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Yusuke Hibino and Seishi Kimura

Full Papers

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Spatiotemporal changes in fish assemblage structures in the Udara River, Amitori Bay, Iriomote Island

Hiroyuki Inoue, Kusuto Nanjo, Akira Mizutani, Tadashi Kitano and Hiroyoshi Kohno

Abstract Fish assemblage structures in estuarine and freshwater areas in the Udara River, Amitori Bay, Iriomote Island, were investigated by visual transect surveys from November 2012 to October 2013. In total, 58 species (26 families) in the estuaries and 12 species (4 families) in freshwater, all comprising native taxa, were observed during the study period. Mean numbers of estuarine species and individuals were significantly higher in the lower and middle estuaries than in the upper estuary, multi–dimensional scaling analysis revealing that fish species compositions clearly differed among each estuarine station. The distribution patterns of the dominant estuarine species (*Neopomacentrus taeniurus* and *Fibramia amboinensis*) and the catadromous species *Kuhlia rupestris* largely explained such spatial variation. The former two species were abundant in the lower and/or middle estuaries with high salinity, whereas the latter was abundant in the low‐salinity upper estuary, suggesting that the salinity gradient may be a factor determining the estuarine fish assemblage. In contrast, the freshwater fish assemblages, largely dominated by small amphidromous gobies, such as *Stiphodon percnopterygionus*, showed neither spatial nor temporal variations, possibly due to the fact that several factors, including water flow and depth, being relatively stable in the freshwater area. The study suggested that the estuarine areas were essential habitats for marine, estuarine and amphidromous freshwater fishes in the river, and should be accorded a level of protection in keeping with a high priority for fish diversity conservation in the small rivers of the Ryukyu Islands.

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Distribution of mitochondrial DNA haplotypes of invasive channel catfish in Japan

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Abstract The North American channel catfish *Ictalurus punctatus*, an invasive freshwater fish introduced to Japan for aquaculture in the 1970s, has become established in several rivers and lakes, with subsequent detrimental effects on local fisheries and other freshwater fauna. The origin and invasive distribution of channel catfish in Japan was assessed from the geographical distribution of mtDNA haplotypes of channel catfish populations, utilizing partial (412 bp) nucleotide sequences of the mtDNA control region from 174 individuals collected from 7 localities. A total of 12 haplotypes (J01–J12) were found in Japanese freshwater systems. Populations in eastern Japan (Fukushima and Ibaraki Prefectures) and a fishing pond in Aichi Prefecture were characterized by many haplotypes, shared among those localities. However, the haplotype compositions of populations in western Japan (Yahagi River, Aichi Prefecture and Lake Biwa water system, Shiga Prefecture) differed from the former and also from each other. A phylogenetic analysis using Japanese (non-indigenous), Chinese (non-indigenous) and United States (indigenous) haplotypes indicated that all of the Asian haplotypes were included in "Lineage VI," distributed over a wide area of the United States, confirming that lineage as the primary source of introduced Asian populations. However, the introduction of channel catfish into Japan occurred on at least three occasions (in eastern Japan, Yahagi River and Lake Biwa water system).

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The importance of habitat continuity between Lake Biwa and inlet rivers with respect to fish fauna

Daisuke Ishizaki, Takeshi Kikko, Yasuhiro Fujioka, Toshiaki Mizuno, Takamaru Nagata, Taiga Yodo and Takuya Okubo

Abstract Although ca. 67 indigenous fish species and subspecies inhabit the Lake Biwa water system, (Shiga Prefecture, central Japan), including many endangered taxa, studies on the continuity of fish habitat between Lake Biwa and inlet rivers are few. The distribution pattern of fishes in 6 inlet rivers around Lake Biwa was examined during 2011–2012, with 32 and 26 fish species/ subspecies being recorded in autumn and spring, respectively. The relationships between presence/absence of these species and 21 physical environmental factors were analyzed by generalized linear mixed model, the results for 12 species in autumn and 4 species in spring being appropriate for predictability. Distance from the river mouth and number of dams from the river mouth were significant variables for *Plecoglossus altivelis altivelis* and *Cottus reinii* in autumn, suggesting that both species were influenced by dams. However, riparian plants were significant for Lake Biwa trout (*Oncorhynchus* sp.) in autumn, suggesting an important "shelter" component. Furthermore, water quality, including electrical conductivity and dissolved organic carbon, were significant for *Tribolodon hakonensis* in autumn. Other environmental conditions were more important for a number of other species. Clearly, active conservation of the inlet river environments and their continuity with Lake Biwa is necessary.

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Population genetic structure of *Sarcocheilichthys variegatus variegatus* in the Tokai region, Japan and invasion of a non-indigenous mitochondrial DNA lineage

Miyu Suzuki, Shigeru Kitanishi, Taiga Yodo and Takahiko Mukai

Abstract *Sarcocheilichthys variegatus variegatus*, an endemic Japanese cyprinid fish distributed from western Honshu (Tokai region) to Kyushu, has recently declined due to environmental damage and reduction of host mussels, and has been designated as a near threatened species in the Red List of the Japan Ministry of Environment. In addition, a recent study has noted the artificial introduction of *S. v. microoculus* from Lake Biwa into the Chubu, Kinki and Kyushu regions, suggesting a threat of genetic introgression. The present study, to investigate the population genetic structure of *S. v. variegatus* and identify invasions of a non-indigenous mtDNA lineage in the Tokai region, involved phylogeographic and population genetic analyses using cytochrome *b* gene sequences of 253 individuals of *S. variegatus* from Gifu, Mie and Shiga Prefectures. In addition, morphological characteristics of *S. v. variegatus* in the Tokai region, and *S. v. microoculus* in and around Lake Biwa, were used to identify instances of hybridization between the two subspecies. Phylogeographic analyses revealed greatest genetic divergence between populations of *S. v. variegatus* in the eastern and western regions of the Suzuka mountain range, and the presence of a non-indigenous mtDNA lineage in *S. v. variegatus* in the Tokai region. Clearly, the latter is characterized by important endemic genetic features, although already suffering from a loss of genetic identity due to the invasion of non-indigenous individuals. Steps are needed for future conservation of native *S. v. variegatus* populations in the Tokai region, including risk assessment and protection from invasive non-indigenous forms.

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Additional records of the snake eel *Ophichthus aphotistos* (Anguilliformes: Ophichthidae) from Japan and Taiwan

Yusuke Hibino, Fumihito Tashiro, Yung-Chieh Chiu and Seishi Kimura

Abstract A single Japanese (469 mm total length) and two Taiwanese (469 and 657 mm total length) specimens of the snake eel *Ophichthus aphotistos* McCosker and Chen, 2000, collected from off Yaku-shima island (East China Sea) and northeastern Taiwan, were newly identified in museum collections. Because known morphological characteristics of the species were based solely on three type specimens, descriptions of the present three additional specimens are provided. The present three specimens differ from the holotype and one of two paratypes of *O. aphotistos* in the arrangement of jaw teeth (biserial anteriorly and uniserial posteriorly vs. biserial), although such can be regarded as an intraspecific variation, remaining paratype having the same tooth-pattern as the newly-found specimens. *Ophichthus aphotistos* is characterized by the following combination of characters: head 7.6–8.5% TL; tail 59–62% TL; body depth at gill opening 2.0–2.9% TL; dorsal fin originating well behind posterior margin of pectoral fin, distance from the origin to the margin almost equal to one pectoral-fin length; pectoral fin rounded, not enlarged distinctly; preoperculomandibular pores 6+2; teeth on maxilla and vomer biserial anteriorly; body uniformly brown, without markings; total vertebrae 157–162 and mean vertebral formula (MVF) 18-59-160. The new Japanese standard name, “Yoiyami-umihebi”, is proposed for the species.

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Short Reports

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Larval development and distributional pattern of the painted sweetlip *Diagramma pictum* in Nakagusuku Bay, Okinawa Island, Ryukyu Archipelago

Masato Uehara, Itaru Ohta, Akihiko Ebisawa, Taiki Ishihara and Katsunori Tachihara

Abstract Larval development and distributional pattern of *Diagramma pictum* are described on the basis of specimens collected from Nakagusuku Bay, Okinawa Island, southwestern Japan. Pre-flexion to post-flexion larvae were readily distinguished from other haemulid larvae by head spination, the number of dorsal spines and pigmentation pattern. The former (3.61 notochord length – 6.36 mm SL) occurred at offshore stations in Nakagusuku Bay from August to October, coinciding with high gonadosomatic index values of adult individuals collected from coastal waters around Okinawa Island. However, no larval *D. pictum* were collected from Nakagusuku Bay tidal flats. Morphological differences were found in supraocular serration and melanophore pattern compared to larvae collected from Tosa Bay (Japan) and the Great Barrier Reef (Australia). Such apparently support a recent division of *D. pictum* into five subspecies, the two larval morphotypes in Japanese waters being suggestive of local populations or subspecies.

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First records of two snake eels, *Phyllophichthus xenodontus* and *Muraenichthys sibogae* (Anguillifornes: Ophichthidae), from the Ryukyu Islands, Japan

Yusuke Hibino and Seishi Kimura

Abstract A taxonomic study of the speciose tropical/temperate water family Ophichthidae, revealed a single specimen of the snake eel, *Phyllophichthus xenodontus* Gosline, 1951 and three specimens of *Muraenichthys sibogae* Weber and de Beaufort, 1916 from the Ryukyu Islands, Japan. Descriptions of the two species based on the Japanese specimens are herein provided. The former, a monotypic species of the genus *Phyllophichthus*, is characterized by a prolonged and pointed snout, well developed eyes and broad anterior nostrils. The present species has been recorded from the Ryukyu Islands in the literature, but with no voucher specimens. The Ryukyu Islands voucher specimen therefore represents the first reliable record of the species from Japan based on the voucher specimen. *Muraenichthys sibogae*, is poorly known species elsewhere in the western-central Pacific Ocean, is recorded from Japan for the first time, bringing the number of Japanese representatives of the Indo-Pacific Ocean genus to three (also *Muraenichthys hattae* Jordan and Snyder, 1901 and *Muraenichthys schultzei* Bleeker, 1857). Although *M. sibogae* is similar to *M. hattae* in small head size [9.7–11% of total length (TL)], position of the dorsal-fin origin (slightly anterior to a vertical through mid anus), and high total vertebrae number (141–150), the former can be easily distinguished from the latter by its longer tail (63–67% TL vs. 56–62%) and a single row of teeth on the upper jaw (vs. 2 rows or more). The new Japanese standard names, “Gettoh-umihebi” and “Shirasu-mimizu-anago”, are proposed for *P. xenodontus* and *M. sibogae*, respectively.

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