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First record of *Conocara kreffti* (Alepocephalidae) collected from off Okinawa Island, Japan

Munehiro Takami, Hiromitsu Endo and Atsushi Fukui

Abstract The family Alepocephalidae, comprising about 23 genera and at least 90 species of benthic and pelagic deep-sea fishes, includes 10 species of the genus *Conocara*, known from about 800 to more than 5000 m depth in the Indo-Pacific and Atlantic oceans. *Conocara* is characterized by the dorsal-fin origin located posterior to the anal-fin origin, the dorsal-fin base length shorter than the anal-fin base length, the body covered with small scales (>80 in longitudinal row above lateral line), tubular scales in lateral line, maxilla toothless, upper jaw length equal to or longer than snout length and photophores absent on body. A single specimen of *Conocara kreffti* Sazonov, 1997 [NSMT-P (National Museum of Nature and Science, Tsukuba) 104036, 329 mm in standard length] was collected from the continental slope of the Ryukyu Trench, Japan in a depth of 1338–1396 m, on 24 May 2005. *Conocara kreffti* is distinguished from all congeners by the following combination of characters: dorsal-fin rays 21–28, anal-fin rays 35–43, number of scales in a longitudinal series above lateral line 190–270, palatine teeth present and premaxilla with a single bony ridge. The species has been previously recorded from tropical and subtropical zones of the Indian Ocean and western central Pacific Ocean, but not from Japanese waters. The present specimen represents the first records of the genus from Japanese waters and the northernmost record of *Conocara kreffti*. The new Japanese names “Yajiri-iwashi-zoku” and “Yajiri-iwashi” are proposed for the genus and species, respectively.

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Upstream migration of adult amago salmon, *Oncorhynchus masou ishikawae* in the Nagara River, central Japan

Tetsuya Tokuhara, Tomonori Kuwada, Ryouji Fujii, Toru Hara, Tetsuji Kariya and Daisuke Kishi

Abstract The ecology of adult amago salmon (*Oncorhynchus masou ishikawae*) after their upstream spawning migration being largely obscure, the study sought to reveal seasonal changes in the longitudinal distribution and abundance of salmon in the upstream spawning area in the Nagara River, Honshu Island, central Japan. The 2004 fish catch record by commercial fishermen and recreational anglers indicated a high level of migration of the salmon from the Ise Bay to the lower section of the Nagara R. in May, with a similarly high level of subsequent upstream migration in late May. Underwater observations in a tributary of the upper Nagara R. revealed that the salmon occupied large deep pools over summer. However, a considerable decrease in salmon numbers occurred in the pools during August, possibly due to bycatch fishing. To maintain wild amago salmon populations, such pool habitats are important refuges and fishing regulations to deter bycatch fishing must be considered.

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Distribution and origin of bagrid catfish *Tachysurus nudiceps* established in the Oita

River system, Kyushu Island, Japan

Hiroki Takano, Kazuo Hoshino, Tetsuya Okura, Toshio Matsuo and Katsutoshi Watanabe

Abstract Field sampling, inquiry to fishermen, and DNA analysis were used to determine the distribution and origin of the bagrid catfish *Tachysurus nudiceps* in the Oita River system, central Oita Prefecture, Kyushu Island, Japan. Specimens were collected from only three adjacent localities (nine localities sampled) in the river system. Localities the species found were cramped and limited in the river system, despite the potential for a greater distribution range. Reproduction in the wild was inferred from the juveniles collected in October 2012 and June 2014. Capture records of the Oita River Fishermen's Association suggested that the species first appeared in the Oita River system in 2004. Stocking records of the association indicated that Funa (*Carassius* sp.) seedlings from a pond in the Yakkan River system (within the native range of *T. nudiceps*; northern Oita Prefecture) were released in 2000, 2001 and 2003. Further inquiries also revealed contamination of the Funa seedlings with *T. nudiceps* and other species. Subsequent sampling of the pond showed the continued presence of *T. nudiceps*. A comparison of DNA data from Oita River specimens with published data for seventeen other localities in Japan were consistent with the scenario of accidental introduction of *T. nudiceps* together with Funa seedlings. These results suggest that *T. nudiceps* is not indigenous to the Oita River system, and its occurrence likely resulted from the introduction of contaminated Funa seedlings released in the early 2000s. Introduced *T. nudiceps* likely compete with native species for some resources, particularly with the sleeper *Eleotris oxycephala* for food and spawning sites in the Oita River system. The establishment of the former in the Oita River system and future ramifications for the freshwater fish fauna of northeastern Kyushu should be noted.

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Effect of dark chub *Nipponocypris temminckii* on feeding behavior of pale chub *Zacco platypus* in experimental ponds influenced by water currents

Hiromu Ogawa and Osamu Katano

Abstract Pale chub *Zacco platypus* is an omnivorous fish, coexisting with dark chub *Nipponocypris temminckii* in the middle reaches of Japanese rivers. Previous studies have examined their feeding behavior, including algal, drift and surface feeding, and aggressive interactions. In particular, algal feeding of pale chub is known to decrease in the presence of algivorous ayu *Plecoglossus altivelis*. Such behavioral shifts may be common in fish communities, but have been little studied among coexisting cyprinid fishes. To determine whether or not feeding behavior of pale chub changed in the presence of dark chub, 8 individuals of the former were established in each of 6 current-influenced ponds. One week later, 8 dark chub individuals each were introduced into 3 (randomly chosen) of the 6 ponds. All fishes were observed during three 5-days periods. Pale chub exhibited predominantly algal and drift feeding, whereas dark chub showed mainly drift feeding. However, following dark chub introduction, pale chub increased algal feeding, but did not change the number of drift feeding acts. The growth rates of pale chub were consistent, regardless of the presence or absence of dark chub. The latter sometimes attacked pale chub, which subsequently moved to the water layer adjacent to the substrate and changed feeding behavior, thus allowing resource partitioning and continued coexistence of the two species.

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High levels of genetic diversity and gene flow in the endangered goby *Hypseleotris cyprinoides* on Okinawajima Island, Ishigakijima Island and Luzon Island

Shumpei Tomita, Shohei Matsuzaki, Shin-ichiro Oka, Minoru Toda and
Hideyuki Imai

Abstract The amphidromous goby *Hypseleotris cyprinoides* is the most widely distributed *Hypseleotris* species in the Indo-Western Pacific Ocean. Recently, the species has declined around Japan because of environmental destruction, overexploitation, water pollution and the effects of invasive fish species, and has been designated as an "endangered species in Japan". Because captive breeding for the preservation of endangered species is considered an indispensable course of action in conservation biology, the Japanese Association of Zoos and Aquariums (JAZA) is currently attempting such for *H. cyprinoides*. Furthermore, there exists an urgent need for comprehensive studies on the genetic population structures and diversity levels of the species for the promotion of effective conservation and management activities. The present study examined the genetic population structure, genetic diversity and gene flow of *H. cyprinoides* from the Philippines to southern Japan, covering the Kuroshio Current region of the western North Pacific. Eight hundred and thirty-five bp of the mtDNA control region were analyzed in 140 specimens taken from three localities: Okinawajima Island and Ishigakijima Island, Ryukyu Archipelago, southern Japan and Luzon Island, Philippines. A total of 113 haplotypes were detected, four to eight shared haplotypes occurring at all localities, which had high levels of genetic diversity (range: $h = 0.9930$–0.9984; $\pi = 0.0133$–0.0153). AMOVA, pairwise F_{ST}, and N_{m} revealed high gene flow among the three localities, suggesting overall genetic homogeneity and a single shared gene pool, due to high dispersal ability during the oceanic larval stage and likely influence of the Kuroshio Current. Conservation and management directives should recognize the potential of these areas for sustainable recruitment of the species.

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A first record of a jawfish (Perciformes: Opistognathidae) *Opistognathus variabilis* from Yonaguni Island, Yaeyama Islands, Japan

Yusuke Hibino, Daichi Sasaki and Seishi Kimura

Abstract The cosmopolitan genus *Opistognathus* Cuvier, 1816, characterized by unforked dorsal-fin spines, currently comprises 64 valid species, including *Opistognathus variabilis* Smith-Vaniz, 2009, described on the basis of 71 specimens and widely known from the Maldives, Andaman Sea, Indonesia, Philippines, Palau, Taiwan, Ryukyu Islands and Vanuatu. However, the Japanese record was based solely on an underwater photograph taken off Iriomote Island, Ryukyu Islands. A single example of the species, collected from Yonaguni Island, Yaeyama Islands, represents the first record of the species from Japan supported by a voucher specimen. *Opistognathus variabilis* closely resembles *Opistognathus albicaudatus* Smith-Vaniz, 2011 and *Opistognathus castelnaui* Bleeker, 1860 in having an elongate upper jaw, numerous longitudinal scales and similar body coloration, including 7–10 dark blotches along the dorsal-fin base. However, the former can be distinguished from *O. albicaudatus* by the poreless Y-shaped area dorsally on the head (vs. absent) and 9–11 procurrent caudal-fin rays (vs. 6–7), and from *O. castelnaui* by having 68–92 longitudinal scale rows (vs. 90–110), the dorsal fin deeper posteriorly (vs. similar depth along entire length), a single stripe on the upper jaw inner surface (vs. two), and seven or eight mid-lateral blotches along the body (vs. three or four irregular dark horizontal lines and/or dark reticulations laterally on body). The new Japanese standard name "Shishidama-ohkuchi-amadai" is proposed for *O. variabilis.*

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