greatly varied in the red lionfish. The specimens of the red lionfish captured from deeper reef areas were larger and older than that from shallow habitats indicated that this species change the main habitat in their lifecycle. This might effect to their diet which main food for both species were crustaceans in small individuals, but the red lionfish switched to fish in large individuals. The proposed fast growth and strong teleostern feeding might be the important factors why the red lionfish could be a successful alien species. Our results indicate that the related species which share the same habitat in the origin, have different risk to be an alien species, and were effected by their growth and food habits.

Comparative life history of sympatric Sillaginidae inhabiting southeast Australian coastal waters

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This study examined whether the coexisting *Sillago robusta* and *S. flindersii* displayed different life-history strategies and depth distributions in coastal waters off eastern Australia. Both species were present year round across sampled depths from 11 to 90 m, however *S. robusta* was most abundant in summer and autumn and *S. flindersii* in winter and spring. Further, *S. robusta* was generally more abundant in the shallow (11-30 m) strata, and *S. flindersii* in the mid (31-60 m) and deep (61-90 m) strata. The size composition of *S. robusta* was generally similar across depth strata, but smaller and immature *S. flindersii* predominantly occurred in the shallow strata, whereas larger and mature individuals occurred in the deeper offshore strata. Growth was faster in *S. flindersii* compared to *S. robusta*, with the maximum age and fork length determined being 6 years and 22 cm for *S. flindersii*, and 10 years and 25 cm for *S. robusta*. For both species, females grew faster and attained a greater maximum length than males. Both species potentially spawned year-round, however a greater proportion of *S. robusta* was is spawning condition between September and March, whereas *S. flindersii* displayed no such temporal pattern. Both species displayed similar ovarian development, with mature gonads having a range of oocytes of different stages and development, indicating potential multiple spawning and indeterminate fecundity, as observed in other sillaginids. Estimated batch fecundity of both species increased with length, and the size and age at maturity was generally smaller and younger, respectively, in males than females. The data provide evidence of potential spatial and temporal partitioning of habitat resources, which may aid species coexistence.

Decadal scale change in biological character of *Lethrinus atkinsoni*, associated with population decline and environment degradations

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The Pacific yellowtail emperor Lethrinus atkinsoni is one of the most important food fishes in the Yaeyama Islands, southwestern Japan. In this region, the Pacific yellowtail emperor is caught by various fishing methods. Their spawning aggregations have often been targeted by local fishers. In recent years, annual landings of the species are approximately 20 tons; however, the landing is decreasing by half over the last two decades, indicating the population decline of the species. Also since 1970s, coral reefs in this region have been heavily damaged by redsoil pollution, outbreaks of crownofthorns starfish, and mass coral bleaching. Thus the population decline may be caused by overfishing and deterioration of environment. To examine the temporal change of biological and demographical characteristics of the species associating with these degradations, this study compared various biological characteristics such as, growth, maturity, sex ratio and condition factors among 1990s, 2000s, and 2010s. Age was determined by sectioned otolith, and growth was expressed in von Bertalanffy's equations. Sex was determined by macroscopic and histological observations of gonads. As these results, the growth gradually became to be slower over time, especially from 1990s to 2000s. In younger ages, ratio of female shifted from 0.7 to 0.5 in gradually. Condition factor was the highest in 2000s, than 2010s, 1990s. These facts may indicate that habitat environment, stock conditions and population density potentially affected on biological characters of the Pacific yellow-tail emperor.

How well do life-history traits explain species' vulnerability to overexploitation in parrotfishes?

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The potential vulnerability of coral reef fishes to overexploitation is a major concern among biologists and resource managers. A variety of factors dictate susceptibility to overfishing in a given species, including life-history traits, ecology, behaviour, and the nature of fisheries themselves. Traits such as growth rate, body size, age and mortality are certainly major drivers of vulnerability between species, but the lack of such data for Indo-Pacific species has hindered quantitative evaluations. Here, we provide an extensive examination of parrotfish life histories for twelve species from Micronesia. Recent work has highlighted both the importance of parrotfish communities in the trophic and structural dynamics of coral reefs as well as their increasing prevalence in fisheries harvests throughout the Indo-Pacific. They have dynamic life histories which include protogynous hermaphroditism, various sexual pathways, strong sexual dimorphism, and complex mating systems. As a group, they encompass a variety of body sizes and can range in longevity from approximately 3 to greater than 30 years. The aim of the present study was to obtain detailed life-history information to predict species' relative vulnerabilities to overfishing along a life-history spectrum. Data were combined with ecological and behavioral information and tested empirically against historical creel survey data as well as spatial demography data using a standardized proxy for differences in fishing pressure. Differences in life-history traits among species explained much of the observed trends in historical and spatial data, while ecological and behavioral traits can also be important predictors. Altogether, this represents the most comprehensive synthesis of parrotfish life history to date and is an invaluable first step before further investigations of community dynamics, fishing effects, or resilience to anthropogenic-induced or environmental change can be conducted.

Demographic variation in a coral reef fish across ocean basins: from the Pacific Ocean to the Red Sea

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Many Indo-Pacific coral reef fishes have geographical distributions that span ocean basins, with some extending into the Red Sea. The demography and life history of species with large distributional patterns vary in response to environmental conditions and ocean evolutionary history. While demographic patterns have been established across the Indo-Pacific, little is known of the demographic response to the comparatively more recent geological history of the Red Sea and Arabian Peninsula region. The Arabian Peninsula, with its past of sea level fluctuations, is a unique environment that provides some of the warmest, most saline and nutrient-poor waters of all marine systems. In this study, we examine the demographic signature of a sister species complex within the coral reef fish family Acanthuridae (surgeonfishes) whose geographical distribution spans the length of the Indo-Pacific, from the Red Sea and Arabian Seas region (*Acanthurus sohal*) to the Indian Ocean and the Pacific (*Acanthurus lineatus*). The two species are abundant in shallow waters where they aggressively defend algal territories, thereby experiencing a range of environmental conditions across their distributional range. Sampling covered four locations from the Red Sea and Gulf of Oman (*A. sohal*), and seven locations across the Indo-Pacific (*A. lineatus*), and was designed (i) to examine patterns of variation in demographic traits of the two species longitudinally across the Indo-Pacific region including the Red Sea, (ii) to establish the demographic signature of the much younger Arabian Peninsula region (*A. sohal*) relative to the Indo-Pacific (*A. lineatus*), and (iii) to explore how bio-physical parameters contribute to demographic variation across the region. We use a broken-stick regression approach to explore which aspects of growth underlie the demographic response and estimate the age at which growth rate switches between rapid initial growth and subsequent slow growth, and the rate at which this switch occurs. Locality-specific estimates of mean size-at-age, growth rate and life span are related to satellite-derived physical (sea surface temperature) and biological (Chlorophyll a) environmental variables to establish general biophysical descriptions of each sampling area (seasonal climatologies), and how these have changed in time (time-series) in relation to the demographic information.

Downstream spawning migration in amphidromous fishes: a link to catadromy through larval transport

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Amphidromous and catadromous fish dominate many freshwater fish communities throughout the Indo-Pacific region. Both groups of fish exhibit a marine pelagic larval phase followed by a period of extended freshwater residency. In amphidromous fish, spawning occurs in freshwater with larval migration to the sea. In contrast, adult catadromous fish migrate and spawn in the sea. The function of the two life cycles has been subject to prolonged debate. A common feature of both life cycles is the production of small pelagic marine larvae. Producing small pelagic larvae enables (often small-bodied) amphidromous and catadromous fish to maintain high levels of fecundity, but limits the capacity of the larvae to survive extended periods of starvation. The New Zealand torrentfish is an endemic amphidromous freshwater fish that can penetrate over 100 km inland. Such extensive inland migrations pose the question, how do larvae get to their marine pelagic rearing habitat before terminal starvation occurs? Our extensive sampling around the South Island of New Zealand confirms that primarily female torrentfish undertake extensive upstream migrations (>100 km), with most males remaining in downstream river reaches. Downstream migration by females to spawning sites in riffles close to the sea occurs from late spring. This pattern of upstream migration by females during growth to maturity, followed by downstream migration to a spawning habitat close to the marine interface is a pattern that is repeated in a number of amphidromous fish species, particularly in species that either penetrate long distances inland or inhabit low gradient landscapes. This pattern of migration also has close parallels with migration in various catadromous fish species – rather than spawning in freshwater, the downstream spawning migration continues into near-shore marine habitats. We discuss possible functions for these downstream migrations and the apparent similarities between amphidromous and catadromous life histories in various Indo-Pacific fish species.

Climate change associated elevated temperatures and variable food supply influence performance of a larval coral reef fish

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Climate change models predict that tropical sea surface temperatures will increase by 2-3°C this century. Warmer ocean temperatures can increase metabolism and energy requirements of ectotherms such as marine fish. Warmer temperatures can also alter plankton communities that are food for many marine fish larvae. However, little is known about the potential interacting effects of ocean warming and changes to food supply on the performance of larval reef fish. We raised coral reef anemonefish (*Amphiprion percula*) larvae in an orthogonal experiment comprising 3 temperatures and 3 feeding schedules. Temperatures were chosen to represent current-day summer averages (29.2°C) and end-ofcentury climate change projections, +1.5°C (30.7°C) and +3°C (32.2°C). Feeding schedule (daily, every 2 days, or every 3 days) was chosen to represent increased variability in food availability. Overall, larvae took longer to settle under high temperatures and less frequent feeding. The time to settlement increased from 10.6± 0.2 days at 29.2°C and high food supply to 15.6 ± 1 days at 32.2°C and low food supply. Fish from the lower feeding regimes had a lower condition and decreased survivorship. Routine oxygen consumption rates ($\dot{M}O_{2Routine}$) were highest (1640±100 mg O_2 kg^{-1} h^{-1}) for fish raised at 32.2°C and fed every third day and lowest (1210 ± 125 mg O_2 kg^{-1} h^{-1}) at 29.2°C and fed daily. Elevated $\dot{M}O_{2Routine}$ and therefore energy use at higher temperatures may leave less energy available for growth, resulting in the longer time to settlement and lower body condition. Increased larval duration and reduced body condition could reduce survivorship during the larval phase and postsettlement, with consequences for population dynamics. This eco-physiological approach has allowed us to highlight important physiological mechanisms that could be impacted in larval fishes under climate change scenarios.

Olfactory discrimination in juvenile coral reef fish: Response to conspecifics and alterations to coral health

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Coral reef fish use olfaction to respond to a variety of chemical cues that allow them to garner critical information regarding their surroundings. Through such processes fish are adept at detecting the presence of predators, resident conspecifics and suitable areas of reef water. The relative importance of chemical cues emitted from habitats versus those from resident individuals toward juvenile reef fish has not been assessed. The ability to distinguish and use such cues could be critical in determining spatial distributions of juveniles across coral reef areas. Here we test olfactory preferences toward conspecifics and coral health in newly recruited juveniles of coral reef fishes. Newly settled juveniles of eight common coral associated species in Kimbe Bay, Papua New Guinea, were subjected to a series of pairwise olfactory choice tests using two-channel choice flume. Focal species were comprised of three common reef fish families; 1) Pomacentridae: *Dascyllus melanurus, D. reticulatus, Chrysiptera parasema, C. aurifons* and *Pomacentrus moluccensis,* 2) Labridae: *Halichoeres melanurus* and *Labrichthys unilineatus* and 3) Chaetodontidae: *Chaetodon octofasciatus.* All species demonstrated a significant dislike for water containing chemical cues derived from degraded coral colonies (≤ 75%), choosing to spend the majority of time in such trials in the water seeded with the chemical cues from healthy coral colonies. The presence of conspecifics also invoked favourable responses from the majority of test species (≥60%). Only three species, *P. moluccensis, H. melanurus* and *L. unilineatus* exhibited either limited or no response to the presence of such cues. Our results indicate olfactory preferences for both conspecifics and live coral may combine to determine juvenile and recruitment distribution patterns in these species and local population declines in response to coral degradation.

The relationship between boldness and learning in a tropical reef fish

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Boldness is known to be a key personality trait dealing with the propensity to take risks and explore new environments. For juvenile organisms undergoing intense predation pressure, there are ecological trade-offs associated with alternative boldness-shyness behavioral strategies. We are only just beginning to understand the relationship between boldness and other behaviors that influence short-term success in complex new environments. Here, we document a laboratory experiment that examines the link between boldness and learning in the juveniles of a common tropical reef fish, *Pomacentrus amboinensis* (Pomacentridae). Newly metamorphosed fish were individually ranked on a boldness-shyness axis on the basis of their willingness to explore a novel environment in an aquarium.. Each fish was then given a simple task four times, which involved learning how to navigate a maze to reach a food source. Fish that were ranked highly in boldness were significantly more successful at navigating the maze in a fewer number of trials compared to shy fish. Boldness is likely to be closely linked with learning appropriate behaviors while exploring new habitats. Although a higher level of boldness is inherently risky, the greater reward associated with this trait may explain why boldness persists as a behavior in natural populations.

Elevated CO2 affects predator-prey interactions through altered performance

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Recent research has shown that elevated dissolved carbon dioxide (CO2) affects how fishes perceive their environment, affecting behavioral and cognitive processes leading to increased prey mortality. However it is unclear if this increased mortality results from changes in the dynamics of predator-prey interactions or due to prey increasing activity levels and moving further away from shelter. Here we demonstrate that levels of dissolved CO2, which may occur by the end of the century, have significant effects on the interactions of a predator-prey pair of common reef fish: the planktivorous damselfish *Pomacentrus amboinensis* and the piscivorous dottyback *Pseudochromis fuscus*. Prey exposed to elevated O2 (880µatm) or a present day control (440µatm) interacted with similarly exposed predators in a cross-factored design. Predators had the lowest capture success when exposed to elevated CO2 and interacting with prey exposed to present day CO2. Prey exposed to elevated CO2 had a reduced escape distance and longer reaction distances compared to prey exposed to present day CO2 conditions, but this was dependent on whether the prey was paired with a CO2 exposed predator or not. The results suggest that the dynamics of predator-prey interactions under future CO2 environments will depend on the extent to which the interacting species are affected and can adapt to the adverse effects of elevated CO2.

Trophic ecology of top predators: what have we learnt in the western Indian Ocean?

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Catches of tunas, billfishes, swordfish and sharks by high-sea fisheries have dramatically increased during the two last decades. Fishing activity cannot be reduced to a simple removal of individuals but might deeply impact population demography and can have strong repercussions on the food web structure through complex trophic controls. However, our knowledge of the biological components and the predator-prey interactions in open-sea ecosystems is still scarce. Comparative studies of the trophic ecology of top predators and the implications for resource partitioning will provide basic elements for an ecosystem approach to high-sea fisheries management. In this work, we investigated the trophic ecology of several marine tropical top predators in the western Indian Ocean. A large sampling programme, covering the last decade and involving the collection of stomachs and fish muscle tissues, has been implemented. The aim was to combine results on diet studies (stomach contents) and stable isotope analysis ($\delta^{15}N$ and $\delta^{13}C$) to explore the feeding habits of large tropical predators, and the food web structures supporting them. Diet studies allowed us to define predator foraging ranges (composition and abundance of prey species, predator-prey size ratios, feeding variability, resource partitioning), and can also provide useful information on species composition, distribution, abundance and ecology of the intermediate trophic levels (pelagic predators used as biological samplers of micronekton organisms). Stable isotope analyses add relevant information to conventional dietary techniques. They permit to conduct community-based investigations of fish diet, feeding ecology and trophic structure (consumer foraging areas and trophic levels). Additional stable isotope analyses were also performed for fish prey, and some results on tropical seabirds of the Indian Ocean allowed us to show that seabirds overall share the same trophic level than several large predatory fishes.

Predator/prey interactions and the effect of harvesting predators on reef fish assemblages on the Great Barrier Reef, Australia

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Predators perform crucial roles in both terrestrial and marine ecosystems, and the interplay between predatory species and their prey can have a profound effect on the community structure of an ecosystem. Predation is an important process structuring coral reef fish assemblages, and piscivores form a substantial component of reef fish assemblages. On the Great Barrier Reef (GBR), important coral reef piscivores such as the coral trout (*Plectropomus leopardus*) are targeted by recreational and commercial fisheries, significantly altering patterns of predation in fished areas. Great variation in predator abundance has been found in and out of marine reserves, however despite the potential for trophic cascades due to this variation, little is known about the potential effects on prey. Classical predictions suggest that removal of large predators may facilitate "prey release", resulting in higher prey abundance in fished areas. An alternative prediction is that predator and prey abundances may be positively correlated, as predators either recruit preferentially, or actively move, to areas of high prey abundance. These processes, however, have the potential to vary according to spatial and temporal scales. The objective of this study was to investigate the interactions between predatory fish and their prey, at multiple spatial scales and between times. Reef fish assemblages were surveyed at multiple locations on the GBR to investigate the influence of marine reserves over a wide latitudinal range. Further, a detailed study at One Tree Island examined local effects and temporal patterns of abundance. Relationships between predators and prey were scale-dependant. At local scales, predator and prey populations were positively correlated, especially in predator dense areas with a history of long-term protection; seasonal effects were also found. At larger spatial scales and across a gradient of fishing intensity, patterns of predator/prey abundance differed, with a variety of trophic effects demonstrated. The abundance and composition of fish assemblages varied according to marine reserve status, and there was evidence of prey release in heavily fished areas. This study demonstrates the potential effects of removal of important predators through fishing, and emphasizes the importance of considering multiple spatial and temporal scales in management of marine protected areas.

Functional diversity of large top predator fish community: monsoon matters in the Indian Ocean

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Environmental changes and human activities can have strong impacts on biodiversity and ecosystem functioning. In this context, while traditionally based on species richness and composition, there is a growing concern to take into account functional diversity (FD) to assess and manage species communities. In spite of their trophic and economic importance in the open-sea ecosystems, FD of large top predator fishes (tunas, billfishes, sharks, etc.) is poorly documented. There is a lack of knowledge and consensus on the impacts of human activities (e.g. fishing) and environmental changes (e.g. induced by monsoon system) on FD of these communities. In this work, we investigated for the first time FD of large top predator communities exploited by longline in the western Indian Ocean, and influences of area (contrasted environment and human activities) and climate (monsoon alternance). Fishes were collected from 120 drifting longline samplings performed during scientific surveys around Seychelles archipelago and in the Mozambique Channel. These areas present contrasted fishing and environmental conditions. A total of 25 species were collected and 20 functional traits were quantified describing 4 main functions: food acquisition, locomotion, social behavior and reproduction. Fish abundances and functional dissimilarities data were combined in a multivariate analysis to investigate area and monsoon effects on functional typology of fish communities. Results highlighted monsoon effects on FD of top predators community, with different functional typology between South West (SW) monsoon and Intermediate SW monsoon. In contrast, no differences in FD were detected between Seychelles archipelago and Mozambique Channel. While this study provide a first view of functional diversity of large top predator community, a similar assessment based on purse-seine samplings could complement our knowledge of this diversity facet in open ocean.

Marine megafauna, *Manta alfredi* target multispecies surgeonfish spawning aggregations as a food source

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Across Micronesia, aggregations of reef-associated manta rays (*Manta alfredi*) occur throughout island groups, atolls, channels, and bays. Predictable assemblages of *M. alfredi* gather along coral and rocky reefs at cleaning stations or areas of high productivity to feed (Homma et al. 1999, Marshall et al 2009). *M. alfredi* are ram-filter feeders that feed on rich sources of zooplankton influencing their distribution and site fidelity (Anderson et al. 2011, Dewar et al. 2008). Recently, on Guam *M. alfredi* have been observed targeting spawning aggregations (SPAGs) of teleost fishes to feed off gamete clouds of numerically abundant acanthurids, *Acanthurus triostegus*, *A. guttatus* and *A. lineatus*. Spawning events occurred on the reef slope of Tumon Bay Marine Preserve, Guam, at a depth of 5-13 m on an outgoing tide. The first spawning events of the year were the largest in size, with fish numbers decreasing in subsequent events throughout the year. Surgeonfish spawning generally lasted approximately 20 minutes, always within the same channel during an outgoing tide. During 13 of the 15 observed SPAGs, up to 12 *M. alfredi* were observed feeding on the gamete clouds. The number of manta rays present was positively correlated with the size of surgeonfish aggregations. Similar to our observations, the whale shark (*Rhincodon typus*) is also known to target teleost spawning aggregations and feed upon fish spawn (Heyman et al. 2001). Given the global decline of reef-fish spawning aggregations, this recent discovery highlights the urgency for further research on (1) marine megafauna, like *M. alfredi,* depend upon spawning aggregations, as a food source; (2) how to predict SPAG patterns for 3 species of surgeonfish; (3) the importance of specific reef habitats used for SPAGs by multiple fish species, and (4) characterizing spawning events within Tumon Bay Marine Preserve.

Ghosts of the coast: A first step toward understanding the ecosystem role of sawfishes

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Top predators in marine systems have been systemically targeted, by often highly unselective fisheries, over the past 500 years. Consequently many species may have disappeared long before today's scientists established personal baselines of ocean structure and function. Looking deeper back in time using historical ecology can reveal predator species whose loss from coastal ecosystems has gone virtually unnoticed. Only by reconstructing their former abundance and distribution can we go on to ask questions as to their ecological role before they disappeared. Here we take that first step and bring to your attention the scale and extent of decline of a once iconic and influential family of chondrichthyans – the sawfishes (Pristdae). Sawfishes were formerly widespread in tropical and subtropical coastal waters of approximately 80 countries, with some species extending into freshwater. However, their long toothed saw and their heavy reliance on shallow nearshore environments, close to human population centres, has led to dramatic declines in their abundance and distribution over the past century. Their distribution is now severely fragmented, and some sawfish species are thought to be locally extinct from large parts of their former range; they are now found in fewer than 25 countries. Because of this, and their slow life histories, there is a very real risk that this ecologically unique and evolutionarily distinct lineage will vanish in our lifetime due to overexploitation and habitat loss. The next step is build upon this comprehensive biological synthesis of diet, abundance and distribution data to develop and understand the historic ecological role of sawfishes in tropical coastal ecosystems.

The role of non-resident sharks in shaping coral reef communities

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The importance of sharks in shaping coral reef communities, and the effects of declines in reef shark numbers, has received increased attention in recent times. Relevant research has focused on reef-resident species of shark, most notably grey reef (*Carcharhinus amblyrhynchos*), whitetip reef (*Triaenodon obesus*) and blacktip reef (*Carcharhinus melanopterus*) sharks. However, a range of other shark species occur around and within coral reefs, and may play an important role as predators of resident reef invertebrates, fish and sharks. This predation may have both direct and indirect effects on the functioning of coral reef communities. Catch data from reefs in the southern Great Barrier Reef indicates that species such as tiger (*Galeocerdo cuvier*), sandbar (*Carcharhinus plumbeus*), blacktip (*Carcharhinus limbatus*), bull (*Carchahinus leucas*) and weasel (*Hemigaleus australiensis*) sharks regularly occupy coral reef ecosystems in which they may play important roles. Acoustic monitoring data that show the space use of non-resident species will be presented. The results of this preliminary work indicates that the role of non-resident shark species is far greater than previously anticipated, and may be an important consideration in the management of coral reef ecosystems.

Hotspots of interactions between whale sharks, marine mammals and tropical tuna purse seine fishery in the Indian and Atlantic Oceans

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The tuna fishing industry holds an important place in the Indian and Atlantic Oceans. Considering log-book data of the French and Spanish tuna purse seine fleets PSF (1980-2011, AVDTH database) and data collected by scientific observers on board (1995-2011, ObServe database), we studied the relationship between fleet, whale sharks WHS and marine mammals. These large marine organisms are indeed observed during activities and are sometimes encircled with the net when fishing tuna schools. However, there is a lack of knowledge on the spatio-temporal distribution (season and year) of co-occurrence frequency between fishing activities and WHS, and the potential impact on their mortality. Distribution maps of Sightings Per Unit of Effort (SPUE, ie. number of WHS observations per PSF activities), supported by multivariate data analysis (PCA), were performed. The results highlight a seasonal and annual variability in the distribution of activities and observations. Areas of aggregations of organisms and specific seasons were highlighted, certainly in relation to structuring environmental parameters. 96% of the whale shark sightings (AVDTH) were associated with fishing activity, and 25% (ObServe) to catches, which is particularly important in comparison to marine mammal sightings (respectively 76% and 6%). No particular association between fishing and dolphins was observed in contrast to the situation known in the Pacific Ocean. The impact of fishing on the mortality of whale sharks and mammals is extremely low, even zero depending the organism, in the studied oceans.

Pelagic diversity highlighted by longline fisheries in the Indian Ocean

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Data collected on board fishing vessels can be used as a tool for documenting species diversity of pelagic ecosystems in open oceans. In this work, scientific-observer records from pelagic longline fisheries allowed us to investigate diversity patterns of large fish predator assemblages in the tropical Indian Ocean. Indeed, pelagic longlines catch a wide range of species in a similar way, and operate at a large spatial scale. Historical and recent data were combined in a dataset of 135 cruises and 3,886 longline sets carried out from 1958 to 2011. The Indian Ocean was partitioned in three embedded groups of zones, taking into account the main pelagic habitat features such as distance from shelf breaks, presence of islands, shoals or seamounts, and Longhurst' s biogeochemical provinces. Longline sets were assigned to one zone and analyzed in terms of species richness. We carefully dealt with the taxonomic identification of individual catches and worked at species level by correcting the higherlevel resolutions. Linear mixed-effect models were used to standardize fishing effort (hook number) and allowed us to predict species richness in the different panels. In addition, stomach contents recovered from some predators were carefully analyzed in the laboratory. Then the prey composition provided unique information on the diversity of the forage fauna. We thus used these top predators as biological samplers of micronekton. More than 2,000 non-empty stomachs recovering 223 preys at the genus level were analyzed in the same way than the fish predators. Our findings highlight regional differences with high species diversity areas that might be used for future conservation issues.

Predicting MPA utilization for reef-associated sharks: an individual-based simulation approach

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Recent studies have reported large population declines of reef-associated sharks. This has raised global concern as some species are thought to play an important role in the stability and functioning of marine ecosystems. Marine protected areas (MPAs) have become a common tool in the management and conservation of coral reefs. However, most MPAs have limited conservation value for highly mobile species such as sharks. Shark species with a higher degree of reef-association (low inter-reef movements and high fidelity to a single reef) are expected to derive greater benefit from MPAs, but this has been poorly quantified. Therefore, a better understanding of the benefits of MPAs to reef-associated sharks will help improve their management and conservation. An individual-based simulation approach was used to evaluate the extent to which no-take zones protect sharks with different degrees of reef association. A negative exponential function and fixed probabilities (e.g. staying at the same reef, moving between reefs, moving in/out, and leaving the system) were used to model shark movements on a reef patch-matrix. We then quantified 1) the proportion of time sharks spent in no-take zones and 2) the number of excursions (moves) from protected to non-protected areas under different management options. The simulation model showed that sharks with the highest site attachment also had the greatest protection from no-take zones in all management scenarios; however, the level of protection decreased rapidly as the probability of moving to a new reef increased. In addition, increasing the amount of protected areas did not really benefit more mobile sharks. These results suggest that existing MPAs may have limited conservation value for sharks with a lower reef association and that increasing the number of MPAs may not result in higher protection.

Relationship between diet composition of pelagic sharks and oceanographic condition around Hachijo Island, Izu Archipelago, Japan

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Hachijo Island is a volcanic island belonging to Fuji volcanic belt in Izu Archipelago, Japan, where is 287 km south off Tokyo. A major warm current, Kuroshio, run across Hachijo Island, and it oscillates between north and south of the island. Some pelagic sharks of Carcharhiniformes (2 families and 9 species), and Lamniformes (2 families and 3 species) inhabit around Hachijo Island showing some seasonal changes of distribution. Previous reports of stomach content analysis revealed differences of the diet composition among these shark species. Seasonal and annual variations of the diet composition have also been detected, but it is still unclear what causes of these differences. Kuroshio Current is a major environmental factor in this area and greatly affects on distributions of sharks and prey fishes. Therefore, the diet composition of sharks may vary with oceanographic conditions such as route of Kuroshio Current and water temperature. We studied relationship between diet composition of sharks and oceanographic conditions, and found some patterns of variations. Dusky shark *Carcharhinus obscurus* and Copper shark *Carcharhinus brachyurus* were found around Hachijo Island from February to May, which fed mainly on coast flying fish *Cypselurus pinnatibarbatus japonicus*. Feeding habits of these sharks are strongly related to seasonal migration of main prey. While, oceanic whitetip shark *Carcharhinus longimanus* always fed mainly on splendid alfonsino *Beryx splendens*, but more frequently on splendid alfonsino when Kuroshio Current running off north of Hachijo Island and warm water predominated. CPUE of splendid alfonsino increased under such condition, which implies they migrate in warm water relating to Kuroshio Current. Contribution of splendid alfonsino to oceanic whitetip shark probably depends on Kuroshio Current and water temperature. These examples suggest possible correlation between variations of oceanographic conditions and diet composition of pelagic sharks around Hachijo Island.

Partitioning and competition for cephalopod resources in top predators of the Indian Ocean

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Exploitation of top predators has dramatically increased during the two last decades in the western Indian Ocean. Such a removal of top predators could impact the food web structure through top-down trophic cascades. However, feeding habits and forage fauna of top predators remains poorly documented. In this work, we investigated the competition and resource partitioning for cephalopod resources among top predators. Cepaholopods are indeed an important component of their diet, and beaks are diagnostic hard part remains commonly recovered in the stomachs. Based on an extensive dataset, our goal then was to highlight the role of pelagic cephalopods in the diet of top predators in the Indian Ocean. From 2000 to 2010, the stomach contents of 35 fishes representing ten families (Xiphiidae, Istiophoridae, Scombridae, Carangidae, Coryphaenidae, Alepisauridae, Dasyatidae, Carcharhinidae, Alopiidae and Sphyrnidae) and of the sooty tern *Onychoprion fuscata* of the Mozambique Channel were analyzed. Using such a combination of diverse large predatory fishes and one seabird, we collected new information on prey composition and the resource partitioning in the western Indian Ocean. Ten species from four Teuthida families (Ommastrephidae, Onychoteuthidae, Histioteuthidae and Ancistrocheiridae), two Octopoda families (Argonautidae and Bolitaenidae) occurred very frequently in the stomach contents, while Sepiida were rare. Ommastrephids were the main cephalopod food sources: the purpleback flying squid *Sthenoteuthis oualaniensis* was the most prevalent prey by far, *Ornithoteuthis volatilis* was important for eleven predators and few but large specimens of the neon flying squid *Ommastrephes bartramii* were recovered in the stomachs of swordfish in the Indian South Subtropical Gyre and East African provinces. Surface predators' diets were characterized by lower cephalopod diversity but greater average numbers of cephalopod prey, whereas the deepdwelling predators (swordfish and bigeye tuna) preyed on larger specimens than surface predators (*O. fuscata* or yellowfin tunas *T. albacares*). The size of beaks collected in the stomachs illustrates the partitioning of the resources among top predators which forage on different part of the population. Our findings shed some light on resource partitioning and competition among large fish predators in the Indian Ocean and emphasized the usefulness of a community of marine predators to gain valuable information on the food-web structure.

Trophic networks involving anguilliform fish in New Caledonian coral reefs: insight from stable isotope analysis

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Anguilliform fish (moray eels, conger eels, snake eels) are high trophic level predators, however their trophic ecology remains largely unknown. This study focused on two anguilliform species: the moray eel *Gymnothorax chilospilus* (Muraenidae) and the conger eel *Conger* spp. (three species of Congridae). Carbon (δ13C) and nitrogen (δ15N) stable isotope ratios were measured in the two species and in various compartments (e.g. sediment, producers, primary consumers), along a coast to barrier reef transect in the southwest lagoon of New Caledonia. The results enabled us to reconstruct the food web architecture and to assess the organic matter pathways inside the lagoon. Significant differences in both C and N along the food web were observed. Particulate organic matter (POM) was C-depleted (-19.53 ± 1.85 ‰) and N-enriched (4.75 ± 1.01 ‰) compared to sediment organic matter (SOM; -14.14 ± 2.77 ‰ and 3.43 ± 1.33 ‰.). For each of these sources, signatures in carbon and nitrogen varied between sites along the coast-barrier reef transect. Other potential sources of organic matter such as *Halodule uninervis* (seagrass), *Padina australis, Halimeda opuntia* (macroalgae) and "algal turf", exhibited distinct C signatures with -8.40, -7.16, -18.43 and -19.46 ‰ respectively. Nevertheless, δ15N values were quite similar between primary producers (~2.20 ‰) and lower than POM and SOM signatures. Invertebrates displayed very different δ13C and δ15N isotopic signatures according to taxa (from -15.96 ‰ for shrimps to -8.61 ‰ for crabs for δ13C, and 3.64 ‰ for gastropods to 5.13 ‰ for crabs for δ15N), with N-enriched values with regard to source compartments. Invertebrates did not show strong variations of their signatures between coast and barrier reef. The isotopic ratios (C and N) of the two anguilliform fishes showed significant differences compared to underlying levels. However, we did not find differences between sites. The moray eel (*G. chilospilus*) showed C-enriched values (-12.81 ± 1.12 ‰) and a trend for N-depleted values (7.80 ± 0.62 ‰) compared to the conger eel (*Conger* spp.; -15.28 ± 2.37 ‰ and 8.52 ± 0.92 ‰), suggesting different diets and reliance upon different sources of organic matter. These divergences suggest the existence of complex food webs.

Feeding habits of the great sculpin *Myoxocephalus polyacanthocephalus* (Cottidae) and its position in the trophic system of Kamchatka waters

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Giant sculpin *Myoxocephalus polyacanthocephalus* (Pallas) is one of largest and widely distributed sculpins (Cottidae) in the North Pacific Ocean being typical representative of demersal ichthyofauna of Kamchatka waters. Taking into account high abundance and biomass of this sculpin, as predator it plays significant role in bottom communities and is considered as a target of coastal fisheries since attains large size (over 90 cm and 10 kg) and has a rather high food value. Nevertheless, data on its role in the trophic system of Kamchatka waters are still very limited. The main goal of this presentation is to analyze feeding habits of giant sculpin off Kamchatka and to present in the rough its position in the trophic system of the Sea of Okhotsk, Bering Sea and Pacific Ocean off Kamchatka. This research is based on the results of analysis of giant sculpin's stomach contents sampled during various seasons of 1978-2002 in 6 different areas of Kamchatka waters: northwestern Kamchatka, southwestern Kamchatka, Pacific waters off the northern Kuril Islands and southeastern Kamchatka, Kronotsky Bay, Karaginsky Bay, and the western Bering Sea. During the period of study over 1,500 stomachs were analyzed using quantity-weighted method. In addition, about 4,000 stomachs of giant sculpin were opened and analyzed in the field that enabled us broaden information on its diet composition and size of its prey. It is shown that despite rather wide food spectrum (over 150 dietary items) fish and decapod crustaceans are most important components of giant sculpin ration. The bulk of the former group consists of walleye pollock *Theragra chalcogramma*, flatfishes Pleuronectidae and sculpins Cottidae, while that of the latter group – of crabs of Majidae family. Seasonal, local, inter-annual and age-dependent changes of diet composition of giant sculpin are considered. The position of species under question in the trophic system of Kamchatka waters is revealed. Giant sculpin is facultative ambush predator with high feeding plasticity that enables it to use variety of food items. Trophic links that form biomass of the giant sculpin are marked out.

Is the elusive freshwater moray a top predator in tropical insular streams?

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Insular streams throughout the tropical Indo-Pacific tend to be numerically dominated by small fishes (especially gobies) and palaemonids (shrimps and prawns), with relatively few large-bodied top predators, eels of the genus *Anguilla* being the exception. A somewhat mystical (elusive) species of moray eel, *Gymnothorax polyranodon* (Bleeker 1853), the only known freshwater moray species, presumably acts as a top predator in these systems, but this has yet to be confirmed. Owing to the secretive nature of this rare species we attempted to piece together its feeding biology using the following tools and methods: maximum daily ration estimation from captive studies; dietary preference in captivity and information on predator and prey species body size to construct a stylised food web; and filming of feeding mode and behaviour in aquaria. Lastly, MRI and CT scans enabled us to examine the cranial morphology for wild caught individuals in order to correlate cranial form with feeding behaviour. Combining multiple information sources enabled us to assemble some understanding of the trophic role this elusive predator has in tropical insular streams.

The importance of resource pulse timing to the response of cutthroat trout

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Resources moving across ecosystem boundaries, known as resource subsidies, can have pronounced effects on consumers in recipient systems. Resource subsidies can induce cascading effects on recipient communities, subsequently altering ecosystem processes. Temporal variation is an inherent quality of resource subsidies, which often occur seasonally or as pulses (short-term, but high magnitude availability)". Recent theory suggests that seasonal timing of pulsed subsidies can be a critical component that determines the magnitude of consumer responses. In forested streams, terrestrial invertebrates entering streams often become an important energy subsidy for stream fishes. These terrestrial prey inputs vary in space and time with timing of peak abundance dependant on insect composition and phenology, or the parasites that drive their hosts into streams. To test the importance of resource pulse timing, we conducted a large-scale field experiment in small forested streams in British Columbia, Canada, to which we artificially added terrestrial invertebrates at different times (i.e., June-August pulse vs. August-October pulse). We found that cutthroat trout grew faster in the subsidized reaches during the early pulse period (June-August). Trout in subsidized reaches also grew faster during the late pulse period (August-October), however the growth rate of subsidized trout was lower during this period when compared with subsidized trout from the early pulse period. The survival rate did not differ significantly among treatments throughout either period. Population biomass was much higher in subsidized reaches after the early pulse period, but did not differ among treatment reaches after the late pulse period. Given that extensive temporal changes in water discharge and temperature occurred during the experiment, our results suggest that the temporal context of the physical environment could be important in determining the effects of subsidy timing on recipient fish consumers.

Location and transport of eggs and larvae of Western Australian dhufish, *Glaucosoma hebraicum* (Richardson, 1845)

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Larval supply can influence recruitment in marine fish population. Standard techniques for conducting quantitative eggs and larvae surveys have been described but it has been noted that documenting the abundance and location of eggs and larvae is difficult because of their patchy distribution and lack of knowledge of spawning locations. Identification of larvae and especially eggs using taxonomy is challenging and time consuming resulting in lag between surveys and data making predictions over annual periods impossible. *Glaucosoma hebraicum* is an iconic species and commercially and recreationally important finfish in Western Australia (WA). Fishing mortality is now exceeding natural mortality and fishers reported that they moved further offshore to catch *G. hebraicum* suggesting that heavy fishing in shallower waters in the west coast of WA had reduced fish abundance. Despite the importance of *G. hebraicum* very little is known about its early life stages and until now no larvae have been found in the wild. We used a combination of hydrodynamic modelling and genetics to locate and identify eggs and larvae of *G. hebraicum,* to unravel their transport and retention areas and to relate oceanographic variables to the abundance of eggs and larvae. This combination of methods allowed us to adjust our oceanographic sampling on a daily basis resulting in the first detailed map of the locations of *G. hebraicum* eggs or larvae at two sites in south-western Australia. Results showed that larvae in nearshore habitats can be rapidly carried offshore by surface Ekman flows unless they vertically migrate and then use onshore return flows to maintain their position on the shelf. The model indicated retention areas around Capes Naturaliste and Leeuwin and in Geographe Bay (SW of WA). We used quantitative PCR to measure the concentration of *G. hebraicum* DNA in mixed zooplankton samples providing a relative index of biomass. The development of these methods opens a route to study larval behaviour and monitor larval dynamics, not only in *G. hebraicum*, but also other species of importance.

A general, yet not universal, β-diversity-stability relationship for coral reef fishes of the Great Barrier Reef, Australia

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Despite important implications for theoretical ecology and conservation biology, the empirical relationship between β-diversity and community stability remains equivocal. For example, β-diversity (the spatial rate of species turnover) underlies most conservation strategies that aim to include the most species in a restricted number of sites. However, whether maximizing β-diversity also maximizes the temporal stability of biological communities, a key predictor of extinction risk, remains largely untested. We compared the spatial and temporal dissimilarity of fish communities inhabiting the largest coral reef ecosystem on Earth, the Great Barrier Reef of Australia. Fish β-diversity, measured as spatial turnover in species composition, and temporal stability (turnover) of communities were inversely related. This indicates that high β-diversity was associated with greater temporal stability, and thus, lower extinction risk. Our results demonstrated a strong β-diversity-stability relationship when all taxa were combined. While β-diversity tended to be associated with greater temporal stability at the community level, for some taxa such as surgeonfishes (Acanthuridae, one of the most abundant reef fish families), this relationship was reversed. We detected no effects of extrinsic factors (latitude, α-diversity or dispersal-related characteristics such as reef area and isolation) on the relationship between spatial *versus* temporal turnover. Therefore, the same β-diversity-stability relationship cannot be indiscriminately assumed for all taxa. We conclude that conservation strategies reliant on β-diversity will need to consider biotic factors such as taxon identity, and possibly functional group membership, to ensure the effectiveness of protection measures.

Important habitat characteristics for three key herbivorous fish species (Kyphosidae) in temperate waters

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Kyphosids are an important family of mainly herbivorous fishes distributed worldwide in both tropical and temperate reefs. Despite their high abundances and wide distribution, very little is still known about their role and interactions in temperate marine systems. For this study, we determined the environmental factors that influence the abundances of juvenile and adults of *Kyphosus sydneyanus/gladius* and *K. cornelii*, the three most common species in the temperate waters of Western Australia. Abundance of fish was assessed at 20 inshore and offshore sites with high and low structural relief using UVC. Environmental data characterising each site (i.e. depth, number and dimension of shelters, abundance of algae, and number of adult *Parma mccullochi*) were also collected. Higher abundances of juvenile and adult *Kyphosus sydneyanus/gladius* and juvenile *K. cornelii* were present on high relief reefs. Variation in abundances was explained predominantly by the number of caves in a reef. This confirms that topographic complexity plays a major role in influencing kyphosid abundances. However, of the variables that represent structural complexity of reef, certain distinctive structures appear to be important. Caves within high relief reefs are likely to provide refuge from predators for these large schooling fish. Since herbivorous fishes play an important role in the removal of algae and transfer of nutrients within and beyond the reef ecosystem, our results suggest key environmental factors, such as large structural attributes need to be considered especially in the process of planning and managing marine protected areas.

Socotra Archipelago: coastal fish community and productivity dynamics in an upwelling environment

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The Socotra Archipelago is a recognised global biodiversity hotspot, situated in the north-western Indian Ocean. These islands are subject to a seasonally variable environment as a result of the reversing monsoon winds, which drive a highly productive coastal upwelling system during the south-west monsoon (May to September). The coastal ecosystems support a diverse array of communities, including non-reefal coral communities with high live hard coral cover, and the highest diversity of marine fishes in the Arabian region with 830-890 species modeled to occur (Chao2, Jacknife2). Also the inshore fish biomass is phenomenally high. Biomass estimates based on visual underwater length frequency counts were started in 2007 as a proxy of coastal productivity, adding to a permanent transect-based monitoring program operated since 2000. Sanding crop in 2007 (pre-monsoon) averaged 2.08 t/ha across eight sites and 3.04 t/ha at five deeper sites (> 6m), with maxima of 5.13 t/ha (SD +- 5.64) at Socotra Island and of 5.95 t/ha (SD +-9.34) at Darsa Island. In 2011 again maxima (post-monsoon) of 5.03 t/ha (SD +1.67) and 6.77 t/ha (SD +-3.06) were recorded. These maxima rank among the highest fish biomass estimates from the Western Indian Ocean. Comparison of pre- and post-monsoon biomass of 113 species in 2011 indicate a very substantial biomass replenishment following the summer monsoon of 1012% (SD +-722%) across 12 relatively undisturbed sites, representing a rise from an average of 0.183 t/ha (SD +-0.275) in May to 2.035 t/ha (SD +-2.052) in November 2011, non-linearly related to increases of abundances by 448% (SD +- 478%) and of species number by 40% (SD +28%). This appears to be mainly attributable to a) upwelling related rises in primary productivity, as inferred from MODIS based productivity models; and, b) the cessation of the local beach-landing fishery during the monsoon. Univariate and multivariate analyses reveal dramatic seasonal community shifts regarding functional, trophic and taxonomic composition, and marked post-monsoonal recovery effects. The islands, however, obviously witness a severe drop in standing crop from 2007 to 2011 by approx. 90%, which is putatively due to recent rises in fishing effort, calling for instant management action.

Spatial patterns of fish assemblage structure in the Hawaiian archipelago: Identifying biogeographic patterns and species affinities

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There are currently a number of disparate data sets for reef fishes around the Hawaiian Islands but no single data set is spatially comprehensive enough to understand the natural and anthropogenic processes that affect the distribution, abundance, and size of reef fishes around the state. This study synthesized underwater-visual survey data into a spatially-comprehensive characterization of reef fish assemblages around the Hawaiian Islands allowing us to define the distribution of fishes across the entire Hawaiian Archipelago, while controlling for habitat, wave exposure and geographic influences. With this robust data set, we developed a biogeographic framework to examine natural and anthropogenic factors that influenced patterns of reef fish assemblage structure across one of the most unique and isolated marine ecosystems on earth. We combined the observational data with information on each species' life history traits and known geographic distributions to develop hypotheses about spatial patterns of abundance and biomass along latitudinal, oceanographic and anthropogenic gradients. Despite high levels of exploitation of fishes in the Main Hawaiian Islands (MHI) compared to the isolated and uninhabited, Northwestern Hawaiian Islands (NWHI), the MHI today has a higher richness of fishes than the NWHI. This pattern among others was explored following a rigorous quantitative approach, with analyses covering various metrics (e.g. numerical density, biomass, trophic structure) bringing in concepts from biogeographic theory. Regional affinities of species within the archipelago were in concordance with the known geographic distributions and hypothesized dispersal of each species to Hawaii. This work serves to identify important faunal breaks and spatial patterns of fish assemblage structure across the archipelago and identifies biodiversity hotspots that will help to define regional management strategies in Hawaii.

The development and validation of a mid-water baited video technique for investigating spatial patterns and human impacts on pelagic fishes

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The development of non-extractive fishery-independent sampling techniques, which are cost effective, repeatable and robust across a range of habitats and depths, is urgently needed for research in the pelagic environment. At present, it is difficult to obtain accurate survey data on pelagic fish assemblages. Studies on pelagic fish often rely exclusively upon longline surveys and catch records from commercial and recreational fishers. However, the use of fishery-dependent techniques alone can lead to sampling biases and is not appropriate in areas that are closed to fishing. The objectives of this study were to develop and validate the use of mid-water stereo Baited Remote Underwater Video systems (stereo-BRUVs) as an effective fishery-independent approach to study pelagic fish assemblages. We describe the design and use of mid-water stereo-BRUVs, investigate optimal soak times and discuss the effects of depth on the ability of this technique to survey pelagic fish. The advantages, limitations and requirements for future development of this emerging sampling technique are also discussed. The application of such novel methods will provide a better understanding about the ecology of pelagic fish assemblages and will allow us to explore their spatial patterns and the effect of human impacts on these pelagic species.

Management and depth protects creatures great and small in Fiji's largest marine reserve

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Protection from fishing generally results in an increase in the abundance and biomass of species targeted by fisheries within marine reserve boundaries. Natural refuges such as depth may also protect such species, yet few studies in the Indo Pacific have investigated the effects of depth concomitant with marine reserves. We studied the effects of artisanal fishing and depth on reef fish and shark assemblages in the Kubulau District of Vanua Levu Island, Fiji, using baited remote underwater stereo-video systems. Video samples were collected from shallow (5–8 m) and deep (25–30 m) sites inside and outside of Namena, Fiji's largest marine reserve (60.6 km2). In the shallow waters, species richness tended to be greater in the Namena reserve when compared to fished areas. In the deeper waters, species richness appeared to be comparable. The difference in shallow waters was driven by species targeted by fisheries, indicative of a depth refuge effect. In contrast, differences in the abundance and composition of the fish assemblage existed between protected and fished areas for deep sites, but not shallow. Fish species targeted by local fisheries were 89% more abundant inside the Namena reserve than surrounding fished areas, while non-targeted species were comparable. The abundance and biomass of reef sharks was approximately two and four times greater in shallow and deep locations, respectively, within the Namena reserve compared to adjacent fished areas. The greater abundance and biomass of reef sharks inside Namena is likely a result of greater prey availability rather than protection from fishing. This study suggests that artisanal fishing impacts on the abundance and species richness of coral reef fish assemblages and that marine reserve protection can benefit reef sharks. Observed effects of protection also vary with depth, highlighting the importance of explicitly incorporating multiple depth strata in studies of marine reserves.

Decreasing beta-diversity in fish communities along a depth gradient: evidence from repeated video deployments off New Zealand

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Continental slopes are among the steepest environmental gradients on earth. However, they still lack finer quantification and characterisation of their faunal diversity patterns for many parts of the world. Changes in fish community structure and diversity along a depth gradient were studied from replicated stereo baited remote underwater video deployments (N=347) within each of seven depth zones (50, 100, 300, 500, 700, 900 and 1200 m) at seven locations in New Zealand (latitudinal span: 21°). A total of 247 fish taxa in 86 families were identified from 7251 individuals after reviewing the videos. Results showed a significant interaction between latitude and depth in fish community structure. This interaction was explained by an increased similarity of fish communities at deeper stations compared to shallower, or in other words, beta-diversity significantly decreased with depth. A null modelling approach was then applied to determine if beta-diversity deviated from the expectations of a random (stochastic) assembly process and whether the magnitude of the deviation varied along the depth gradient. Using this approach, we showed that specimens tended to be more aggregated than expected in the shallow. However, at sites deeper than 700m, specimens were not aggregating and were even showing a pattern of over-dispersion (specimens were less aggregated than expected just by chance). It is then possible that mechanisms at depth operate to optimize maximal distances between individuals. We hypothesize that this pattern could be a feature of extreme environments.

Trophic function of reef fish in tropical seagrass beds

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Seagrass beds are important habitats or nursery grounds for coastal fish species. To understand the ecological function of different fish species in tropical seagrass ecosystems, we surveyed dominant organisms of seagrass beds for trophic modeling at Dongsha Island, the South China Sea by using Ecopath with Ecosim. Our results indicate that the assemblages of the seagrass beds in Dongsha could be divided into three different regions: inner lagoon, lagoon inlet and coastal area. The results of feeding analysis showed 2 herbivorous, 4 carnivorous, 1omivorous and 1 detrivorous feeding groups in the Dongsha seagrass beds. Very few animals fed seagrass directly in the seagrass beds except the parrot fish. Most of energy in the seagrass beds was mainly transferred from detrital litters to small benthic invertebrates, and then transferred to larger-sized animals through predation. Benthic invertebrate feeding fish was the most dominant fish feeding groups in the seagrass beds, including Lethrinidae, Mullidae and Labridae. The polychaetes and crustaceans were the most important food items for these fish species. The top predators of the Dongsha seagrass beds were piscivorous fish, and they were also the keystone species in the seagrass beds. Large-sized piscivorous fish like lemon shark and barracuda fed mostly on other fish in the seagrass beds. They exerted a strong top-down control on the abundance of many trophic groups. The results suggest abundant benthic invertebrates and piscivorous fish is key factors in maintaining the trophic structure of the seagrass ecosystems.

Spatial and ontogenetic variation in the trophodynamics of a coral reef fish community

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Coral reef scientists increasingly are using stable isotopes, primarily $\delta^{15}N$ and $\delta^{13}C$, to investigate the trophodynamics of reef fish communities and answer a variety of other ecological questions such as the relative importance of oceanic versus reef-derived primary productivity to reef fish. Most reef fishes, however, feed at multiple trophic levels throughout their lifetimes and the resulting ontogenetic variation in stable isotope values can lead to confusion in the construction of reef-based food webs or mask potentially useful patterns of spatial variation in isotope values. In order to investigate the relative strengths of ontogenetic and spatial variation in stable isotope values, we sampled 2,100 individuals representing just over 200 species of reef fishes from a single atoll in the southern Tuamotu Archipeligo, French Polynesia. Species sampled included representatives of all of the common Pacific reef fish families and encompassed the full range of body sizes and trophic levels present in the community. Collections were made at 13 locations within the lagoon of the atoll and at one site on the outer barrier reef. Lagoon locations sampled differed in their proximity to oceanic passes and underlying reef habitat, and several were situated on pinnacles that arose from the deeper lagoon floor. A sub-set of all individuals collected at a given location was selected from each collection to ensure that the full size range of each species in the catch was included in the sub-sample chosen for tissue isotopic analysis (both $\delta^{15}N$ and $\delta^{13}C$). Simultaneous collections of coral, macro-algal turf, reef epifauna, POM and zooplankton were made at each location for similar analysis. In general, we detected a large degree of both spatial and ontogenetic variation in values of $\delta^{15}N$, although the relative amounts varied among families. Ontogenetic variation in values of $\delta^{13}C$ was less than that for $\delta^{15}N$, but did show a significant degree of spatial variation for some species. Our results suggest that while the use of stable isotope values remains a valuable tool in studies involving the trophodynamics of reef fishes, care should be taken to minimize potentially confounding effects arising from simple ontogenetic shifts in diet.

Temperate reef fish diversity associated to large brown macroalgae: ecological and evolutionary explanations of a longitudinal trend in the South Pacific Ocean

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The causes of the species distribution in local communities depend on the resolution and the scale of observation. Several hypotheses have been proposed in order to explain trends in species richness, diversity and co-occurrence in natural communities. Given that most of these have been tested at local scales, our capacity to identify boundaries at which small-scale patterns can be generalized over large areas may be compromised. By using hierarchical sampling, incorporating several spatial scales (metres to thousands of kilometres) from Continental and Oceanic (Juan Fernández Islands) Chile, Northern and Southern North Island New Zealand, and Tasmania (Australia), we explored the differences in number of species, diversity and patterns of co-occurrence of temperate reef fish assemblages associated to large brown macroalgae. At broader spatial scales we identify a significant longitudinal westward range in fish species richness. Western temperate fish fauna have significantly more species in Tasmania and New Zealand than in Continental and Oceanic Chile. Evolutionary parameters such as ages of fish families and taxonomic distinctness gave a strong plausible explanation of this trend. Western reef fish faunas have older representatives than eastern ones. Ecological factors were fundamental in explaining species co-occurrence. Patterns of co-occurrence, for instance, were not related to numbers of species but to primary productivity. Species tend to have a random distribution at regions with high primary production. We highlights the importance of hierarchical sampling, most of patterns were obscure or absent at small or intermediate spatial scales. By sampling at multiple levels of spatial resolution we were able to understand biogeographic patterns of temperate reef fishes.

Effects of structural complexity of mangrove roots on fish assemblage structure and predation risk: a field experimental approach

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Mangrove estuaries often support large numbers of fish species and individuals compared to nearby open mud-or sand-flats. Though the sheltering effect of habitat complexity against predators is considered as an especially important factor responsible for such differences, such an effect has seldom been examined by field experiments. In order to clarify the effects of mangrove-root structure on the predation risk of small fishes in addition to fish assemblage structure, field experiments using experimental units (50×50 cm), in which artificial mangrove roots (PVC pipe) being planted with 4 density levels, were conducted in the Urauchi River mangrove estuary, Iriomote Island, southern Japan. In the first experiment, fishes that occurred in the units were recorded by visual census. In the second experiment (tethering), the predation risk for the small resident fish *Apogon amboinensis*, which frequented the mangrove-root areas in the study site, was compared among the units with different complexity levels. Numbers of fish species and individuals were highest in the unit with highest root density, although few fishes occurred in the unit lacking root structure. The predation mortality rate of *A. amboinensis* was lower in the unit with highest complexity than other units. These results supported the generally believed idea that the sheltering effect of mangrove-root structure may at least partly explain the higher fish diversity/abundance in the mangrove areas.

Fish4Knowledge - large scale coral reef fish monitoring using undersea computer vision methods

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The Fish4Knowledge project (www.Fish4Knowledge.eu) is developing automatic software for analyzing coral reef fish in underwater video recordings. These recordings are obtained from a set of permanent, fixed undersea cameras that observe portions of coral reef. The fixed cameras allow continuous monitoring in the 12 daylight hours for the past 3 years, which avoids the disturbance caused by short-term diver observations. The video streams are analyzed by automatic software which finds and follows individual fish and identifies the species. Approximately 100K hours of video have been recorded of which 3% have been analyzed so far giving about 6 million observations of the local fish population. 35 species of fish have been identified so far and the software is currently able to recognize 15 species representing more than 96% of the observed fish (many of these are resident species so are frequently re-observed). Ultimately, this software is expected to analyze close to 1 billion observations. Given the analyzed data, an interface has been developed that allows ichthyologists to study fish behavior or ecology from the following questions: 1) How does the number of observations of each species vary throughout the day, 2) or across the year, 3) or between different recording sites, 4) or between consecutive years?, 5) How are observations affected after a major event such as a typhoon? Data collection uses 10 undersea cameras at 3 sites in Taiwan (HoBiHu harbor, LanYu Island, Kenting). The videos are upload to a data server with 200 Tb data storage and 100 processors to run the analysis software on. By exploiting the stationary background, fish can be found in the recordings. Individual fish are followed across consecutive frames, and then identified as one of (currently) 15 species. Detection rate (for finding the fish) is 75% together with 10% false alarms, and individual fish recognition accuracy is 97% (however species that are less common are sometimes more difficult to recognize, so the average species recognition accuracy is 90%). Each fish is recorded in an database. The data can be explored using our web-based interface.

Shifting of Fish Species Composition in Ambon Bay (Indonesia); 1996 -2012

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Ambon Bay consists of two parts linked by a narrow channel with approximately 0.8 km long and 0.6 km wide. In Ambon Inner Bay (AIB), the deepest water is around 42 m, while in Ambon Outer Bay (AOB), it is at least 600 m, and the channel has variation in depth, 9-13 m. Fishery is an important activity by local fishers along the coastal area of Ambon Bay. They are usually operated gillnets, hand line or beach seines for catching fish in the bay. Since 1996, we have observed the fish composition taken by beach seine in the coastal area of AIB. Fish samples were collected monthly in three executive periods, such as 1996-1997, 2005-2006 and 2010-2012. The totals of 327 species of fish belonging to 67 families were identified from the fish samples. The 10 dominant species (in term of individual numbers and weights) seemed to be inconsistent in the catch composition. This slightly change in fish species composition was possible related to extend on upper land clearing and sedimentation that would be impacted on decrease of water quality in the Ambon Bay. Therefore, sustainable management for Ambon Bay is needed to enhance.

The taxonomy of ocean sunfishes (Tetraodontiformes: Molidae) with notes on changes in morphological characteristics with growth

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The ocean sunfishes (Molidae) are widely distributed in warm and temperate zones of all over the world. Some molid species, genus *Mola*, are known as the world's largest bony fish. For the taxonomy of the family, Fraser-Brunner (1951) ever proposed 3 genera including 3-5 species. As for the growth patterns, Martin and Drewry (1978) compiled morphological characteristics of various stages, i.e., from egg to adult. Both studies provided important biological information of the family, but contained not a few problems in the taxonomical methodology and in the lack of data in some growth stages. To discover the biological mysteries of the family, we adopt the molecular phylogenetic analysis using mtDNA focusing on the genus *Mola*. We found that *Mola* sunfish comprises at least 3 species (*Mola* spp. A-C) all over the world (Yoshita et al., 2009), which would pull the trigger at taxonomical reexamination of ocean sunfishes because Fraser-Brunner (1951) proposed that *Mola* includes only two species (*Mola mola*, *M. ramsayi*). We have taxonomically approached also to the biology of other two genera, i.e., Masturus and Ranzania, by the same methodology. In addition, we tried to reexamine morphological characteristics clarifying species-identification and growth patterns. With showing these results, we will provide new biological information of molid fishes.

What a drag: Large ectoparasites affect fish swimming performance and behavioural lateralization

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Ectoparasites can reduce individual fitness by negatively affecting behavioural, morphological and physiological traits. In fishes, there are potential additional costs if ectoparasites decrease streamlining, thereby directly affecting activities involving swimming. Few studies have examined the effects of ectoparasites on fish swimming performance and none distinguish between energetic costs imposed by changes in streamlining and effects on host physiology. Furthermore, no study has examined the effect of an asymmetrically attached parasite on individual turning bias (lateralization). On the Great Barrier Reef, the bridled monocle bream (*Scolopsis bilineatus*) is parasitized by an isopod (*Anilocra nemipteri),* which attaches above the eye. We show that parasitized fish have higher standard metabolic rates (SMR), poorer aerobic capacities and lower maximum swimming speeds than non-parasitized fish. Adding a model parasite did not affect SMR, but reduced maximum swimming speed and elevated oxygen consumption rates at high speeds to levels observed in naturally-parasitized fish. This demonstrates that ectoparasites create drag effects that are energetically important at high speeds. Although we found fish had no preference for turning in the direction of their attached parasite, the presence of the isopod resulted in increased lateralization in parasitized fish compared to unparasitized or parasite-removed fish. Together, these results demonstrate profound effects of ectoparasites both on fish swimming performance and behaviour, which has important implications for host demographics and survival.

Interactive drivers of activity in a free-ranging estuarine predator

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Animal activity patterns evolve as an optimal balance between energy use, energy acquisition, and predation risk, so understanding how animals partition activity relative to extrinsic environmental fluctuations is central to understanding their ecology, biology and physiology. Here we use accelerometry to examine the degree to which activity patterns of an estuarine predator are driven by a series of rhythmic and arrhythmic environmental fluctuations. We implanted free-ranging yellowfin bream *Acanthopagrus australis* with acoustic transmitters that measured biaxial acceleration and pressure (depth), and simultaneously monitored a series of environmental variables (photosynthetically active radiation, tidal height, temperature, turbidity, and lunar phase) for a period of approximately four months. Linear modeling showed an interaction between fish activity, light level and tidal height; with activity rates also negatively correlated with fish depth. These patterns highlight the relatively-complex trade-offs that are required to persist in highly variable environments. This study demonstrates how novel acoustic sensor tags can reveal interactive links between environmental cycles and animal behavior.

Habitat preferences of a corallivorous reef fish: predation risk versus food quality

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Many animals preferentially select a habitat from a range of those potentially available. However, the consequences of these preferences for distribution and abundance, and the underlying basis of habitat preferences are often unknown. The present study examined how distribution and abundance of an obligate corallivorous filefish, *Oxymonacanthus longirostris*, relates to coral architecture and diversity. Quantitative field surveys determined that individuals were almost exclusively associated with branching *Acropora* species, primarily *Acropora nobilis*. The main drivers of the distribution and abundance of *O. longirostris* were coral species richness and availability of branching coral. A series of pairwise choice experiments in which both structural complexity and coral tissue quality were independently manipulated showed that habitat choice was primarily based on structural complexity and shelter characteristics. In addition, the choice for the preferred coral (*A. nobilis*) was stronger in the presence of a piscivorous fish. These results indicate that species diverse coral habitats, that provide sufficient structural complexity along with nutritionally important prey, are essential for population persistence of this small, corallivorous reef fish.

Removal of temperate predators opens opportunity for range shifts in tropical fishes

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Tropical fishes are shifting their distribution into temperate waters in response to climate change. However, successful shifts may be constrained by access to suitable resources (i.e. food). We can predict that high levels of predation, in conjunction with seasonal temperature fluctuations may reduce potential foraging activities of tropical fishes in temperate environments. We tested the effects of temperate predators and seasonal water temperature change on the foraging behaviour of the tropical damselfish, *Abudefduf vaigiensis*. This species recruits to temperate, SE Australian waters throughout the Austral summer. Behaviour of *A. vaigiensis* was compared inside and outside of Marine Park Areas (MPAs) at the start (22°C water) and end of summer (18°C water). *A. vaigiensis* foraged at greater distances from reef substrate outside than inside MPAs, with foraging movement highest in the warmer water temperature. Within an aquaria trial foraging distance was greater when exposed to a temperate herbivore than when exposed to the temperate predator. These results suggest that protecting predatory fishes from fishing activities may improve resilience of temperate ecosystems to range-expansions of tropical fishes through controlling their capacity to access necessary resources.

The evolutionary and behavioral origin of fish migration: Escapement hypothesis

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Diadromous migration of fishes is the subject of active research, but there has been much less attention on the evolutionary or behavioral origins of diadromy. Diadromy likely evolved as a result of adaptive advantage of using higher productivity habitats for growth, but the reason the first individuals left their habitat to enter a new one is unknown. Eels likely evolved in tropics from a marine ancestor and salmon evolved in temperate regions from a freshwater ancestor. Evidence of ancestral life history states of these fishes can be seen in geographic clines of migratory patterns of the sympatric Japanese eel, *Anguilla japonica*, and masu salmon, *Oncorhynchus masou*. After analyzing otolith Sr/Ca ratios of catadromous Japanese eels that estimate their migratory history, a latitudinal cline of a higher proportion of sea eels (residents in marine habitat) was found in northern areas. The geographic variation in migratory pattern of anadromous masu salmon showed a mirror image phenomenon with the proportion of migrants to the sea decreasing in southern areas. The triggering mechanism of upstream migration in the amphidromous ayu, *Plecoglossus altivelis*, was studied to explore the behavioral origins of migration, and could be explained by a three step model of necessary conditions for starting migration: (1) age and body size, (2) endocrinological condition, and (3) psychological process. A behavioral model of drive was proposed to explain the last step that was influenced by exogenous/endogenous factors such as water temperature, fish density, hunger level etc. The drive of upstream migration behavior appears to be a psychological "repulsion" that occurs in stressed fish when the behavioral rule of optimum inter-individual distance is broken, since fish with stronger repulsion (large distance) showed active jumping behavior and stronger upstream migration. A vacuum activity of jumping behavior of ayu contained in a limited space occurred in random directions without any stimuli when water temperature increased. This vacuum activity can be interpreted as an escapement behavior of fish that bolt out of unfavorable environments, and this "escapement" might be a behavioral origin of fish migration that may also help to understand the evolutionary origin of migration (Random Escapement Hypothesis).

Effects of global warming on coral trout populations (*Plectropomus leopardus*)

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Global warming is increasingly affecting coral reef ecosystems and resulting habitat degradation has already had dramatic effects on fish communities. Less well known are the direct impacts of increasing temperatures on fishes. Coral trout (*Plectropomus leopardus*) is an ecologically important predator on coral reefs, but also one of the most sought-after species on Asian fish markets. Understanding how coral trout will respond to climate change is of ecological and economic importance and we investigated the thermal tolerance of this species using a number of physiological and biochemical parameters. *P. leopardus* were sourced from the northern and southern Great Barrier Reef (GBR), with the northern population experiencing temperatures on average 2.2°C higher than in the South. Fish were kept in experimental tanks for two months at 24°, 27°C, 30°C and 33°C. Despite the difference in acclimation temperatures between the two populations, we found no difference in aerobic performance at the different temperatures. Aerobic scope was highest at 30°C, but dropped markedly at 33°C. Interestingly, the combined stress of elevated temperatures and strenuous physical activity caused high mortality rates at 30°C and even more so at 33°C, suggesting that 30°C is already outside the optimal temperature range for this species. Critical thermal maxima comparisons between a number of large carnivorous coral reef fish indicate that the thermal tolerance of coral trout is relatively low. Furthermore, the lack of differences in metabolic rates of northern versus southern populations suggests a limited capacity for acclimation to higher temperatures. Coral trout in coral reef systems closer to the equator may therefore already be experiencing conditions at the limit of their thermal tolerance and will struggle to cope with the increased in temperature predicted by the end of the century.

Diversity and risk of extinction in Indo-West Pacific Sciaenidae

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Sciaenidae (croakers & drums) are a major capture fishery resource found along warm to temperate continental coasts, estuaries and river basins. World fishery productions of croakers are on the rise and have reached near two million metric tons in 2010 (FAO). About 70 to 80% of reported catches are Indo-West Pacific species (14 taxa). Globally, most of the 280 sciaenid species are targeted by industrial or artisanal fisheries. Three phylogeographic regions, New World, East Atlantic and Indo-West Pacific have been proposed for the family. The New World has the richest Sciaenidae diversity (~170 species), while the East Atlantic (includingthe Mediterranean) has the poorest with only 18 species. Under the auspice of IUCN, Global Marine Species Assessment (GMSA) and the Sciaenidae Red List Authority, the first global assessments of population status and risk of extinction for 275 of 280 known species of sciaenids were completed. In 2012, the Brazilian threatened marine species program has thoroughly reviewed the 52 sciaenid species from Brazilian waters, resulting in the following IUCN Red List categories; one species is Endangered (EN-1.9%), 2 Near Threatened (NE-3.8%), 35 Least Concern (LC-67.3%), 12 Data Deficient (DD-23.1%) and 2 Not Applicable (NE-3.8%). Of the 95 species known from the Indo-West Pacific region, 2 species are Critically Endangered (CR-2.1%), 3 EN (3.2%), 1 VU (1.1%), 46 LC (48.4%), 38 DD (40%) and 5 NE (5.3%). The Chinese Red Book (2009) included 4 EN (10.5%) and 15 VU (39.5) out of total 38 sciaenid species reported in Chinese waters. The discrepancies on frequency distributions of categories, or the category *per se* for some species, may be due to differences in applying IUCN criteria at regional or national vs. global levels, or to the lack of adequate data to evaluate population trends of many Sciaenidae. It may also reflect the risk of extinction is more severe in certain regions. Proper evaluation of the risk of extinction is extremely important to set priorities on biodiversity conservation. An improved practice of applying and interpreting IUCN criteria on Indo-West Pacific Sciaenidae is urgently needed to resolve these discrepancies.

Assessment of an exploited *Cheilinus undulatus* population in Fiji -underwater visual census and catch data from a remote fishing community

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The humphead wrasse *Cheilinus undulatus* (Rüppell, 1835) is the largest member of the Labridae family and is currently listed as endangered (IUCN Red List) and in CITES Appendix II. *C. undulatus* is likely to be a key species for long-term ecosystem stability and its life history characteristics make it very susceptible to fisheries exploitation at any level. In Fiji *C. undulatus* continues to be consumed locally and sold illegally since poor rural fishers are easily convinced by middlemen to catch large numbers for relatively substantial payment. Research is required to fill several knowledge gaps globally and specific data for the Fiji Islands are lacking. The Great Sea Reef is an international hotspot for marine biodiversity, where a major *C. undulatus* landing site was monitored on a daily basis for a complete year and fisheries and morphometric data was recorded for approximately 200 fishes from January to December 2012. To complement these data, *C. undulatus* populations were also examined using fishery-independent underwater visual census (UVC) within and outside a customary marine closure on the Great Sea Reef. Survey sites focused on areas where *C. undulatus* were most commonly caught and/or seen and were identified through local expert knowledge and landing site data. Five replicate timed swims were conducted at each of three sites, representing typical *C. undulatus* home ranges in protected and unprotected areas with structurally intact reef crests. At low tide, data were recorded on the number of individuals, size, maturity (phase A-D), behaviour, depth and habitat utilization. Very low densities on the heavily fished reef and relatively low densities in 'protected' sites were consistent with exploitation in this poorly managed customary closure. A broad range of sizes were caught during the year in contrast with a narrower range of smaller phase C individuals observed on the reef. The general absence of live mature males (phase D) and difference with caught sizes can be attributed to intensive extraction of this threatened species and highlights the need for enforcement of fisheries regulations in these communities.

Umbrellas can work underwater: bumphead parrotfish and seascape conservation

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Marine ecosystems have been subjected to a long history of degradation and are now threatened by rising sea temperatures, ocean acidification and extreme weather. With the increasing human footprint, conservation effort is focused on maintaining biodiversity and ecosystem functioning. It is, however, limited by gaps in our knowledge of species biology and ecological processes. Consequently, spatial conservation planning requires the making of critical ecological decisions in the absence of key information on species and ecosystem ecology. For this reason focal species and habitats are used as surrogates for biodiversity and ecological processes. Enhancing connectivity is also favored in conservation because it provides the mechanism for reserves to influence populations and ecosystems beyond their borders. We examined the effects of connectivity among tropical reefs, mangroves and seagrass on the performance of marine reserves in the Solomon Islands. These reserves were designed using indigenous ecological knowledge to conserve bumphead parrotfish (*Bolbometopon muricatum*) and protect food security. The large size, exploitation and cultural significance of this species makes it a flagship for conservation, the bio-eroding function these fish perform means they are keystone species on coral reefs, and their diverse ontogenetic habitat requirements suggest they may also be important umbrella species for biodiversity conservation. We demonstrate that seascape connectivity improved the ability of marine reserves to promote bumphead parrotfish abundance, and confirm that this species can be an important umbrella for conservation of local reef fish diversity. Connectivity among reef, seagrass and mangroves also enhanced reserve effects on 17 harvested fish species. This has implications for both local biodiversity and socio-ecological resilience because many of these species support extensive subsistence fisheries. These results support the assertion that habitat connectivity and heterogeneity can improve reserve performance and indicate that we may further enhance ecosystem functioning by managing reefs and adjacent habitats together as functional seascape units. Umbrella species are often adopted in terrestrial conservation programs. They are, however, not typically utilized in marine spatial planning, and we suggest that their incorporation may improve conservation outcomes in other heterogeneous seascapes.

The sustainability myth: making management and conservation decisions in a reproductive biology information vacuum

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Population sustainability in the face of fishing impact and both biotic and abiotic environmental changes is dependent upon population replacement capacity. The latter consists of the ability to produce compensatory numbers of offspring that survive to adulthood and have sufficient individual lifetime reproductive output (LRO) to offset population losses. Ova are the limiting gamete in most commercially important species, so an understanding of female reproductive biology is critical to making valid estimates of population replacement capacity. Individual LRO among females varies according to the number of ova released during a single ovulation event (instantaneous fecundity), the quality of ova produced, the degree of fertilization success, the number of spawning events in a spawning season, and the number of spawning seasons a female remains reproductively active. However, for many commercial species, much of this information is unknown. We do know that all of the factors listed above can have significant individual variation which will compound sources of error in estimates of individual LRO and population replacement capacity. In addition, there are likely to be as-of-yet undetermined interaction effects among reproductive factors and changing environmental conditions associated with climate change. Consequently, current positive statements as to the health and sustainability of either commercially important or presently unexploited fish populations are likely to be unfounded and premature.

Marine reserves can reverse the effects of fishing on protogynous coral reef fishes

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Intense fishing can decrease the size at sex change, alter the sex ratio, and possibly reduce the relative egg output of protogynous coral reef fishes. Can no-take marine reserves reverse these effects? We surveyed parrotfish (Labridae, Scarinae) populations within 28 no-take marine reserves and 32 reefs open to fishing in the central Philippines. Densities and size (TL) at transition from the predominantly female intermediate phase (IP) to the entirely male terminal phase (TP) of four species (*Chlorurus bleekeri, C. spilurus, Scarus dimidiatus*, and *S. rivulatus*) were compared among sites open to fishing and reserves protected for 1-2, 3-5, and 6-10 years. Three species showed 3- to 6-fold greater densities in 3-5 year old reserves relative to fished sites, in contrast to *C. spilurus* which had a significantly greater density in 6-10 year old reserves. For all four species, the size at sex change was greater by 5 cm in 3-5 year old reserves compared to fished sites. In addition, the size at sex change was greater by 10 cm in three species except *C. spilurus* in 6-10 year old reserves. Greater size at sex change in these protogynous species inside reserves will likely have a positive effect on the relative egg output of individual females. This effect, coupled with higher parrotfish densities in reserves may also enhance egg output per unit area from reserves compared to fished sites. Our initial findings strongly indicate that marine reserves can reverse some of the detrimental effects of fishing on protogynous species.

Connectivity of cryptobenthic fishes in Australian Marine Parks

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Cryptobenthic reef fishes comprise the most diverse families of marine teleost worldwide. Their ecological traits have shown to be an advantage to inhabit different marine environments along an extended latitudinal gradient. Although highly abundant, diverse, and presenting crucial symbiosis with other fishes they are often not considered key species for marine fish conservation. The New South Wales coast, Australia, presents four main Marine Protected Areas that aim to preserve the Australian marine biodiversity. However, there is no study that evaluates the efficiency of Marine Protected Areas on the population connectivity of cryptobenthic fishes. Self-recruitment, short home range, upwelling and depth are the main boundaries likely limiting the gene flow among populations of the cryptobenthic fishes. I herein present the genetic structure of the three most abundant species of cryptobenthic fishes found along the New South Wales marine parks, eastern Australia. This study investigates population connectivity based on three mtDNA regions, considered to be highly variable among these species. Results suggest that the four Marine Protected Areas have been providing high connectivity among the populations of the three species, despite of the numerous biogeographic boundaries found along the Eastern coast of Australia, and the ecological characteristics of these fishes. There is, however, a strong difference in the genetic diversity among species, showing for example a very homogeneous population of Australian endemic fishes along the entire NSW coast. Patterns of genetic diversity and population structure of the cryptobenthic fishes are an important aspect to evaluate the efficiency of marine protected areas in maintaining population connectivity and investigate the phylogenetic trends of mtDNA among different species of fish.

Climate change and the effects of sea-surface temperature and current flow on the growth and future productivity of fishes in a boundary current

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Climate change is having major effects on the world's marine ecosystems and it is predicted that the severity of this problem will increase rapidly in coming years. For fishes, changes in temperature regimes and patterns of ocean circulation driven by climate change are likely to lead to shifts in latitude and depth distributions and to changes in growth rates. Ultimately, this will have major implications for any fished species, since growth, productivity and sustainable yield of populations are tightly linked. To predict how marine species will respond to climate change, we applied dendrochronological techniques to develop records of growth from the otoliths of three long-lived (up to 70 years) fishes from the southern coast of Western Australia. These were a shallow water (<100 m) carnivore (western blue groper *Achoerodus gouldii*), a deep water (>250 m) carnivore (hapuku, *Polyprion oxygeneios*) and an omnivore (sea sweep *Scorpis aequipinnis*). We compared growth biochronologies of these species to a variety of instrumental records of the physical oceanography of the west coast of Australia. Growth of blue groper was strongly correlated with sea surface temperature off the south-west coast in the region where these animals were collected. In contrast, growth of hapuku and sea sweep was strongly correlated with Fremantle sea level (a proxy of Leeuwin Current strength). For both of these latter species, correlations were strongest with current strength measured in the previous year. In the case of hapuku, this lag probably reflects the time required for peaks in productivity generated by the current system to be propagated up the food chain to forage species such as squid. Scenarios of future climate change have contrasting implications for these fishes. For blue groper, warming temperature may lead to sizes-at-age that are 5% larger than in earlier records. However, the growth of sea sweep and hapuku should be reduced, given predictions that the strength of the Leeuwin Current will decline by an average of 15% by 2060.

Monitoring of pelagic species in large marine reserves: the missing piece in open ocean management

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Pelagic fishes and sharks have been the target of an expanding industrial fishing fleet for the last 60 years, leading to depletions and in some cases, trophic cascades. Following widespread collapse of coastal fish populations, no-take marine protected areas (MPAs) are increasingly recognised as an integral part of ecosystem based management strategies, in combination with fisheries management. Empirical evidence of biomass recovery in coastal MPAs is now ample. With the relatively recent establishment of large open-ocean MPAs, there is a need to establish effective monitoring approaches to establish how pelagic species respond to this new protection. Here we demonstrate a novel approach to the sampling of pelagic species in two recently implemented MPAs, following mid-water baited camera trials in Shark Bay, Western Australia. These include: 1) A mid-water baited camera survey conducted in Australia's newly established MPA in the Timor Sea, the Oceanic Shoal Commonwealth Marine Reserve (>70,000 km^2), to assess spatial heterogeneity in pelagic species and their distribution relative to seabed features. A hundred and seventeen moored mid-water baited cameras were successfully deployed in seabed depths to 165 m; 2) A multidisciplinary sampling regime undertaken in a large (>500,000 km^2) MPA, the British Indian Ocean Territory Marine Reserve, to establish techniques for monitoring pelagic species with respect to their distribution, abundance and biomass. Our approach combined mid-water baited cameras, hydro-acoustics and seabird surveys. A hundred and forty-four mid-water camera deployments were made, both moored to the seabed (n=30) and drifting in a long-line formation (n=105). Our approach establishes that information on spatial heterogeneity and long term monitoring of pelagic species can be attained using nonextractive means only. The implementation of large-scale open-ocean MPAs closed to extractive activities means that monitoring methods and metrics pertaining to the efficiency of closures are needed. Ideally, such methods would also become standardized between regions and oceans. We recommend similar multifaceted, and non-extractive approaches in other large open-ocean MPAs.

Poster Presentations
(Tuesday 25 June 2013)

25-01

Cryptic species and unique lineages in a number of reef fish species in the Western Indian Ocean revealed by broad-scale phylogeographic studies

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Numerous broad-scale and coarse-grained phylogeographic studies of putatively-widespread, reef-associated species have been conducted across the Western Indian Ocean (WIO) portion of their distributions, under the ambit of a large research programme initiated in 2008. The broader programme has used a multi-taxon approach and the analysis of data from multiple molecular markers to examine patterns of contemporary and historical connectivity among the regions of the WIO in order to elucidate the biogeographic history of the region and the evolutionary origins of its diversity and endemism. Individual species, representing the Apogonidae, Holocentridae, Labridae, Lutjanidae, Mullidae, Pomacentridae, Scaridae and Serranidae, have shown patterns varying from genetic homogeneity and panmixia to marked regional intraspecific genetic structure. However, several species have demonstrated substantial and deep genetic structure, suggesting the presence of hidden taxonomic diversity. Sequence data from one nuclear (S7 intron I) and two mitochondrial (ATPase 6 and cytochrome *b*) gene fragments revealed three deeply, divergent lineages of the sergeant major (*Abudefduf vaigiensis*) occurring in the WIO. One of the lineages was widespread, occurring across the WIO. The two others were restricted in distribution, occurring only at the Kenya and Seychelles sampling localities and in sympatry with the widespread lineage. Through the analysis of the same gene fragments, the sharptooth cardinalfish (*Cheilodipterus quinquelineatus*) was found to comprise of two lineages, inhabiting the northern and southern WIO, respectively. The two lineages occurred in sympatry at the Kenyan sampling locality. Despite sequence divergences in excess of 8% for the mitochondrial markers, nuclear data provided evidence of hybridization among the two lineages at this locality. This presentation will detail the genetic evidence for hidden diversity and present the results of ongoing morphological and morphometric comparisons among the various lineages within these and other species. The unexpected identification of cryptic species has been ancillary to the original aims, but this suggests that more diversity remains to be discovered in the WIO through studies such as the present.

25-02

A poster on the forthcoming book, *Coastal Fishes of the Western Indian Ocean*

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This book will be a multi-authored guide to the 3000 + fishes that inhabit the continental shelf, upper slope, islands and sea mounts of the Western Indian Ocean (WIO), including the Red Sea, Persian Gulf and Arabian Sea. Despite the considerable efforts of ichthyologists over the past two centuries, the taxonomy of WIO fishes is still a "work in progress". The systematic section of this new WIO fish book will cover details of the classes, orders, families, genera and species of the fishes in the region. Family accounts will include keys to genera and/or species. Examples of illustrations, photographs and text are shown on the poster.

25-03

The Fishes of New Zealand: a comprehensive guidebook

Clive D Roberts, Andrew L. Stewart, Carl D. Struthers (editors)

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New Zealand is an exciting and dynamic place to study fish diversity and systematics. A targeted, long-term programme of collecting and taxonomic research has significantly increased our knowledge of the fish fauna, which has so far doubled the total number of species known, despite many deep-sea habitats remaining unsampled. In order to fully document this growth, indicated by the consistent rate of discovery since the 1970s of 15–20 species per year, the fish team at Te Papa, together with 40 collaborating specialists worldwide, have been working on a government funded study since 1996 to collect, identify, and describe this diversity. To date, a total of over 1300 fish species in 252 families have been discovered within New Zealand waters, including 141 new to science (73 of these endemic) and 189 new records for the area; concurrently the number of voucher specimens registered into the National Fish Collection at Te Papa has doubled, by 47,000 specimens. Scientific outputs of the programme include 95 refereed papers, 261 popular articles, and submission of a 2000-page guidebook to enable the accurate identification of the fish fauna, with which to underpin the sustainable management and conservation of this important natural resource. Authors have prepared family accounts and species treatments, with illustrated keys, diagnoses, distribution maps, and accounts of habitat and biology for each species. This material is currently being produced by the fish team and Te Papa Press for publication in 2014. Further details of the guidebook and example pages are presented. Funding through contracts with New Zealand's Foundation for Research Science and Technology and National Institute for Water and Atmosphere Research is gratefully acknowledged.

25-04

Demersal fish community in nearshore waters off Niigata in the northern Sea of Japan

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Species composition of demersal fishes was investigated in nearshore waters (39–148 m depth) off northern Niigata by conducting 40 bottom trawls in March, May and August 2012. Water temperature and salinity just above the sea bottom were 9.2–9.5°C and 33.8–34.1 psu in March, 9.0–11.6°C and 33.9–34.2 psu in May, and 10.9–23.8°C and 33.6–34.4 psu in August, respectively. A total of 19,293 individuals belonging to over 105 species in 59 families were collected during the study period, with species richness and overall fish density peaking in August. Cluster analysis based on species composition revealed that the demersal fish community consisted of three groups which varied based on study site depth, with each site dominated by *Trachurus japonicas* and *Pseudorhombus pentophthalmus*, *Pagrus major* and *Apogon lineatus*, and *Glossanodon semifasciatus* and *Cottiusculus nihonkaiensis*, respectively. Indicator species analysis, which involves using a particular species to differentiate between groups, showed that gobiid (*Amblychaeturichthys hexanema* and *A. sciistius*), cottid (*C. nihonkaiensis* and *Ricuzenius pinetorum*) and pleuronectid (*Glyptocephalus stelleri, Pseudopleuronectes herzensteini* and *Tanakius kitaharai*) fishes contributed largely to the groupings. The obtained results described the depth-gradient structure of the demersal fish community on the continental shelf of this region.

25-05

Biological survey of the Al Zubarah, Qatar, UNESCO buffer zone, 2012 – Fishes

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Al Zubarah is a former pearl fishing settlement in northern Qatar. In 2013 it will be a new UNESCO world heritage site. Extensive archeological excavations are being done, but knowledge about the marine environment has remained unknown. The buffer zone contains a wide range of habitats covering bottoms with sea grass, sand, mud, rocks, sea weed and small reefs of peal oysters. The zone seems to be in a healthy environmental shape, although a few signs of human impact were noted. No oil spills were observed in the water, in sharp contrast to the situation on shore. In order to provide a first overview of the fish fauna in the Al Zubarah buffer zone, we used multi-mesh gill-net, baited traps, snorkeling and scuba diving. From 6-23 March 2012 a total of ca. 48 identified fish species in 33 families were observed, photographed and/ or caught within the buffer zone. Most effective method was the night snorkelling. A total of 33 species were collected for museum collections and tissue was sampled for DNA sequencing. A total of 35 species were UV-photographed. The most diverse families were seabreams (Sparidae) with 5 species, followed by stingrays (Dasyatidae), Blennies (Blennidae) and emperors (Lethrinidae) all with 3 species. Two species of stingray (*Himantura gerrardi* and *Himantura uarnak* (Fig. 3) are considered Vulnerable (VU), a shark *Chiloscyllium arabicum* (Fig. 2) and a labrid *Halichoeres leptotaenia* are considered Near threatened (NT), a butterflyfish *Chaetodon nigropunctatus* and a angelfish *Pomacanthus maculosus* are placed in the Least Concern (LC) category, whereas another stingray *Pastinachus sephen*, a flathead *Platycephalus indicus* and a grouper *Epinephelus tauvina* are currently Data Deficient (DD). More seasons need to be sampled in order to get at more complete species list.

25-06

Nonindigenous *Rhinogobius* gobies replaced indigenous congener species in Japanese streams

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Yoshinobori gobies (genus *Rhinogobius*, Gobioidei, Perciformes) are diadromous or genuine freshwater gobies and are common in various inland waters in East Asia. In Japan, there are 14 morphologically similar species, and many studies have suggested that they often compete ecologically with each other. Therefore, these species show different distribution patterns within and between rivers. Although some of these gobies have been reported to be introduced in nonindigenous areas, the ecological and/or genetic impacts on the indigenous congener species have not been well elucidated. We aimed to show the ecological impacts of introduced *Rhinogobius* gobies on indigenous congener species and propose the necessity of management of these gobies as invasive alien species. Case 1. Kuro-yoshinobori *Rhinogobius brunneus* is a diadromous species, and it mainly inhabits small streams (<10 km) that flow directly into the open sea. In contrast, kawa-yoshinobori *Rhinogobius flumineus* is a genuine freshwater species, and it inhabits various scales of streams. It is uncommon for both of these species to occur in the same stream because of competitive exclusion. *R. flumineus* had not been collected before 2001 in 2 small streams (Ido and Kumano-Miya Rivers, respectively, Mie Prefecture, central Japan) where *R. brunneus* was found. However, in 2009 and 2010, we collected *R. flumineus* individuals from the 2 streams and found that *R. brunneus* had disappeared. It is supposed that *R. flumineus* invaded the streams after 2001 and replaced *R. brunneus*. Case 2. In 1 stream (Ano River, Mie Prefecture), many *R. flumineus* and few tou-yoshinobori *Rhinogobius kurodai* had inhabited sympatrically, at least before 1988. However, *R. kurodai* has become the dominant *Rhinogobius* species in some areas, especially around the reservoir constructed in the upper reach of the river in 1989. mtDNA analysis indicated that *R. kurodai* is a nonindigenous species in the river (originated from the Lake Biwa population). We suppose that *R. kurodai* was introduced unintentionally as a result of fishery stocking of ayu from Lake Biwa in the river (a very common stocking program in Japan); *R. kurodai* became dominant over the indigenous *R. flumineus* locally, because *R. kurodai* is more adaptive to limnetic habitats such as lakes or reservoirs than to riverine habitats.

25-07

Current status and perspective of digital archives of Taiwan fishes

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Sponsored by Taiwan e-Learning and Digital Archives Program (TELDAP, 2002-2012), and on the basis of *The Fish Database of Taiwan* (http://fishdb.sinica.edu.tw) which was established in the early 1990s, the Biodiversity Research Center, Academia Sinica (BRCAS) has collected and integrated information such as classification, distribution, specimens, and references on 3,090 fishes of Taiwan. The contents of the database include specimen descriptions, images, skeletal X-rays, otoliths, COI gene sequences, and field collecting data; all are made accessible online and constantly updated. In addition to provide academic services to promote academic exchanges and raise research quality, the database also has popular science material such as "The Seafood Guide" so that it can contribute to the research, education, and conservation of marine resources. In 1994, *The Fish Database of Taiwan* started a long-term partnership with the global FishBase. It continues to actively collaborate with other international biodiversity databases and projects, including GBIF, Barcode of Life, and Fish4Knowledge. It conducts cross-strait collaboration with China to exchange fish specimen data and establish a parallel list of traditional and simplified Chinese fish names. The repatriation of 323 type specimens of Taiwan fishes from more than ten institutions abroad is another achievement. As to the value-added creations and applications, many educational products, e.g. Taiwan Fish Multimedia Dictionary, Taiwan Fish Culture and Nature Knowledge Base, Intellectual Restaurant, Augmented Reality Knowledge Cards, e-books and e-magazines, were developed via different channels provided by TELDAP. After TELDAP ended in 2012, Academia Sinica's Sustainable Management of Digital Archives Project began to provide funding so the work can continue. A cell phone version of *The Fish Database of Taiwan* will be developed to conform to the trend of querying real-time data. Other promotional applications being considered are in the areas of eco-tourism (diving, fishing, etc.), catch statistics, aquatic products transactions, aquarium trade, customs quarantine control, and marine conservation and education.

25-08

Coreoleucisucs namdongensis, a new species of Korean splendid dace (Cypriniformes: Cyprinidae)

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We describe a new species of splendid dace, *Coreoleucisucs namdongensis,* from rivers and independent tributaries of the southern coasts and Namhae Island of Korea with the exception of the Yeongsan River. The new species can be differentiated from its congener, *C. splendidus*, by the following characters: the pectoral fin with one or two black crossbars (mostly one); the pectoral and anal fins with a black crossbar; the caudal fin with two crossbars-an outer continuous curved black crossbar and an inner separate black crossbar not connected between the upper and lower lobes; short fin rays in the longest fin ray; a short distance from the dorsal-fin origin to the pelvic origin (16.8–20.2 % SL), the pre-dorsal length (47.8–51.7 % SL) equal to or slightly less than the pre-pelvic length (48.6–52.4 % SL), and a narrow interorbital width (23.5–30.2 % SL).

25-09

Taxonomic status of Megalonibea fusca Chu, Lo and Wu 1963 and *Protonibea diacanthus* (Lacepède 1802) (Perciformes Sciaenidae)

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Protonbea diacanthus (Lacepède 1802) is a large-size sciaenid (maximum length: 150cm SL), widely distributed in Indo-Western Pacific. *Megalonibea fusca* Chu, Lo and Wu 1963 is another large-size sciaenid (holotype: 143 cm SL) in Western Pacific with more restrict distribution in East China Sea. These two species bear similar types of sagitta, but different characteristics of swimbladder. Desse and Desse-Derset (1999) suggested that they may be the same species and their difference in swimbladders could be resulted from ontogenic modification. The similar sagitta implies a congernerous possibility for two species. The aim of this study is to clarify their taxonomic status based on DNA sequences including the mitochondrial 16S rRNA, COI and cytochrome *b* genes and the nuclear EGR1, EGR2B, RAG1 and rhodopsin genes for the samples collected from their range of distribution including Taiwan, China, India and Australia. The possibility of ontogenic changes in shape and appendage numbers of swimbladder of the species was investigated. Our joint evidence of morphological variation of sagitta and swimbladder in different-size specimens and molecular phylogenetic analysis demonstrate that *M. fusca* is the large-size adult *of Protonibea diacanthus. Megalonibea nibea* should not be considered as valid species.

25-10

Spatial and temporal characteristics of distribution of two seahorses, *Hippocampus coronatus* and *Hippocampus mohnikei* in the coastal waters of Korea

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The purpose of this study was to investigate the occurrence patterns on winter season in relation to seasonal variation of fishes at 4 sites of seagrass beds and unvegetated area in Gamark Bay (southern Korea), in September and December 2008. A total of 1,608 fishes of seahorses belong to 11 families, 13 species were collected, during the study period. In September, *Hippocampus coronatus* was observed difference in abundance between seagrass beds (above 1.4 seahorse 100 m^{-2}) and unvegetated area (approximately 0.3 seahorse 100 m^{-2}), while have no difference in *H. mohnikei*. In December, seahorses were not different in abundance by habitats (observed 2 seahorses in *H. coronatus* at Seagrass beds and unvegetaed area, zero in *H. mohnikei*). The results presented that occurrence of *H. coronatus* which was temporal species were closer correlated with decline of seagrass. However, our knowledge was limited on distribution patterns of *H. coronatus* and *H. mohnikei* in winter season, it needed to further study in seasonal variation of seahorses on seagrass beds.

25-11

Taxonomic review of *Kyphosus* species (Perciformes, Kyphosidae) from the Indo-Pacific and Atlantic Oceans

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A taxonomic review of the genus *Kyphosus* disclosed eleven species, including *K. bigibbus* Lacepède, 1801, *K. cinerascens* (Forsskål, 1775), *K. vaigiensis* (Quoy and Gaimard, 1825), *K. analogus* (Gill, 1862), *K. elegans* (Peters, 1869), *K. sydneyanus* (Günther, 1886), *K. pacificus* Sakai and Nakabo, 2004 and *K. hawaiiensis* Sakai and Nakabo, 2004 (Indo-Pacific), and *K. bosquii* (Lacepède, 1802), *K. incisor* (Cuvier, 1831) and *K. metzelaari* Jordan and Evermann, 1927 (Atlantic). An additional Atlantic species, reported as *K. sectatrix* by Moore (1962), comprises the two previously described species, *K. bosquii* and *K. metzelaari*. *Kyphosus* is defined by the following characters: both jaws with single lanceolate, incisor-like teeth with a horizontal base in individuals > ca. 50 mm SL (tri- or poly-cuspate, incisor-like teeth in juveniles), dorsal fin with 11 spines and 12-14 soft rays, anal fin with 3 spines and 11-13 soft rays, pectoral fin with 16-20 soft rays, branchiostegals seven, vertebral number 10+16 or 11+15=26, caudal fin moderately forked, body covered by transforming ctenoid scales, and interorbital space of head and maxilla scaled in post-juveniles. The species of *Kyphosus* are distinguished from each other by a combination of dorsal and anal fin soft ray counts, and counts of longitudinal row scales along the midbody (LR) and gillrakers in the first gill-arch (Gr). Four species groups are recognized: Group A (*K. vaigiensis*, *K. analogus* and *K. incisor*) with 14 dorsal-fin rays and 13 anal-fin rays; Group B (*K. cinerascens*, *K. elegans* and *K. metzelaari*) with 12-13 dorsal-fin rays, 11–12 anal-fin rays, LR ≤57 and Gr ≥23; Group C (*K. bigibbus*, *K. pacificus*, *K. hawaiiensis* and *K. bosquii*) with 12 dorsal-fin rays, 11 anal-fin rays, LR ≥58 and Gr ≥21; and Group D (*K. sydneyanus*) with 12 dorsal-fin rays, 11 anal-fin rays, LR ≤58 and Gr ≤21. The species of *Kyphosus* may have originated from a herbivorous species inhabiting coastal rocky reefs, later becoming broadly distributed worldwide by an association with floating drift materials. This is discussed on the basis of morphological and genetic analyses.

25-12

A review of the red-fin *Decapterus* group with an undescribed species (Perciformes: Carangidae)

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The carangid genus *Decapterus* can be defined by having a single finlet behind both the second dorsal and anal fins, and lacking scutes on anterior curved part of lateral line. We revised taxonomically the species of *Decapterus* with red-colored caudal fins (the red-fin *Decapterus* group) and revealed that the group consisted of following four species: *D. akaadsi* Abe 1958, distributed in the eastern Indian Ocean and West Pacific from the Andaman Sea to Indonesia, north to central Japan; *D. kurroides* Bleeker 1855, distributed in the Indo-West Pacific from Red Sea and eastern coast of Africa to eastern Australia, north to Philippines; *D. tabl* Berry 1968, distributed circumglobally in tropical and subtropical seas; and an undescribed species, occurring in the Andaman Sea, the South China Sea, and Indonesia. Diagnositic characters of those species are as follows: *D. akaadsi*—curved part of lateral line with 43–53 cycloid scales, straight part of lateral line with 26–29 scutes, head length 26.7–30.1% SL, and body depth 24.0–27.9% SL; *D. kurroides*—curved part of lateral line with 45–51 cycloid scales, straight part of lateral line with 30–32 scutes, head length 30.3–33.0% SL, and body depth 23.4–26.4% SL; *D. tabl*—tip of upper jaw usually hooked and opercular membrane partly serrated in larger specimens, lower gill rakers 28–33, curved part of lateral line with 61–72 cycloid scales, body depth 16.6–23.0% SL, pectoral-fin tip not reaching to a level of second dorsal-fin origin; undescribed species—lower gill rakers 25–31; curved part of lateral line with 54–62 cycloid scales, body depth 19.4–22.5% SL, pectoral-fin tip usually beyond a level of second dorsal-fin origin.

25-13

Coilia macrognathus aequidentata Chabanaud, 1924, a junior synonym of *Coilia lindmani* Bleeker, 1857 and comparisons with *Coilia grayii* Richardson, 1845 (Clupeiformes: Engraulidae)

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The taxonomic status of *Coilia macrognathus aequidentata* Chabanaud, 1924, originally described from southern Vietnam, has been in doubt. Detailed examination of the three syntypes of *C. m. aequidentata*, and the holotype and 66 non-type specimens of *Coilia lindmani* Bleeker, 1857 (type locality: Palembrang, Indonesia) shows that *C. m. aequidentata* is a junior synonym of *C. lindmani*. Examination of specimens of *C. lindmani* showed that the body depth, pectoral-fin length, upper-jaw length, and a distance between the posterior ends of the supramaxilla and maxilla tended to become greater proportionally with growth. Although *C. lindmani* is similar to *Coilia grayii* Richardson, 1845, sharing almost same the numbers of scutes and gill rakers and the maxilla extending posteriorly beyond the opercular margin, the two species have never been compared with each other in detail; the only known difference between them is the number of the pectoral-fin filaments (6 vs. 7, respectively). Comparisons of *C. lindmani* with *C. grayii* based on 70 and 6 specimens, respectively, including the type-specimens, from the western Pacific revealed that the former has a relatively deeper body (depth 91.5–138.1%, mean 112.8% of head length vs. 92.0–108.3%, 100.8% in *C. grayii*), a longer upper jaw (length 87.3–128.1%, 107.1% vs. 85.6–112.8%, 102.5%), a longer first branched pectoral-fin ray (length 69.1–99.2%, 84.3% vs. 57.7–58.6%, 58.2%), a longer longest pectoral-fin filament (length 164.6–293.4%, 232.3% vs. 164.8–180.6%, 172.7%), a shorter anal-fin base (length 252.2–303.3%, 280.7% vs. 311.7–342.3%, 324.4%), a deeper caudal peduncle (depth 15.7–22.4%, 18.3% vs. 12.6–15.1%, 13.6%), and a higher number of caudal-peduncle scales (9–11, mode 9 vs. 7–8, 7). *Coilia lindmani* is distributed in rivers and estuaries in Thailand, Cambodia, Vietnam, and Indonesia (Sumatra), whereas *C. grayii* occurs in estuaries and coastal waters in China from Suchow to Hainan.

25-14

Review of the *Chromis xanthura* species group, based on morphological and molecular analyses, with the identification of an undescribed species (Perciformes: Pomacentridae)

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Chromis xanthura (Bleeker, 1854), originally described from a single Indonesian specimen, has been regarded as a valid, widely distributed Indo-West Pacific species, with two color forms. One of the two color forms has a white caudal peduncle and fin; and the other has a black caudal peduncle and fin. *Chromis opercularis* (Günther, 1867), originally described from a single Tanzanian specimen, has been recognized as a valid Indian Ocean species that is closely related to *C. xanthura*, although detailed comparisons of the two species have not been published. The two species, including the color forms, are herein defined as a *C. xanthura* species group characterized by the presence of two black bands along the preopercular margin and upper opercular margin, respectively, in adults and the yellow upper and lower margins of the caudal fin in juveniles. An examination of the holotypes and non-type specimens of *C. opercularis* and *C. xanthura*, including its two color forms, across their distributional ranges revealed the two color forms of *C. xanthura* to be identical and the two species to be distinct with allopatric distributions. *Chromis opercularis* is distributed in the Indian Ocean and *C. xanthura* in the western Pacific Ocean and Christmas Island. A molecular analysis and underwater observations also support the recognition of two color forms as the same species. During this study, a species similar to the black-tail form of *C. xanthura* was found in the Ryukyu Islands, Palau, and French Polynesia. Underwater observations of the species of *Chromis* by the authors in the Ryukyu Islands revealed that it schools with *C. xanthura*. Despite this, the *Chromis* is distinguished from the latter species in having a higher gill raker count (mode 30 vs. 28 in *C. xanthura*), a wider black band along the preopercular margin, shorter longest dorsal-fin soft ray (mean 22.4% of SL vs. 30.6%) and first anal-fin spine (mean 5.6% vs. 7.0%), the posterior tips of the caudal fin densely black (vs. tips the same color as the rest of the fin), two triangular blotches at the upper and lower ends of the caudal-fin base (vs. no blotches), and a sequence divergence of mitochondrial COI (greater than 6% between the two species).

25-15

Revision of the *Minous trachycephalus* complex, with two undescribed species (Scorpaeniformes: Synanceiidae)

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The Indo-Pacific stonefish genus *Minous* comprises 10 valid species. The *Minous trachycephalus* complex is herein defined by the following combination of characters: first dorsal-fin spine short, its base close to second spine base; dorsal spine strong and hard; and no transverse dark bars on the caudal fin. The complex comprises six valid species: *M. coccineus* Alcock, 1890 (distributed in the Indian Ocean and South China Sea) characterized by the inside of the pectoral fin yellow with irregular black blotches, and posterior lacrimal spine longer than anterior lacrimal spine; *M. dempsterae* Eschmeyer, Hallacher and Rama-Rao, 1979 (western Indian Ocean)—inside of pectoral fin brownish-black with small irregular pale spots, and posterior lacrimal spine longer than anterior lacrimal spine; *M. inermis* Alcock, 1889 (Indian Ocean)—inside of pectoral fin brown, pectoral fin very long, and anterior and posterior lacrimal spines relatively short; *M. longimanus* Regan, 1908 (Saya de Malha Bank)—inside of pectoral fin brown, pectoral fin very long, and posterior lacrimal spine longer than anterior lacrimal spine; *M. pictus* Günther, 1880 (western Pacific)—inside of pectoral fin yellow with black lines along the fin rays and posterior lacrimal spine longer than anterior lacrimal spine; and *M. trachycephalus* (Bleeker, 1854) (eastern Indian and western Pacific oceans)—inside of pectoral fin brown with hexagon-shaped white blotches, and caudal fin with small brown spots. In addition to these six species, two undescribed species, *Minous* sp. 1 (northwestern Australia and Indonesia) and *Minous* sp. 2 (northern Australia), are recognized in the *M. trachycephalus* complex. *Minous* sp. 1 differs from all other members of the complex in having the anterior and posterior lacrimal spines relatively short; preopercular spines not developed; inside of pectoral fin yellow with black lines along the fin rays; body brown with whitish-brown blotches dorsally; and caudal fin pal e brown. *Minous* sp. 2 is distinguished by having a short first dorsal-fin spine (3.4–4.8% of standard length); posterior lacrimal spine longer than anterior lacrimal spine; inside of pectoral fin yellow, with large black blotches in three rows; a pale brown body; and caudal fin whitish, with small black spots dorsally.

25-16

Revision of the *Scolecenchelys gymnota* species group (Anguilliformes: Ophichthidae)

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The worm eels belonging to the genus *Scolecenchelys* are widely distributed in Indo-Pacific from tropical to warm-temperate area. Most part of species of the genus inhabit in shallow water, others in deep water limit to about a depth of 800 m. The genus is characterized by the absence of pectoral fins; the center of eye located posterior to the mid-point of the upper jaw; the upper-jaw and the vomerine teeth conical, pointed, and arranged in single to triple rows; the posterior nostril situated on the inner fold or margin of the upper lip; three preopercular sensory pores; and two infraorbital sensory pores between anterior and posterior nostrils. The genus can be divided into two morphological groups by the position of the dorsal-fin origin: *S. gymnota* species group (the origin posterior to the level of anus) and *S. macroptera* species group (the origin anterior to the level of anus). The *Scolecenchelys gymnota* species group consists of the following 10 species: *S. aoki* (Jordan and Snyder, 1901), *S. australis* (Macleay, 1881), *S. chilensis* (McCosker, 1970), *S. fuscogularis* Hibino, Kai and Kimura, 2013, *S. gymnota* (Bleeker, 1857), *S. iredalei* (Whitley, 1927), *S. japonica* (Machida and Ohta, 1993), *S. laticaudata* (Ogilby, 1897), *S. profundorum* (McCosker and Parin, 1995), and an undescribed species. *Scolecenchelys aoki* and *S. iredalei* are regarded as valid species, but *S. borealis* (Machida and Shiogaki, 1990), *S. erythraeensis* (Bauchot and Maugé, 1980), and *S. tasmaniensis* (McCulloch, 1911) as junior synonyms of *S. aoki*, *S. iredalei*, and *S. australis*, respectively. Although the undescribed species from South Africa, Réunion and Mauritius resembles *S. laticaudata*, the former can be distinguished from the latter by fewer vertebral counts and a larger head.

25-17

Polyphyly and paraphyly found in the genus *Carangoides* (Carangidae, Perciformes) and the phylogenetic position of the type species

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The carangid genus *Carangoides* was established by Bleeker (1851), subsequently Jordan (1919) defined its type species as *Carangoides praeustus* [Anonymous (Bennett), 1830]. Although the genus are characterized by having scutes present only on posterior straight part of lateral line, undeveloped adipose eyelid, and falcate or sometimes prolonged anterior second dorsal and anal fins (Gushiken, 1983), Kimura et al. (2011) doubted its monophyly. In this presentation, we show the polyphyly and paraphyly of the genus *Carangoides* and phylogenetic relationship between the type species and other *Carangoide*s species, using molecular phylogenetic [mitochondrial DNA (Cyt-*b*, 16s rRNA, COI) and nuclear DNA (RAG2)] and morphological methods. All *Carangoides* species excluding *C. praeustus* compose a large clade with six other genera of Caranginae: *Alectis*, *Atropus*, *Caragichthys*, *Parastromateus*, *Ulua* and *Uraspis*, but these *Carangoides* species are arranged dispersively in the clade, showing distinct paraphyly. The type species *C. praeustus* separates phylogenetically far from other *Carangoides* species and composes a different clade. *Carangoides praeustus* also differs morphologically from other *Carangoides* species in having an anchor-shaped vomerine tooth patch (vs. triangle or V-shaped tooth patch) and narrow neural-and hemal-spine tips of ninth caudal vertebra (vs. paddle-like or blade-like tips). From these facts, the genus *Carangoides* should be monotypic, including only *C. praeustus* and other *Carangoides* species should belong several different genera.

25-18

Review of the triplefin genus *Enneapterygius* in the Ryukyu Islands with three undescribed species (Tripterygiidae)

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The triplefins of the genus *Enneapterygius* are widely distributed in the tropical to temperate Indo-Pacific. Eleven species in the genus were previously known from the Ryukyu Islands: *Enneapterygius bahasa* Fricke, 1997, *E. elegans* (Peters, 1877), *E. etheostoma* (Jordan & Snyder, 1903), *E. flavoccipitis* Shen, 1994, *E. hemimelas* (Kner & Steindachner, 1867), *E. leucopunctatus* Shen, 1994, *E. philippinus* (Peters, 1869), *E. rhabdotus* Fricke, 1994, *E. signicauda* Fricke, 1997, *E. similis* Fricke, 1997, and *E. tutuilae* (Jordan & Seale, 1906). During ichthyological surveys in the Ryukyu Islands, *E. erythrosoma* Shen, 1994 and *E. fuscoventer* Fricke, 1997 were recorded from Japan for the first time and three undescribed species, *Enneapterygius* sp. 1–3, are recognized. *Enneapterygius* sp. 1 (collected from Osumi Peninsula, and Amami-oshima and Yoronjima islands) is similar to *E. atriceps* (Hawaiian endemic) in nuptial coloration of males, but can be easily distinguished by usually having 12 second dorsal-fin spines (vs. 13–14 in *E. atriceps*), usually 17 anal fin rays (vs. usually 19), and an unbranched anterior nostril tentacle (vs. branched). *Enneapterygius* sp. 2 (collected only from Yaku-shima Island) and *Enneapterygius* sp. 3 (Okinawa-jima Island) are members of the *E. tutuilae* species group, which is characterized by having unbranched pectoral fin rays, 2 + 2 + 2 mandibular pores, 8 caudal peduncle scales. In this species group, *Enneapterygius* sp. 2 is very similar to *E. tutuilae* in sharing the similar meristics and morphometrics, but differs in having a black spot on the first dorsal fin (vs. absent in *E. tutuilae*), a black band on the caudal peduncle (vs. absent), and scales on the ventral surface of the body (vs. no scales). *Enneapterygius* sp. 3 is similar to *E. mirabilis* in having an elongated first dorsal fin, but is separated in having 16 anal fin rays (vs. 19–20 in *E. mirabilis*), 22 notched lateral-line scales (vs. 23–27), and 4 pores at center of the parietal sensory system (vs. 3). This study brings the total number of species of, *Enneapterygius* in the Ryukyu Islands to 16.

25-19

Taxonomic revision of bar-tailed species of the genus *Platycephalus* Bloch, 1785 from Australia (Scorpaeniformes: Platycephalidae)

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The platycephalid genus *Platycephalus* Bloch, 1785 is characterized by having usually 60 or more pored lateral line scales, and 13–14 second dorsal and anal fin rays, a single tooth plate on the vomer, and two distinct preopercular spines. Of the members of *Platycephalus*, species having some longitudinal dark bars or stripes on the caudal fin well resemble each other and have much taxonomic confusion (e.g., Imamura, 2008). In this study, "bar-tailed species" of *Platycephalus* from Australia, having the richest species diversity of the genus, is taxonomically revised. After the detailed examination of about 360 specimens of the genus from Australia, the following four bar-tailed species were recognized form the area: *P. angustus* Steindachner, 1866, *P. endrachtensis* Quoy & Gaimard, 1825 (sensu Imamura, 2008), *P. westraliae* (Whitley, 1938) and undescribed *Platycephalus* sp. *Platycephalus angustus* was confused with *P. indicus* (Linnaeus, 1758) in some museums in Australia. The former is separable from all other congeners in having teeth on the dorsal surface of the premaxilla anterolaterally on the edge of the upper jaw. Until Imamura (2008) was published, *P. endrachtensis* and *P. westraliae* were mistakenly identified as *P. arenarius* Ramsay & Ogilby, 1886 and *P. endrachtensis*, respectively. *Platycephalus endrachtensis* is a senior synonym of *P. arenarius* and separable from other bar-tailed species in having characters such as a narrower interorbital width, fewer vomerine teeth, and four or more dark bands on the caudal fin. Although this species has been considered to distribute from New South Wales, across northern Australia to Hamelin Bay, Western Australia, and also from Bali, no reliable records from northern Australia were recognized in this study. *Platycephalus westraliae* easily differs from other three bar-tailed species in having the upper iris lappet broad and usually slightly bilobed. Although *Platycephalus* sp. has been mistakenly identified as *P. indicus* by previous authors, the former can be distinguished from the latter by having a larger number of pectoral fin rays, fewer gill rakers, longer postorbital length and narrower suborbital width.

25-20

Morphological and genetic divergence in *Crystallichthys matsushimae* (Cottoidei, Liparidae)

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Crystallichthys matsushimae is distributed in the Seas of Japan and Okhotsk, and off the Pacific coast of northern Japan. In the Sea of Okhotsk and off northern Japan, the species is characterized by round red markings on the body. However, recently we found specimens with yellow body stripes in the southern Sea of Japan. In a study of morphological and genetic divergence between the two morphotypes, clear differences were found in the numbers of dorsal, anal and pectoral fin rays, but not so for morphometric characters. The genetic analysis disclosed two highly divergent mitochondrial lineages, on the basis of sequence variations on the cytochrome *b* and COI genes, although not necessarily corresponding to the two morphotypes. Specimens belonging to one lineage included both morphotypes (collected from the Seas of Japan and Okhotsk), whereas the other included only the red morphotype (collected from the Pacific coast of Japan and the Sea of Okhotsk). Gene flow restrictions between the two morphotypes and the geographic populations were determined from significant ΦST estimates.

25-21

Fish species diversity between the present and 200 years ago at Heuk-san Do, Korea

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In 1814, Jeong Yak-Jeon compiled a book (titled *Ja-San-Eo-Bo*) concerning the natural history of fishes of Heuk-san Do, which is an island located some distance west of the southwestern coast of Korea. During the persecution of Catholics at the time of the Cho-sun Dynasty, Jeong Yak-Jeon was exiled to Heuk-san Do for a period of 15 years. In his monograph he recorded 227 species from waters adjacent to the island, including 70 scaled fishes, 42 scaleless fishes, 69 shellfish, and 46 other species. *Ja-San-Eo-Bo* is one of the five oldest fisheries books concerning Korea, but because it was written entirely in old Chinese characters it was regarded as largely inaccessible. Jeon Moon-Gi translated the book into modern Korean language in 1977, enabling the contents to be widely read, but this translation did not include scientific names or pictures, or identify relationships to currently recognized Korean species. To address these problems, in 1997 an updated version (*Sang-Hae-JaSan-Eo-Bo*) was published by Jeon Seok-Jo, but in this publication some Korean fish names remained unclear. The aim of our study was to collect fish specimens from Heuk-san Do and compare them with 104 nominal species recorded in *Ja-San-Eo-Bo*. From August to December 2012 we collected fishes at Heuk-san Do using gill net, bag net, trap net and long line methods. We identified a total of 70 species, of which 36 species corresponded to fishes recorded in *Ja-San-Eo-Bo*. We investigated the identity of the remaining 68 nominal species, based on scientific publications, and as a result we confirmed the identity of an additional 21 species, 27 were ambiguous, 13 were uncertain, and 7 were unable to be identified.

25-22

Attempts to improve the Internet atlas of Japanese fishes from web 1.0 to web 2.0

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The Internet has changed the way we communicate. Information on fish biology is not an exception to this subject. For instance, the prevalence of online ichthyological databases, such as FishBase and Catalog of Fishes, has considerably contributed to our understanding of fish taxonomy and ecology. The Japanese Internet atlas of fishes, WEB sakana-zukan, has been in operation since 2002 by us and several volunteers, and aims to provide an opportunity to communicate and accumulate information on fish biology by amateur users consisting mainly of sports fishing fans. To date, more than 35,000 photographs of fishes have been registered by more than 1,000 unique users. This site has functioned not only as an entertainment but also as an educational tool for the environment and ichthyology. However, it has several problems, including the accuracy of species identification and improper biology descriptions of some fish species. Because over 1 million page views per month have been recorded since *ca.* 2005, these problems threaten to influence the main purpose of the site, as well as members of the Japanese society, including ichthyologists. An increase in the registration numbers of fish photographs makes it more difficult for website staff, which spends a significant amount of time arranging and revising its contents. Supervising editors, descriptions, and identification of past systems of our site were web 1.0, whereas the other systems were almost web 2.0 since day one. Since 2013, we have improved the system from web 1.0 to web 2.0 to extend its targets. According to past activities and experiences and previous instances, this improvement should resolve the problems mentioned above. This presentation will introduce detailed information of the past activity, methods for improvement, and agendas regarding education for the environment and ichthyology.

25-23

Preliminary study on taxonomic status of spotted sea bass using molecular markers

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Spotted sea bass, often used as *Lateolabrax maculatus*, is characterized by many clear black dots on dorso-lateral body, whereas sea bass, *Lateolabrax japonicus*, is missing or faded as they get older. So, it was used to separate between two species according to whether they have black spots or not. But, because some individuals of *L. japonicus* have black spots on the dorso-lateral body even after they grew to adult, it is not easy to distinguish the two species by only color. There have been many studies on taxonomic review regarding the genus *Lateolabrax*, but there seems to be no distinct external features distinguishing the two species except some internal features such as the number of vertebrae (36 in *L. japonicus* vs. 35 in *L. maculatus*), gill rakers (24~30 vs. 19~24), and genetic structure (not isolation by distance vs. isolation by distance). According to Yokogawa (1997, 2004), some meristic characters and genetic structure of sea bass from the Ariake sea showed intermediate forms between the two species. To clarify if a natural hybridization between two species exist or not, we analyzed 4 specimens for spotted sea bass and 10 specimens for sea bass using partial mitochondrial COI and nuclear RAG2 sequences. We found that single specimen, having many spots on its dorso-lateral body, identified as *L. japonicus* in mtDNA COI, but identified as hybrid between the two species in nDNA RAG2, showing double peaks at one position. This result showed that there is a possibility that a natural hybridization might occur between two species.

25-24

Gymnocranius sp., a sibling species of lethrinid fish (Perciformes: Lethrinidae)

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The genus *Gymnocranius* (the family Lethrinidae) is distributed from tropical to temperate area in Indo-West Pacific. This genus was diagnosed by the following characteristics in smooth maxilla surface, 5–7 transverse scale rows on rear part of cheek, scaleless on inner surface of pectoral-fin base, dorsal fin with 10 spines and 10 soft rays, and anal fin with 3 spines and 10 (occasionally 9) soft rays. The authors noticed that some specimens, having long been identified as *G. griseus,* had subtle different bands on the body and reddish hind margin of caudal fin. *Gymnocranius* sp. is most similar to *Gymnocranius griseus* (Temminck and Schlegel 1843). Both *Gymnocranius* sp. and *G. griseus* have straight hind margins of upper and lower caudal-fin lobes, and then, clearly longer lengths of middle or shortest caudal-fin rays than dermal eye opening. Both species do not have outstanding, wavy and blue longitudinal-lines or tens of blue spots from snout to cheek below eye. However, *Gymnocranius* sp. differs from *G. griseus* in having slender body, no scales' extension area of posterior part of dorsal head view almost reaching to vertically posterior margin of eye, and reddish color at posterior part of all fins except pectoral fins (*vs.* deep body, no scales' extension area posteriorly, being beyond posterior margin of eye vertically, and yellowish color at hind margins of all fins except pectoral fins in *G. griseus*). Moreover, the DNA barcode region of cytochrome oxidase subunit 1 showed distinction of sequence (9.2 % by 590 bp) between *Gymnocranius* sp. and *G. griseus*. *Gymnocranius* sp. seems to be widely distributed in Indian Ocean and western Pacific from East Africa to southeastern Oceania in addition to Australia and southern japan.

25-25

The HUMZ Fish Collection and its contributions to systematic ichthyology

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More than 210,000 fish specimens, including about 2,900 species, are deposited in the Fisheries Science Center of the Hokkaido University Museum, Hakodate, Japan, registered under the international collection code "HUMZ." The material has been collected from marine and freshwater habitats around the world, not only by organized scientific expeditions (e.g., to the Kuril Islands, Shantar Islands in the Okhotsk Sea, Southeast Asia, and Lake Baikal) but also by deep-water surveys in search of unexploited fisheries resources (e.g., in the Okhotsk Sea, Indian Ocean, Greenland, Indonesia, and Peru) and educational cruises such as the T/V Oshoro-maru of Hokakido University (e.g., expeditions around Hokkaido, the Ogasawara Islands, and the Bering and Chukchi seas). Through use of the HUMZ collections, professors and graduate students of the Laboratory of Marine Biology and Biodiversity (Systematic Ichthyology), Hokkaido University, have been studying the phylogenetic systematics of fishes, especially from the standpoint of comparative morphology. Since 1974, 41 doctoral dissertations have been completed by successive members of the laboratory under the directions of two emeritus professors, K. Amaoka and K. Nakaya, as well as by the present curators. Most of the doctoral students responsible for this work have studied the species diversity of fishes morphologically, and reconstructed new classifications based on phylogenetic relationships by incorporating primarily osteological and myological observations. During these studies, more than 150 new species in various fish groups, including sharks and rays, scorpaeniforms, cottiforms, perciforms and pleuronectiforms, have been described on the basis of HUMZ collections, and about 1,000 individual specimens have been designated as primary or secondary types. We strongly encourage active exchanges with institutions and researchers around the world to further advance the science of systematic ichthyology.

25-26

Taxonomic review of the genus *Neoscopelus* (Myctophiformes: Neoscopelidae)

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The Neoscopelidae consists of three genera and six described species. *Neoscopelus*, with three described species, are benthopelagic over the continental slope in tropical and subtropical waters of all three oceans. The genus has a single series of photophores along the edge of the tongue and also a midventral series and a few bilateral series of photophores on the body. One undescribed species was reported from Kyushu–Palau Ridge in 1982. The genus has not been reviewed until now. This study re-examines the genus used specimens from all three oceans. We recognize four undescribed species: *N.* sp. 1 (n=65), *N.* sp. 2 (n=3), *N.* sp. 3 (n=40) and *N.* sp. 4 (n=5), in addition to the three described species: *N. macrolepidotus* Johnson, 1863, *N. microchir* Matsubara, 1943, and *N. porosus* Arai, 1969. Three of the undescribed species are similar to *N. macrolepidotus* in that the lateral series of photophores does not reach anal fin base. *N.* sp. 1 differs from it in having a large number of circum anal photophores, fewer gill rakers (10–12 vs. *N. macrolepidotus* 13–15) and black body color. *N.* sp. 2 differs from it in having a small number of anteromedial photophores and fewer gill rakers (10–11), *N.* sp. 3 has series of photophores the same as *N. macrolepidotus* but fewer gill rakers (11) and black operculum. Additionally, the photophores are fragile. *N.* sp. 4 is similar to *N. microchir* in having the lateral series of photophores reaching about end of anal fin base. *N.* sp. 4 differs from it in having fewer gill rakers (14 vs. *N. microchir* 15–18) and black operculum and abdomen.

25-27

Homology of lateral line canals in the subfamily Stichaeinae (Cottiformes: Stichaeidae)

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The species of stichaeid subfamily Stichaeinae have distinct lateral line canal system on the body. Characters associated with the canals have been recognized as being useful in defining genera and identifying species (Makushok, 1958; Hatooka, 2002). The following terms have been used for each lateral line canal in some studies: "upper lateral line canal" for the horizontal canal on the dorsal side of the body; "middle lateral line canal" for the canal on the midside of the body; "lower lateral line canal" for the canal on the lower side of the body; and "ventral lateral line canal" for the canal on the ventral surface of the body. However, the homology and definition of these canals have not been discussed in detail. In this study, the definition and homology of the lateral line canals are discussed based on detailed morphological observations and ontogenetic development in several species. The study revealed that the "upper and middle lateral line canals" in the subfamily are homologous, respectively, because they have same position and ontogenetic process. Based on the ontogenetic development, the "lower lateral line canal" may be divided into two types, the "straight type" and "zigzag type". It was also concluded that the "mid-ventral lateral line canal" was derived independently in several species. In this study, we estimate the phylogenetic relationships of the subfamily Stichaeinae and related taxa based on morphological characters, including those of the lateral line canals. In this study, we also refer to the evolution of lateral line canal patterns based on the estimated phylogenetic relationships.

25-28

Phylogeny of the cyprinid subfamily Cultrinae and related taxa (Ostariophysi: Cypriniformes)

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The phylogenetic relationships of the cyprinid subfamily Cultrinae (*sensu* Luo and Chen, 1998) and related taxa were estimated cladistically based on 66 phenotypic characters derived mainly from osteology. Three equally parsimonious trees of 97 steps (CI = 0.86, RI = 0.94) were found. Based on the strict consensus tree of the three equally parsimonious trees, not all of the putative members of the Cultrinae were resolved as a monophyletic group. However, a major clade containing the bulk of cultrin diversity was recovered. This group, termed here the Cultrinae in my sense includes: *Anabarilius*, *Culter* (including *Chanodichthys* and *Ancherythroculter*), *Hemiculter*, *Hemiculterella*, *Ischikauia*, *Megalobrama*, *Parabramis*, *Pseudohemiculter*, *Pseudolaubuca*, *Sinibrama*, and *Toxabramis*. Based on the phylogeny, two major groups are recognized within the Cultrinae termed as follows: the first lineage is the "cultrine group" including large and compressed fishes such as *Culter*, *Megalobrama*, *Parabramis*, *Sinibrama*, and *Ischikauia*, whereas the second is the "hemicultrine group" including small and slender fishes such as *Hemiculter*, *Toxabramis*, *Hemiculterella*, *Pseudolaubuca*, *Pseudohemiculter*, and *Anabarilius*. A number of taxa are not found in the Cultrinae that have been previously classified in the subfamily: *Macrochirichthys*, *Metzia*, and *Paralaubuca*. Following the results of the cladistic analysis, the classification and nomenclature of the Cultrinae and related taxa were discussed.

25-29

A new species of the genus *Glossanodon* off Western Australia (Protacanthopterygii: Argentinidae)

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The argentinid genus *Glossanodon* consists of 15 species. Among them, 12 species occur in the Indo-Pacific: *G. australis* (NWP), *G. danieli* (SEP), *G. elongatus* (SWP), *G. kotakamaru* (NWP), *G. lineatus* (NWP), *G. melanomanus* (NWI), *G. microcephalus* (NWP), *G. mildredae* (WI), *G. nazca* (SEP), *G. pseudolineatus* (SEI) *G. semifasciatus* (NWP), and *G. struhsakeri* (CP). During a workshop on demersal fishes of the southern Australia held at the National Museum of Nature and Science, Tsukuba (NSMT, Japan) in 2012, an undescribed species of *Glossanodon* was found: 38 specimens were collected from off the western Australia by R/V Kaiyo-maru (177–190 m depths) in November of 1975. These specimens were a part of the fish collection had deposited in the former Far Seas Fisheries Research Laboratory, Shimizu (FSFL, Fisheries Research Agency, Japan), being recently transferred to NSMT. This undescribed species, ranging from 60 to 98 mm in standard length (SL), differs from the congeners in having the following combination of characters: counts of dorsal fin rays (11–12), anal fin rays (11–12), pectoral fin rays (20–23), pelvic fin rays (12–13), branchiostegal rays (5), gill-rakers on first arch (31–35), and vertebrae (47–49); dentition on lower jaws (teeth on middle) and tongue (0–1); some proportions; anus immediately located on anal fin origin; a black stripe on sides of body; no blotch on dorsum of body; no external pigmentation on ventral side of body from isthmus to anus.

25-30

Taxonomy and conservation of Japanese freshwater fishes

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About 400 species of freshwater fishes has been recorded from the Japanese Archipelago so far. Among them, 144 species are listed in the Red List of the Ministry of the Environment. This has been urging every prefecture to make a local Red lists. Considering the number of species in these lists, we obviously can recognize how much those endangered freshwater fishes exist in Japan. On the other hand, current taxonomic studies are failing to define the exact situation with endangered fishes. There still remain many endangered species which are not mentioned at all. Taxonomic study is not so well advanced, that difficulty may arise in the definition and management for conservation. Even when a unique population with genetic markers happens to be discovered, it is not sufficient in taxonomic treatment that the arrangement may contribute to the actual conservation. Japanese common names vaguely are used to the groups which are recognized by the ecological and genetic characteristics. Therefore, this turns out that the recognition of the state of the conservation target is unstable as ever. Domestic laws to protect these endangered species including Ex-situ preservation, are reviced. Nomenclature for their target species always owe to taxonomy. It is important not only for foreign countries. In order to achieve the conservation of biodiversity, it is necessary to recognize clearly the groups which become targets, then promote observations of the specimens in a lot of old original descriptions. Conservation biology, taxonomy plays a role by providing the basis. However, many subjects with concreteness are seen. Also, we provide a scenealio for improvement on the conservation taxonomists.

25-31

First finding of the separated eggs of *Lophius litulon* (Lophiiformes; Lophiidae) by DNA-based identification from Korea in Northwest Pacific

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The separated pelagic eggs of *Lophius litulon* were first found by DNA-based identification. The eggs were sorted from the sample collected around the Gageo-rock in Yellow Sea from Korea. The morphology of eggs was described. For the verification of species identification, the 16SrDNA and COI genes of mitochondrial DNA were used as a molecular marker. The 16SrDNA sequences agreed with that of *L. litulon* (JQ178228) deposited in NCBI (http://www.ncbi.nlm.nih.gov/). However, the 16SrDNA phylogenetic tree by NJ method showed that there were suspicious sequences in the other species in the same genus, such as *L. piscatorius, L. americanus,* and *L. budegassa.* The COI gene was amplified with specific primer sets designed in this study referring to the sequences of adult specimens of *L. litulon*. The adult specimens were verified by morphology. The adult sequences had two haplotypes, A and B. They were same to those of *L. litulon* (haplotype A; EU660720, JF952786/ haplotype B;EU660703). The sequences of eggs were identical to the haplotype A. Eggs were identified as *L. litulon.* From the phylogenetic relationship of COI gene among Lophiidae, the COI gene showed that it was the adequate molecular marker for species identification of *L. litulon* as well as Lophiidae spp. Consequently, in order to make it clear to identify fish eggs into species level, it needs to consider the reliability of sequences deposited in database and the effectiveness of amplification according the molecular marker. When identifying species of unknown fish eggs, it is suggested to pre-sequence with 16SrDNA and to sequence with specific primer like COI gene.

25-32

Patterns of evolutionary diversification in Red Sea fishes as revealed by phylogeographic analyses of DNA barcoding sequences

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Barcoding of mitochondrial DNA has been applied in analyses of genetic diversity and diversification in many groups of organisms with the aim to assess genetic diversity, to identify species and to analyze spatial patterns of evolutionary divergence. In marine fishes from the Indo-Pacific, DNA barcoding studies already focused on specific regions such as the coastal waters of the South Western Indian Ocean or the South West Pacific. Hitherto, the fish fauna of the Red Sea has not been the focus of DNA barcoding and only few sequence information was available from marine fishes for analyses of evolutionary divergence and large scale phylogeographic patterns. In the frame of an ongoing research project, we collected voucher specimens and archived tissue samples of more than two hundred of fish species from the Northern, Central and/or Southern Red Sea. Tissue samples of voucher specimens were used for the generation of partial mitochondrial cytochrome oxidase subunit1 sequences as DNA barcodes. Phylogenetic analyses of the barcoding region of fishes from the Red Sea and available sequences from several other regions of the Indian and Pacific Oceans revealed distinctive phylogeographic patterns. In their extremes, Red Sea species with broad Indo-Pacific distribution showed either no marked diversification when compared with their conspecifics from more closely or even from highly distantly located regions. Or they showed patterns of strong evolutionary divergence, separating for example Red Sea populations from most closely located populations from the Indian Ocean or showing no marked evolutionary divergence of Red Sea and Indian Ocean populations, but showing evidence for a marked divergence from their Pacific conspecifics. In order to assess the value of genetic information for future taxonomic studies, we correlated phylogeographic patterns with taxonomic information on morphological divergence on the subspecific level. The results are discussed in a comparative frame work and a broad taxonomic perspective. The utility of short mitochondrial DNA sequences for phylogenetic comparisons is evaluated and critically discussed with respect to the taxonomic range of its application and the context of specific evolutionary questions such as species delimitation and timing of species divergence.

25-33

Molecular systematics and speciation in sharpnose pufferfishes (Tetraodontidae: Canthigasteridae: *Canthigaster*)

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The genus *Canthigaster* Swainson (1839), known popularly as the Tobies or Sharpnose puffers, is a monophyletic genus which currently consists of 36 nominal valid species. These fishes are small (usually under 12cm), omnivorous, highly derived teleosts which are primarily found in shallow waters associated with coral or rocky reefs. The genus reaches its highest diversity in the Indo-Pacific region. *Canthigaster* are morphologically conserved, and are notable for the "monotonous sameness of external morphology from species to species" (Allen and Randall, 1977). Consequently, color is used as the primary tool for delineating species boundaries. Here, we take initial steps towards developing the first comprehensive phylogeny of the genus *Canthigaster* based on mitochondrial (CO1) and nuclear (RAG1) markers. Some hypothesized relationships, such as that between the restricted-range *C. natalensis,* endemic to South Africa and the wide-ranging *C. amboinensis,* are well supported by the molecular phylogeny. Some species complexes, such as the *C. coronata* complex, the *C. janthinoptera* complex, and the shallow-water Atlantic *Canthigaster* species, show minimal genetic divergence despite differentiation in color, supporting the hypothesis that this group undergoes fast color differentiation and slow mTDNA evolution. In contrast, significant divergence in the CO1 gene was observed between Indian Ocean and Pacific Ocean populations of the widely distributed *C. solandri*. This prompted a morphological examination of *C. solandri* specimens which resulted in corroborating lines of evidence supporting the taxonomic validity of the Indian Ocean *C. petersii.* A complete phylogeny of this genus will ultimately contribute to our growing understanding of evolutionary processes in the marine environment and of the role of ecology and behavior in maintaining the diversity of reef fishes with high disbursal potential. This phylogeny will also be relevant in the discussion of color as a diagnostic for detecting evolutionary partitions and delineating taxonomic species units.

25-34

Using satellite telemetry to understand movements of whale sharks (*Rhincodon typus*) in the Red Sea

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Despite the appeal associated with charismatic megafuana, surprisingly little is known about the ecology of the world's largest fish. We lack a basic understanding of whale shark (*Rhincodon typus*) behavior and life history characteristics such as maturation size, lifespan, regional movements, and habitat use. Our understanding of population dynamics is hindered by a circumtropical distribution, deep diving ability, and capacity for large-scale movements (>1000s of kms). In addition, rising demand for shark fins maintains pressure on an already vulnerable species. Thus, an understanding of whale shark movements is critical to understanding their ecology and developing effective species management techniques. We will describe our ongoing studies to address horizontal and vertical movements of whale sharks in and around the Red Sea using satellite telemetry techniques. These findings suggest a collaborative, multi-national effort is required to adequately conserve these wide-ranging fish that regularly traverse international borders. Improved strategies could be developed exploiting their higher value alive as targets of the ecotourism trade rather than dead for consumption or medicinal uses.

25-35

Observations on the embryo of *Manta alfredi* using ultrasonographic imaging

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Successful captive reproduction of *Manta alfredi* has been recorded at the Okinawa Churaumi Aquarium since 2007. Mating behavior, gestation period (363 to 374 days), and annual reproductive cycle were observed. However, the development of the embryo was not observed until 2011. The subject of this study was a female that copulated with a male every year from 2007 to 2012, and gave birth annually for the past 6 years. We monitored embryonic development inside the uterus using a sonography diagnostic imaging system (Fuji Film Medical, FAZONE-M) with a transducer placed on the dorsal surface of the body above the uterus. We succeeded in the long-term observation of an embryo for the first time in 2011, and examined its morphology and motion in the uterus. The embryo was first observed 70 days after copulation. The cephalic and dorsal fins were first observed at 102 days. The mouth opening/closing cycle was first observed at 141 days. The embryo turned around in the uterus several times in a day; its orientation in the uterus was settled at 188 days. From the 188th day, it was not possible to make ultrasonic images of the whole body of the embryo because its size exceeded 70 cm in disk width. The ultrasonic images were effective for observation of early embryonic development and the position of the embryo in the uterus. The neonates were born at an average disk width of 185.6 cm and body weight of 66.25 kg. Three of them are maintained in the 7500 m^3 exhibit tank at the Okinawa Churaumi Aquarium.

25-36

Cospeciation of onchobothriid tapeworms and elasmobranchs

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In elasmobranchs, various parasites have been observed on the body surface and in internal organ. Tapeworms of family Onchobothriidae (Cestoda, Tetraphyllidea) are highly host specific and dominant parasites in the spinal valve of elasmobranchs. In the present study, therefore, we performed a molecular phylogeny and analyzed the cospeciation of onchobothriid tapeworms and their host elasmbranchs to clarify the evolution of onchobothriids. A total of 715 elasmobranch specimens of 49 species of 35 genera were examined from costal waters of central Japan. From 8 species of 7 genera of elasmobranchs, we found 8 onchobothriid species (including 3 undescribed species) of 4 genera. *Acanthobothrium* is parasitic for wide range of elasmobranch taxa, and 4 species infected 2 ray and 2 shark species: *A. microcephalum* in *Myliobatis tobijei* (Myliobatidae), *Acanthobothrium* sp. in *Dasyatis akajei* (Dasyatidae), *A. cestraciontis* in *Heterodontus japonicus* (Heterodontidae), and *A.* cf. *ijimaii* in *Pristiophorus japonicus* (Pristiophoridae). *Platybothrium auriculatum* infected *Prionace glauca* (Carcharhinidae). *Calliobothrium* infected *Mustelus* (Triakidae): *C. tylotocepalum* and *C. varticillatum* in *M. manazo*, and *Calliobothrium* sp. in *M. griseus*. 2 *Erudituncus* species infected *Hemitriakis japanica* (Triakidae). Molecular phylogeny of these eight examined species and 4 species from GenBank using nuclear 18S rDNA (1004 bp) showed that *Acanthobothrium* was most basal and that *Calliobothrium* and *Erudituncus* were monophyletic and most closely related with each other. Cospeciation analysis of this phylogenetic tree of onchobothriids and the tree of elasmobranchs using mitchondrial cytochrome b (494 bp) suggested that 7 cospeciations, 4 host switches and 1 sorting were recognized in the evolution of onchobothriids. Cospeciation was observed in basal branchings including genus-level diversifications, while host switch was observed only in species-level diversifications. Cospeciation is probably the most important process in the evolution of onchobothriid tapeworms.

25-37

The importance of Ariake Bay, western Kyushu, Japan, as a nursery ground for many sharks and rays

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Coastal shallow areas such as estuaries and mangrove swamps have been widely recognized to function as ideal nursery grounds for many elasmobranchs. The study area, Ariake Bay, is located in the west part of Japan, next to the East China Sea. The bay has a great tidal range (approximately 6 m) that creates large mudflats in the innermost area. In this study, we demonstrated that the innermost area of Ariake Bay is used as nursery grounds by many elasmobranchs. For example, scalloped hammerhead shark, *Sphyrna lewini* immigrate into the innermost areas of the bay during the summer season for parturition. In Ariake Bay, stingrays belonging to the genus *Dasyatis* are abundantly distributed, and some of them are economically important. We confirmed that 6 *Dasyatis* species (*Dasyatis acutirostra*, *Dasyatis akajei*, *Dasyatis izuensis*, *Dasyatis laevigata*, *Dasyatis zugei*, and *Dasyatis* sp.) inhabit the bay. The *Dasyatis* species, except *D. izuensis*, also give birth to neonates in the bay, mainly between June and August, and the neonates are found in the innermost area, including the estuaries. The neonates feed mainly on gammarids, mysids, and small fish. In addition to its high productivity, the environmental conditions of the innermost area are characterized by highly turbid waters, which may provide suitable feeding grounds and shelters against predatory sharks to the neonates.

25-38

Comparison for residues of PCBs and DDTs in six deep sea sharks in Suruga Bay, Japan

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This study provides information on concentration of Polychlorinated biphenyls (PCBs) and Dichloro diphenyl trichloroethanes (DDTs) in six deep sea sharks, *Galeus eastmani* (n=37), *G. nipponensis* (n=86), *Etmopterus brachyurus* (n=41), *E. molleri* (n=42), *Squalus mitsukurii* (n=77) and *S. japonicus* (n=74), collected from Suruga Bay, Japan. Lipids in liver, ovum and embryo were extracted by hexan and aceton. The lipid was saponified by 1M-KOH EtOH and cleaned by silica gel colum. Quantification of PCBs and DDTs was performed on a gas chromatograph equipped with a electron capture detecter (GC-ECD). The ranges of concentration on lipid weight basis in liver was as following (PCBs / DDTs). *G. eastmani* 63 - 2400 / 17 - 660 ng/g, *G. nipponensis* 16 - 1700 / 3.7 – 400 ng/g, *E. brachyurus* 60 – 2700 / 6.4 - 400ng/g, *E. molleri* 180 - 3200 / 14 - 290, *S. mitsukurii* 250 - 4800 / 30 - 890 ng/g, and *S. japonicus* 350 - 3000 / 50 - 710 mg/g. Although the range of concentration had overlapped, residue levels of organochlorines were approximately in the order of *Squalus*, *Galeus* and *Etmopterus.* These are considered to be the difference in the food habits by size of body. The concentration of both organochlorines was higher for the smaller shark and decreased with growth. Concentration of organochlorines for mature males was higher than mature females. The organochlorines shifted from mother to ova or embryos at high concentration. The relationship between PCBs and DDTs concentration indicated significant correlation. These relations differed between the species or sex. This suggests that their habitat and behavior are dissimilar.

25-39

Geographical, seasonal and sexual effects on length-weight relationship for blue shark *Prionace glauca* in the North Pacific Ocean

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Blue shark is a large pelagic shark and distributed in the world's oceans. In the North Pacific Ocean, the stock assessment of this species is ongoing as a cooperative work among WCPFC, ISC as well as IATTC. The length-weight relationship is one of the important biological information to estimate the stock biomass. For the large pelagic fishes, it is generally considered that this relationship is affected by sex, season and area which are associated with their lifecycles. Thus the effects of these factors on the length-weight relationship were investigated by applying GLM analysis. The sexed size (pre caudal length; cm), whole weight (kg) and the location of operation data were collected through variety of longline research and training cruises conducted by the national and relational research organizations and by fisheries high schools in Japan during 1994 -2012. The starting point of the model involve a response variable natural log transformed weight and explanatory variables four main effects (natural log transformed length, sex, season (parturition season or not) and area (parturition ground (>N30) or not)) and their two way interactions. The step-wise method with BIC was applied for the first model to select the best fit model. The four main effects and three two way interactions (log(length)*area, log(length)*sex and area*season) were remained. The results of our analysis indicated that the length-weight relationship largely changed by the parturition ground than others, and this tendency is more apparent in the season of nonparturition. The sex difference was also significant. Females were indicated to be slightly heavier than males in the size range to approximately 180 cm PCL.

25-40

Bioaccumulation of PCBs and DDTs in the sharpnose sevengill shark *Heptranchias perlo* in Suruga Bay, Japan

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This study provides information on bioaccumulation of Polychlorinated biphenyls (PCBs) and Dichloro diphenyl trichloroethanes (DDTs) in the sharpnose sevengill shark, *Heptranchias perlo,* collected from Suruga Bay, Japan. A total of 103 (9male and 94female) shark was sampled by deep sea bottom trawlers between September 2007 to December 2012. Lipids in liver and ovum were extracted by hexan and aceton. The lipid was saponified by 1M-KOH EtOH and cleaned by silica gel colum. Quantification of PCBs and DDTs was performed on a gas chromatograph equipped with a electron capture detecter (GC-ECD). The range of concentration on lipid weight basis in liver was 0.037 – 17μg/g at PCBs and 0.024 – 7.3μg/g at DDTs. The concentrations of both organochlorine were higher for the smaller shark and decreased with growth. However, burden of organochlorines in liver was increased with growth as an exponential function. PCBs congener in liver was dominated by HxCB and HpCB. The relationship between PCBs and DDTs concentrations indicated a significant correlation. Two mature sharks had 15 to 20 large yolky ova. The range of cocentration in ovum was 0.52 – 1.7μg/g at PCBs and 0.18 – 1.1μg/g at DDTs. Burden of the organochlorines in ovum was over 10% of liver. These were thought that the concentration of mature female was low, and small shark was high for their shift from parent. We considered to be the characteristic of the shark which breeds large embryos. These are anxious about the influence by high concentration exposure in the embryonic growth.

25-41

Age and growth of the tawny nurse shark, *Nebrius ferrugineus*, around the Yaeyama Islands, Okinawa

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The tawny nurse shark, *Nebrius ferrugineus* is currently listed as vulnerable by the IUCN. This shark is known to inhabit the coral reef waters and bear one or two young. The Yaeyama fisherman's cooperative has captured a total of 56 tawny nurse sharks by longline at the riddance of sharks once or twice in a year from 1996 to 2012 around the Yaeyama Islands. In order to acquire insight into the life history of this species, age and growth were estimated by counting growth band in the vertebral sections from 25 males (103–209 cm in precaudal length: PCL) and 7 females (151–180 cm PCL). The maximum number of growth band was counted to be 25 and 17 for males and females, respectively. Growth models were fitted using the traditional von Bertalanffy growth equation and a modification of this equation using estimated size at birth. The von Bertalanffy parameters for sexes combined were L_∞=228.5cm PCL, K=0.08 year^{-1}. In the Yaeyama Islands water, age at maturity for males was assumed 11–13 years (162–179cm PCL) by a state of calcified claspers.

25-42

Species composition of sharks in Southeast Asian region: Reanalysis of the study on sharks in 2003 and 2004 by SEAFDEC and ASEAN-SEAFDEC member countries

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One hundred seventy-four species of sharks have been recognized in Southeast Asian region. Moreover, about 126 thousand tons of sharks, rays and chimaeras were captured in 2009 in Southeast Asia. High demands for shark fin in Asia raise a concern about shark populations. However, most sharks were obtained by by-catch and all parts of sharks have been fully utilized in the region. In 1998, FAO proposed International Plan of Action for the Conservation and Management of Sharks (IPOA-SHARKS) corresponds to increase of shark catch. SEAFDEC and ASEANSEAFDEC member countries conducted the basic study of sharks in the ASEAN region in 2003-2004. Species composition and their abundance at landing sites were available for one year at major ports in Indonesia, Malaysia, Philippines, Thailand and Vietnam. Although those results have been published in 2006, mathematical comparisons among those countries have been never conducted. Because sustainable utilization of sharks and rays has been required in the region, it is important to know the characteristics of shark species composition in the region. Using the data taken in 2003 and 2004, the diversity index by Shannon-Weaver and similarity index by Pianka (1973) were calculated for 10 dominant shark species for the countries. Other minor species were not included for those calculations. In the diversity index, Indonesia has the highest score (6.54) followed by Malaysia (6.24), the Philippines (4.62), Thailand (4.41) and Vietnam (2.95). For the similarity index between Malaysia and Thailand has a high number (0.665). The other numbers between countries were relatively low (0.001-0.185). Most shark landings in Malaysia and Thailand came from trawl fisheries and they included high proportions of *Chiloscyllium punctatum*, inshore bottom dweller. However, long-line and gillnet were mainly used in Indonesia, the Philippines and Vietnam. Those results indicate that there is similarity in species composition between Malaysia and Thailand, and that species compositions of other countries and Malaysia and Thailand combined are different. Therefore, it is important to have both national and regional management plans in the ASEAN-SEAFDEC member countries for sustainable utilization of sharks. This work was supported by the Japanese Trust Fund of Fishery Agency, Japan.

25-43

Diet composition of the tiger shark, *Galeocerdo cuvier*, around Yaeyama islands, Okinawa, Japan

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The tiger shark, *Galeocerdo cuvier*, has a circumglobal distribution in tropical and temperate seas. The variety of prey groups have been reported for tiger shark in the past, namely teleost fishes, turtles, sea snakes, sea birds, crustaceans, other elasmobranchs, cephalopods and marine mammals, though it has been unknown about the diet of this species around Japan. Thus we examined the diet of tiger shark in Yaeyama islands waters to obtain basic information necessary for the population analysis and compared it between 1990's and 2000's. A total of 1073 specimens were captured by longline of Yaeyama fisherman's cooperative from August to October in 1996-2012. Stomach contents were obtained from 406 specimens (214 specimens for male and 192 specimens for female) between 86 and 315cm precaudal length (PCL). Prey items were identified as 12 groups. The importance of prey items was evaluated by the percent frequency of occurrence (%F), the percent total number (%N), the percent total wet weight (%W) and the index of relative importance adjusted to 100% (%IRI). For the tiger shark inhabited around Yaeyama islands, the most dominant prey in their diet composition was teleost fishes which showed more than 70% for %IRI estimated by the groups combined year, sex and size, and the second was birds (approximately 10%). The other prey groups were less than 5%. The diet composition for each size group was differed by sex. Males fed teleost fishes more than 75% for %IRI in the size categories <150cm PCL and 150-200cm PCL, then decreased about 50% in 200-250cm PCL and ≧250cm PCL. Females also mainly fed teleost fishes to 250cm PCL but decreased over 250cm PCL. These results indicate that the difference of maturation size by sex would affect their diet. The large shift of diet composition between 1990's and 2000's was not observed.

25-44

Authentication of the dried seahorses in the Taiwanese traditional Chinese medicine market by molecular forensics

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In addition to the unique appearance and male pregnancy exhibited by the seahorse, it is a material for traditional Chinese medicine (TCM). Inasmuch as the demand for TCM is growing, vast amounts of seahorses are harvested from the wild every year and traded internationally. This study investigated 58 dried seahorse samples collected from 23 Chinese herbal medicine stores across Taiwan by molecular forensics. Results showed that eight seahorse species were present in the Taiwanese TCM market. Among them, Knysa seahorse (*Hippocampus capensis*) has an the endangered status according to the IUCN Red List, while the tiger tail seahorse (*H. comes*), yellow seahorse (*H. kuda*), hedgehog seahorse (*H. spinosissimus*), and three-spot seahorse (*H. trimaculatus*) have a the vulnerable status, and the remaining three species, West African seahorse (*H. algiricus*), thorny seahorse (*H. histrix*), and great seahorse (*H. kelloggi*), are listed as having insufficient data. Based on the study results, we call on the Taiwanese government to take more measures to regulate the exploitation of seahorse resources.

The abundance of herbivorous fish on coral communities in the Gulf of Thailand following the 2010 coral bleaching event

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A healthy coral community usually dominates by a high diversity of live hard corals and a low coverage of macroalgae. Abundance of herbivores is an important factor for the resilience of a coral community following severe natural or anthropogenic disturbances. The high seawater temperature anomalies in 2010 caused severe coral bleaching in the Gulf of Thailand, especially in the eastern and western Gulf of Thailand. The most susceptible coral species were *Acropora* spp. and *Pocillopora damicornis*. The dominant corals in the Gulf of Thailand, such as *Porites lutea* also showed high mortality rates following the bleaching event at several reef sites. The abundance of herbivorous fish on coral communities in the Gulf of Thailand following the 2010 severe coral bleaching event was investigated. Fourteen coral communities were selected in the present study, i.e. Ko Khang Khao, Ko Lan, Ko Khrok, Ko Sak, Hin Phanang and Hin Hu Chang, in the inner Gulf of Thailand, Hin Gurk Maa, Hin Baidung and Ko Kut (Ao PhakWaeng, Ao Phrao, Ao Kralang) in the eastern Gulf of Thailand and Ko Samui (Laem Sed, Ao Thong Tanote) and Ko Taen in the western Gulf of Thailand. Densities of herbivorous fish in the western Gulf of Thailand were much lower than other regions. The low densities of herbivorous fish were also observed at Ko Khang Khao and Hin Hu Chang in the inner Gulf of Thailand and Hin Baidung in the eastern Gulf of Thailand. The abundant herbivorous fish on coral communities in the Gulf of Thailand included Silver demoiselle (*Neopomacentrus anabatoides*), Yellowtail demoiselle (*Neopomacentrus azysron*), Chinese demoiselle (*Neopomacentrus bankieri*), Wedgespot damsel (*Pomacentrus cuneatus*) and Whitetail damsel (*Pomacentrus chrysurus*). The sea urchin *Diadema setosum* may play a major role in maintaining herbivory, especially in the inner Gulf of Thailand. The effective law enforcement to protect herbivorous fish and other fishery resources from overfishing is urgently required. The proposed coral reef management actions under the coral bleaching crisis in Thailand should be properly implemented. It is also necessary to have effective mechanisms for project implementation under Thailand's national coral reef management plan.

Poster Presentations
(Wednesday 26 June 2013)

26-01

Morphological phylogeny of the hexanchiform sharks (Squalomorphii: Hexanchiformes)

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The order Hexanchiformes (sensu Nelson 2006) is characterized by having six to seven gill arches, terminal or subterminal mouth opening, only a single spineless dorsal fin, and anal fin. The order is composed of two families, the Chlamydoselachidae, including a single genus *Chlamydoselachus* and two species, and Hexanchidae, containing three genera, *Heptranchias*, *Hexanchus*, and *Notorynchus*, and four species. The sharks were estimated their phylogenetic position by many authors because of having peculiar morphology. Currently, molecular studies consider to be monophyly (single order Hexanchiformes) of the sharks, however, previous morphological studies propose monophyly and paraphyly (two orders Chlamydoselachiformes and Hexanchiformes). This study reconstructed phylogenetic position in the hexanchiform sharks among superorder Squalomorphii (bramble sharks, dogfishes, angel sharks, and saw sharks) based on 78 morphological characters including new characters (cartilages between pelvic basipterygium and clasper and circulatory system around gill) and characters being considered its homology (dorsal fin, components of gill cartilages, and sensory system in head). As a result of parsimonious analysis, 10 most parsimonious trees with 180 steps are obtained (CI=0.66, RI=0.77, RC=0.51). The strict consensus tree based on these trees is presented as the phylogenetic relationships of the Hexanchiformes and related taxa. The strict consensus tree suggests that the hexanchiform sharks is monophyletic group based on 6 synapomorphies (infraorbital nerve passing below ectethmoid process, preorbitalis inserting onto antorbital process, pectoral propterygium separated from radials, rostral canals on both sides separated each other, connection between ultimate and penultimate efferent branchial arteries, and one dorsal fin present). The number of gill arches of the order is considered to be increase of 'β' arches (sensu Shirai 1992), however, it is undeterminable whether the increase of β arches is a synapomorphy of the Hexanchiformes or not. Consequently, classification of the hexanchiform sharks are regarded as single order Hexanchiformes, besides, the following orders, the Echinorhiniformes, Squaliformes, Pristiophoriformes, and Squatiniformes are also regarded as order ranks in the superorder Squalomorphii.

26-02

Sexual dimorphism in scales of marbled flounder *Pseudopleuronectes yokohamae* (Pleuronectiformes: Pleuronectidae): possible relevance to their spawning behaviour

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The marbled flounder, *Pseudopleuronectes yokohamae*, is an important flatfish for coastal fisheries in Japan. Although sexual dimorphism in external morphology has rarely been reported in pleuronectid flatfishes, fishermen discriminate male and female *P. yokohamae* by palpation texture of the blind side: usually rough in males due to the presence of ctenoid scales and smooth in females due to their cycloid scales. To test the sexual difference in the skin morphology, I sampled 646 individuals of *P. yokohamae* (155-463 mm standard length) caught by commercial fisheries off Fukushima, Japan (35° 45'-38° 05' N; 140° 50'-141° 50' E) from 2008 to 2011. The scales on the blind side of *P. yokohamae* varied in relation to maturity and body size. Immature males often had cycloid scales, while mature males had mostly ctenoid scales. Large females also often had ctenoid scales, but small females had mostly cycloid scales on their blind side. The number of spines on blind-side scales increased with body size, indicating an ontogenetic change in the scale morphology. As *P. yokohamae* spawn demersal eggs and males position above a female's ocular side to press against the female's body, it was hypothesized that the ctenoid scales on the blind side in mature males function for maintaining contact with females during spawning.

26-03

Trunk lateral line system in three basal gobioids (Teleostei: Perciformes)

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The trunk lateral line system was studied in three basal gobioids included in Rhyacichthyidae and Eleotridae. In *Rhyacichthys aspro*, the trunk lateral line is canalized: the anterior part is a single dermal tube extending posteriorly below the end of the first dorsal fin base, with distally pored 16 short sub-tubes detaching above and below; the posterior part comprises 20 scales, each with an ossified canal. Scales bearing an ossified canal are also present on other parts of the body: one below the first dorsal fin base and two on the caudal peduncle. The anterior part of the line includes a total of 31 canal neuromasts, with 1–6 neuromasts on each scale; the posterior part includes a total of 114 canal neuromasts, with 3–7 neuromasts on each scale. These canal neuromasts are arranged horizontally, following orientation of the tube and ossified canals. Superficial neuromasts also develop along the entire length of the trunk lateral line, mostly being immediately lateral to the tube and canals. In *Eleotris oxycephala* and *Hypseleotris cyprinoides* (Eleotridae), tubular and canalized parts are absent in the trunk lateral line, ca. 20 vertical rows of the superficial neuromasts are arranged along the mid-lateral surface of the body, the pattern being typical in Gobiidae. It is suggested that the loss of the tube and canalized scales allowed a change from the horizontal canal neuromast rows to the vertical superficial neuromast rows, possibly related with a habitat shift from a rapid stream to more or less still-water.

26-04

Functions of pelvic fins during the fast escape response in a tropical wrasse, black-spot tuskfish *Choerodon schoenleinii*

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Pelvic fins of teleost fish are paired appendages that are considered to be homologous to the limbs of tetrapods, and evolutionary aspects of the fin structures have been thoroughly studied in model species. However, pelvic fin function in fish has been the subject of few studies because the pelvic fins of most teleosts are considered to be of little importance for swimming compared with the other fins. Here, we challenged this notion through the detailed kinematic analysis of black-spot tuskfish during the fast escape response which is crucial for predator evasion. To investigate whether the pelvic fin is important for the fast escape response, we first removed the left pelvic fins of black-spot tuskfish, and compared the escape response of the modified fish with control fish. The modified fish and the control fish showed C-starts that consisted of a sudden turn (stage 1) and a rapid acceleration (stage 2). The fish without the inside pelvic fin had a greater stage 1 angle and escape trajectory angle compared with the control fish. In contrast, the stage 1 angle and the escape trajectory angle were similar for the fish without the outside fin and the control fish. We then monitored the movement of the pelvic fins of the control fish during the fast escape response. The both inside and outside fins were extended during the stage 1; however, during the stage 2, the extensions depended on the subsequent behavior (swim, glide or stop). Given that the both pelvic fins were extended during the stage 1, the inside pelvic fin had probably increased the inside drag to maintain the turning angle and the subsequent escape trajectory angle. The probability of evasion from a scoop net was also analyzed to test whether the pelvic fin influenced the escape performance. The fish without one pelvic fin were more likely to be captured than the control fish. These results suggest that the pelvic fins have a significant role for the fast escape response.

26-05

Comparisons of osmoregulatory mechanisms between two closely related euryhaline teleosts from different natural habitats

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Euryhaline teleosts that survive in a variety of habitats have to regulate their internal water and ion concentrations in order to maintain the blood and tissue fluid osmolality within the range of physiological homeostasis. Na^+/K^+-ATPase (NKA) in osmoregulatory organs (e.g., gills, kidneys, and intestines) is crucial for maintaining intracellular homeostasis because it provides a driving force for many ion-transporting systems. Among the regulators of NKA, the FXYD protein family was found to be the novel regulator and was widely studied in mammals and sharks. Although teleostean FXYD proteins have recently been identified and investigated, those papers focused mainly on gills of limited species. Moreover, few studies compared simultaneously differential osmoregulatory capabilities and diverse natural habitats between two or among more fish species. Hence the purposes of the present study were to investigate the diversity of teleostean FXYD expression profiles by comparing two closely related euryhaline model teleosts (*Oryzias dancena* and *O. latipes*) from different natural habitats and to research the expression of the FXYD protein family in the osmoregulatory organs for illustrating the correlation between NKA and FXYD proteins of these two medaka species in response to salinity changes. Fourteen members of the FXYD protein family were cloned from the two medaka species. Across all FXYD family members, higher identities were found between the homologous FXYD proteins of the *O. dancena* and *O. latipes* as compared with the other FXYD homologues from teleosts and mammals. In the osmoregulatory organs of the two medaka species, moreover, most of the *fxyd* genes were expressed. The protein sequences and tissue distributions of the FXYD proteins were very similar between the two medaka species, but different expression profiles were observed upon salinity challenge for most *fxyd* genes of the osmoregulatory organs. These results revealed that, in these osmoregulatory organs of the two medaka species from different natural habitats, different strategies may be taken to modulate the expression of FXYD proteins and NKA for maintaining internal homeostasis. Future studies will focus on the molecular regulatory mechanisms of FXYD protein and NKA expression of euryhaline teleosts.

26-06

Learning from the bodies of fishes: introduction to a biomimetics project in Japan

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Biomimetics is the study of structure and function of organisms as models for design and engineering of materials and/or machines, bridging biology, engineering and industry. A well-known example of biomimetics is the hook-and-loop fastener which mimics plant seeds sticking to clothes and animal furs. Skins of rapidly swimming fishes (e.g., some sharks and tunas) have been studied to develop a mechanism for reducing skin friction drag. This has been applied to swimming suites and others. On the other hand, the shape of boxfishes recently inspired a new car design (the Bionic Car) that combined robust structure and friction-drag reduction. Since 2012, the authors together with Japanese physicists have been collaborating in a Biomimetics Project that is investigating body surface structures of various Japanese fishes using digital microscopy and SEM in order to comprehend the morphological diversity. Digital images of skins collected from fish specimens in our museums and data on biology of fishes are being stored in a biomimetic database. The biomimetic database will not only be a repository for resources about the morphological structures of fishes, but will also provide many opportunities for interdisciplinary studies between scientists in different fields. A progress report of the newly started Biomimetics Project is presented.

26-07

Morphological review of the *Comephorus*, the endemic sculpin of Lake Baikal (Cottiformes, Comephoridae)

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Thirty-three cottoid species inhabit in Lake Baikal, and most of which are endemic to the lake. Among them, the endemic genus *Comephorus*, comprising *C. baicalensis* and *C. dybowski*, has an extremely different morphology to other Baikalian sculpins. The two species also have a unique pelagic mode of life and ovoviviparous form of reproduction. For these reasons, it has been hypothesized that *Comephorus* does not share the common ancestory with other Baikalian sculpins (Sideleva, 1982; Yabe and Sideleva, 2000). Recently, however, molecular studies have suggested that Baikalian sculpins are a monophyletic group that share a common ancestry (Kontula, 2003; Smith and Wheeler, 2004; Kinziger, 2005). To test these hypotheses, we reviewed the morphology of *Comephorus* and compared it with that of other Baikalian sculpins. We found a number of unique characters in *Comephorus*, including a well developed lateral line system on the head with large cavities on the cranium, the lack of a suborbital stay, the upper jaw structure not protruding forward, the mandibular sensory canals of both sides connected at the tip of lower jaw, the adductor mandibulae section 1 completely separated from other sections, the protractor hyoidei limited to an extremely thin muscle, the scapula foramen placed on the scapula, no pelvic fin rays or the muscles that are normally connected to the rays, a lack of preural ribs and the obliquus superioris inserting on the ventrolateral surface of the cranium. Of these characters, conditions of the scapula foramen and the obliquus superioris, at the very least, maybe primitive for cottoid fishes. Remaining Baikalian sculpins share derived conditions for these two characters with most cottid fishes, except for *Jordania* which is regarded as the most primitive. These results place doubt on the monophyly of Baikalian sculpins, including *Comephorus*.

26-08

Reevaluation of the monophyly of the family Congridae

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The family Congridae, one of the most speciated groups in the order Anguilliformes, contains 32 genera and roughly 160 species, and is distributed in tropical and temperate zones (Asano, 1962; Nelson, 2006). Asano (1962) and Smith (1989) regarded the Congridae as a monophyletic group, and Smith (1989) recognized three subfamilies, Heterocongrinae, Bathymyrinae and Congrinae, in it. However, recent molecular phylogenetic studies (e.g., Inoue et al., 2010) inferred that the Congridae is either paraphyletic or polyphyletic. In this study, we reevaluated the monophyly of the Congridae based on morphological characters, including osteology and myology. Our study failed to identify synapomorphies supporting the monophyly of the Congridae. Although Smith (1989) suggested that the loss of the hypohyal is one of the synapomorphies of the Congridae, this character is known in many anguilliform families and its state as a synapomorphy is unclear. Therefore, the congrid monophyly is still questionable. In contrast, Asano (1962) and Smith (1989) provided good support for the monophyly of each of the three subfamilies (e.g., quadrate condyle well projected anteriorly in the Heterocongrinae, gas bladder attached to vertebra in the Bathymyrinae and posterior urohyal projecting like spatulate in the Congrinae). We discovered several additional apomorphic characters in the three subfamilies (e.g., adductor mandibula section 2 attached to only half of the margin of the suspensorium in Heterocongrinae, arrector dorsalis extending to the cleithrum in the Bathymyrinae and the absence of an intermandibularis in the Congrinae). This further supports the previously suggested monophyly of the three subfamilies.

26-09

Finding the best estimates of metabolic rates in a coral reef fish

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Swimming and resting respirometry, two techniques that use oxygen consumption rates ($\dot{M}O_2$) to estimate metabolic rates in aquatic organisms, are increasingly used to study physiological responses to environmental stressors. However, there have been few attempts to verify whether these techniques yield comparable results. We examined whether two fundamental $\dot{M}O_2$ measures, standard metabolic rate (SMR) and maximum metabolic rate (MMR), vary according to the type of respirometry used. Ten bridled monocle bream (*Scolopsis bilineatus*) were exercised using (1) a critical swimming speed (U_{crit}) protocol in a swimming respirometer and (2) a 15 min exhaustive exercise protocol and (3) a 3 min exhaustive exercise protocol followed by 1 min of air exposure and in resting respirometry. SMR estimates obtained using swimming respirometry were not significantly different from those in resting respirometry when a three parameter exponential function was used to extrapolate the swimming speed-$\dot{M}O_2$ relationship to zero. In contrast, MMR measured with the U_{crit} protocol was 36% higher than MMR measured in the 15 min exercise protocol and 23% higher than MMR in the 3 min exercise, 1 min air exposure protocol. For fish like *S. bilineatus* that are good steady (endurance) swimmers, swimming respirometry can produce more accurate MMR estimates than exhaustive exercise protocols since oxygen consumption is measured directly during exertion. However, when swimming respirometry is impractical, exhaustive exercise protocols should be supplemented with a brief period of air exposure to improve accuracy. Nevertheless, caution is warranted when comparing MMR estimates obtained with different respirometry methods unless they have been cross-validated on a species-specific basis.

26-10

Cenozoic teleostean fish fossils from Japan

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Yabumoto and Uyeno (1994) provided a review of the chondrichthyan and osteichthyan fish fossils found from the Late Mesozoic and Cenozoic beds of Japan in the form of a series of tabular compilations and demonstrated that a number of cartilaginous fishes disappeared at the end of the Cretaceous Period. Then modern sharks, including the family Carcharhinidae, increased from the Oligocene to the Miocene, whereas the Hexanchidae and Lamnidae declined. However, as to teleostean fishes, it was only mentioned that most Miocene species differ from the Recent congeners at the species level. In the last two decades, teleostean fish fossils have been described as a new species and some new genera have been established from Cenozoic beds in Japan. These are *Sardinella miyanoshitaensis* Sato and Uyeno, 1999; *Spirinchus akagii* Uyeno and Sakamoto, 1999; *Inabaperca taniurai* Yabumoto and Uyeno, 2000; *Euleiognathus tottori* (Yabumoto and Uyeno, 1994); and *Tottoriblennius hiraoi* Yabumoto and Uyeno, 2007 from the Middle Miocene marine sediments, the Iwami Formation, at Kokufu, Tottori Prefecture and *Ikiculter chojabaruensis* Yabumoto, 2010; *Pseudobagrus ikiensis* Watanabe and Uyeno, 1999; *Coreoperca maruoi* Yabumoto and Uyeno, 2009 from the Middle Miocene freshwater sediments, the Chojabaru Formation, in Iki Island, Nagasaki Prefecture in the western part of Japan. In addition, there are studies of the Pleistocene freshwater fish fossil assemblage from Kusu basin, Oita Prefecture (Uyeno, et al., 2000) and a Pleistocene clupeid fish, *Clupanodon tanegashimaensis* (Saeki, 1929) in the marine fish fossil assemblage from Tanegashima Island, Kagoshima Prefecture (Yabumoto, et al., 2005). These studies provide some clues to understand the origin and history of Recent fish fauna of the Indo-Pacific region and the freshwater fish fauna in Japan and East Asia.

26-11

Revision of a cyprinid fish, *Zacco* cf. *Zacco temminckii* from the Middle Pleistocene Nogami Formation, Kusu Basin, Oita Prefecture, Kyusyu, Japan

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Many well preserved freshwater fishes have been found from the Middle Pleistocene Nogami Formation, which is a lacustrine diatomaceous bed in Kusu Basin, Oita Prefecture in the northern Kyushu, Japan (Uyeno et al., 1975; Takahashi and Okumura, 1998; Uyeno, et al., 2000). These are *Oncorhynchus masou* of the family Salmonidae; *Hemibarbus barbus* or *H. labeo*, *Zacco* cf. *Z. temminckii*, and *Acheilognathus* sp. of the family Cyprinidae, and *Rhinogobius giurinus* or *R. brunneus* of the family Gobiidae (see Yabumoto, 1987; Uyeno, et al., 2000). Among these species, *Zacco* cf. *Z. temminckii* is reviewed with comparison to allied extant cyprinids (*Opsariichthys*, *Nipponocypris*, *Candidia* and *Parazacco*) in the present study. *Zacco* cf. *Z. temminckii* from the Nogami Formation is considered to be a member of the genus *Nipponocypris*, because the number of vertebra and supraneural bones, the position of dorsal fin base, the parietal cannel, and the shape of dentary are almost the same as those of the genus. The genus *Nipponocypris* consists of three extant species, *Nipponocypris temminckii, N. sieboldii* and *N. koreanus*. *Zacco* cf. *Z. temminckii* has the same number of the anal fin proximal pterygiophores with *N. temminckii* and *N. koreanus*. Furthermore it is similar to *N. temminckii* in having the notch on the lateral margin of the frontal. However, it differs in the neural spines of the second and third preural centra. Several fossils of the genus *Zacco* have been described or reported from Paleogene and Neogene in East Asia. These are *Zacco honggangensis* Li and Wang, 1981 from the lower Eocene Buxin Formation, China; *Zacco* sp. from Isikawa Prefecture, Japan (Nakajima, 1975; Tomoda and Nakajima, 1975) and others. It is necessary to review these fossils with comparison to allied fossil and recent cyprinid fishes.

26-12

Evolutionary trends of the intestinal coiling pattern in the family Cyprinidae (Ostariophysi: Cypriniformes)

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The fishes of the family Cyprinidae is one of the most diverse freshwater fish groups in the world with more than 2000 species in 200 genera. This fish group exhibits a variation in feeding habits, *i.e.*, *Culter*, *Elopichthys*, and *Aspius* are carnivorous, feeding on fishes, crustaceans, and insects; whereas *Ctenopharyngodon* and *Hypophthalmichthys* are herbivorous, feeding on aquatic plants and algae. The external (*e.g.*, shape, size and position of mouth) and internal (*e.g.*, length and shape of digestive tract) morphology provide useful information to demonstrate their feeding habits, ecological adaptation or speciation. Especially, the morphological data on the intestinal coiling pattern is absolutely necessary. In this study, the intestinal coiling patterns in the family Cyprinidae are reviewed, and the evolutionary trends within the family are estimated on the phylogenetic tree. The intestinal coiling patterns in cyprinid fishes traits generally fall into six categories tentatively proposed by Kafuku (1958). Based on the reconstruction of ancestral character state on the molecular phylogenetic tree provided the hypothesis that the common ancestor of all cyprinids has simple intestine. The simple intestinal structures is found in majority of cyprinids (Danioninae, Xenocyprinae, Tinincinae, Tanichthyinae, Leuciscinae, and Gobioninae), whereas the complex patterns were recognized in the subfamily Cyprininae, several groups of Xenocyprinae, and Acheilognathinae on the phylogenetic tree.

26-13

Comparisons of the ion transporter expression in the pseudobranchs of the seawater- and fresh water-acclimated milkfish

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In euryhaline milkfish, the pseudobranch is a reduced mandibular gill arch with proposed multiple functions. Our results showed that, the pseudobranchial epithelium of the milkfish contained the mitochondria-rich cells (MRCs) and a unique cell type, the pseudobranch type cells (PSCs). Therefore, we compared the differences of ion transporter expression between PSCs and MRCs of the pseudobranchs in the seawater (SW)- and fresh water (FW)-acclimated milkfish. Both types of cells showed high NKA protein expression while only MRCs exhibited NKCC on the basolateral membrane and CFTR on the apical membrane in SW-acclimated individuals. In contrast, few and smaller MRCs in the filaments close to the afferent artery exhibited NCC on the apical membrane of the pseudobranchs from the FW-acclimated milkfish. In addition, the size of PSCs became larger in the FW- than SW-acclimated fish, but their numbers per 100μm interval in the lamellae were not significantly different. Taken together, our results revealed that the MRCs in the pseudobranch exhibited similar ion transporters like the MRCs in gills of the milkfish. Moreover, changes in numbers and morphology of MRCs and the ion transporter expression in the pseudobranchs of the milkfish upon salinity challenge indicated the potential roles of pseudobranchs for hypo-osmoregulation of this euryhaline teleostean species.

26-14

Growth performance, body composition and stress responses of olive flounder *Paralichthys olivaceus* held under different water pH levels

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The growth performance, body composition and stress responses of olive flounder, *Paralichthys olivaceus* (50.8 g mean body weight) reared under three different water pH levels (8.0, 7.5 and 6.5) were investigated. Fish in each pH level were stocked at a density 8 fish per rectangular aquarium (96 L) with triplicate, and were fed with a commercial diet (54.4% protein) to apparent satiation, two times a day for 6 weeks. At the end of experiment, blood sample was collected from 4 fish of each aquarium for haematological analysis and the other 4 fish were sacrificed for chemical body composition analysis. After blood sampling from each experimental fish, the fish were sacrificed for histological analysis of its gill, liver and kidney. Before the sampling, all fish were measured and weighed individually. There were no significant differences in weight gain, feed efficiency, specific growth rate and feed intake in fish exposed to 8.0, 7.5 and 6.5 pH levels ($P > 0.05$). Moisture and protein content of fish were not significantly ($P > 0.05$) affected by pH levels. However, decrease in the pH level provoked significant ($P < 0.05$) increase of lipid and decrease of ash content in fish. Hemoglobin (Hb) content of fish in pH 6.5 was significantly ($P < 0.05$) lower than those of fish in pH 8.0 and 7.5, but no significant difference was observed in Hb between the fish raised at pH 8.0 and 7.5. Although the histological changes of liver and kidney were not observed in all treatments, gill of fish at pH 6.5 was observed with some damaged. These results indicate that decrease of water pH from 8.0 to 6.5 caused gill damage as well as change of body composition and haematology of *P. olivaceus*.

26-15

Hypotonic acclimation induces stress responses, expression of branchial Na^+/K^+-ATPase and proliferating cell nuclear antigen in *Takifugu niphobles*

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Almost the whole life cycle of the grass puffer (*Takifugu niphobles*) occurs in seawater (SW), but it is also sometimes found in fresh water (FW) rivers. This study aims to evaluate the effects of FW exposure on the stress, osmoregulatory and physiological responses of the grass puffer. The grass puffers were captured from a local wetland and acclimated to SW (35‰) or FW in the laboratory. In the stress responses, plasma glucose concentrations and the abundances of hepatic and branchial heat shock proteins (HSPs) (i.e., HSP70 and HSP90) were higher in the FW group than in the SW group. Furthermore, FW acclimation led to a significant increase in the protein abundance and the specific activity of branchial Na^+/K^+-ATPase (NKA). Immunochemical staining showed that the NKA immunoreactive (NKIR) cells of the FW and SW puffer were distributed mainly in gill filaments. Although the number of NKIR cells was similar in the two groups, the protein levels of proliferating cell nuclear antigen (PCNA) of nuclear fractions were elevated in the gills of the FW puffers. The induction of gill PCNA might contribute to cell proliferation, which would maintain the amount of NKIR cells, or repair DNA when the puffers were exposed to FW, an osmotically stressful environment. Taken together, activation of stress responses would provide the osmoprotection associated with FW adaptation of the grass puffer. Changes of branchial NKA expression and activity for osmoregulatory adjustment were required for physiological homeostasis (stable blood osmolality and muscle water content). Based on our findings, the grass puffer is a euryhaline teleost with SW preference was suggested.

26-16

Molecular phylogeny and origin of Sulawesian adrianichthyids

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Seventeen species of Adrianichthyidae, more than half of the members of this family, are known from Sulawesi, an island in the Malay Archipelago. Interestingly, 16 of those species are endemic to Sulawesi, suggesting that they have diverged within this island. However, little is known of their divergence history nor their geographic origins. Molecular phylogenies of 15 Sulawesian and six non-Sulawesian adrianichthyid species based on mitochondrial DNA sequences revealed that species endemic to Sulawesi (14 species) form a monophyletic group, supporting the hypothesis of within-island diversification. Species basal within the Sulawesian clade tended to be distributed in the southeastern part of the island, while derived species had restricted distributions at tectonic lakes in the central part. This finding suggests that the common ancestor of the Sulawesian adrianichthyids originated in the southeast and that physical isolation drove allopatric speciation in landlocked lakes. The phylogenies also revealed that the non-Sulawesian adrianichthyids form two major clades. However, phylogenetic relationships among the Sulawesian and the two non-Sulawesian clades were not clear, obscuring the origin of the Sulawesian adrianichthyids. To resolve the deeper phylogeny of these fishes, more species must be sampled from both Sulawesi and other regions.

26-17

Genetic divergence in the *Careproctus rastrinus* species complex (Liparidae) inferred from AFLP: evidence of secondary contact in the Bering Sea

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Careproctus rastrinus is one of the most common snailfishes in the North Pacific, widely distributed in the Sea of Japan, along the Pacific coast of Japan, in the Sea of Okhotsk, Bering Sea, Gulf of Alaska, and Arctic Ocean. However, the taxonomy of the species has been confused with the related species *C. trachysoma*, *C. scottae*, *C. pellucidus*, *C. phasma,* and *C. acanthodes*, because of their similar appearance and overlapping counts. In our recent study, the species complex was demonstrated to include nine mitochondrial lineages, but some of them did not show any morphological differences. In our previous study, the absence of morphological divergence between two mitochondrial lineages in the Sea of Japan was explained by the extensive gene flow resulting from secondary contact, using nuclear DNA analysis. In order to examine the possibility of secondary contact among other lineages of the species complex, we herein attempted to elucidate nuclear DNA divergence within the *C. rastrinus* species complex on the basis of AFLP. The neighbor-joining tree within the *C. rastrinus* species complex inferred from the AFLP banding pattern revealed six divergent clusters, three of the original nine mitochondrial lineages being collapsed. One of the collapsed mitochondrial lineages was found in the Sea of Japan, as previously demonstrated, and the other two were found in the Bering Sea. This suggests that the extensive gene flow between mitochondrial lineages in the Bering Sea is a result of secondary contact following past isolation. The secondary contact of these mitochondrial lineages in the Bering Sea was also supported by the absence of morphological divergence. Because both the Sea of Japan and the Bering Sea are marginal seas of the North Pacific, the divergence pattern of the *C. rastrinus* species complex may be formed by repeated isolation and migration between these and neighboring areas caused by sea level fluctuations during glacial periods.

26-18

Comparative phylogeography of *Pomacanthus imperator* and *P. semicirculatus* in the Indo-Pacific Ocean

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Pomacanthus imperator and *Pomacanthus semicirculatus* are two of the biggest and most widely distributed marine angelfish (Pomacanthidae) in the Indo-west Pacific Ocean. In order to understand their phylogeography, evolutionary direction and demographic history, 114 and 138 individuals of *P. imperator* and *P. semicirculatus* were collected since July 2007 until June 2012 from their native distribution range that includes Kenya, Maldives, Sri Lanka in the Indian Ocean to Indonesia, the Philippines, Vietnam, Taiwan, Japan, Australia and Kiribati in the Pacific Ocean, respectively. A total of 599bp and 596bp of cytochrome c oxidase I (COI) sequences of *P. imperator* and *P. semicirculatus* were PCR amplified, respectively, of which 11 and 13 haplotypes were obtained. The haplotype diversities (h) of the two species were estimated to be 0.578 and 0.464, respectively, while the nucleotide diversities (π) were 0.00308 and 0.00153. The neighbor-joining (NJ) tree of *P. imperator* suggested that the species originated from mid-Indian Ocean then spread into two directions, one to the western Indian Ocean and the other one to the Pacific Ocean. On the other hand, the NJ tree of *P. semicirculatus* suggested a different evolutionary direction wherein the species originated from the western Indian Ocean and then spread to eastern Indian Ocean and the Pacific Ocean. The results of evolutionary direction indicated contrasting evolutionary patterns between these two angelfishes. The NJ tree and haplotype network all suggested that there is a potential barrier which restricted the gene flow of these two species between the Indian Ocean and the Pacific Ocean. The Indian and the Pacific Ocean populations of the two species all overlapped in Indonesia indicating a possibility of Centre-of-overlap hypothesis. Tajima's D and Fu's Fs analyses of neutrality tests both suggested a recent population expansion for *P. imperator* and *P. semicirculatus*. This study provides information on the evolutionary patterns of the biggest marine angelfish in the Indo-western Pacific Ocean.

26-19

A new species of Pomacanthidae from Cocos Island with emphasis on its phylogenetic relationship to its sister species in the Pacific

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A new *Centropyge* angelfish species was found in the Cocos Islands in the Indian Ocean. This species is rare and is endemic only to the Christmas and Cocos-Keeling Islands of the East Indian Ocean. It was previously regarded as a color variant of its Pacific Ocean counterpart, the lemonpeel angelfish *C. flavissima* but differs in having a blue iris and a faint blue eye ring. Genetic analyses of the mitochondrial 16S and Cytochrome c oxidase subunit I (COI) genes and nuclear intron ETS2 confirmed a species-level separation of this new species from *C. flavissima*. The phylogenetic relationships between the new species and the other yellow Pacific *Centropyge* spp. (*C. flavissima*, *C. heraldi*, and *C. woodheadi*) also suggested closer genetic relationships between the new species and *C. flavissima* and between *C. heraldi* and *C. woodheadi*. We also found a color variant of *C. woodheadi* from Queensland, Australia that is starting to diverge from the *C. woodheadi* from Vanuatu. Key words: *Centropyge flavissima*, *C. heraldi*, *C. woodheadi*, New species, Cocos Island.

26-20

Formation of freshwater fish fauna in western Japan

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The Japanese Archipelago harbors a freshwater biome with high endemicity in East Asia. Specifically, high species richness is found in the fresh waters of western Japan. To elucidate the formation process of freshwater ichthyofauna in western Japan, we conducted comparative phylogeographic analysis and ecological niche modeling for many freshwater fishes (for ~20 and ~60 spp./sspp., respectively) occurring in this region. The results of phylogeographic analysis revealed various patterns; some species sharing similar geographic distribution differed in genetic population structure and inferred divergence times. Allopatric fragmentation corresponding to major watersheds was inferred to be the dominant process for population structure, with secondary contact between divergent lineages also being inferred in specific areas. The distribution and phylogeographic patterns of fish species showed some relations to their ecological traits. Ecological niche models using a few (4–7) geotopographical and climatic factors exhibited high predictivity for the present distributions (average AUC ~0.9). The change in potential distributions extrapolated under regression and transgression scenarios exhibited some relevance to the present distribution patterns. Although no simple pattern was found for the distribution and phylogeography in freshwater fishes in western Japan, our results showed that the integration of historical processes and ecological traits of species will contribute to an understanding of the formation process of freshwater fish assemblies.

26-21

Local populations found in the catshark *Scyliorhinus torazame* in Japan

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The Japanese catshark, *Scyliorhinus torazame* (Tanaka, 1908) is a common benthic shark found on the western Pacific continental shelf, and it is known that there are some morphological differences among individuals in this species. In the present study the population structure of *S. torazame* around Japan was assessed. We collected individuals of *S. torazame* from six localities around the coasts of Japan (Hokkaido, Boso, Sagami Bay, Shimane, East China Sea and Okinawa) and compared the mitochondrial nucleotide sequences of 16S rRNA (380 bp), cytochrome *b* (321 bp) and control region (332 bp), and also several morphological characters among them. As a result, nucleotide substitution rates of 16S rRNA and cytochrome *b* showed that the differences found in *S. torazame* are at an intra-specific level. Phylogenetic trees constructed using the neighbor-joining methods consistently indicate that *S. torazame* collected from Japan can be divided into the following three clades; ''Hokkaido, Shimane and East China Sea group'', ''Boso and Sagami Bay group'', and ''Okinawa group''. Especially ''Okinawa group'' was different from the other two groups and characterized in having, 1) more tooth counts in both jaws, 2) dark blotches on ventral surface of the body, and 3) unique and endemic haplotypes in 16S rRNA, cytochrome *b* and control region. The unique ''Okinawa group'' is distributed southward the Kuroshio Current which separates Okinawa and Amami Islands from main islands of Japan and might act as a barrier to prevent genetic exchange between the ''Okinawa group'' and the other two groups. Additionally, based on the morphological observations, the previously recognized differences in meristic counts (number of vertebrae, intestinal valve turns and so on) between two nominal Japanese *Scyliorhinus* species (*S. torazame* and *S. tokubee* Shirai, Hagiwara and Nakaya, 1992) have become unclear. Also, some specimens having very similar coloration to *S. tokubee* were genetically identified as the members of the ''Boso and Sagami Bay group'' by the present molecular analysis.

26-22

Phylogeographical and morphological analyses of the mottled spinefoot *Siganus fuscescens* in the Indo-West Pacific, with comments on synonyms

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Mottled spinefoot *Siganus fuscescens* (Houttuyn, 1782) is a species belonging to the family Siganidae with the greatest latitude range lives in shallow coastal habitats throughout the tropical, subtropical, and temperate Indo-West Pacific region. It is economically important as aquatic resource in many countries and regions, and needed to conserve due to overfishing, especially around Southeast Asia. On the other hand, browsing by herbivorous fishes has been paid attention as a causative agent of seaweed/seagrass bed reduction in warm temperate waters on the coastal area of Japan, recently. This species is regards as harmful, because it has been reported that their browsing has been kept throughout the year with rising seawater temperature due to global warming, and has caused rocky-shore denudation. Thus, revealing and understanding genetic structure and connectivity are needed to manage commercial marine fishes properly and monitor population dynamics. *Siganus fuscescens* has been taxonomically confused with white-spotted spinefoot *S. canaliculatus* (Park, 1797). They are morphologically very similar, and their distributions overlap. Because the taxonomical status of the two species is unresolved, we did not distinguish them and treated as unity for analysis. The objective of this study is to reveal genetic population structure and demographic history in *S. fuscescens* by phylogeographical analysis based on the mitochondrial DNA control region sequences. Moreover, we discuss taxonomic treatment about *S. fuscescens* and *S. canaliculatus* in terms of population genetics and morphological studies. In total, 715 individuals were collected from 16 localities distributed throughout the Indo-West Pacific. Sequence analysis indicated that haplotypes were clearly divided into three lineages, and populations were grouped due to different frequencies of appearance of the above three lineages into three clades as following: (1) Indian Ocean (2) Ryukyus (3) West Pacific. Morphological analysis based on 30 morphometric characters indicated that no significant differences were found in measurements for three genetically divergent lineages. In conclusion, each lineage had once been isolated, and former allopatric lineages may have resulted in the sympatric distribution of lineages due to secondary contact. Moreover, it should be appropriate that *S. fuscescens* and *S. canaliculatus* are considered as a single biological species.

26-23

Molecular phylogeny of the cardinalfishes (Percomorpha: Apogonidae): revisions for genus/subgenus systematics

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Cardinalfishes (Apogonidae) are one of the most numerically dominant reef fish families, mostly nocturnal, and many known to be mouthbrooders. The family has 505 nominal species, 348 as valid species. There are about 69 nominal genera/subgenera with generally less than half as valid genera/subgenera. The genus *Apogon* sensu lato, historically, has been the most speciose genus, with more than163 and less than 200 recognized species in the 10 subgenera proposed in 1972. The limits of *Apogon*, as well as some of the subgenera, are unsettled. A few authors elevated some subgenera to genera following an unpublished doctoral dissertation on the cephalic lateralis system in 2004. A molecular paper in 2006 supported the non-monophyletic nature for the subgenus *Ostorhinchus*, while monophyly of *Apogon* sensu lato had too few species represented to be adequately evaluated. Based on morphological characters, about 30 species formerly in *Apogon* have been placed in *Nectamia* and *Apogonichthyoides* in 2008 and 2010. Thus, we conducted a molecular phylogenetic analysis using about 130 species representing about 17 genera. Over seventy species of *Apogon* sensu lato, representing about 13 subgenera, were included in this study. Using three gobioids as collective outgroups, the monophyly of *Apogon* was evaluated phylogenetically based on mitochondrial and nuclear DNA sequence data. Preliminary molecular phylogeny inferred by Bayesian method based on ca. 1500bp of mitochondrially encoded 12S and 16S rRNA genes demonstrated that the genus *Apogon* was polyphyletic with over 10 well-supported monophyletic groups being recognized from the genus. While some of the monophyletic groups corresponded to existing subgenera (e.g. *Pristiapogon*, *Zoramia*), some subgenera (e.g. *Ostorhinchus*, *Apogon*) were respectively divided into multiple independent groups, some forming well-supported monophyletic groups with non-*Apogon* sensu stricto species. The result, consistent with morphological evidence, supports revising the generic/subgeneric systematics for the family.

26-24

Phylogeny of the lefteye flounders (family Bothidae): a mitogenomic perspective

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The marine fish family Bothidae (lefteye flounders) is the largest group in the Pleuronectiformes including 20 genera and about 160 species. Widely distributed in tropical and temperate waters all over the world, the majority of species are found in the Indo-Pacific oceans. The habitats are widely variable, they are found in both shallow reef area and bathyal zone (over 3,000 meters). Most bothids lie on the sea bottom on their right side, with both eyes on the left side. They also have synapomorphy of having pelvic fin base on eyed side longer than on blind side and at least two series of intermuscular bones etc.. And bothids contain many species with unique characters, such as a dorsal fin ray has evolved like lure and changes in secondary sex characteristics. Moreover, in the course of our comprehensive phylogenetic analysis for fishes using the whole mitochondrial (mt-) genome, we found that mt-genomes from a bothid species, exhibited the identical gene order which greatly differed from that of any other vertebrates. The gene order was quite unusual compared to those of known vertebrate mt-genomes. In order to study how these various traits are shared in this family, and how they has evolved, the higher level of molecular phylogenetic trees is absolutely imperative. Therefore, we determined the whole mt-genome sequences of over 30 species of 16 genera representing this family. In addition, the data of closely related species such as Achiropsettidae, formaly belonged the Bothidae, were also determined in this study. And then we conducted molecular phylogenetic analysis using their all data (50 and up). In this study, we also estimated divergence time within the family Bothidae. The combined results of all these, we consider the pattern of evolution of the various features for the Bothidae.

26-25

Molecular phylogeny of the caesionid fishes (fusilier fish or Gurukun) based on mitochondrial and nuclear DNA sequences

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The fishes of the family Caesionidae are broadly distributed in the tropical Indo-Pacific Oceans, inhabiting coral reefs in large aggregations (often mixed species) and mass-spawning. This family consists of four genera (*Caesio*, *Pterocaesio*, *Dipterygonotus*, and *Gymnocaesio*) with 23 known species. Ten species (four genera) of them are distributed in Japan (Okinawa, Ogasawara and southwestern coast of main lands). These are exploited by both small-scale and commercial fisheries. In Okinawa, Japan, the caesionid is also an important fishery fish and referred to "Gurukun", then it has been designated as the Okinawan Prefectural fish. The logo for IPFC 9 is based on one of the caesinonid fish, *Pterocaesio digramma* (Bleeker, 1864). Phylogenetic analysis of this well-known fish has been conducted mainly based on the morphological characters. Molecular phylogenetic analysis, however, is also necessary for the elucidation of evolution and diversification pattern of this group. Here we aimed to obtain robust phylogenetic tree of the family Caesionidae, by applying mitochondrial DNA (mtDNA) and nuclear DNA (nucDNA) sequencing. Today, many partial sequences of mtDNA of fishes have been deposited in DDBJ/EMBL/GenBank. We performed a comprehensive investigation of the phylogenetic relationships among them on a world wide basis using the best-scoring ML tree topology obtained by mtDNA sequencing as a backbone constraint and a "supermatrix" comprising the downloaded partial mtDNA sequences from the database and the newly determined ones. As a result, we obtained a combined total of 3601 base pairs from three mitochondrial (16S ribosomal RNA, cytochrome b and cytochrome oxidase I) and three nuclear (TMO-4C4, recombination-activating gene 2 and S7 intron 1) regions. In both mtDNA and nucDNA resultant trees, Caesio and Pterocaesio did not form reciprocally monophyletic clades, suggesting the necessity for generic and subfamilial reevaluation of the Caesionidae. Discordance between mtDNA and nucDNA trees might have been associated with hybridization or mtDNA introgressions among species in the Caesionidae.

26-26

Dates and rates of major pelagic deep-sea fish radiations

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The pelagic realm of the deep-sea is home to some of the most spectacular fishes in terms of morphological adaptations, a probable consequence of the distinct hostile living conditions in this poorly known habitat. Detecting speciation patterns in open ocean fishes is often complicated from the lack of defined physical barriers inhibiting gene flow, resulting in difficulties when establishing species richness and ecology, a particularly evident problem when considering volume of habitat available in the deep-sea. However, considering the "hostile" factors such as scarce prey and infrequent sexual encounters, comparing species richness and habitat alone tells us little about successful speciation in the pelagic deep-sea environment. The last two decades has expanded our knowledge on teleostean phylogeny from molecular data, although comparing nuclear, mitochondrial and hundreds of years of morphological work on both extant and extinct fishes, clearly illustrates numerous discrepancies between these three phylogenetic hypotheses. The phylogenetic results, updated paleontological information, a continuous production of new molecular data and advanced relaxed clock analysis provide us with the opportunity to initiate the calculation of speciation rates across independent fish lineages occupying similar habitats. In this study we produced new mitogenomic data of previously insufficiently sampled deep-sea fish lineages, and constructed a dataset of over 250 taxa to represent the current mitogenomic view of actinopterygian phylogeny. Taxon sampling was chosen with special emphasis on recent results, that showed phylogeny and age estimates from nuclear evidence, allowing us to compare the ages of stem- and crown group nodes of all major deep-sea pelagic fish radiations. Two extreme extinction rates were used to calculate the diversification rates of all major deep-sea fish radiations using the different phylogenetic hypotheses and associated estimates of divergence time. Two deep-sea radiations, the order Stomiiformes and the deep-sea Anglerfishes in the suborder Ceratoidei, were found to present higher diversification rates than all other lineages in this habitat when compared to a background diversification rate of pelagic deep-sea fishes in the Teleostei.

26-27

Phylogenetic positions of American sparid genera inferred from multi gene sequences (Actinopterygii, Perciformes)

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The family Sparidae is currently thought to consist of six subfamilies with 33 genera. Previous molecular phylogenetic studies have indicated that some taxa are not monophyletic and that two or three clades may be recognized in the family. Although two clades have wide distributions in the tropical and temperate coastal regions of the Atlantic, Indian and Pacific oceans, their monophyly has been well supported. The third clade is endemic to the Pacific and Atlantic coasts of the American continents and comprises four genera: *Archosargus*, *Calamus*, *Lagodon*, and *Stenotomus*. These genera have been placed in different phylogenetic positions, depending on data sets and analysis methods. Some studies placed these genera in a monophyletic clade that is a sister group of one of the first two clades. A recent study placed these genera in three basal clades and hypothesized that the genera were isolated by the formation of the Atlantic Ocean in the early stages of their evolutionary history. In the present study, a two step sampling was employed to address the phylogenetic position of these genera. First, a taxon sampling of representative species of major sparid lineages was undertaken and a data matrix of their mitochondrial protein coding gene and putative single-copy nuclear gene sequences constructed. A broad taxon sampling of sparids was then undertaken the resultant data matrix was combined with published mitochondrial cytochrome b sequences registered in GenBank. This data set was analyzed as a super-matrix according to maximum likelihood methods. The phylogenetic positions of the genera in the third clade are discussed with respect to the resulting more robust phylogenetic tree.

26-28

Classical complement activity in the skin mucus of Siberian sturgeon (*Acipensre baerii*)

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Fish skin mucus includes a number of non-specific immune components, but whether classical component pathway exists in skin mucus remains unknown. In this study, we found that Siberian sturgeon (*Acipenser baerii*) skin mucus was able to inhibit the growth of Escherichia coli, and the bacteriostatic activity of the skin mucus was reduced by heating, and pre-incubating with EDTA and with mouse anti-C1q antibody. Meanwhile, we observed that C1q was present in the skin mucus. In addition, full-length cDNA of C1qC of Siberian sturgeon was cloned, revealing the conservation of their structure and expression pattern among Siberian sturgeon, teleosts, and mammals. Taken together, our data suggested that the presence of classical complement pathway in Siberian sturgeon skin mucus, and the key component of classical complement pathway C1qC in Siberian sturgeon represents an ancestor of actinopterygian and sarcopterygian C1qC.

26-29

Molecular genetic study on the origin of endemic fishes in Lake Biwa

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Lake Biwa, located in central Japan, is a representative ancient lake in East Asia. Lake Biwa harbors about 70 fish species/subspecies, including endemics of diverse taxa (~16 species/subspecies). The organisms endemic to Lake Biwa are often divided into two categories, i.e., "species that evolved in the lake" and "relic species". Among them, the former have been presumed to have differentiated from their ancestors through ecological adaptation to the particular environments of the lake. To obtain insight regarding the origin and evolution of endemic fishes, we conducted phylogenetic and population demographic analyses for about 10 endemic species based on about 5,000 bp mitochondrial DNA sequences and partial cyt *b* sequences, respectively. Bayesian phylogenetic analysis with a relaxed molecular clock model suggested that some endemic species, including "species that evolved in the lake", diverged from closely related species rather early (in the Pliocene or at the beginning of the Pleistocene), while others did so more recently (in the late Pleistocene). The divergence time of the former preceded the formation of the present Lake Biwa environment with an extensive deep pelagic area (0.3–0.4 Mya). Demographic parameters from mismatch distribution and Bayesian skyline plot analyses suggested that both the endemic species that diverged early and recently, expanded their populations after experiencing a bottleneck. All expansions were inferred to have occurred after the development of the present Lake Biwa environment. These results suggest that adaptive phenotypic traits of some endemic species in the lake may have evolved much later than the divergence of these endemic lineages. It is necessary to reconsider the previous scenario for the origin of endemic species in Lake Biwa. We are also focusing on mitochondrial functions as adaptive traits because some of the fishes in Lake Biwa have been required to improve their exercise and metabolic capacity to utilize a large pelagic area and/or deep-water habitat. Our ongoing mitogenomic analysis has detected evidence of adaptive molecular evolution in mitochondrial genes, which may be related to their lacustrine life.

26-30

Mitogenomic phylogeny of acanthuroid fishes (Actinopterygii: Perciformes) and evolutionary origins of distinct larvae

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Acanthuroidei is one of the perciform suborders and currently consists of 129 species placed in six families: Acanthuridae (surgeonfishes), Ephippidae (spadefishes), Luvaridae (louvars), Scatophagidae (scats), Siganidae (rabitfishes), Zanclidae (moorish idol). Most acanthuroids inhabit tropic and temperate coastal waters including coral reefs. Some families exhibit spectacular larval stages: "acronurus" for acanthurids, and zanclids and luvarids, while "tholichthys" for scatophagids. Their phylogeny has been estimated by several morphological and molecular studies and their monophyly was proposed based on morphological synapomorphies, but was not supported by molecular data. To estimate their phylogenetic relationships, we assembled whole mitogenome sequences from 15 acanthuroids representing all the six families. Unambiguously aligned whole mitogenome sequences from 47 higher teleosts including 15 acanthuroids were subjected to phylogenetic analysis. Partitioned ML and Bayesian analyses recover monophyly of the six families, but fail to do so for the suborder. Those species with the acronurus larval stage are demonstrably monophyletic as indicated by the previous studies. Also ephippids are sister to drepaneids (concertina fishes) with high statistic values, which was removed from the suborder based on cladistic analyses of morphological characters. In addition, we found a close relationship between scatophagids and chaetodontids (butterflyfishes), both of which exhibit the tholichthys larval stage but Chaetodontidae is not included in Acanthuroidei based on adult morphology. Our phylogenetic analysis indicates that each of the two larval traits has a single origin, and the current classification of acanthuroid fishes should be revised in the future.

26-31

Phenotypic and molecular characterization of hybrid catfish from fish farms in Abia and Akwa Ibom States of Nigeria

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This study was carried out to characterize clariid catfish hybrids produced in Abia and Akwa Ibom states of Nigeria using phenotypic and molecular approaches. Two farms were chosen from each state. Ten juveniles of the hybrids were obtained from each of the farms to give a total of forty. Thirty morphometric and meristic characters were measured. The data obtained were subjected to different statistical techniques. Analysis of variance (ANOVA) showed that dorsal fin ray number was significant in Abia1 (53.79) than Abia 2 (48.05), Akwa Ibom1 (49.04) and Akwa Ibom 2 (47.00). Adipose fin length which is a major distinguishing character among "Heterobranchus x Clarias" hybrids were observed to have varying proportions among the farms with Abia 2 having a significant length of 9.8cm followed by Abia 1 (8.09cm), Akwa Ibom 1 (6.12cm) and Akwa Ibom 2 having the least (3.32cm). Molecular analysis was carried out to ascertain differences in the hybrids from the farms and between the states using randomly polymorphic DNA-polymerase chain reaction (RAPD-PCR). Seven out of the ten primers used annealed to the genomic DNA of the hybrids indicating that all the hybrids had similar DNA sequence.

26-32

A hypothetical mechanism of making NORs variability on chromosomes in bitterlings (Cyprinidae, Acheilognathinae)

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Bitterlings are freshwater fish species, ascribed to the sub-family Acheilognathinae (Cyprinidae), and consist of three genera, *Acheilognathus*, *Rhodeus* and *Tanakia*. The approximately 60 species or subspecies are widely distributed in Eurasia, with most occurring in East Asia. Karyotypes of some species or subspecies of bitterlings, collected from China, Italy, Japan and South Korea, were studied. Chromosome preparations were obtained using air-drying techniques from gastrula cells and kidney cells of fishes. Metaphases were analyzed by stainings with chromomycin A_3 (CMA_3) and silver nitrate. C-banding of chromosomes was also obtained. Mapping of 18S rDNA was performed by means of fluorescence *in situ* hybridization (FISH). The Ag-positive sites were corresponded to the CMA_3-positive sites. The CMA_3-positive sites were corresponded to the FISH signals with 18S rDNA. C-banding heterochromatin was observed at nucleolar organizer regions (NORs). It is supposed that NORs variability is a common feature in bitterlings. Moreover, inter- and intra-individual polymorphisms of NORs were recognized. A decrease in NORs during early development was suggested. This phenomenon might be concerned with germ cell differentiation in bitterlings.

26-33

The genetic architecture of the latitudinal variation in sexual dimorphism of medaka

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Sexual dimorphism, morphological differences between the sexes, is widespread a throughout the animal kingdom. However, the degree of sexual dimorphism varies considerably among closely-related species or even populations. Although there are many theoretical genetic models that can explain the genetic mechanisms of variation in sexual dimorphism, little empirical studies have been conducted to investigate the genetic basis of the variation in sexual dimorphism among natural populations. How many genes are involved in the variation in sexual dimorphism? Are they localized at particular chromosomal regions, such as sex chromosomes? Are different dimorphic traits regulated by different genes? In the Japanese medaka (*Oryzias latipes*), populations at lower latitude are more sexually dimorphic than populations at higher latitude. For example, anal and dorsal fins of mature males in low-latitude populations are longer than that of the higher-latitude males. Laboratory rearing experiments revealed that these differences in male fin length is mediated by the difference in the rate of fin elongation during development, in particular after a certain body size which probably represents sexual maturation. Furthermore, males from lower-latitude populations show more frequent fighting and courtship behaviors than males from higher-latitude populations. In this study, genetic basis for these morphological and behavioral differences were investigated using QTL mapping. We crossed two populations of medaka from habitats of different latitude (Aomori and Okinawa) and quantified several traits related to fin elongation process and mating behavior in F2 progenies. We next designed custom SNP assay system to create a linkage map and conduct QTL mapping. We will report the results of QTL analysis, such as identification of responsible chromosomal regions and effect sizes of each QTL.

26-34

Lineage-specific adaptive evolution in a unique sea basin: insights from phylogeography, phenotypic pattern and genome scan of an anadromous goby *Leucopsarion petersii*

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Climate changes on various time scales often shape genetic novelty and adaptive variation in many biotas. In the marine realms, low sea levels during Pleistocene glacial periods created land bridges that could effectively divide populations of marine organisms with high potential for dispersal and widespread distribution. Genetic divergence was often promoted by the historical isolation of the ocean (sea) basins. Such allopatric lineages that might have experienced different selective regimes by past climatic and current oceanographic factors provide valuable examples that advance our understanding of climate change–phenotypic diversity relationships. Marine organisms around the Japanese Archipelago can be excellent models to investigate adaptive divergence in relation to the isolation of sea basins. We explored lineage-specific adaptive evolution in a unique sea basin, the Sea of Japan, where severe environmental conditions existed in the Pleistocene in relation to repeated glaciations, using the ice goby *Leucopsarion petersii* as a model system. Phylogeographic analyses showed that this species consisted of two historically allopatric lineages, the Japan Sea (JS) and Pacific Ocean (PO) lineages that have lived under past and current contrasting environments. Two lineages are not reproductively isolated because hybrid swarms are formed in secondary contact zones. Populations of the JS lineage are characterized by larger body size with higher number of vertebrates and greater cold tolerance. Common garden experiment revealed genetic control of such phenotypic divergence, suggesting that the JS lineage is a cold-adapted lineage. A limited genome-scan approach using candidate genes for phenotypic variation between two lineages in combination with 100 anonymous microsatellite loci showed that *NPY* gene, which is an important regulator of food intake and potent orexigenic agent, and three anonymous microsatellites were identified as robust outliers, that is, candidate loci potentially under directional selection. For these outlier loci, populations of the JS lineage had putative signals of selective sweeps. Also, the JS fish reared in a common environment showed a higher expression level for *NPY* gene. Thus, this study succeeded in identifying molecular signatures of directional selection across populations of the JS lineage and provided evidence for lineage-specific adaptive evolution in this unique sea basin.

26-35

Population differentiation of Moses Perch (*Lutjanus russelli*) in Thailand

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Moses Perch (*Lutjanus russelli*) is a common fish that supports the livelihoods of many thousands of local artisanal fishers and is a principal form of local food security in coastal Thailand. The heavy reliance on these fishes potentially places them at risk of overfishing if the regional stocks are largely self-seeding; despite its ubiquity, *L. russelli* displays evidence of regionalization. Thailand is a unique geographic location that includes differently-coloured populations from two oceans divided by the Thai-Malay Peninsula and connected only via a narrow waterway. Therefore, in this study we focused on examining genetic differences between populations from the Gulf of Thailand (western Pacific Ocean/ South China Sea) and the Andaman Sea (east Indian Ocean). A study of 300 individuals using 9 microsatellite loci showed that the *L. russelli* population in the Gulf of Thailand is genetically distinct from the populations in the Andaman Sea, possibly indicating the existence of geographical barriers hitherto unsuspected between the Gulf of Thailand and populations within the Andaman Sea. Moreover, morphometric examination revealed consistent differences between fishes from two coasts of Thailand. These results raise all sorts of questions not only about additional management policies which might need to be implemented to safeguard resource security for local fishers in Thailand, but also about the taxonomic stability and potential need for taxonomic re-evaluation of this species.

26-36

DNA species identification of fish-remains from South Pacific Island

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DNA analyses on the fish-remains have the unique potential to provide insight into the biology of extinct organisms and evolution of living species and ethno-ecological study. We tried to DNA extraction and PCR amplification of excavated fish-remains (estimating about 600 years ago) from Atafu Atoll, Tokelau in 2008 and 2009. To select most suitable DNA extraction method from fish-hard tissue sample, we applied to seven DNA extraction methods classifiable four categories (spin-column, ethanol precipitation, adsorption and spin-column plus adsorption method) on the present shark teeth and vertebra bone materials. The extracted DNA samples from present bone materials were quantified DNA concentration and purity using UV spectrophotometry. In addition, PCR amplification were conducted on the all DNA samples of seven DNA extraction methods, and judged the most suitable DNA extraction method for fishhard tissue sample. Fish-remains, which were morphologically identified as shark tooth and vertebra (genus *Carcharhinus*) and parrotfish tooth bone (family Scaridae) from archaeological approach, were used and grinded to a fine bone powder after decontamination. PCR amplifications for species identification of fish-remains were conducted using universal primers located on 12S and 16S ribosomal RNA gene region of mitochondrial DNA, and nucleotide sequence were detected by direct or cloning sequencing. The obtained nucleotide sequences were checked through the BLAST search within DDBJ database to examine whether the sequence would match to any species. The resultant DNA extraction method of spin-column plus adsorption method was showed clearly high concentration and good PCR amplification, thus this method applied following fish-remains. PCR amplification of fish-remains DNA was successful, but many unexpected species such as *Homo sapience* and Acidimicrobidae were identified by BLAST search. On the other hand, two positive results were obtained from shark vertebra and parrotfish tooth bone. These two sequences were identified as three species (*C. melanopterus, C. brevipinna, C. plumbeus*) genus *Carcharhinus* and one species (*Scarus schlegeli*) family Scaridae, respectively. These results mean that both morphological identification from archaeological approach and molecular analysis basically correspond, and DNA analysis would enable the further detail identification from fish-remains.

26-37

Population structure and sequence divergence in the mitochondrial DNA control region of Gizzard shad *Konosirus punctatus* in Korea and Japan

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To investigate the extent of genetic differentiation among populations, genetic polymorphism in Gizzard shad, collected from wild populations of eight locations (Youngheungdo, Hongwon in the West Sea, Boseong, Daepo, Yeosu, Jinhae in the South Sea, and Busan, Jukbyun in the East Sea) in Korea and two locations (Ariake, Genkainada) in Japan, were examined using mitochondrial DNA (mtDNA) control region. Nucleotide sequence analysis of 403 bps in the variable portion of the 5 end of the mtDNA control region revealed 87 variable nucleotide sites among 309 individuals, which defined higher number of haplotypes 23-28 from the samples of 30-32, except for Busan and Jukbyun samples. In addition, haplotype diversity of the samples from eight locations was also much higher than those of Busan and Jukbyun samples which indicate 0.876 ± 0.044 and 0.893 ± 0.037, respectively. Analysis of mtDNA control region indicates that Gizzard shad in 5 groups of sample (Youngheungdo, Hongwon, Boseong, Daepo, Yeosu), Jinhae, 2 groups of sample (Busan, Jukbyun), and 2 groups of sample (Ariake, Genkainada) are genetically different populations.

26-38

Complex genetic structure of a catadromous fish in temporarily open closed estuaries of Socotra Island and the northern Gulf of Aden

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Temporarily open/closed estuaries (TOCEs) are major ecosystems of the Indian Ocean coastal zone, in particular of the wider Gulf of Aden including Socotra Island. Climatic events like monsoons and storms are the main forces responsible of the particular functioning of those ecosystems which can close up for prolonged and variable periods of time, thus limiting their connectivity with the marine environment. The aim of this study was to test the hypothesis that the particular functioning of TOCEs can promote population genetic differentiation of estuarine fishes. To reach this aim, the genetic structure of 288 individuals of *Terapon jarbua*, a widely distributed fish species in the region was assessed using two types of genetic markers (i.e.: mitochondrial Cytochrome c Oxidase I (COI) gene and eight microsatellites). The first marker allowed inferring 1) a high haplotype diversity and reduced nucleotide diversity over the whole data set and 2) a "star-like" shape of the haplotype network, putatively interpreted as resulting from a recent population expansion following sea-level rises after local extinctions during the Pleistocene glaciations. The genotyping of the latter markers detected a significant genetic differentiation between *T. jarbua* populations in the wider Gulf of Aden ($F_{ST} = 0{,}035$, $p < 0.01$). Significant multi-locus deficits in heterozygotes at particular locations displaying high levels of F_{IS} were recorded. It is suggested that a possible Wahlund effect took place in those TOCEs which could gather several cohorts of larvae originating from different marine sub-populations over the sampled area. The present study emphasizes: 1) the presence of a past and recent genetic structure of *T. jarbua* in the wider Gulf of Aden, 2) the necessity to improve our knowledge on the role of the opening-closing timing of the TOCEs on the genetic structure of fish populations and 3) the urgent need for a better conservation program of TOCEs as potential reservoirs of biodiversity in this region, in order to avoid habitat fragmentation and permanent closure of those nursery areas by human activities.

26-39

The hypothesis of establishment of the Pacific cod modern population structure in the North Pacific

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The modern population structure of Pacific cod was formed in the Pleistocene-Holocene period, with its features of transgressions and regressions of the World ocean waters, and forming of the relief in the north Pacific region. Summarizing the results of the few populationgenetic studies of Pacific cod, a generalized scheme of the organization of Pacific cod population might be presented in as the following. There exists a central grouping, which can be traced back to ancestral forms, which colonized the North Pacific from the Arctic after the Bering Strait opened 5.4-5.5 million years ago (according to updated data). This subunit combines the modern population of Pacific cod from deep-sea Okhotsk and Bering Seas, Gulf of Alaska and coastal waters of the Pacific, living at stable temperature and salinity conditions, exposed to relatively weak changes, even during periods of global glaciation maxima and accompanying oceanic regressions. Some internal differentiation can be determined by the power of gene flow between different parts of the range, which are under the effect of various factors from the water current systems to the biological characteristics of individual stocks. The next subunit is the group of the Sea of Japan, which may have acquired its individual genotype characteristics in the process of repeated isolation of the Sea of Japan from the Pacific (for example, in glacial ages). The last and most heterogeneous subunit (which could be named as "Holocene invaders") is a kind of mixture of small "young" groups distributed now in the Yellow Sea, in shallow waters of the Okhotsk and Bering Seas, in the coastal fjord-like waters from the Georgia basin (Strait of Georgia, Canada, and Puget Sound, USA) in the south to the Gulf of Alaska in the north. They colonized these regions during the postglacial transgression, and formed their morpho-biological and genetic characteristics under a wide range of conditions under the impact of environmental factors, often located on the boundaries of tolerance for Pacific cod.

26-40

Preliminary review of the gobiid fish genus *Paratrypauchen* of Japan with a comment on the validity of *P. wakae* (Jordan and Snyder, 1901)

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The gobiid fish genus *Paratrypauchen* is a unique within the *Trypauchen* group and characterized in having a scaleless abdomen, frontal crest without serrations and emarginated pelvic fins. Although there is wide variation in meristic characters, *Paratrypauchen* is thought to be composed by only one species in recent revision by Murdy (2008). Based on more than 260 specimens of the genus collected from Japan, morphological observation showed the presence of two distinct species, which were also detected by the analyses of partial mitochondrial 16S rRNA and ND2 gene sequences. Morphological differences between them are counts of caudal vertebrae (24-26, mode 25 vs. 26-28, mode 27) and longitudinal scale rows (49-59 vs. 60-76). The species with fewer counts is identified as *Paratrypauchen wakae* (Jordan and Snyder, 1901) and the other one is identified as *P. microcephalus* (Bleeker, 1860) because each holotype of the former (SU 6515, type locality: Wakanoura, Japan) and the latter (RMNH 4671, type locality: Sungiduri, Indonesia) species has 25 and 28 caudal vertebrae, respectively. Other three nominal species or subspecies, *P. raha* (Popta, 1922), *P. barnardi* (Hora, 1926), and *P. wakae chantungensis* (Fang, 1942), might be identified as either one of the two valid species based on the counts of caudal vertebrae or longitudinal scale rows. However, further study of molecular-morphological combined approach is required for samples from Southeast Asian and South African regions to clarify the taxonomy of the members of *Paratrypauchen*.

26-41

Phylogenetic relationships of *Rhinogobius* gobies in Japan, inferred from multiple nuclear gene sequences

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The gobies of the genus *Rhinogobius* (Gobiidae) are distributed widely in fresh waters of East and Southeast Asia, and represent the most species-rich group of freshwater gobies. Their life history and egg size are diversified, so the process of diversification is worth studying in terms of adaptation and speciation. However, their taxonomy is very confused and limited information is available about their ecology. To investigate the process of their ecological diversification, we first estimated the phylogenetic relationships and life history evolution of the Japanese *Rhinogobius* gobies, for which ecological information has been relatively well accumulated. We analyzed all 15 species known from Japan. We sequenced four mitochondrial and six nuclear loci, and reconstructed phylogenetic trees for each genomic dataset. The ancestral states for the life history pattern and egg size were reconstructed based on the nuclear DNA phylogeny. As partially suggested in previous studies, the mitochondrial DNA (mtDNA) phylogeny indicated that some widely distributed species are polyphyletic; three regional mtDNA clades (i.e., the mainland, Ryukyu Archipelago, and Bonin Island clades) including some distinct morphological species were revealed. On the other hand, the nuclear DNA phylogeny was essentially concordant with the morphological species. This conflict between the mtDNA and nuclear DNA phylogenies strongly suggests mitochondrial introgression through interspecific hybridization within each region. The hybridization was inferred to have occurred in the early–middle Pleistocene, based on molecular dating using geological data. Reconstruction of the ancestral states revealed that the evolutionary change from amphidromous to freshwater life histories accompanied by change in egg size occurred independently in at least three lineages. In one of these lineages, two life historical changes were estimated; i.e., from amphidromous (small egg) to lentic (small egg) through fluvial (large egg). Although congeneric species outside Japan should be analyzed further, the present results suggest that an important factor for species diversification in this genus is the life history evolution associated with high adaptability to freshwater environments. Reproductive isolation may have easily been established under such ecological divergence.

26-42

Structure of egg envelope in rice-fish *Oryzias sinensis* (Adrianichthyidae)

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The filaments surrounding the entire egg envelope of *Oryzias sinensis* could be categorized into two topographically distinct types: attaching and non-attaching filaments. The attaching filaments were twisted together tightly above the egg envelope surface to form massive bundles of filaments opposite the animal pole that were visible to the naked eye. These bundles were inserted into the gonoduct to suspend the egg cluster. The attaching filaments consisted of bundles of filaments were at least three to five times longer than the non-attaching filaments. The remainder of the egg envelope surface was covered with non-attaching filaments, which were shorter and more numerous than the attaching filaments. Both the attaching and non-attaching filaments could be divided into basal and distal segments based on the presence of a "bamboo joint-like structure". The basal segments, closest to the egg envelope, had a round cylinder-like appearance, were short and nearly constant in length. Hairlike micro-protrusions were visible on the basal segments of the attaching filaments whereas no such protrusions were present on the basal non-attaching filaments. Meanwhile, the long distal segments had a tapering structure of variable length and frequently terminated in a threadlike projection. The egg envelope of *O. sinensis* has a flat or smooth surface.

26-43

Effects of human-made obstructions on the distribution and density of the amphidromous sculpin, *Cottus* sp. ME

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In the 20th century, many rivers in Japan have been equipped with locks, dams, or weirs to optimize water levels for navigation, generating electricity, or for agricultural land-use. Such human-made obstructions interrupt the migration and dispersal of many fish species, with a height of 25–30 cm being considered as the critical limit that is impassable by small fish species. The amphidromous sculpin, *Cottus* sp. ME, is a poor swimmer relative to most large-bodied fish. Jungwirth (1996) reported that vertical drops of just 25 cm were impassable for bullheads (*Cottus gobio*) moving upstream. Here, we studied the effects of human-made obstructions on the distribution and density of *Cottus* sp. ME in three rivers (the Kita, Minami, and Kuzuryu rivers) in Fukui Prefecture, Japan. Two or three-pass electrofishing surveys were performed at specific sites up to the 2nd or 3rd weir from the mouth of each river. The first weir from the river mouth of the Minami and Kuzuryu rivers was equipped with two fishways on both banks whereas just one fishway was placed on the right-hand bank of the Kita River. The inlet arranged at the fishway exit on the first weir of the Kita River because of the intake of water from a river used for agriculture. Sculpin density above the first weir decreased to about 60% of that below the weir at both the Minami and Kuzuryu rivers. Therefore, fish density above the first weir decreased by about half, despite there being two fishways on either side of the first weir. Fish density was higher below the first weir of the Kita River compared to the other two rivers. However, above the first weir of the Kita River, fish density declined to about 90% that below first the weir. The major decline in fish density may be related to the fishway exit being closed by human-activity. Our results suggest that sculpin passage is even prevented by instream obstructions equipped with fishways. Further study is necessary to develop a fishway suitable for the passage of small benthic fishes, including freshwater sculpins.

26-44

Morphological and genetic variation of domestic alien species, *Pseudorasbora parva,* in Matsumoto Castle Moat

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Pseudorasbora parva is very common freshwater minnow in the ponds and rivers of eastern Asia, including western Japan, where it occurs naturally in the Kanto region, western Honshu, Shikoku and Kyushu (Nakamura 1969). Over the last several decades, the distribution of *P. parva* has rapidly expanded toward eastern Japan as domestic invasive species, resulting from accidental introductions during transplantation of other commercial fish. In recent years, *P. parva* is known as one of the most famous invasive fish not only in Japan but also in Europe and central Asia etc.. In the present study, to evaluate phenotypic plasticity which could contribute to such a high establishing ability and rapidly widespread expansion, we examined morphological and genetic variation among populations collected from central Japan (two site within Matsumoto Castle moat and one pond in Nagano City), using morphometric method measuring length and angles between 27 landmarks, 6 meristic characters, and mitochondrial haplotypes compositions estimated by partial sequences and RFLP of cytochrome *b* gene. Genetic analysis revealed that both moat populations suffered extensive genetic disturbance among 3 genetic gropes (central Japan, western Japan and China) and all individuals from pond population had a haplotype peculiar to western Japan group. It was not observed significant difference in haplotype compositions between two moat populations. We found a great variation in morphometric characteristics, especially dorsal shape and the central part of body shape, between three populations using principle component analysis with multiple comparisons test. This variation was estimated to associate with variation of environmental factors, such as electrical conductivity and PO^4-P. The number of pored lateral line scales as meristic character differed between moat and pond populations. It was not observed that morphological variation among three genetic groups, considering that individuals having different diverged haplotype could perform almost random mating. These strongly suggested that *P. parva* as Japanese (domestic) alien species suffered extensive genetic disturbance and would have ability to form flexibly their body shape.

26-45

Review of wedgefish family Rhynchobatidae (Elasmobranchii: Rajiformes) of Taiwan

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The wedgefish family Rhynchobatidae in Taiwan is reviewed. Four species are recognized, including a new species and two new records. *Rhynchobatus palpebratus*, based on 2 specimens, has 146 total centra, 60-64 total basal radials, origin of first dorsal fin over origin of pelvic fin, and females usually with two eyebrow spots; *R. springeri*, based on 2 specimens, has 126-134 total centra, 60 total basal radials, a robust snout, and prominent black pectoral marking, usually closely surrounded with 3-4 white spots. A new species, which is recognized based on 10 specimens collected from Taiwan, can be distinguished from its sympatric congeners by having 179–184 total centra and in lacking a dark pectoral spot in specimens smaller than 1 m TL. It most closely resembles *R. palpebratus* in body shape in having a dark, eye-brow like marking on its orbital membrane, but differs from this species in having a higher vertebral count (160–170 vs. 130–139 total free centra). A fourth species, *R. australiae*, is also listed based on a validated literature record. No specimens of the first recorded member of the genus, *R. djiddensis*, an Indian Ocean species, have been found. This is a likely misidentification and this species should be excluded from the Taiwanese ichthyofauna.

Poster Presentations
(Thursday 27 June 2013)

27-01

Spawning ecology of *Maurolicus japonicus* in the Korea Strait and the Ulleng Basin

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In order to investigate the spawning ecology of *M. japonicus* in the Korea Strait (KS) and the Ulleung Basin (UB), we collected the eggs and larvae of *M. japonicus*, and measured the water temperature and salinity from 1992 to 2003. We analyze the distribution pattern on the eggs and larvae, and the density changes and distribution pattern according to the developmental stages of eggs. There were two types of water masses such as the Tsushima Warm Current (TWC) and the Korea Strait Bottom Cold Water (KSBCW). Their two currents were opposite in flow direction. *M. japonicus* was a year-round spawning between the KS and the UB. The eggs were mainly distributed in the UB and the northern Korea Strait (NKS) including the western channel. The distribution range of eggs was widely in the fall but most narrowly in the winter. The range of egg density was 1.0235 to 1.0266g/cm3, which was increased as eggs developed. The egg density was higher than that of the surface water but similar to the ambient water in 55-140m depth. The composition of eggs with early, middle, and late developmental stages had similar ratios to each other in the NKS. But the relative egg ratios of the middle and late developmental stages were slightly increased into the western KS away from the NKS located in the southern Ulleung Basin (SUB). The distribution pattern of larvae was similar to those of eggs. But the larvae were not found in the WKS and only found rarely in the eastern KS in the winter. Most larvae were less than 5mm body length between the NKS and the SUB but more than 5mm body length in the UB. The distribution depth of larvae was mainly below the seasonal thermocline in the daytime but went up to the top of the thermocline at night. The estimated spawning and hatching ground using the biological information from eggs and larvae, and the environmental factors was in the lower part of the seasonal thermocline located between the SUB and the NKS except the WKS and the northern UB. Based on the biological information of *M. japonicus* and the environmental conditions, the spawning and hatching ground seems to be kept constantly by the interaction of the two water masses, TWC and KSBCW, and the spawning strategy of *M. japonicus*.

27-02

Reproductive biology and growth of blue stripe herring, *Herklotsichthys quadrimaculatus* (Clupeidae), in coastal water of Okinawa Island, southern Japan

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Blue stripe herring, *Herklotsichthys quadrimaculatus*, is an important commercial fish popularly eaten and used as live bait for bonito fishery in Okinawa Island. However, little is known about life history of this species in Japanese water. To study their life history, monthly fish sampling was carried out at coastal water of northern Okinawa Island. Larvae were collected using an aquatic lamp at fishing port. Juvenile and adult fish were sampled from commercial catches by the aquatic lamp and the set net at offshore. Hatch dates, estimated from daily increments of larval otolith, ranged from middle February to early August, and frequency of these occurrences peaked from middle March to July. High gonadosomatic index (GSI) appeared from March to August and peaked from April to July. Thus, their spawning season was between middle March and August. It is possible that larvae hatching at February were transferred from warm southern area. Both sexes were estimated to begin to mature at ca. 80 mm SL based on histological observation of gonads and relationship between size and GSI. Female would spawn several times during spawning season, because mature and spent ovary also had immature oocyte. Batch fecundity of female was estimated 1200-10000. Larvae (< 25 mm SL) occurred between March and September. Monthly changes of size frequency indicated that larvae grew rapidly, and growth stagnates since winter. Also decrease in adult size indicating change of age cohort was found after spawning season. Largest adult in our study was ca. 120 mm. The age determination by increment counts of otolith showed increasing linear growth up to 80 mm (ca. 150 days after hatching) and the growth was almost stagnant after then. And no fish lived more than ca. 1 year. These facts suggested that this fish was an "annual_ species in study area.

27-03

Taxonomic studies on the larval clupeoid fishes from the Ryukyu Islands based on mtDNA 16S and morphological data

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Many ontogenetic studies on clupeoid fishes have been done especially in temperate waters including Japan, EU, US, Canada and Australia. However, little is known about the early life history of clupeoid fishes found in tropical waters. Identification of the larval clupeoid fishes found in tropical waters has been often limited to family level (i.e. Cluepidae spp. or Engraulidae spp.) due to the lacking of basal information about morphological characters and genetic markers for species identification. The chaotic state of taxonomy of Indo-Pacific clupeoid fishes with high species diversity is another obstacle to identification of those larvae. In some cases different species may share identical morphological characters especially in the same genus, so identification using morphological characters is better applied to the categories of family or genus at field work, and molecular sequencing provide correct identification to the species level in laboratory. The goal of my study is to accumulate the morphological data and partial mtDNA 16S sequences for the larvae of clupeoid fishes from the Ryukyus to identify to the species level. To establish fish identification using molecular genetic data, we collected four families 20 genera 40 species such as *Chirocentrus* (Chirocentridae); *Dussumieria, Spratelloides, Herklotsichthys, Amblygaster, Sardinella, Escualosa, Hilsa, Tenualosa, Clupanodon, Nematalosa,* and *Anodontstoma* (Clupeidae); *Ilisha* and *Opisthopterus* (Pristigasteridae); *Encracicholina, Stolephorus, Thryssa, Setipinna,* and *Coilia* (Engraulididae). About 500 bp sequences of partial mitochiondrial 16S rRNA were determined from the adult specimens and six genera 12 species were referred from Genebank such as *Etrumeus*, *Sardinops*, *Clupea*, and *Konosirus* (Clupeidae); *Engraulis*, and *Lycothrissa* (Engraulididae). Thus 26 of 28 genera in tropical western Pacific are covered and each genus and species was distinguished from each other by the sequence data. Until now, I recognize that 3 families 12 genera 21 species (including 2 undiscribed *Sardinella*) of clupeoid fishes are distributed in the Ryukyu Islands, where most species share with tropical western Pacific. In this presentation, we introduce 16 clupeoid species of larvae and juveniles identified to the species level.

27-04

Recruitment of *Anguilla* spp. (Anguillidae) in Takase river, Wakayama, Central Japan

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Two species of freshwater eels occur in Wakayama Prefecture, Honshu, Japan: *Anguilla japonica* and *A. marmorata*. The former is the more common species in Wakayama. However, populations of both species are declining critically. *Anguilla marmorata* is a rare species in Wakayama and is listed as "Near Threatened" in the Red Data Book of Wakayama Prefecture. A portion of the Tonda River in southern Wakayama, where this species occurs, is a protected area, however after 1985, large *A. marmorata* (> 1m) have not been found there. The basic ecology for both species in Wakayama is poorly known. We studied individual body size ratios, recruitment season, and condition of *Anguilla* spp. that recruit to selected streams there. Monitoring of glass eel recruitment was conducted for 2h each night on two consecutive days per a month between January-December, 2012. Two monitoring stations were set across the estuary of the Takase River, a branch of the Tonda River. A total of 198 glass eels were collected by underwater lamplight during this sampling period. *Anguilla japonica* (n=195:98.5% of the total glass eels collected) was collected between January and June, and also in September. The peak of recruitment (n=72) was in February and March. There was no recruitment peak in June. The total length (TL) and wet body weight (WBW) of *A. japonica* were 58.5±2.5mm (mean±S.D.; range 50.3-63.8) and 137±19mg (91-197), respectively. The TL and WBW tended to become smaller later in the season. Pigmentation varied in a range between stages VA and VIB. A single individual was collected in September; its body was small and thin (TL 56.4mm WBW 91.2mg). The pigmentation stage was not fully developed (VIAiv). Only a few *Anguilla marmorata* (n=3:1.5%) were collected during February, May and October. The TL and WBW of this species were 51.3±3.7mm (47.3-54.7) and 168±40mg (126-207), respectively. The pigmentation stages were young, VA (n=1) and VB (n=2). No recruitment peak was observed. We suggest that monitoring continue in order to obtain additional data that may indicate a pattern of recruitment, growth, and pigmentation for these two species in this protected river system within Wakayama Prefecture.

27-05

Early development and occurrence pattern of two *Nematalosa* species in Nakagusuku Bay, Okinawa Island, Ryukyu Archipelago

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The genus *Nematalosa* (Clupeiformes: Clupeidae) is widespread throughout the tropical and subtropical Indo-Pacific regions. Two particular *Nematalosa* species, *N. come* and *N. japonica* are sympatrically distributed around Okinawa Island, Ryukyu Archipelago, southwestern Japan. These fishes are important target species for gill net and small set net fisheries in Okinawa Prefecture. In Okinawa Island, their habitat is rapidly decreasing in size because of recent reclamation and land exploitation. Given this status, the fundamental studies will provide valuable information, particularly with regard to the increasing need for their conservation and management. In present study, the early development and occurrence pattern of these two species are described and compared in detail. A total of 1258 larvae and juveniles of two *Nemtalosa* species were collected at the surf zones as sandy beach and tidal mudflat of Nakagusuku Bay from April 2005 to April 2006. These larvae and juveniles were identified as 482 *N. come* (8.9-41.5 mm SL) and 776 *N. japonica* (11.2-47.4 mm SL), based on morphological and molecular methods. They were very similar in general morphological characteristics such as body shape and pigment patterns, but could be distinguished between the two species by the differences in myomers or a timing of occurrence in the surf zones. Their developmental stages collected at the surf zones were postflexion larva to juvenile. The larvae and juveniles of *N. come* occurred year-round with two peaks in April and July, and those of *N. japonica* occurred from January to June, peaking in April. Postflexion and metamorphosis larvae of both species at first occurred in the sandy beaches, and then most of metamorphosis larvae and juveniles occurred in the tidal mudflats. It suggested that two species moved from sandy beaches to tidal mudflats during the metamorphosis stage. Juveniles of the two species grew up in shallow area and reached at 80-115 mm SL in one year after hatching. These results revealed that coastal shallow area such as the surf zones was important nursery ground to support their early life history.

27-06

Short-term temporal and spatial variations in larval fish community in estuary of Tamsui River, northern Taiwan, and relations in sampling designs

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Researches on larval fish provide important and fundamental information for fisheries management and marine conservations. However, the accuracy of the information will affect the subsequent efficiency of management. In the past, the majority of the time unit in larval fish sampling in Taiwan was seasonally or monthly based, and thus, the representative samples might be biased. The objective of this research is to evaluate, through high frequency sampling, the larval fish assemblage variations in short-term temporal and spatial intervals and to discuss the relations in sampling designs. Larval fish were collected from 3 stations (array in line, 2 km apart from each) in the coastal waters of Tamsui River estuary, Northern Taiwan, with different sampling frequencies (2~12 hours across day and night, and 2~43 days intervals) and in early June to mid-July 2012. Afterward, the larval fish assemblage variations in different temporal and spatial scales were evaluated. The preliminary results showed that the fluctuations in the catches were large. In the temporal scale, the most important factor that resulted in community variations in the fish assemblages was day-night; the next important factors were the hourly-and daily-intervals. In the spatial scale, there were no significant assemblage differences among the 3 stations. This preliminary result suggests that, to correctly reflect the larval fish assemblages in the Tamsui River estuary, the sampling designs in the future must firstly cover the day-night interval and secondly increase the hourly and daily sampling frequencies, as well as decrease the number of sampling stations.

27-07

Spawning migrations in a mildly catadromous fish species: we know the destination, but where is the source?

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The diadromous fish *Galaxias maculatus* (inanga) is one of the most widely distributed fishes in the world, occurring throughout the southern hemisphere. The post-larval juveniles of this species form the basis of New Zealand's whitebait fishery as they migrate back into freshwater. This essentially annual species spawns exclusively in tidally inundated riparian vegetation in upper estuaries. The success of spawning is closely linked to the availability and composition of suitable riparian vegetation. It has been widely assumed that after entering a river as whitebait, mature fish do not migrate to other waterways before spawning. Therefore, whitebait that enter a waterway are committed to finding critical spawning habitat in that river if they are to spawn successfully when they mature. If spawning habitat is absent or degraded, their ability to contribute to future generations is compromised. Consequently, degradation or reduction of spawning habitat in individual estuaries can lead to the formation of 'sink' populations. Here we present the results of a tagging study to track adult fish across waterways during the spawning season. This study will provide a measure of stream fidelity in adult fish along with basic population characteristics and dynamics. This knowledge will allow whitebait conservation and habitat rehabilitation to be targeted at productive waterways and estuaries.

27-08

Early life history of deep-sea demersal fishes collected in the near-bottom on the upper continental slope of Suruga Bay, Japan

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The early life histories of most deep-sea demersal fishes remain unknown, despite some epipelagic larvae having been collected (e.g., Ipnopidae). We undertook a near-bottom larval sampling programme on the upper continental slope (100–1053 m depth) of Suruga Bay, southern Japan, during monthly cruises of the T/V *Hokuto* (Tokai University). The sampling devices used included a larval net (1.3 m in diameter) equipped with a depth meter and deep-sea floats, and joined by chain to a depressor (36 kg) just above a columnar weight (235 kg) developed in our laboratory. A total 261 larvae and juveniles of demersal fishes, representing 27 species (including unidentified 12) of 16 genera in 13 families, were collected from 74 tows between 2006 and 2009. Three distribution patterns related to the water column were determined: Type A, larvae to adults occurring only near-bottom, e.g., alepocephalids (*Leptoderma lubricum* and *L. retropinnum*) and liparids (*Paraliparis dipterus*); Type B-1, larvae and early juveniles rising to shallower depths in the water column, late juveniles and adults occurring near-bottom, e.g., macrourids (*Coryphaenoides marginatus* and *Coelorinchus kishinouyei*); Type B-2, juveniles and adults collected near-bottom, no larvae collected to date, e.g., synaphobranchids (*Synaphobranchus affinis*) and ophidioids (*Dicrolene tristis*). The ontogeny of Type A is characterized by the acquisition of general adult characters, such as fin-ray numbers and body proportions, during an early developmental (e.g., yolk-sac) stage and indistinct transformation thereafter, its members spawning a few large-diameter demersal eggs and living near-bottom throughout life. The acquisition of general adult characters, related to the advancement of swimming ability, seems to contribute to the improvement of predatory ability and the mitigation of predation pressure in the early growth stages.

27-09

Classification of gonadal development patterns in Cyprinidae

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The family Cyprinidae has undergone extensive speciation. Most cyprinids spawn from spring to summer, but some variability exists depending on gonadal maturation. To clarify the taxonomic and ecological relationships between six cyprinid species, we examined gonadal maturation in *Gnathopogon elongatus elongatus, Nipponocypris temminckii*, *Phoxinus logowskii steindachneri*, *Pseudogobio esocinus esocinus*, *Tanakia lanceolata*, and *Zacco platypus*. Wild specimens were caught over a 12-month period in the Kiso River system in central Japan and gonad development was examined histologically. Gonadal development was classified into the following four patterns based on the onset of vitellogenesis and meiosis in females and males, respectively. 1) Autumn-onset pattern, as observed in both sexes of *Gnathopogon* and *Phoxinus*. Gonadal development begins in October to November in response to decreased temperatures and day length, with spawning after 5 to 6 months. This pattern has been reported in both sexes of some Gobioninae and Leuciscinae. 2) Winter-onset pattern, as observed in both sexes of *Tanakia* and in males of *Pseudogobio*: gonadal growth occurs in December to January in response to decreasing temperatures and day length, with spawning occurring after 3 to 4 months. This spawning pattern has been reported in males of some Acheilognathinae. 3) Spring-onset pattern, as observed in both sexes of *Nipponocypris* and *Zacco*. Gonadal development occurs from February to March in response to low temperatures and increased day length, with spawning after several months. This pattern may be shared with the Danioninae as well as females of some Acheilognathinae. 4) Simultaneous pattern, as observed in females of *Pseudogobio*, where gonadal development is initiated immediately before the spawning season in April to June in response to rising temperatures and increased day length, and simultaneously process during spawning season. No information on this pattern of gonad development has yet been reported. Except for the Gobioninae, the patterns of gonadal development were similar in almost the same subfamilies and sexes. The observed variation in gonadal development patterns may reflect the disparate biogeographic histories of the various taxa, which would account for differences in growth patterns, maturation size, and length of spawning season.

27-10

Histological characteristics of the mature ovaries of three sharks

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To obtain basic information on reproduction in sharks, we examined mature ovarian tissues of three viviparous species, *Carcharhinus leucas*, *C. limbatus* and *Negaprion acutidens.* These tissues contained many large yolky oocytes distributed on the surface of the anterior part of the epigonal organ. Ovarian tissues from all three species were red in color due to well-developed blood vessels, and were therefore easy to distinguish the epigonal organ. To avoid any regional bias in the development and distribution of tissues in the ovary, many tissue fragments (1x1x2cm) were examined from each whole ovary. Tissues were fixed with Bouin's solution and observed by routine microscopy methods. No significant differences were found in the uneven distribution of oocytes at various stages in the ovaries from anterior to posterior. The outer surfaces of the ovaries were covered with a layer of epithelial cells. Smooth muscle tissue (SMT), stained with eosin, was present beneath the epithelial cells. Some young oocytes at the peri-nucleolus stage were distributed in contact with the SMT. H Oocytes developed in size gradually in concert with migration to the interior of the ovary. Many traces of young oocytes were present around the developing young oocytes. Some yolky and mature oocytes were seen inside of the ovary. Follicle tissue, which is the site of steroid hormone production, enclosed the yolky oocytes and was composed basically of two layers, an inner layer of granulosa cells and an outer layer of theca cells. The theca layer was divided into two layers, with a thin layer of SMT between the two theca layers. Many presumptive steroid-producing theca cells were present and were distributed mainly in the outer theca layer compared to the inner layer. Many degenerating yolky oocytes, together with developing yolky oocytes, were present in the whole ovary. Granulosa cells, which enclosed degenerating oocytes that were hypertrophied, actively phagocytosed the yolk granules. The granulosa cells eventually formed a cluster similar to the structure of the corpus luteum of the mammalian ovary. However, it is not yet evident if these clusters function in steroid hormone production for maintaining pregnancy.

27-11

Skeletal anatomy of the caudal fin of sharks of the order Carcharhiniformes (Chondrichthyes, Elasmobranchii)

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Sharks typically exhibit a heterocercal tail divided in epaxial and hypaxial portions. The epaxial portion consists of the supraneural spine, basidorsal and interdorsal components. The basidorsal and interdorsal are distally jointed forming the neural arch. The hypaxial portion consists of basiventrals (forming the haemal arch), the haemal spine, and reduced hypural and haemal elements situated just distally to each basiventral. The new term parahaemal spine is proposed for that haemal element ventral to the basiventral. The tail of Scyliorhinidae does not present parahaemal spines and the haemal spine is smaller and wider than in all other carcharhiniforms. Only *Galeocerdo* presents a reduced and flattened prehypochordal cartilage distal to the parahaemal spine. The tail of Carcharhiniformes, with exception of Scyliorhinidae, can be divided into anterior and posterior diplospondylic caudal regions. The anterior diplospondylic caudal region is characterized by the presence of the parahaemal spine. The posterior diplospondylic caudal region may be divided into as many as three subregions. Subregion 1 is characterized by convex haemal spines. In subregion 2, the haemal element is >-shaped. Subregion 3 is confined to the terminal lobe and displays reduced haemal spines and hypurals. In Carcharhiniformes there are four main types of caudal fin: 1. Scyliorhinoid (Scyliorhinidae), with an undivided diplospondylic caudal region, subregion 1 extending almost throughout the entire tail length, haemal spines plate-like, presence of subregion 3, and lacking subregion 2; 2. Triakoid (Triakidae), with anterior and posterior diplospondylic caudal regions, parahaemal spines, presence of subregion 1, reduced subregion 3, and lacking subregion 2; 3. Carcharhinoid (Hemigaleidae, Carcharhinidae, *Sphyrna tiburo* and *S. tudes*), with anterior and posterior diplospondylic caudal regions, presence of parahaemal spines, reduced subregion 1, and well-developed subregions 2 and 3; 4. Sphyrnoid (*S. lewini* and *S. zygaena*), with the greatest anterior diplospondylic caudal region (almost 37% of total tail length), posterior diplospondylic caudal region, parahaemal spines, presence of subregions 2 and 3, and lacking subregion 1. The caudal skeleton of triakids appears to be intermediate between basal and higher carcharhiniforms. The same caudal fin pattern found in carcharhinids, *Sphyrna tiburo* and *S. tudes* suggests a fairly close relationship between these taxa. The internal structure of the caudal fin has great value in taxonomy and provides useful phylogenetic characters that may help elucidate unclear relationships.

27-12

Sexual dimorphisms of spined loach, *Cobitis kaibarai* (Teleostei: Cobitidae) in the Rokkaku river system, northwestern Kyushu Island, Japan

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The sexual dimorphisms of *Cobitis* fishes have been reported on several morphological characteristics such as the size, sex ratio, presence/absence of the lamina circularis on pectoral fin ray, and color pattern on the lateral side of body.The lines of males in several *Cobitis* species are known to change to striated line in spawning season. These characteristics are also important keys on the taxonomic identifications *Cobitis* fishes. The sexual dimorphism of spined loach, *Cobitis kaibarai* was studied on the basis of measurements and observations of 224 specimens collected monthly from April 2007 to March 2008 in an irrigation ditch. This spined loach is endemic species in northwestern part of Kyushu, Japan. We distinguish easily between 95 males and 129 females by presence/absence of the lamina circularis on the secondary pectoral fin ray. The GSI (Gonadosomatic index) of both males and females indicated high from April to August and low from September to March. Although the SL (Standard Length) had significant differences between males and females in high GSI season, those had no availability for the sexual discrimination. In the PFL (Pectoral Fin Length / SL), the statistical results indicated the PFL/SL was available for sexual discrimination in all season. The color patterns of lateral body in males showed the changes from dotted to striated types in June, while the pattern in females had no changes. The changes of males indicated the highest accuracy for the random generated GSI of females.

27-13

Reproductive peculiarity of the Okinawan population of paradise fish *Macropodus opercularis* (L., 1758)

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Paradise fish, *Macropodus opercularis* is distributed from the northern part of Vietnam though Asian continent, Taiwan to Okinawa, and tentatively categorized as a Critical Endangered Species in Japan. Because the Okinawan population is so obscure that it often is regarded as immigrants from Taiwan or mainland China. Then it is necessary to inspect its peculiarity, in order to elucidate its origin and then provide a relevant protective measure. Some reproductive characteristics were compared between the Okinawan and the Chinese populations. During the breeding trials, a pair of broodstocks were reared under constant environments (25.5 ± 0.5 °C, 14 h L – 10 h D). In this study, it was clarified that the Okinawan population is different from the Chinese population by following characteristics; internesting intervals were shorter by 16 – 35 days than the Chinese, fertilized eggs were larger by about 36 %, and buoyancy was tenuous in the Okinawan than the Chinese. The filial cannibalism was observed each populations. Overall, the local differentiations were recognized on reproductive characteristics.

27-14

Group specific sexual maturation in female and life history traits, in the yellowscale parrotfish, *Scarus ghobban* around the Okinawa Island

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Yellowscale parrotfish, *Scarus ghobban*, has particularly high commercial value among more than 30 species of parrot fishes caught in Okinawa, southwestern Japan. To understand the fundamental biology for stock evaluation and management of the species, growth, sexual maturity, and sexuality were studied based on 302specimens collected between 1990 and 2002 caught by local fishermen around the Okinawa Island. The analysis of the sectioned otolith revealed that opaque bands were formed once a year and that the von Bertalanffy growth parameters were $L\infty$=48.5 cm in fork length (LF), k=0.389, t0=-1.1, with the maximum age of 14 yr. Specimens of which sex and developmental stages were determined based on histological observation of gonads were divided into two groups: 127 individuals of females were originated from the groups which comprised of only female, caught inner ward of relatively large bay area (female unity group), and 152 individuals including 41 male and 3 transitional phase were originated from the groups, in which male and female were mixed (mixed group), captured at areas facing to open sea apart from the bay area. Mature females were found in the mixed group year round, but never found in the female unity group, even though they attained to the size and age of sexual maturation, with the largest female 43cm LF and 4 yr. The size of 50% maturity of female in the mixed group was 33 cm LF. All males had secondary testes and were larger than 39cm LF, with the age of 2 yr. These facts indicated that *S ghobban* is substantially protogynous hermaphrodite, but sexual maturity and sexuality would be influenced by sexual composition of group associated with their habitats. The number of male caught by fishermen around the Okinawa Island was relatively few at about 3% in the total catches of *S. ghobban*. Accordingly, fishing pressure to mature females accompanied with mature male inhabiting open sea area of the reefs would be relatively low comparing to that to immature females inhabiting inside the reefs. Currently, the low fishing pressure to the mature individuals of the species may contribute conservation of their reproduction.

27-15

Mechanisms determining the distribution patterns of filefish *Rudarius ercodes* in and around seagrass habitats

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Mechanisms determining the distribution patterns of filefish *Rudarius ercodes*, one of the most dominant seagrass habitat fishes in temperate Japan, were examined by field/laboratory experiments. Few individuals were preyed upon in a field tethering experiment, suggesting a relatively low predation risk, even in open bare sandy areas around seagrass habitats. In the laboratory, predator presence/absence did not affect filefish distribution, the latter mostly staying in the area planted with seagrass, even when predators were absent in the open bare area. Filefish showed a strong preference for the seagrass habitat structure itself, staying significantly longer in the seagrass area (despite a lack of food) than in the area with food but devoid of seagrass. Faced with the choice of both seagrass and food, and seagrass without food, even satiated filefish, which showed lower foraging activity, remained significantly longer in the former area, suggesting an additional preference for seagrass with abundant epiphytic food. Accordingly, habitat preference may be the most important factor determining the distribution patterns of filefish, which may primarily select seagrass habitats via an intrinsic preference for seagrass structure, their distribution pattern subsequently being modified by food availability via a preference for seagrass with abundant epiphytic food.

27-16

Quantitative Analysis on Environmental Factors Regarding the Habitat Selection by Red Spotted Masu Salmon

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Red spotted masu salmon *Onchorynchus masou isikawae* is classified into a cold water species which mainly distributes in mountain streams and adjacent coastal waters of western Japan. In recent times, the stream habitats have been degraded by fragmentation, embankment, dam construction and decreased extent of riparian forest. We focus on environmental factors that might influence habitat selection of species at the pool habitat. Two fixed study sites for biological observation were defined in tributaries of the Fuji- and the Tenryu-river systems located in eastern and western district of Shizuoka prefecture, respectively. The basic phase of these two sites can be characterized as follows: The study site in the Fuji-river system has gradient of 13.5% in average, an annual water temperature is ranging from 4.8 to 20.1 ℃. The other site in the Tenryu-river system has gradient of 5.8% in average, and 4.6–22.1 ℃ water temperature. Whereas the former is free of dams and artifacts, the latter has small dams every 30 meters within the lower half area. The life history type of study site stock closed in these two areas could be surely identified as fluvial form. Based on various biological information and relating physical and hydro-dynamical measurements collected by seasonal survey, we constructed regression models that describe a relationship between environmental fluctuation and habitat selection. Habitat selection by red spotted masu salmon is discussed by statistical treatment from the perspective of future needs for habitat improvement.

27-17

Monogamous mating system in the gobiid fish, *Ptereleotris hanae* (Gobiidae) and territorial defense requirement

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Ptereleotris hanae is a swimming goby and inhabiting edge of coral reefs and shore reefs, in the central and western Pacific. Young generally make school together, while adult fish often form a pair using nests of the snapping shrimp symbiotic with the gobies, without digging nests by themselves. We have observed adult *P. hanae* with individual recognition by the difference of long soft ray of the caudal fin in scuba diving at Kochi, Japan since 2011. Our study area was set in the wharf where many pairing of this speacies use the nests of *Amblyeleotris japonica* and *Alpheus bellulus*. Any observed pairs (n=15) didn't change a partner during one reproductive seasons, demonstrating their monogamy. One of the hypotheses which explain evolution of monogamous pair bonds is territory defending hypothesis (Whiteman, 2004). Their nests are suggested to be important as their shelters and spawning beds for *P. hanae*. It may force them into monogamous and we thought this hypothesis suit for this species. Because aggressions toward conspecific individual approaching their nests were exhibited by the females as well as the males, two individuals may necessary in defending nest. After removal experiments (removing an individual from 15 pairs) (six males and nine females), 12 gobies formed pairs with a new partner in the old nest, two gobies formed pairs with a new partner in the new nest within a short term (2–5days), and one goby went away. Only an individual of a pair was not observed to maintain the nest for a long time. We suggested the possibility that remaining individuals accept a new partner against its will, or induce a new partner to the nest, and disappear due to it couldn't defend the nest. We discuss the pair forming behavior and examine a cause of monogamy.

27-18

Reproductive behavior of frogfish: spinning ejaculation and male-male competition

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The behavioral ecology of frogfish, *Antennarius striatus*, was studied in aquaria, sequences of reproductive behavior being revealed by video recording for 3-6 hours at night. Five to 10 frogfishes were randomly housed in each of four aquaria. Nine fish were observed spawning, including two pair spawning, five pair-spawning with a sneaker, and the remaining two each with several males in group. Typically the body of spawning females became much enlarged, being almost spherical due to ripened eggs. An attentive male kept a close position, nudging the female's abdomen with his snout. Spawning resulted in a veil-like egg mass, the male exhibiting irregular spinning movements that reeled off the egg mass veil from the female body when he ejaculated. No significant differences were apparent between males involved in pair spawning or sneaking, either in SL or spinning behavior (duration, number of spins and spinning rate). However, spinning duration and SL tended to show a positive correlation. Microhabitat selection in *A. striatus* was examined, and substrate preference and the relationship between substrate and reproduction during the breeding period discussed.

27-19

Homing and foraging behavior of the symbiotically luminous cardinalfish *Siphamia versicolor* (Perciformes: Apogonidae)

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The sea urchin cardinalfish, *Siphamia versicolor*, like other *Siphamia* species, is unusual among apogonids for forming a bioluminescent symbiosis with light-emitting bacteria, which it harbors in a ventral light organ connected to the intestine. Observations in aquaria indicate *S. versicolor* emits ventral luminescence during feeding at dusk and the following morning, release feces rich in their symbiotic bacteria. We used mark and recapture methods along with field observations of the fish and gut content analysis to begin gaining insight on the behavior of *S. versicolor* in the wild. During daylight hours, *S. versicolor* aggregated in groups among the spines of the long-spined sea urchin, *Diadema setosum,* and the banded sea urchin, *Echinothrix calamaris*, both abundant on reefs at our study site along the northern Motobu Peninsula, Okinawa, Japan. A distinct preference for associating with *D. setosum* ($P < 0.001$) was evident, especially among larger individuals (>28 mm SL, $P < 0.01$). At dusk, the fish began emitting ventral luminescence and left the urchins to forage and returned to an urchin at dawn. Stomach contents of the returned fish (N=28) were composed primarily of benthic zooplankton, including crab zooea and carid and mysid shrimps. Occasional teleost eggs and larvae were also observed within *S. versicolor* stomachs. An average of 33% (21-54%) of tagged individuals were found at the same urchin or reef site over a one week period, and when displaced 1 km and 2 km, 34% (23-40%) and 29% (27-31%) of tagged individuals, respectively, returned to their site of origin within two days. These results indicate a high level of site fidelity and imply the use of site-specific environmental cues by the fish to home. Furthermore, the homing behavior of *S. versicolor* following nocturnal foraging and their tendency to aggregate in groups indicates the potential for the adults to enrich their home sites with strains of symbiotic bacteria released from their light organs throughout the day. The behavior of adult *S. versicolor* might therefore have implications for the acquisition of the symbiotic bacteria by the next generation of larval fish.

27-20

Neural basis of the 'puffing'behavior in the pufferfish *Takifugu obscurus*

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The "puffing" behavior is an unique defensive behavior of the pufferfish when sudden stimulation occurred. According to our previous study and the observation/recording during the inflation/deflation action in the pufferfish Takifugu obscurus, the mechanism of puffing is due to the rapid movement of buccal cavity. However, the neural base behind the action is still unknown. Here, we report our new findings from current neuroanatomical study by tracing the nerves of innervating the buccal muscles that are involved into the puffing action, from peripheral to central of the nerve system. Our primary data indicate that during inflation behavior, the buccal cavity expanded and compressed as a pump, and drew in/out the water. The inflation is involved a suite of major anatomical modification of the head of the pufferfish. A greatly enlarged the first branchiostegal ray and its associated hyohyoideus abductor muscle are the key modification for this behavior. The nerve branch innervating hyohyoideus abductor muscle is highly developed and its central projection pathway is revealed by the DiI neural tracing. The central origin is the motor nuclei of VII and the descending projection was to several motor nuclei in the medulla and the spinal cord, and the ascending path was to the nuclei of IV and III in the mesencephalon and then to the nucleus pretectalis superficialis and the periventricular preoptic nucleus in diencephalon. According to the results, we speculate that both the sympathetic cells and parvocellular part of periventricular preoptic nucleus are playing the neuroendocrine role in the rapid movement of buccal cavity of the puffing behavior in the pufferfish.

27-21

The processing of electrosensory information related to prey in the hindbrain of sturgeon (*Acipenser transmontanus*)

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Sturgeons are known to detect th eir prey fish by using passive el ectrosensory system. In general, the electric fields of prey fish were dipolar features with negative potential on head and positive potential on tail, and m odulated by the respiratory rhythm of the fish. In this study, two sinusoidal dipoles fields sim ulating the prey fish with dif ferent direction w ere applied to dete rmine the neu rons' preference of field orientation in dorsal octavolateral nucleus (DON) of white stur geon, Acipenser transmontanus. We founded that DON neurons showe d regular spontaneous activity and could be classified into two types: neurons with a low spont aneous rate (<10 Hz) and those with a high spontaneous rate (>10 Hz). The neurons with high spontaneous activity had the higher relative evoked rates during the stimulus; the degree of phase locking response was decreased with the spontaneous rate. And there was no significant difference in increasing evoked discharge rates with two dipolar stimulations (Mann Whitney U test, U=6.00, Z=-0.577, P>0.05), but existed two kinds of phase locking response in DON units. With one dipole field axis paralleling to the fish body, the units were found to increase the spike rate at the positive half cycle, showing two peaks at angles 200° and 270° in the phase plot. For the perpendicular to the fish body, firing suppressed in the positive cycle, and the spikes appeared at the negative half cycle and at a phase angle of approximately 90°. It was possible that the neurons with high spontaneous activity preferred to rate coding and used in electrosensory avoidance behaviors to predator or m etal obstacles. But the ne urons with low spontaneous activity prefer red to phase coding for orientating the prey fish or pr edator. The results suggested that two mode s of electrosensory processing were adapte d for rapid response of different behaviors.

27-22

Sound production in marbled rockfish, *Sebasticus marmoratus*

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Many fish are capable of producing sounds for communication and some rockfishes have been reported to be soniferous. The sounds which associated with different behaviors were produced by the interaction between the sonic muscles and swim bladder. Recroding and analyzing the occurrence of sounds can provide as a remotly monitor of fish populations. The marbled rockfish *Sebasticus marmoratus* is an important commerical species in southeast coastal of China. It has a pair of sonic muscles originated on the pterotic bones and extened to the anterodorsal surface of the swim bladder. But little-known is about their acoustical behavior. In this study, sound production of marbled rockfish was investigated under disturbance with tactile stimulus (disturbance sound) and free-ranging fishes in large tank (voluntary sound). These sounds consisted of a series of sound pulses with 3-5 acoustic energy cycles per pulse. The disturbance sounds consist of a burst of pulses wih decreaing interpulse interval from 196 to 10 ms (42±63ms), and the mean dominant frequency was 175.5±3.1 Hz, pulse period of 30.3±2.8 ms. For the voluntary sounds, they were individual pulsed sounds with mean dominant frequency of 49.2±3.2 Hz, pulse period of 75.5±20.2 ms. The differences between two type of sounds suggested that the sounds of fish reflects some behavior contexts. And it is possible to use passive acoustics to monitor the population and distribution of marbled rockfish based the species-specific and behavior-specific sounds.

27-23

First record of the small (Age-0) Pacific bluefin tuna (*Thunnus orientalis*) migration in the sea off Kochi revealed by archival tags

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Pacific bluefin tuna (*Thunnus orientalis*, PBT) juveniles, hatched in the area around the Philippines and Nansei islands in the North Pacific Ocean, migrate to Kochi and Nagasaki coastal areas 2 to 3 months after hatch and are targeted by troll fishing for farming. During this period, the juveniles are still small (about 20cm in FL) and so weak that even direct touch to the fish can cause fatal damage. Their vulnerability makes it difficult to attach archival tags and release to the ocean collecting vital data in the natural environment. We developed an operational instrument for smooth and quick attachment of tags. Fish was kept in the water even during the operation and we shorten the operation time to be 30-60 seconds. As a result of this technical progress, the survival rate of the tagged fish significantly increased. Also, the mechanical progress contributed to the survival rate; archival tags downsized dramatically in recent years. These innovations made it possible to attach archival tags to the smallest 0-year-old PBT (23-33cm in FL). Kochi trolling fishery gives young distribution information, but it is limited to coastal area. Now we can track migrations of very young PBT in and out of the fishing grounds, according to the archival tag data. Our data showed that the tagged juvenile migrated between coastal areas and offshore into the Kuroshio Current during summer to fall season, the experienced average temperatures were 26.2 C (ranged from 8.5 to 30.1 C). We will be able to see the relationship between their swimming behavior, migration route and the oceanographic conditions such as the Kuroshio Current off Kochi, which is a north-flowing ocean current on the west side of the North Pacific Ocean

27-24

Polygamy and social promiscuity in the gorgonian-associated pygmy seahorse *Hippocampus denise* (Actinopterygii, Syngnathiformes)

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A wide range of mating systems have been recorded in syngnathids; however, despite some social promiscuity and mate switching, all studies of seahorse reproduction to date have revealed ubiquitous genetic monogamy. Denise's pygmy seahorse (*Hippocampus denise*) is among the smallest (maximum standard length 24 mm) and most habitat-specific of all seahorses, with individuals spending their entire adult life isolated in small groups on a single gorgonian coral host. We investigated whether the reproductive strategies and social interactions of this species align with those of its congeners. During 217 thirty-minute observation periods we recorded the reproductive and social behaviour of 18 adult *H. denise* in four groups of differing sex ratio in a wild population of seahorses in southeast Sulawesi, Indonesia. We found social polygamy and sequential polyandry to feature in the species' reproductive strategies, although monogamy was dominant. Social and reproductive behaviours were described for the first time and characterised by daily interactions between reproductively active partners at dawn and dusk conducted in a core area. The use of core areas, a term used for protected regions of the gorgonian host shared for the most part by reproductively active individuals, may have been pivotal in enabling a stable polyandry to develop. Conventional sex roles were observed, with males competing for access to females. The ecology of *H. denise* appears to have favoured the evolution of mating system plasticity and the maximisation of reproductive output, which may be explained by the species' small size, skewed sex ratios and density of individuals sharing a single host.

27-25

Ecological mechanism for genetic introgression from orange-red commercial variety himedaka to wild population of medaka in Japan

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Medaka, *Oryzias latipes* complex, is small freshwater fish inhabiting paddy fields and irrigation canals in the eastern part of Asia. In Japan, while wild populations of medaka are endangered, the orange-red commercial variety of medaka (called himedaka) are cultured on a large scale in freshwater fish farming and sold at pet shops having aquariums. Recently, genetic disturbance in the wild populations of medaka because of the introduction of himedaka was shown. Since some fish types are ecologically affected by their body color differences, himedaka could be subjected to negative selection pressure such that the hybridization between the wild type and himedaka are restricted. However, the extent of the effect caused by this difference in the body color has not been shown. In this study, wild-type medaka and himedaka were used to verify 3 factors: predation pressure, mate preference, and schooling behavior, in relation with survival and reproduction by using laboratory experiments and field research. During predation pressure examination by using the dark chub *Zacco temminckii* as the model predator, himedaka was preyed upon more than the wild-type medaka. In the mate preference examination, no relationship was observed between the body color and selected partner by both males and females. The assessment of schooling behavior by using video cameras showed no differences in distances between each individual within schools and between school types of mixed populations of both medaka and himedaka, irrespective of their body color. These results indicated that occasional hybridization could easily occur, despite himedaka being under negative selection pressure because of the predators. Further, genetic structure analysis was performed on a field-sampled population, and a lesser number of himedaka individuals were observed than that estimated by the allele frequency in the population. This observation supports the result of our predation pressure examination. However, to reduce the introgression of himedaka, it is necessary to assess the risk of genetic disturbance in the wild populations of medaka.

27-26

Size-advantage in nest-holding tactics in the dusky frillgoby *Bathygobius fuscus* males: mating and parental care success

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Parasitic spawning is a common alternative reproductive tactic in fish, especially in species with external fertilization. Relatively large males in the dusky frillgoby *Bathygobius fuscus* occupy spawning nests and spawn in pairs with several females (nest-holding males). After spawning, eggs are tended only by the nest-holding males until they hatch (4-5days). Relatively small males, on the other hand, do not occupy nest, but intrude into a nest where spawning is occurring and quickly fertilize the eggs (sneaking tactic). Higher fertilization success of nest-holding males compared with sneaker males has been estimated in some fishes, however, sneaker *B. fuscus* males do not always change their tactics into nest-holding even when nests and females are available. This may be attributed to low reproductive success of small nest-holding males. In this study, to examine the effects of body size of nest-holding males on male reproductive success, field investigation using artificial spawning nests were conducted in intertidal pools on the Miezaki coasts, Nagasaki, Japan, from early June to early September in 2012. We measured total length of nest-holding males (n=37), the number of eggs in their nests (mating success) and survival rate of the eggs (parental care success). Larger nest-holding males showed significantly higher mating and parental care success. As sneaker males are generally smaller than nest-holding males, they may not be expected to have high mating and parental care success even if they become nest-holders at that time. To understand the difference in reproductive success not only between tactics but also within each tactic is important to consider the timing of change in tactics and evolution of alternative reproductive tactic.

27-27

Underlying modality in the complex swimming behaviours of foraging coral reef fishes

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Foraging behaviours in fishes can be incredibly complex due to various intrinsic and extrinsic drivers. In coral reef fishes we see a diversity of body and fin movement patterns (gaits) as they forage, and these gaits can be broadly categorized into median-and-paired fin (MPF) or body-caudal fin (BCF) swimming. While these gait groups are widely thought to be optimized for either slow swimming and manoeuvrability (MPF) or high-speed cruising (BCF), very few empirical studies have examined whether fish undergo patterns of gait-switching according to the optimal fin movements needed to achieve each foraging activity. We employed field-based surveys on the Great Barrier Reef to explore whether eight species of coral reef fish utilize different swimming gaits while undertaking specific foraging tasks. While species tended to use a specific pattern of fin use during steady swimming (either MPF or BCF), most fishes converged in their fin use during activities requiring slow-speed interaction with the reef. For instance, during searching all species tended to use median and/or paired fins (e.g. pelvic fins). Likewise, during high-speed activities such as chasing, almost every species utilized their caudal fin, even in labriform-swimming species that use solely the pectoral fins during routine steady swimming. Lending support to the MPF-BCF performance paradigm, we found consistent gait-switching patterns during foraging that transcended taxonomic, trophic and life history (juvenile-adult) differences among our study species. Such overarching modality in swimming behaviour sheds light on the biomechanical constraints underlying each type of foraging activity and helps explain the intrinsic drivers that underpin the diversity of foraging patterns displayed by demersal fishes.

27-28

Genetic population structure of the fourspine sculpin, *Cottus kazika* inferred from mitochondrial DNA control region haplotypes

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The fourspine sculpin, *Cottus kazika* (Scorpaeniformes, Cottidae) is endemic to Japans, distributing on the Pacific side of Honshu from Ibaraki Prefecture southward, the side of Sea of Japan in of Honshu from Aomori Prefecture southward, Shikoku, and Kyushu. The life cycle is catadromous, and the adults move down to river estuaries in winter, to spawn in brackish water, and the larvae go to sea. The juveniles return at a length of 15-30mm, during the spring. In this study, we determined the sequences of the mitochondrial DNA (mtDNA) control region for 30 river populations in 16 prefectures. A total of 13 haplotypes (seven variable nucleotide sites) were detected in 414 specimens. Nineteen river populations of ten prefectures were shown to have same haplotype. On the other hand, Ooyodo river (Miyazaki prefecture) and five river populations of Wakayama Prefecture were prefecture endemic. Haplotype diversity was 0-0.75, and nucleotide diversity was 0-0.002. The pairwise *F*st showed a significant difference between the most Japan group, Wakayama group (Wakayama populations) and Miyazaki group (Miyazaki populations). Accordingly, the three groups seemed to be genetically differentiated from each other.

27-29

Distribution and abundance of larval fish assemblages in the Kuroshio waters east of Taiwan

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We investigated the changes in assemblages of larval fish from February 2003 to November 2004 and evaluated their relationships with the hydrographic conditions of the waters off eastern Taiwan. Three hundred and ninety-three larval fish taxa were identified in this study, belonging to 106 families and 204 genera. *Maurolicus* sp. (7.8%), *Vinciguerria nimbaria* (7.4%), *Sigmops gracilis* (6.5%), *Cyclothone alba* (5.5%), and *Neoscopelus microchir* (3.9%) were the five most abundant taxa. The composition of the predominant taxa of larval fish was similar between seasons; however, the abundance of larval fish was significantly lower in summer than in other seasons. The distribution pattern of larval fish in the waters east of Taiwan appears to depend on the prevailing oceanographic processes of the area. Larval fish were transported by the Kuroshio Current from waters southeast into northeast of Taiwan. This study not only has expanded our knowledge on the larval fish distribution in the Kuroshio waters east of Taiwan, but also provided good evidence for the responses of larval fish to the hydrological conditions.

27-30

Genetic population structure of the yellowfin tuna *Thunnus albacares* in the North Pacific Ocean

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The yellowfin tuna (YFT), *Thunnus albacares*, is a commercially important species world-wide and catches have been on the rise in recent years. This trend has led to increased concern for the proper management of this species. Elucidation of genetic population structure is indispensable for sustainable management of YFT. There are two microsatellite studies that estimate genetic variations of YFT in the Pacific Ocean: one that uses samples collected from the Philippines, Indonesia, Oceania and North America (Appleyard et al. 2001), and one that uses samples collected from the eastern Pacific Ocean (Diaz-Jaimes et al. 2006). However, there is no genetic information for the species in Northeast Asia. In this study, we investigated genetic population structure of YFT in the North Pacific Ocean including samples collected near Japan. Specimens were collected around Japan (n = 25) and Central America (n = 20). A 396-bp fragment of the mitochondrial control region (mtCR) was obtained from those 45 specimens. In the analysis of mtCR, the sequences of 20 individuals sampled near the Philippines were added. A neighbor-joining (NJ) tree was constructed from evolutionary distances calculated based on Kimura's two-parameter model, using PHYLIP 3.65. A minimum spanning network (MSN) tree based on the minimum sequence differences between haplotypes was constructed using TCS 1.21. Pairwise F_{ST} values among the three geographic populations were estimated using ARLEQUIN 3.5. Haplotype diversity was high in each geographic population (1.000±0.011 in Japan; 1.000±0.015 in Central America; 1.000±0.015 in the Philippines). No significant difference of nucleotide diversity among geographic populations was revealed (0.031±0.016 in Japan; 0.044±0.023 in Central America; 0.037±0.019 in the Philippines). Neither the NJ tree nor the MSN tree showed genetic differentiation among the geographic populations. The pairwise F_{ST} values among the geographic populations were low and not significant (-0.01798 between Japan and Central America; -0.01551 between Japan and the Philippines; -0.02104 between the Philippines and Central America). In YFT, genetic differentiation was not evident among the geographic populations around Japan, Central America and the Philippines.

27-31

Fluctuations in abundance and intra-and interspecific population synchrony of four bitterling species and two non-bitterling species in Lake Kasumigaura, Japan

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In freshwater ecosystems, seasonal fluctuations in environments such as water level and water temperature often regulate population dynamics of many fish species at regional scales. Bitterling species often form assemblages of two to six species in rivers, lakes and ponds in Japan. These habitats are highly fluctuating conditions. The aims of this study were (1) to investigate the population fluctuation patterns in four bitterlings including three endangered native and an alien species, and two non-bitterling species, (2) to identify whether bitterlings show intraspecific and interspecific population synchrony and (3) to assess what processes operate spatial population dynamics of bitterlings by comparing the spatiotemporal fluctuation patterns between bitterlings and non-bitterling species. Field surveys were conducted in nine sites around Lake Kasumigaura every September from 2005 to 2012, and the spatiotemporal fluctuation patterns in abundanceof fish were examined at thewhole-lake scale. Large fluctuations in the abundance of four bitterling species were observed during survey years, specifically two native bitterlings, *Acheilognathus tabira erythropterus* (CV=106%) and *A. melanogaster* (CV=102%), showed large fluctuation. The abundances of *A. t. erythropterus* and *A. melanogaster* were regionally synchronized among the nine sites. Synchrony of *A. t. erythropterus* and *A. melangasgter* declined with increasing distance. In addition to intraspecific synchrony, interspecific synchrony was detected among all bitterling species examined except *T. lanceolata*. However, no significant synchrony was observed between bitterlings and the two non-bitterling species. The overall results supported the contribution of both regional climatic factor (the Moran effect) and dispersal in population synchrony of bitterlings. Consequently, regional processes (the Moran effect and dispersal) at a whole-lake scale are considered to affect the population and assemblage dynamics of bitterlings.

27-32

Influence of environmental parameters on fish larval abundance and distribution in the seagrass-mangrove ecosystem of Gelang Patah, Johor, Malaysia

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Fish larval assemblages and their relationships with surrounding water parameters (temperature, salinity, DO, pH, conductivity and TSS) were determined by analyzing larval abundance data versus environmental parameters. Research data were collected from the seagrass-mangrove ecosystem fringing the Johor Strait between October 2007 and September 2008. The study was aimed at determining the influence of environmental parameters to the abundance and distribution of fish larvae. Five stations were pre-selected namely upper estuary (S1), middle estuary (S2) and lower estuary (S3) of the Pendas River; seagrass beds (S4) and open seas (S5). Each sampling station was approximately chosen to be 1 km apart from each other. Fish larvae were collected by subsurface towing of bongo net equipped with a flow meter. A total of 24 families were recorded and 18 familes showed both positive and negative correlation with the water parameters. It is found that five families (Carangidae, Gobiidae, Monacanthidae, Syngnathidae and Uranoscopeidae) were negatively correlated with temperature. None of the families recorded were significantly correlated with temperature. Salinity showed positive significant correlation with Clupeidae ($r = 0.345$, $p < 0.01$). Terapontidae was significantly correlated with dissolved oxygen ($r = 0.27$, $p < 0.01$). Mullidae and Syngnathidae were significantly correlated with pH ($p < 0.05$). Positive highly significant correlations were also observed between conductivity and five families that was Cynoglossidae ($r = 0.489$, $p < 0.01$), Engraulidae ($r = 0.823$, $p < 0.01$), Leiognathidae ($r = 0.271$, $p < 0.05$), Sillaginidae ($r = 0.844$, $p < 0.05$) and Terapontidae ($r = 0.579$, $p < 0.05$). The highest and significant regression coefficient ($R2 = 0.72$) was observed in Sillaginidae which indicated 72% abundance of Sillaginidae was influenced by the major six water parameters.

27-33

Speciation on converging plates - a case study from Dinematichthyini in the West Pacific

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A review of the fishes of the Dinematichthyini (Bythitidae; Ophidiiformes) published in the years 2005 through 2011 has revealed certain recurring geographical species distribution patterns in the West Pacific clearly visible on a geographic overlay map of individual species. Cluster of related species occur along the island chains of the western margin of the Pacific plate including the northern coast of New Guinea and the Philippines (Alionematichthys crassiceps) or parts of the chain (A. plicatosurculus, Diancistrus karinae in the north, and D. eremitus, Eusurculus pristinus in the south) or are found endemic to the Riukius, Philippines, Fiji or Tonga respectively. A few species are only distributed ocean wards along the Caroline and/or Marshall and/or Gilbert Islands and/or Society and Tuamotu Islands (Diancistrus atollorum, D. katrineae, D. mennei, D. pohnpeiensis). This contrasts with only few widely distributed Indo-West Pacific species (Alionematichthys piger, Diancistrus alleni, Dinematichthys iluocoeteoides). The highlighted area represents a zone of plate convergence between the underthrusting Pacific Plate and the approaching Asian and Australian Plates for more than 50 million years. Island arcs have been amalgamated to the northern coast of New Guinea several times and plate segments have agglomerated to form the Philippine archipelago, while other regions became separated (Fiji and Tonga) or new arc systems were generated through volcanic activities along the ocean ward western approaches of the Pacific Plate. It is here assumed that species distribution paths like those of the Dinematichthyini went through a phase of expansion thereby populating more remote locations and island arcs. Once firmly established in an area, the immigration barrier for related newcomers would become raised. During a subsequent stable phase, population interaction would become restricted and endemics developed as has been reported so many times. However, the plate converging process along the western edge of the Pacific Plate would bring once separated endemics together again, when the island "rafts" collided, for instance, with the Australian plate along the northern shore of New Guinea. This mechanism in our opinion is responsible for a good proportion of the unusual high account of closely related species in such areas as the Philippines or the northern coast of New Guinea.

27-34

Residency, movement, migration and the genetic stock structure of an endemic South Africa sparid, the black musselcracker (*Cymatoceps nasutus*)

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Black musselcracker (*Cymatoceps nasutus*), an endemic South African sparid, is an important component of the recreational line-fishery, targeted predominantly by the shore-and boat-angling sectors. The life history of this species (slow-growing, long-lived, late-maturing and sex-changing) has made it vulnerable to exploitation. Trends in catch per unit effort have reflected a severe stock decline over the past two decades. This has not been arrested, despite the imposition of daily bag and minimum size limits. Information on the movement ecology (residency, movement and migrations) and the genetic structure of the stock have been identified as critical gaps for the management of this fishery. This study aimed to examine patterns of movement and connectivity along the South African coast from two perspectives. Data from three long-term mark-recapture (conventional dart-tagging) studies were analysed to examine movement over contemporary timescales. This data (189 recaptures from 2 704 tagged fish) indicated high levels of residency. Larger adults moved greater distances while juveniles and sub-adults showed higher degrees of residency. Several adults underwent large easterly displacements, potentially representing unidirectional migrations up the coastline towards the former Transkei, where individuals may settle for the remainder of their lives. Genetic data from a 334 bp fragment of the mitochondrial DNA control region and 404 bp of the first intron of the ribosomal nuclear S7 gene were used to assess differentiation and historical and contemporary gene flow among eight regions along the South African coast. These analyses revealed high levels of diversity for this species, and little evidence of genetic differentiation and spatial structure – with the exception of the Western Cape, for which features of the Agulhas Current may form a soft barrier. No patterns of isolation by distance were detected, suggesting unimpeded gene-flow throughout the species range. The observed patterns of extreme residency have contributed to the species' over-exploitation and decline, and suggest that the species should benefit from 'no-take zones' within Marine Protected Areas. Simultaneously, the observed larger scale movements of adults, coupled with movement of larvae, have been sufficient to maintain the genetic homogeneity of the stock; these movements should be accommodated in a reserve network.

27-35

Experimental evaluation of inorganic fertilization in larval orange-spotted grouper (*Epinephelus coioides*) production

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A major constraint in successful larviculture of groupers has been the small gape of the larvae and hence the requirement for small prey at first feeding. In this study, we examined how maintaining a phosphate concentration of 100 μg P L^{-1} and an inorganic nitrogen level of 700 μg N L^{-1} via weekly fertilization with inorganic fertilizers affected phytoplankton, zooplankton, and orange-spotted grouper (*Epinephelus coioides*) larval survival in relation to a control group that was provided with rotifers immediately after larvae hatched. Chl a in the range of 0.2~3.0 μm, unicellular algae, and survival of giant grouper larvae were all significantly higher in the fertilized treatment compared to the control. Stomach analysis revealed that ciliates and flagellates were actively consumed by larval fish in the fertilized group. We conclude that the inorganic fertilization method provides suitable-sized prey for larval groupers at the onset of exogenous feeding before they are able to consume larger, commercially available rotifers and copepods.

27-36

Natural spawning and early life history of the bluestreak cleaner wrasse, *Labroides dimidiatus* (Valenciennes, 1839) in captivity

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Successful natural spawning of *Labroides dimidiatus* in captivity at water temperature of 24.1-29.2 °C from 1 May 2011 to 30 April 2012 was described. Four broodfish (1♂: 3♀) laid 647,900 eggs, mean fertilization rate of 96.9%, and the hatching rate of 2-100%. Results indicate *L. dimidiatus* spawn daily throughout the lunar cycle as wild. Fertilized eggs, with a mean diameter of 0.65 ± 0.01 mm, were spherical, transparent and buoyant. Embryonic development lasted 18h 30 min at 27.3 ± 0.3 °C. Newly hatched larvae were 1.65 ± 0.07 mm in total length (TL) with 29 myomeres and had an oil globule in the ventroanterior area of the yolk sac. Transformation of larvae to the juvenile stage was completed at 7.84±0.69 mm TL. Under the scanning electron microscope, the micropyle was cylinder shape, about 6.9 μm in diameter. There were ridge substances with a sharp circular triangle inside the micropyle. The pores on the egg surface were uniform in size and were protrudent, with a density about 61 pieces /100 μm2. The accessory opening numbers were about 500 pieces. A few neuromasts were observed on the body surface of newly hatched larvae. The effects of temperature (14, 17, 20, 23, 26, 29, 32, 35 and 38 °C) on hatching rate and hatching time were assessed. And the effect of salinity (10, 15, 20, 25, 30, 35 and 40 ppt) on hatching rate was also assessed. Results indicate significant (p<0.05) higher hatching rate (78.9%) in temperature 20 to 32°C, and showed the significantly (p<0.05) longer hatching time in 17 °C (39.22 h). In the salinity trail, egg showed the significantly (p<0.05) higher hatching rate (74.4%) at 30 and 35 ppt. These results indicate that the optimal temperature and salinity for embryonic and larval development of *L. dimidiatus* are 26.1 °C and 30-35 ppt, respectively. The present study provides a starting point for successful spawning and rearing of *L. dimidiatus* in the first time.

27-37

TRUSS analysis and biology of spotted scat, *Scatophagus argus* (Linnaeus 1766)

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Scatophagus argus also known as spotted scat is an euryhaline fish that can be found in mangroves, port, estuaries and marine habitats which widely distributed throughout the Indo-Pacific Ocean, Malay Archipelago, Philippines, Australia and Southeast Asia especially India. This paper aimed to study and analyse TRUSS morpho-meristic, the feeding and reproduction potential of spotted scat collected from Peninsular Malaysia coastal waters. There is no issue on the systematic revision of this species. However Truss analysis is performed to validate sexual differences of the species. The growth pattern of scats is allometric negative where regression coefficient of 'a' is 0.04252(± 0.00633) and 'b' is 2.92021(± 0.05201), meanwhile r^2 value is 0.9598. Stomach content analysis denying the belief that scats is a feces eater as its get from the word *Scatophagus* literally where in the present study found that they are mainly seaweed, acetes shrimps and some other minutes crustacean eater. The result of reproductive potential assessment shows that the total gross fecundity ranged from 21,000 to 74,000 eggs with oocyte diameter is 0.4282±0.02 mm while estimation of length at first maturity for female is at 11.0 cm SL. Studies on the breeding patterns of this species will require further indepth study in the Malaysian coastal waters.

27-38

On the resiliency of the Halfbeak fish *Zenarchopterus buffonis* (VALENCIENNES 1847) in the coastal waters of Peninsular Malaysia

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Studies on halfbeaks (*Zenarchopterus buffonis*) has been conducted in the coastal areas of Peninsular Malaysia. Information on the feeding mechanism and relationship to the resiliency of halfbeak fish species in harsh environment of estuarine ecosystem is still lacking. The present study investigates the fine structure of tooth systems in halfbeak fish species in an effort to understand the feeding mechanisms and their relatonship to the prey items. Adaptation and changes in feeding habit may contribute high degree of resiliency in this species. A total of 84 halfbeak fish specimens have been collected throughout the studies. The results of the study showed that their teeth in the posteromedial region of the pharyngeal jaw apparatus (PJA) are eroded into an occlusion zone where the teeth of the third pharyngobranchial are spatulate incisiform and face posteriorly in opposition to the rostrally oriented spatulate incisiform teeth in the wear zone of the fifth ceratobranchial. The shape of the teeth and their pedestals (bone of attachment) is consistent with the model and with the forces likely to operate on the elements of the PJA during mastication. The alimentary tract of *Z. buffonis* is stomachless but has a cylindrical intestine which consists of folded mucosal layer to provide a larger surface area, thus increase the effectiveness of the digestive system. The average number of the trophic level for *Z. buffonis* is 3.2±0.55, which denote them as carnivorous. Further analysis of prey items in the halfbeak's alimentary tract denoted 85.73% of insects and 12.2% of crustaceans respectively.

27-39

Observations on the enigmatic tissue on the tongue of fishes of the genus *Siphamia* (Perciformes, Apogonidae)

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Several years ago examination of preserved specimens for a taxonomic revision of the cardindalfish genus *Siphamia* (Apogonidae) revealed an unusual whitish tissue on the tongue of many specimens. It was illustrated and the external morphology described briefly by Fishelson et al. (2005) and in the revision of this genus by Gon & Allen (2012); the former paper also forwarded ideas on the potential function of this tissue. This presentation reports on work currently in progress on this tissue. Tissue samples were examined using light microscopy, as well as scanning and transmission electron microscopy. Light microscopy preparations included staining with Toluidine Blue, combined Alcian Blue-PAS for acid and neutral mucins, combined Aldehyde Fuchsin-Alcian Blue for sulphated and carboxylated mucins, Ninhydrin-Schiff for amino groups and Bromophenol Blue for proteins. Careful gross examination of specimens found this tissue also in the gill chamber of some fish. The numerous foldes, ridges and crevasses, with large cells arranged in globular clusters suggest a mucosa-like secretory tissue. The absence of macrophage cells in the histological preparations indicates that the tissue is not pathogenic. The secretory cells contain rough endoplasmic reticulation indicative of protein synthesis. The material contained in the secretory granules appears very heterogeneous, possibly an indication of more than one type of secretion.

27-40

Assessment of carbon and nitrogen isotopic ratio within food webs ending to groupers in coral reefs of Wallis Island, Pacific Ocean

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The stable isotope signatures for carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) were measured in various compartments of food webs ending to two carnivorous serranid fishes (*Epinephelus merra* and *Cephalopholis argus*) in two contrasted coral reefs sites of Wallis Island, Pacific Ocean. One site, close to the city of Mata Utu which has no sewage treatment, was impacted by anthropogenic activities. The second site, located further south, was considered as not impacted by anthropogenic activities. Isotopic signatures of sources of organic matter differed between sites. For instance, particulate organic matter (POM) was C-enriched and N-depleted in the impacted site compared to the non impacted, with respectively -14.43 (±0.30) ‰ vs. -20.32 (± 0.56) ‰ and 3.65 (±0.08) ‰vs. 4.65 (±0.07) ‰. Other potential sources of organic matter (*Syringodium isoetifolium* seagrasses, *Padina australis* macroalgae and algal turfs) did not display strong differences according to sites. Their $\delta^{15}N$ values were relatively close to those of POM, but their $\delta^{13}C$ values were much more C-enriched (-6.19 to -5.01 ‰) except for algal turfs (~ -15‰). Invertebrates were also studied, exhibiting similar signatures between sites, although varying among taxa. The studied groupers displayed similar $\delta^{13}C$ and $\delta^{15}N$ values in both sites, i.e. around -11.90 ‰ and 9.75 ‰, respectively for *E. merra* and -11.75 ‰ and 10.25 ‰, respectively for *C. argus*. Other fish species were also sampled but did not shown significant differences between sites in their carbon and nitrogen isotopic ratio. These results suggest that *S. isoetifolium* and *P. australis* are likely poorly used in food webs ending to *E. merra* and *C. argus*, whereas POM and algal turfs may represent major sources for trophic networks ending to these species. In addition, and despite differences in $\delta^{13}C$ and $\delta^{15}N$ values between impacted and non impacted sites in POM, our results showed that this difference decreased at higher trophic levels, suggesting that POM might be of a lesser importance than algal turfs in the studied food webs.

27-41

Natural spawning and early life history of the palette surgeonfish, *Paracanthurus hepatus* (Linnaeus, 1766) in captivity

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Successful natural spawning of *Paracanthurus hepatus* in captivity at water temperature of 26.0-29.4℃from 1 June 2011 to 31 May 2012 was described for the first time. Nine broodfish spawning about 8.26×10^5 eggs, mean fertilization rate of 96.26%, and the hatching rate of 12.596.5%. The greatest amounts of spawning occurred during the full- to new moon and suggested that *P. hepatu* exhibited a semi-lunar spawning rhythm. Fertilized eggs, with a mean diameter of 0.69 mm, were spherical, transparent and buoyant. Embryonic development lasted 24 h at 25 ± 1 ℃. Newly hatched larvae were 1.55 mm in total length (TL) with 25-27 myomeres and had an oil globule in the ventroposterior area of the yolk sac. At 5.04 mm TL, the notochord was slightly flexed, and the hypural bones and caudal-fin rays had begun to develop. The larvae was diamond-shaped and strongly laterally compressed, with a prominent serrated dorsal spine, two equally large and serrated pelvic fin spines, and a single smoother spine at the anal fin. Under the scanning electron microscope, the surface of fertilized egg has a few star lines. The micropyle was cylinder shape, about 5.9 μm in diameter. The pores on the egg surface were uniform in size and were protrudent, with a density about 44 pieces /100 μm^2. The accessory pores on the micropyle region were larger than in the other regions, with a number about 200 pieces. At 2 DPH, a few neuromasts were observed on the body surface, and increased as the fish growing. The effects of temperature (19, 22, 25, 28, 31, 34 and 37℃) on hatching rate and the time to hatch were assessed. Results indicate significantly ($p<0.05$) higher hatching rate (92.7 %) in temperatures ranging from 25-34℃. The effects of salinity (5, 10, 15, 20, 25, 30, 35 and 40 ppt) on hatching rate and the time to hatch were also assessed. Results indicate significantly ($p<0.05$) higher hatching rate (98.7 %) in salinity ranging from 20-35 ppt. These results indicate that the optimal temperature and salinity for embryonic and larval development of *P. hepatus* are 28.2℃ and 30.0 ppt, respectively.

27-42

Small-scale fishery using fish trap in adjacent coral communities in Trat Province, Thailand

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Reef fish resources in the Gulf of Thailand are declining, as demonstrated by reduced total catches, a decline in average size of many species, and a change in catch composition from high valued species to low valued ones. Trap fishing is the primary method which has been practiced for catching reef fishes in Trat Province, and throughout most of the coral communities in the Gulf of Thailand. A number of small-scale fishermen in Thailand rely on their incomes from trap fishing in adjacent coral communities. The present study aimed to assess the status of trap fishing in adjacent coral communities in Trat Province, Thailand and to provide information for future management plan for marine and coastal resources. Traps were constructed of local wood and fishing net, with 2.5x2x1 m in size. They were not baited, allowed to soak for approximately one week, placed at the edge of coral communities, about 5 – 15 m in depth. The number of traps deployed per fishing boat varied between 50 – 100 depending on the size of fishing boat and manpower. The trap fishing was done throughout the year if the weather condition permitted. Most of the total catches were commercial fish species, dominated by several carnivorous fish such as the Greasy grouper (*Epinephelus tauvina*) and Leopard grouper (*Plectropomus pessuliferus*). There were high diversity of fish species in the traps, including Copperband butterflyfish (*Chelmon rostratus*), Horn-nosed boxfish (*Ostracion rhinorhynchos*), Barhead spinefoot (*Siganus virgatus*) and Streaked spinefoot (*Siganus javus*). The implications for the future of fishery resources in the Gulf of Thailand are challenging. The management of trap fishing is urgently needed to ensure sustainability of coral reef fishing, including establishment of marine reserve networks. They will play a major role as natural refuges for reef fish populations. Rebuilding and protecting reef fish stocks should be important and urgent efforts for marine national parks and provincial fishery offices.

27-43

Captive biology of deep-sea fishes using a gravity-produced compression chamber for treating decompression sickness

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Most deep-sea fishes inhabiting in depths below 200m have generally been considered unsuitable for keeping in aquariums worldwide, owing to the difficulties in providing them a habitat with adequate pressure for survival. However, *in-situ* observations on the deep-sea inhabitants are still quite limited, because of the constraints on viewing time and points of observation. According to our observations made on dead samples, the "decompression sickness" is the most significant factor prohibiting long-term keeping of deep-sea fish. The symptoms such as bleeding at the fin edges, invasion and infection of the necrotic tissue by bacteria etc., invariably result in death. For our research, we turned to studies of decompression sickness and successful recompression attempts in humans, and to apply some of the same principles and solutions to our design for a recompression facility for deep-sea animals. Here we introduce our concept for a newly designed pressurized tank, the Simple Gravity Pressure Treatment (SGPT) Chamber, and report an example of successful treatment of decompression sickness of deep-water fishes. The chamber system consists of a 300 L and 3000L holding tanks on the ground floor of the aquarium, with two polyvinyl chloride columns reaching up to smaller tanks on the fourth floor (18.5 m above the ground, 0.185Mpa), and three smaller satellite tanks each on the third (10m), the second (5.5m) and ground (2m) floors. It is a circulating system, each tank with life support system, and with shut-off valves on each floor to create variable pressures in the holding tank. Results indicate that recompression is successful for keeping over 100 species from depths of 200 to 650m around Okinawa, such as *Etelis* spp., *Thysitoides marleyi* and *Triodon macropterus*. This chamber also shows great effectiveness in resolving other problems related to keeping both shallow-water and deep-sea animals, such as bulgy eyes, wounds and abnormal swim bladder metabolism.

27-44

Hyperbaric chambers for rockfish (Northeast Pacific *Sebastes*)

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The Monterey Bay includes extensive Continental Shelf (30 to 200m) fish communities where the rockfishes (*Sebastes*) can be especially diverse and numerous. These fishes and their habitats have been under-represented in the Monterey Bay Aquarium's exhibits partly because of the difficulty in collecting and holding physoclistic fish from these depths. Previously aquarium divers vented rockfish swim bladders using hypodermic needles as the fish came up long lines from deep water. More recently, Jeff Smiley (Hubbs-Sea World, San Diego, CA.) brought large (≤90cm) *S. levis* straight to the surface from over 100m. These fish were quickly moved into pressure vessels for eventual acclimatization to surface pressure. Inspired by Smiley's efforts, collectors at the Monterey Bay Aquarium have developed and employed two types of pressure vessels: One is stainless steel and is pressurized with oxygen gas; the other is built of PVC pipe components, has a staging chamber and pressurized water flow-through. These vessels work well rockfish up to 40cm, are portable, easy to build and operate, and inexpensive. We have collected rockfish with hook and line, trawls, or traps from depths to 150m. These fish show a variety of barotrauma including exophthalmia, corneal emphysema, subcutaneous emphysema and stomach eversion. On the boat the fish are quickly recompressed to between 4 and 9 atmospheres in the vessels which are then brought back to the Aquarium and attached to a seawater flow-through system where the pressure is staged-down over a period of three to five days. Monterey Bay shelf rockfish species that have been successfully acclimated to the surface in these vessels include *S. chlorostictus*, *constellatus, elongatus, entomelas, goodei, hopkinsi, paucispinus, pinniger, rosaceus,* and *semicinctus*. Some of these fishes have only rarely, if ever, been exhibited live before. This increased post-barotrauma survivorship has important implications for rockfish conservation.

27-45

Reproductive biology of Ceratioid Anglerfishes. Are males really parasites? Or is there something more to the story?

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Teleosts are by far the most specious and prosperous of vertebrates, having conquered every part of the Earth's aquatic environments. Currently, ca 32,400 species are recognized. Among Teleosts, suborder Ceratioidei, commonly known as Ceratioid anglerfishes or deep sea anglerfishes, are an unique presence. They are the most specious Teleost suborder at depth greater than 2,500 m, and currently, 11 families, 35 genera and 160 species are reported. Ceratioid anglerfishes are high ranking predators of the deep sea ecosystem, cunningly luring their prey using a bioluminescent luring apparatus called the esca, which is attached to the tip of the modified first dorsal fin ray. However, the most unique characteristic of this suborder is in its mode of reproduction; male parasitizing the female's body surface. This is the only such example known among the vertebrates. This unique mode of reproduction is reported from 6 families and 24 species of Ceratioids. Although reports on male parasitism and parasitized females are being accumulated, studies on the mechanism of parasitism are scarce. How parasitic males obtain nutrients from the host female is still not known. A series of studies were conducted by the author during the past decade on reproductive biology of Ceratioid Anglerfishes. Efforts were focused on *Cryptopsaras couseii*, a species most numerous in museum collections. Newly acquired specimens as well as specimens cataloged at fish collections of Hokkaido University and National Science Museum, Tokyo were used. Other than microscopic observations and morphological measurements of specimens, sibling analysis, TEM observation on sperm ultra-microstructure, and stable isotope analysis between host female and parasitized males were carried out. Results of these studies will be presented, providing new insights into the reproductive biology of this truly unique suborder. And discussions will be made whether parasitic males are actually just parasites or not.

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