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First Japanese record of *Sargocentron iota* (Beryciformes: Holocentridae) from Kakeroma Island, Amami Islands, Japan

Kiyoshi Hagiwara* and Hiroyuki Motomura

Abstract To clarify the ichthyofauna of the Amami Island Ryukyu Archipelago, fish specimens from the region were examined in museums throughout Japan resulting in the discovery of a single specimen (75.9 mm standard length; SL) of the dwarf squirrelifish *Sargocentron iota* Randall, 1998 (Beryciformes, Holocentridae) in the Yokosuka City Museum. Collected from a deep (23 m) dark recess in a rocky reef grotto at a rocky reef off Kakeroma Island. The specimen was characterized by XI, 13 dorsal-fin rays, IV, 9 anal-fin rays, 15 pectoral-fin rays, I, 7 pelvic-fin rays, 6 + 10 + 9 + 5 caudal-fin rays, 45 lateral-line scales, 3.5 scale rows between the mid base of the spinous dorsal fin and the lateral line, 9 scale rows between the lateral line and anal-fin origin, 4 oblique scale rows on the cheek, 5 + 10 gill rakers, 11 + 16 vertebrae, body depth 2.5 in SL, head length 2.7 in SL, head depth 3.6 in body depth, snout length less than half orbital diameter, upper-jaw length 2.6 in head length, fourth dorsal-spine longest, third dorsal-fin soft ray longest, a pair of retrorse spines on the edge of the premaxillary groove, a spine on the upper edge of the lacrimal absent, and a bright red body coloration when fresh. The longest anal-fin soft ray length of the Kakeroma Island specimen was slightly shorter than that of the type specimens of *S. iota* which is likely to be an individual or geographic variation. Although *S. iota* is distributed in the Indo-Pacific, it has been recorded only from the Hawaiian Islands and Palau within the North Pacific Ocean. Accordingly, the Kakeroma Island specimen represents the first record of *S. iota* from Japanese waters and the northernmost record for the species. The new standard Japanese name “Kogashira-ebisu” is proposed for the species.

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Host mussel suitability for the endangered Itasenpara bitterling *Acheilognathus longipinnis* (Cyprinidae, Acheilognathinae) in the Moo River and a conservation pond in Himi, Toyama

Masaki Nishio*, Ryosuke Kawakami and Tomonori Kawamoto

Abstract The Itasenpara bitterling *Acheilognathus longipinnis* is a small cyprinid fish belonging to the Acheilognathinae, a subfamily that has an unusual symbiotic spawning relationship with freshwater mussels. During the spawning period, mature males select a mussel to accommodate spawning of a female. Because females possess short ovipositors for inserting their eggs inside the suprabranchial cavity of the host mussel via the exhalant siphon, the pattern of mussel utilization by spawning Itasenpara bitterling was investigated in the Moo River and a conservation pond (Himi City, Toyama Prefecture, Japan), so as to clarify the most preferred mussel size. In the Moo River (lotic environment), *Nodularia douglasiae nipponensis* (38.8% of total 747 individuals) was the major host of *A. longipinnis* larvae, there being no obvious size preference, possibly because neither eggs nor larvae of *A. longipinnis* could be readily ejected from the host in the lotic environment. By contrast, in the conservation pond (lentic environment), where *N. d. nipponensis* (24.3% of total 136 individuals) was again the main host of *A. longipinnis* larvae, a tendency to prefer smaller-sized mussels was apparent, due to the ease of ejection of eggs and larvae of *A. longipinnis* from larger-sized hosts (shell length >66 mm) in the lentic environment. Accordingly, differences in host mussel suitability are suggested as being related to habitat differences.

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Current status of two closely related *Phoxinus* species, in the Ishi River (Yamato River basin), Osaka Prefecture, Japan

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Abstract Difficulties in distinguishing between morphologically similar species, such as *Phoxinus lagowskii steindachneri* and *Phoxinus oxycephalus jouyi*, whose distributions overlap in the Kinki region, are significant for assessments of biodiversity and conservation, in addition to taxonomic status. Morphological analyses were undertaken on *Phoxinus* specimens (*n* = 75) collected in the Ishi and Chihaya rivers (Yamato River basin, Osaka Prefecture), and compared with type specimens (syntypes of *Phoxinus steindachneri*, Sauvage, 1883 and paratypes of *Leusiscus jouyi*, Jordan and Snyder, 1991) and non-type museum specimens (*Phoxinus oxycephalus jouyi*). Mitochondrial DNA (mtDNA) analyses of 16 individuals were also undertaken. Two distinct types of *Phoxinus* were recognized, differing morphologically in the presence or absence of a black horizontal band on the side of the body and scale numbers above the lateral line, and separated by a principal component analysis of 9 characters. In addition, 12 haplotypes (identified in the present and previous studies) were variously associated within two genetically different groups, corresponding to two ecological types that inhabit the upper and middle parts of the Yamato River, respectively. Because reproductive isolation is already clearly established between the two types, their recognition as separate species (*Phoxinus lagowskii steindachneri* and *P. oxycephalus jouyi*) in the Ishi and Chihaya rivers is upheld.

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Genetic population structure and morphological differences in the mottled skate *Beringraja pulchra*

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Abstract The mottled skate *Beringraja pulchra*, distributed in the western North Pacific, is a commercially important species, directly targeted by Japanese and Korean fisheries. Despite a recently decreasing catch rate, no studies of population structure, crucial to sustainable fisheries management and conservation practices, are known to have been made. Because skates generally have low dispersal ability and are likely to have an extensive population structure, due to large benthic egg capsules and no pelagic larval stage, the population structure of the species was assessed on the basis of sequence variations of the mitochondrial DNA cytochrome *c* oxidase subunit I (COI) 592 bp (in 166 individuals) and morphological variations in seven morphometric characters (in 192 individuals), representing five areas, including Hokkaido, Japan [coasts along Sea of Okhotsk, Pacific Ocean, and Sea of Japan (the East Sea of Korea)], western Sea of Japan, and Yellow Sea. The genetic analysis detected 12 haplotypes, six being shared among the sampling areas, although significant pairwise Φ_{ST} estimates indicated restricted gene flow among the sampling areas (excluding those off the Hokkaido). The extensive population structure of the species was also supported by morphological differences in several characters, such as disc length, disc width, and eye diameter. Beringraja pulchra was concluded as being clearly structured into three populations for future management, viz. Hokkaido, western Sea of Japan, and Yellow Sea populations. This population structure may have been shaped by the Tsushima Current flowing between the Korean Peninsula and the Japanese Archipelago, the species generally inhabiting colder water.

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Ontogenetic morphological changes in artificially-reared larvae and juveniles of the freshwater goby *Rhinogobius kurodai*

Kentarou Hirashima*

Abstract The genus *Rhinogobius* is widely distributed across Japan and East Asia, including Japan, comprises amphidromous, fluvial, lacustrine, and land-locked species. Because *R. kurodai* (Tanaka 1808) an endemic species formerly known as *Rhinogobius* sp. OR (Tou–yoshinobori species complex), in the Kanto region, central Japan, but recently re-assessed taxonomically, has been less studied from ecological, taxonomic and genetic perspectives than other *Rhinogobius* species, this study investigated ontogenetic morphological changes in artificially-reared larvae and juveniles of the former, in addition to larval salinity tolerance. Larval salinity tolerance is described for artificially-reared newly -hatched larvae reared in eight tanks (0, 5, 10, 15, 20, 25, 30, and 35 psu). Newly-hatched *R. kurodai* larvae (3.2 ± 0.1 mm in notochord length) had one or two symmetrical pairs of cupulae, (free neuromast organs), on the trunk around the anus or tail region, such having been previously reported in the genus only from larvae of *R.* sp. BF, a lacustrine species Nine days after hatching (4.5 mm in standard length: SL), the notochord tip projected upwards, and the second dorsal and anal fin ray were formed. Between eighteen (5.6 mm SL) to twenty-one days (6.4 mm SL), the larvae settled to the bottom of the aquarium tank. At thirty-five days (11.2 mm SL), all fins and scales were formed (juvenile stage). All larvae subjected to salinities of 20 to 35 psu died within three days, evidence (together with than of small sized-eggs and ealy presence of larval cupulae) suggesting that *R. kurodai* is a lacustrine -type species.

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Molecular identification of the closely related gobies *Tridentiger brevispinis* and *T. obscurus* using nuclear DNA markers

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Abstract Nuclear DNA (nDNA) markers were developed to distinguish between the closely related brackish water gobies *Tridentiger brevispinis* and *T. obscurus*. Although genetic differentiation of the two species has already been demonstrated by allozyme analysis in previous studies, the nucleotide sequences of mitochondrial DNA (mtDNA) haplotypes were similar and often shared by introgressive hybridization, obscuring the identification of the two species by mtDNA markers. In this study, one mtDNA gene [cytochrome *b* (cyt*b*)] and four nuclear DNA gene regions [G protein-coupled receptor 85 (gpr85), ryanodine receptor 3 (ryr3), recombination activating protein 1 (rag1) and zic family member 1 (zic1)] were sequenced in 11 to 17 individuals, respectively, of *T. brevispinis* and *T. obscurus*, collected from the Mukogawa River, Hyogo Prefecture, Japan. The results for the mtDNA cyt*b* region matched those of previous studies, the nucleotide sequences being very similar, with haplotypes shared among species. On the other hand, two (gpr85 and ryr3) of the four nDNA regions clearly differed between the two species, PCR-RFLP conducted on the former also showing specifically-different electrophoretic patterns. In order to confirm that nDNA PCR-RFLP could distinguish between the two species in other populations, additional samples of both from the Shonai River, Aichi Prefecture were subjected to and identified by the above method. In addition, eight individuals of putative F1 hybrid identified by allozyme analysis (three diagnostic loci) were also investigated. Although six of the eight putative hybrids included heterozygotes at both of the two nDNA PCR-RFLP loci, two individuals were characterized by a heterozygotic pattern at one locus, homozygotic at the other, both individuals possibly being F2 or backcross progeny, although initially misidentified as F1. The results indicated that nDNA markers may be helpful in distinguishing closely related *Tridentiger* species, which cannot be identified by mtDNA markers.

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Rhinogobius biwaensis **(“Biwayoshinobori”) ×** ***Rhinogobius*** **sp. BF (“Shimahireyoshinobori”) hybrids from the ponds of Sento Imperial Palace, Kyoto City, Japan**

Akihito, Masahiro Aizawa, Yuji Ikeda*, Munenori Kishida, Masayoshi Hayashi, Kouji Nakayama and Tetsuji Nakabo

Abstract Hybrids of *Rhinogobius biwaensis* and *Rhinogobius* sp. BF were identified in the ponds of Sento Imperial Palace, Kyoto City, Japan, from microsatellite and mitochondrial DNA markers. Mitochondrial DNA analysis indicated that five of seven *Rhinogobius* specimens had *R. biwaensis* haplotypes, the remaining specimens having those of *Rhinogobius* sp. BF. In DAPC and STRUCTURE analyses based on microsatellite data, all specimens examined showed intermediate status between *R. biwaensis* and *Rhinogobius* sp. BF, the two species being considered to have formed a hybrid swarm in the ponds because genetically pure individuals of either were not found. This is the first report of recent hybridization under field conditions in *Rhinogobius* fishes from Japan, confirmed by nuclear and mitochondrial DNA data. Hybrid *Rhinogobius* specimens from the ponds had 5–17 predorsal scales, an intermediate range between those of non-hybrid *R. biwaensis* (0–6) and *Rhinogobius* sp. BF (11–20). However, in appearance they were more similar to *R. biwaensis* than *Rhinogobius* sp. BF, having bluish-white distal coloring anteriorly on the first and second dorsal fins, a reduced reddish longitudinal band on the anal fin, and lacking yellowish dorsal and posterior margins on the caudal fin. However, they differed from *R. biwaensis* in having a narrower white posterior caudal fin margin. Further morphological differentiation of the hybrid specimens was not apparent.

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Effects of fixed and seasonal weirs on the distribution and movements of the endangered freshwater bagrid catfish *Tachysurus tokiensis* in rural streams

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Abstract The effects of small weirs on freshwater fishes of little or no commercial value have received scant attention, despite the enormous volume of literature on the negative impacts of dams and weirs on fishes generally. The distribution and movements of the endangered bagrid catfish *Tachysurus tokiensis* in a rural area on the Kanto Plain, Japan were examined, focusing on fish mobility and the effects of small weirs on local abundance. Thirty survey stations were selected along 3 tributaries of the Koise River (feeding Lake Kasumigaura). There were 20 weirs, of which 8 functioned only during the irrigation period from late April to early September. Catfish were caught by electrofishing along 25 m of stream length at each station in December 2010, and April, July, and October 2011. In total, 483 catfish were caught (average 4.4 fish per survey). Catfish were recorded in all four surveys at 15 stations (50%) and at least once at 27 stations (90%). Of 298 catfish individually marked with elastomer color tags, 12 were recaptured once and 2 twice at the same station as the first capture. Analysis of the relationship between numbers of catfish captured and environmental factors using generalized linear mixed models (GLMMs) suggested that the number of downstream weirs might have negatively influenced catfish numbers, whereas vegetation cover, bottom material, gap height of weirs, and velocity had little apparent influence. The results suggested that *T. tokiensis* showed little mobility and occurred widely throughout the river system, although possibly being negatively affected by weirs.

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Record of the epigonid fish *Epigonus fragilis* off northeast Marcus Island, western North Pacific

Makoto Okamoto*

Abstract In an on-going study of the taxonomy of the genus *Epigonus* (Perciformes: Epigonidae), the author found two specimens of *E. fragilis* (Jordan and Jordan, 1922) collected off northeast Marcus Island (Minami Torishima), western North Pacific, were found in the Fish Collection of Kyoto University, Maizuru Fisheries Research Station, Kyoto (FAKU). The species having been previously reported from Johnston Atoll, the Hawaiian Islands, and the Colahan Seamount, and Milwaukee Bank (Emperor Seamount chain), the specimens represent the first report of the species from waters adjacent to Japan. The new standard Japanese name "Ibushigin-yasemutsu" is proposed for the species, which belongs to the *E. pandionis* group, defined by Okamoto and Motomura (2013), and is characterized by the following combination of characters: dorsal fin rays VII-I, 10; pectoral fin rays 17 or 18; gill rakers 25–27; vertebrae 10 + 15; pyloric caeca 7 or 8; pored lateral-line scales 46–49 + 3 or 4; pungent opercular spine absent; maxillary mustache-like process absent; lingual teeth absent; small conical teeth on lower jaw; pair of ribs present on last abdominal vertebra; tubercle on inner symphysis of lower jaw absent; orbital diameter 13.5–15.2% SL; and pectoral-fin length 22.8–26.1% SL. Besides *E. fragilis*, four species of *Epigonus* have been recorded from Japan, viz., *E. atherinoides* (Gilbert, 1905); *E. ctenolepis* Mochizuki and Shirakihara, 1983; *E. denticulatus* Dieuzeide, 1950; and *E. pectinifer* Mayer, 1974. A key to the Japanese species of *Epigonus* and list of Japanese standard names of *Epigonus* species worldwide is included.

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Notes

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Distribution of the topmouth gudgeon (*Pseudorasbora parva*) in the Okhotsk region, Hokkaido

Takahisa Kanno, Atsuya Yamamoto and Minoru Kanaiwa*

Abstract Topmouth gudgeon (*Pseudorasbora parva*; Japanese name, motsugo), originally distributed in western Honshu, Shikoku and Kyushu, has been artificially introduced well north of its natural distribution area, to the Tohoku region and Hokkaido. The occurrence of topmouth gudgeon in the pond of Notsukeushi park at Kitami City, Hokkaido, the first record of the species in the Okhotsk region, was established and the population size estimated using the mark-recapture method. Although more than 2,000 fish between 1 and 4 years old were determined as living in the pond, none were found in either the inflow and outflow rivers, despite their apparent suitability. Further efforts in public educations are required to prevent further spreading of this fish.

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Record of *Cobitis matsubarae* (Cypriniformes, Cobitidae) from the Shonai River, Oyodo River system, Kagoshima Prefecture, southern Kyushu, Japan

Jun Nakajima, Yasuyuki Hashiguchi, Satoru Sugio, Takashi Higashi, Yukari Koshizako and Tomoya Taguchi*

Abstract Two voucher specimens of the spined loach, *Cobitis matsubarae* Okada and Ikeda, 1939, collected from the Shonai River, a branch river of the Oyodo River system, southern Kyushu, Japan, represent the first reliable record of that species from the Oyodo River system. Morphological features of the male lamina circularis, prepelvic myotome number, maxillary barbel length, snout length, body pigmentation patterns, and genetic characteristics of mtDNA cyt*b* sequences were in close agreement with characters those of *C. matsubarae*. Together with *C. sakahoko, C. matsubarae*, is considered to be distributed naturally in the Oyodo River system

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Variations in otolith morphology of three species of *Ammodytes* (Perciformes: Ammodytidae) from the Sea of Okhotsk coast of Hokkaido, Japan

Nozomu Muto* and Misa Yamada

Abstract Inter- and intraspecific variations in 2-dimensional otolith morphology were investigated in three sympatric species of *Ammodytes* (Perciformes: Ammodytidae) from Japan, viz., *A. japonicus* Duncker and Mohr, 1939, *A. hexapterus* Pallas, 1814 and *A. heian* Orr, Wildes and Kai, 2015. Size-dependent measurements and elliptic Fourier analyses of otolith outlines failed to show significant differences among the three species. However, both investigating methods revealed intraspecific variations relative to body length in each species, indicating ontogenetic changes in otolith morphology. The occurrence of several outlier specimens suggested a variable pattern of ontogenetic changes among individuals and/or between developmental stages

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Second record of Japanese snook *Lates japonicus* from Osaka Bay, Japan

Yuki Kimura*, Tomoyuki Yamanaka and Shoko Matsui

Abstract A single female specimen (724 mm SL) of Japanese snook, *Lates japonicus* Katayama and Taki, 1984, was corrected in the mouth of the Ajigawa river, Osaka Bay, Japan on 20th August 2018, representing the second record of the species from Osaka Bay. The present record implicates that this fish was not resident but appeared accidentally in Osaka bay, because the bay lacks no suitable over-wintering habitat for *L. japonicus.*

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Marking pattern variants of the pike gudgeon *Pseudogobio esocinus* from streams in Niigata and Kyoto Prefectures, Japan

Koji Tominaga* and Yuichi Kano

Abstract Marking pattern variants of the pike gudgeon *Pseudogobio esocinus* are reported from streams in Niigata and Kyoto Prefectures, Japan. The variant specimens have lost most of the body markings observed in normal specimens, i.e., dark blotches and small black spots on the lateral and dorsal sides of the body, and small black spots on the dorsal, pectoral, and caudal fins. In addition, a specimen from Kyoto Prefecture had a narrow black lateral stripe on the body instead of a narrow yellow-gold stripe under dark blotches. Mitochondrial DNA sequence variations seen in the variant specimens from the two streams suggest that they were derived from their respective indigenous populations.

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