Papers Published in *Japanese Journal of Ichthyology*

Vol. 56, No. 2 November 5, 2009

CONTENTS

Review

Full Papers

Short Reports

Naoto Koyama and Tadao Kitagawa

Reproductive biology of the lumpsucker fish *Lethotremus awae* in Sizugawa Bay, northern Honshu, Japan
Takuzo Abe and Nagaaki Sato

Size homoplasy at microsatellite loci in two rose bittering subspecies, *Rhodeus ocellatus kurumeus* and *R. o. ocellatus*
Yasuko Shirai, Shigeru Ikeda and Shigeyuki Tajima

Review

Japanese Journal of Ichthyology

Vol. 56, No. 2, pp. 89–109

Whole genome duplication and the evolution of fishes

Yukuto Sato and Mutsumi Nishida

Abstract Whole-genome duplication (WGD), which produces a massive number of duplicated genes, is believed to be one of the major evolutionary events that shaped the vertebrate genome organizations. Here, we integrate information from recent researches on WGDs in vertebrate evolution, specifically focusing on the studies of teleost fish genomes. Recent whole-genome analyses confirmed that the jawed vertebrates, including chondrichthyans, sarcopterygians and actinopterygians, experienced two rounds of WGD (i.e., first-round [1R]- and second-round [2R]-WGD) early in their evolution, and that teleost ancestor experienced a subsequent additional WGD (3R-WGD). The 3R-WGD was initially supported by phylogenetic analysis and generation-time inferences for teleost-specific duplicate genes, implying that the 3R-WGD occurred 320–400 million years ago in a teleost ancestor, but after its divergence from living non-teleost actinopterygians (bichir, sturgeon, bowfin and gar). The 3R-WGD was confirmed by detailed whole genome analyses of *Tetraodon* and medaka. The teleost ancestor was shown to have had 12–13 chromosomes per haploid set, all of which were duplicated by the 3R-WGD before the divergence of the modern teleost lineages. On the other hand, although most of tetrapods (excluding a few lineages of amphibians and reptiles) have not experienced an additional WGD, they have experienced repeated inter-chromosomal rearrangements throughout the whole genome. Therefore, different types of chromosomal events appear to have characterized the genome organization of teleosts and tetrapods. The 3R-WGD is an evolutionarily recent WGD. Consequently, teleost genomes retain many more WGD-derived duplicates and “traces” of their evolution than those of tetrapods, suggesting the usefulness of teleosts for investigating the consequences of WGD. In addition, the remarkable morphological, physiological and ecological diversity of teleosts may facilitate future studies regarding macro-phenotypic evolution on the basis of genetic/genomic information. We highlight the teleosts with 3R-WGD as unique models for understanding vertebrate ecology and evolution.

(Corresponding author: Yukuto Sato, Division of Population Genetics, National Institute of Genetics, Yata 1111, Mishima, Shizuoka 411−8540, Japan; e-mail: yuksato@lab.nig.ac.jp)

Full Papers

Japanese Journal of Ichthyology

Vol. 56, No. 2, pp. 111−118

Foraging microhabitat of Japanese charr, *Salvelinus leucomaenis,* in a mountain stream

Masayuki Yagyu

Abstract To clarify the foraging microhabitat of the Japanese charr, *Salvelinus leucomaenis*, I investigated focal point depths and velocities in a 730-m reach of a typical mountain stream in central Japan in the spring and summer of 2004. The water depths and velocities of focal points used by 123 fish (> 9-cm fork length) were compared to data for random points in the stream. The charr utilized focal points with depths > 10 cm and velocities < 60 cm/s. The preferred habitat was comparatively deeper (21–60 cm) and

moving at a slower velocity (11–20 cm/s). The proportion of favorable foraging habitat in the study reach was calculated to be 15% in July and 18% in August based on focal points. This habitat was dispersed in small patches and distributed randomly throughout the reach. In small mountain streams such as the one studied here, there are repeated small steps and pools. Most of the favorable foraging habitat was in the pools. Therefore, charr density may be affected by river morphology, such as the number of pools or steps in a reach.

(National Research Institute of Fisheries Science, Fisheries Research Agency, Chugushi 2482–3, Nikko, Tochigi 321–1661, Japan; e-mail: gyuyagyu@yahoo.co.jp)

Japanese Journal of Ichthyology
Vol. 56, No. 2, pp. 119−133

Ultrastructure of the spermatozoa in Japanese Osmeridae

Masako Hara

Abstract The fine structures of mature spermatozoa of 13 Japanese osmerid and salmonid species (and subspecies) were studied with TEM and SEM. Three types were recognized, based on combinations of morphological characters, such as nucleus shape, number, size and arrangement of mitochondria, and numbers of flagella, as follows: Osmeridae type (7 species, including *Osmerus eperlanus mordax, Hypomesus nipponensis, Hypomesus japonicus, Spirinchus lanceolatus, Mallotus villosus, Plecoglossus altivelis altivelis* and *Plecoglossu altivelis ryukyuensis*), characterized by an elongated ovoid nucleus with a deep cylindrical basal fossa, a single mitochondrion, located along the base of the flagellum, and a single finned flagellum; Salangidae type (4 species, including *Salangichthys microdon*, *Salangichthys ishikawae*, *Salanx ariakensis* and *Neosalanx reganius*), characterized by a spherical nucleus with a partly invaginated, moderately deep conical basal fossa, multiple mitochondria surrounding the flagellum; and a single finned flagellum; Salmonidae type (2 species, including *Oncorhynchus* *masou masou* and *Oncorhynchus mykiss*) being characterized by a depressed ovoid nucleus with a shallow cylindrical basal fossa, a single mitochondrion, annular around the base of the flagellum; and a single finned flagellum. A comparison between these types and currently-recognised osmerid and salmonid systematics revealed the following: (1) The Osmeridae type variously included Hypomesinae, Osmerini (Osmerinae) and Precoglossinae sperm morphs; (2) the present grouping of sperm morphs is less supportive of some recently proposed systematics of relevant taxa, although concurring with a recent molecular phylogenetic study. It is suggested that spermatozoa are potentially useful in evaluating generic relationships within Osmeridae.

(Ocean Research Institute, University of Tokyo, 1−15−1, Minamidai, Nakano, Tokyo 164−8639, Japan; e-mail: mhara@ori.u-tokyo.ac.jp)

Japanese Journal of Ichthyology

Vol. 56, No. 2, pp. 135−*143*

Growth and habitat of the green chub, *Aphyocypris chinensis*, in northern Kyushu Island, Japan

Jun Nakajima and Norio Onikura

Abstract The natural growth and habitat selection of the green chub, *Aphyocypris chinensis*, an endangered species in Japan, was investigated in an agricultural waterway located in northern Kyushu Island, Japan. From April 2007 to March 2008, green chub were captured by hand net and 5 physical environmental variables measured (water temperature, water depth, water current velocity, connection to paddy field, and presence or absence of tunnel-like cover) at 10 survey sites every month. After obtaining an image of the captured fish with a digital camera, all individuals were released alive at their capture location. The standard lengths of 823 individuals were later determined from the images. Monthly changes in the standard length distribution showed that green chub had a life-span of 1 year, the spawning season occurring from mid-June to August. Multiple linear regression analysis applied to the 5 environmental variables separately in the irrigation (from June to September) and non-irrigation seasons (from October to May), showed water depth to be most significant in the former and absence of water movement in the latter. Fish occurrence patterns indicated that temporary waters were utilized as spawning sites and permanent waters for overwintering. Accordingly, continued ease of movement between temporary and permanent waters is essential for future conservation of the species.

(Corresponding author: Jun Nakajima, Faculty of Engineering, Kyushu University, Motooka 744, Fukuoka 819−0395, Japan; e-mail: cyprin@kyudai.jp)

Short Reports

Japanese Journal of Ichthyology

Vol. 56, No. 2, pp. 145−148

First record of a blenny, *Cirripectes filamentosus* (Perciformes, Blenniidae), from Yaku-shima Island, southern Japan

Atsunobu Murase, Masatoshi Meguro and Hiroyuki Motomura

Abstract A single specimen of the blenniid fish, *Cirripectes filamentosus*, was collected from a relatively large-sized rockpool in Yaku-shima Island, southern Japan. This species is characterized by the following combination of characters: lower lip entire medially; dorsal fin distinctly notched above last dorsal-fin spine; cephalic sensory pore system simple; 2 pores behind nuchal flap; last lateral-line tube usually lying between verticals from 2nd and 6th dorsal-fin soft rays; small red spots on cheek and snout in life and when fresh. Description of the specimen is provided, and new Japanese name, “Oboroge-tategamikaeruuo”, is proposed for the species. The specimen from Yaku-shima Island represents both the northernmost record in the western Pacific and the first Japanese record of the species.

(Corresponding author: Atsunobu Murase, Tateyama Station, Field Science Center, Tokyo

University of Marine Science and Technology, 670 Banda, Tateyama, Chiba 294–0308, Japan; e-mail: atsunobum@yahoo.co.jp)

Japanese Journal of Ichthyology

Vol. 56, No. 2, pp. 149–*152*

First Japanese record of a spookfish, *Dolichopteryx parini* (Argentinoidei: Opisthoproctidae), from off the Pacific coast of Aomori Prefecture

Nobuyuki Mizusawa and Atsushi Fukui

Abstract An opisthoproctid fish, *Dolichopteryx parini*, was reported for the first time from Japanese waters, on the basis of a single specimen collected off the Pacific coast of Aomori Prefecture. The species has previously been recorded from the northern part of the Sea of Okhotsk, and other northern and eastern regions in the North Pacific Ocean. The Aomori specimen represents the southernmost record of the species.

(Corresponding author: Nobuyuki Mizusawa, Graduate School of Marine Science and Technology, Tokai University, 3–20–1 Orido, Shimizu-ku, Shizuoka 424–8610, Japan; e-mail: thccp601@yahoo.co.jp)

Japanese Journal of Ichthyology

Vol. 56, No. 2, pp. 153–*157*

Mitochondrial DNA originating from the orange-red type commercial strains of *Oryzias latipes* (himedaka) detected in the wild populations inhabiting the Yamato River system, Nara Prefecture

Naoto Koyama and Tadao Kitagawa

Abstract In order to examine genetic introgression from the orange-red type commercial strain of *Oryzias latipes* (himedaka) to wild medaka populations, a polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) analysis of the mitochondrial cytochrome *b* gene was conducted for 45 populations from the Yamato River system, Nara Prefecture and two fish farm populations from special product grounds of himedaka (Yamatokoriyama and Yatomi Cities). Orange-red type fish only were collected from three sites, and a mixture of wild and orange-red types from sympatric populations at four other sites in the Yamato R. system. Most orange-red type specimens had the B27 mitotype, being identical with that of the typical orange-red type Hd-rR strain. Although most of the wild type fish individuals had mitotype B1a, inferred as one of the native mitotypes in the Yamato R., four from three sites had mitotype B27, implying genetic introgression from himedaka to wild medaka populations.

(Corresponding author: Tadao Kitagawa, Graduate School of Agriculture, Kinki University, 3327–204 Nakamachi, Nara 631–8505, Japan; e-mail: tkitagaw@nara.kindai.ac.jp)

Japanese Journal of Ichthyology

Vol. 56, No. 2, pp. 159–163

Reproductive biology of the lumpsucker fish *Lethotremus awae* in Shizugawa Bay, northern Honshu, Japan

Takuzo Abe and Nagaaki Sato

Abstract Reproductive patterns in the lumpsucker fish *Lethotremus awae* were investigated by field observations and histological analyses. Males guarded egg masses in empty shells of the ribbed barnacle *Balanus rostratus* or in an empty hole, bored in offshore rocks by the boring bivalve *Penitella kamakurensis*, at 7–17 m water depth. The number of egg batches per nest was ranged 1–5, and the number of eggs per batch was 66–133. Eggs shaped sphere with 1.6 to 1.9 mm diameter and adhered to each other. Histological observation on ovaries indicated that females are multiple spawners within a single mating season. The male first dorsal fin was enlarged and crown-like, being a conspicuous feature of sexual dimorphism.

(Corresponding author: Takuzo Abe, Faculty of Fisheries Science, Hokkaido University,

Hakodate 041−8611, Japan; e-mail: takuzo@fish.hokudai.ac.jp)

Japanese Journal of Ichthyology

Vol. 56, No. 2, pp. 165‒169

Size homoplasy at microsatellite loci in two rose bittering subspecies, *Rhodeus ocellatus kurumeus* and *R. o. ocellatus*

Yasuko Shirai, Shigeru Ikeda and Shigeyuki Tajima

Abstract Molecular markers which clearly discriminate between the endangered Japanese rose bitterling *Rhodeus ocellatus kurumeus* and an introduced exotic subspecies, *Rhodeus ocellatus ocellatus*, are very useful for the continued conservation of the former. From this standpoint, the development of microsatellite markers for *R. ocellatus* have already been reported elesewhere. However, electropherograms showed that 9 pairs of alleles at 7 out of 11 loci had a common size in both subspecies. Six pairs of the 9 were homoplasic and 2 pairs had identical sequences between the subspecies. The presence of allelic microsatellite fragments having the same electrophoretic mobility in both subspecies does not necessarily indicate a hybridization or introgression event between the two subspecies.

(Corresponding author: Yasuko Shirai, Environment and Forestry Section, Shozu Regional Office, Kagawa Prefectural Government, 2079−5 Fuchizaki-ko, Tonosho-cho, Shozu-gun, Kagawa 761−4121, Japan; e-mail: vg7552@pref.kagawa.lg.jp)