

# Program and Abstracts

Commemoration of the 130th Anniversary of the National Museum of Nature and Science

## **International Symposium on Systematics and Diversity of Fishes**



National Museum of Nature and Science  
Ichthyological Society of Japan  
Tokyo, 3-4 March 2008

# Symposium Organizers

## **Chair: Keiichi Matsuura**

*Collection Director, National Museum of Nature and  
Science*

## **Vice-chair: Mutsumi Nishida**

*President, Ichthyological Society of Japan  
Ocean Research Institute, University of Tokyo*

## **Organizing Committee Members**

*Takeshi Kon, Kohji Mabuchi, Takashi P. Sato, and  
Gento Shinohara*

# Program

**Sunday, March 2**

14:00–17:00     **Registration** (for Invited Speakers)

**Monday, March 3**

09:00–09:30     **Registration**

09:30–09:40     **Opening Address**

*Mutsumi Nishida*

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**Session 1     Biogeography of Fishes**

Chair: Jeffrey M. Leis/Gento Shinohara

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09:40–10:10     **A tale of two fishes: Unseen and unsung heroes on the Great Barrier Reef—Lessons we can learn from gobies and batfishes**

*David R. Bellwood*

10:10–10:40     **Inferring multi-scale habitat distributions from species ranges—An Australian perspective**

*Martin F. Gomon*

10:40–11:10     **Seasonal and interannual variation of subtidal fish assemblages in Wakasa Bay revealed by underwater visual census with reference to the warming trend in the Sea of Japan**

*Reiji Masuda*

11:10–11:30     **COFFEE BREAK**

11:30–12:00     **Zoogeographical role of the Kuroshio Current: Transportation system and barrier for coastal fishes of southern Japan**

*Keiichi Matsuura & Hiroshi Senou*

12:00–12:30     **Migratory behavior has driven the evolution in anguillid eels**

*Katsumi Tsukamoto*

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12:30–14:00      LUNCH

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**Session 2      Diversity and Taxonomy of Fishes**

Chair: Gento Shinohara/Douglass F. Hoese

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14:00–14:30      **Ask not what evolution can do for *Trimma*—Ask what *Trimma* can do for evolution**

*Richard Winterbottom*

14:30–15:00      **Gobioid genera need re-examination: A case study of *Gobiopsis***

*Naomi Delventhal & Randall D. Mooi*

15:00–15:30      **Radiation of *Glossogobius* in freshwaters of the Indo-west Pacific**

*Douglass F. Hoese*

15:30–16:00      **COFFEE BREAK**

16:00–16:30      **The goby genus *Redigobius* and its relationships—A work in progress**

*Helen K. Larson*

16:30–17:00      **Phylogenetics of the gobioid fishes: Diversity, taxonomy, and ecology**

*Christine Thacker*

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**Poster Session (17:05–17:55)**

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18:15–20:00      **RECEPTION**

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## **Tuesday, March 4**

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**Session 3      Evolution and Systematics of Fishes**

Chair: John R. Paxton/Mutsumi Nishida

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09:00–09:30      **Windows into the architecture of fishes**

*Paula Mabee*

09:30–10:00      **Evolutionary history of modern ray-finned fishes: An overview based**

**on 327 whole mitogenome sequences**

*Masaki Miya & Mutsumi Nishida*

10:00–10:30 **The evolution of fish diversity: Lessons from large-scale comparative analysis**

*Judith E. Mank & John C. Avise*

10:30–10:45 **COFFEE BREAK**

10:45–11:15 **Refining our understanding of the limits and relationships of Percormorpha: Discovering large clades and the taxonomic challenges they present**

*Wm. Leo Smith*

11:15–11:45 **Evolutionary origin and phylogenetic relationships of the Cypriniformes: A multi-gene approach to resolving the evolution of the world's most diverse group of freshwater fishes**

*Richard Mayden*

11:45–12:15 ***Paedocypris*—A developmentally truncated miniature cyprinid with astonishingly complex novel structures**

*Ralf Britz*

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12:15–13:15 **LUNCH**

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**Poster Session (13:15–14:05)**

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**Session 4 Phylogeny and Ontogeny of Fishes**

Chair: Keiichi Matsuura/Ralf Britz

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14:15–14:45 **Phylogeny of the Medaka and relatives: Molecules versus morphology**

*Lynne R. Parenti*

14:45–15:15 **“Scorpaeniform” phylogeny: Morphological approach to a question of its monophyly**

*Hisashi Imamura*

15:15–15:30 **COFFEE BREAK**

15:30–16:00 **Tigerfishes, Tripletails, and Velvetchins form a clade: Morphological evidence from adults and larvae**

*Jeffrey M. Leis & Anthony C. Gill*

- 16:00–16:30      **The cetomimoid conundrum resolved—Whalefishes (Cetomimidae), Tapetails (Mirapinnidae), and Bignose fishes (Megalomycteridae): Amazing larval transformations and striking sexual dimorphism**  
*John R. Paxton & G. David Johnson*
- 16:30–17:00      **Rare, interesting, and scientifically valuable larval fish specimens from the collections of the Far Seas Fisheries Research Laboratory, now housed at the National Museum of Nature and Science**  
*G. David Johnson*
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- 17:00–17:10      **Closing Remarks**  
*Keiichi Matsuura*

**Wednesday, March 5**

**Workshop** (Excursion for Invited Speakers)

# Abstracts of Oral Presentations

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## Session 1 Biogeography of Fishes

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09:40–10:10 (Monday)

### **A tale of two fishes: Unseen and unsung heroes on the Great Barrier Reef— Lessons we can learn from gobies and batfishes**

David R. Bellwood

*Australian Research Council Centre of Excellence for Coral Reef Studies and  
School of Marine and Tropical Biology, James Cook University  
E-mail: david.bellwood@jcu.edu.au*

Our understanding of reef fishes is largely driven by what we can see. In most coral reef regions, research is focussed on the visually apparent component of the fauna, often with an emphasis on the more colourful species. This presentation will examine the overlooked and undervalued fishes of the Great Barrier Reef. Ecological studies of the cryptobenthic fishes have revealed their unusual life history traits and exceptional importance in coral reef ecosystem processes. On the GBR, the cryptobenthic fauna is dominated by gobies, with the most abundant species belonging in the genus *Eviota*. One species in this genus lives for just 59 days, the shortest recorded lifespan for a vertebrate, and spends less than 35 days on the reef. This short lifespan is reflected in an exceptionally fast growth rate, high daily mortality rates and limited lifetime fecundity. These traits have important ramifications. Evolutionarily, they make phylogenetic reconstructions problematical when using traditional molecular methods, as the short generation times appear to result in rapid saturation. Ecologically, however, they underpin significant trends. In terms of their contribution to biomass gobies only comprise 2.4% of the fish assemblage, yet they have the 4th greatest capacity for daily growth in mass (1st in length). Gobies are the powerhouse of the reef. On the reef base half the weekly increase in fish mass can be attributed to cryptobenthic fishes (primarily gobies). If gobies are overlooked because of their size batfishes are overlooked because they are shy. Today's reefs are threatened by overfishing and phase-shifts, with reefs being dominated by algae. By studying experimentally induced phase-shifts we were able to identify the fishes responsible for reversing these phase-shifts. Remarkably, despite having over 47 herbivorous fish species in the vicinity, the reversal of our experimentally-induced phase-shift was primarily driven by just one species: the pinnate batfish (*Platax pinnatus*); a previously unrecorded herbivore. The presence of this species and its activity was only revealed using remote underwater video cameras, in the absence of divers. Overall, if we only understand reefs by what we can see with our own eyes we may enjoy the bright colours but miss the most important messages.

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10:10–10:40 (Monday)

## **Inferring multi-scale habitat distributions from species ranges—An Australian perspective**

Martin F. Gomon

*Ichthyology, Sciences Department, Museum Victoria*

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Recent awareness of the world's rapidly declining biodiversity and our resulting need for establishing protected areas to redress it has brought about an increased urgency to map the full spectrum of biogeographical distributions, from broadscale bioregions to microhabitats. As distributions of marine organisms are even now considered to be poorly documented, more freely available physical data have often been used as surrogates for modelling recurrent biotic distributions in our seas. However, the use of physical surrogacy makes untested assumptions about the affects of physical parameters on the distribution of organisms. Attempts over the past ten years to use existing perceptions of the distributions of Australia's approximately 4500 species of marine fishes living around the island continent have generated bioregional models from coastal habitats to well down Australia's continental slope. Some conform with those in historical biogeographical literature, while others represent new hypotheses. The results of these studies have been incorporated in bioregionalisations that form the basis for developing regional and national management strategies for Australian territorial waters.

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10:40–11:10 (Monday)

## **Seasonal and interannual variation of subtidal fish assemblages in Wakasa Bay revealed by underwater visual census with reference to the warming trend in the Sea of Japan**

Reiji Masuda

*Maizuru Fisheries Research Station, Kyoto University*

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A bi-monthly underwater visual census was conducted in the subtidal reef habitat of Nagahama, Wakasa Bay, Sea of Japan, over 6 years from January 2002 to December 2007. A total of 90 fish species and 72247 individuals were recorded over 144 1-hr visual censuses composed of three 2×200m transects. The number of both total individuals (abundance) and species (richness) was greatest in summer (July–September), with 10–20 species per 400 m<sup>2</sup>, when the sea-bottom temperature was highest (24–28°C), and lowest in winter (January–March), with 1–8 species per 400 m<sup>2</sup>, when the temperature was lowest (10–12°C). Five species, i.e. rockfish (*Sebastes inermis*), wrasse (*Pseudolabrus sieboldi*), two species of goby (*Acentrogobius pflaumii* and *Tridentiger trigonocephalus*), and pygmy filefish (*Rudarius ercodes*) were frequently observed and present in more than 250 of the total of 432 total transects. While the presence of most fish species was dependent on water temperature, some species were independent of water temperature, including anchovy (*Engraulis japonicus*), *S. inermis*, wasp fish (*Hypodytes rubripinnis*), *A. pflaumii*, and pufferfish (*Takifugu poecilonotus*). Jack mackerel (*Trachurus japonicus*) was the most abundant fish, being most typically seen from spring through autumn. Some species such as red sea bream (*Pagrus major*) showed strong annual fluctuations in abundance. The interannual stability in fish abundance and species richness was probably because the fish assemblage was composed of a sufficiently large number of species, but with the number of each species fluctuating over time. The species composition of the present research was compared to the results of marine faunal survey conducted in the same area from 1970 to 1972 (Nishida et al., 1977). The median of the center of distribution (COD: the average of the northern and the southern limit of distribution in northern hemisphere in each species) for fish observed from 2002 to 2007 was 30.5°N, which was significantly lower latitude than the COD for 1970–1972, which was 33.5°N. This indicates that over the last 30 years southern fish species have significantly increased whereas those indigenous to northern waters

have decreased in accordance with the warming trend in the Sea of Japan.

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11:30–12:00 (Monday)

## **Zoogeographical role of the Kuroshio Current: Transportation system and barrier for coastal fishes of southern Japan**

Keiichi Matsuura<sup>1</sup> & Hiroshi Senou<sup>2</sup>

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<sup>2</sup>*Kanagawa Prefectural Museum of Natural History*

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Many SCUBA divers have discovered new information about fishes including new species and new records in rocky and coral reefs with complex topographies being impossible for ichthyologists to access by other collecting gear. They also provided many excellent underwater photographs of fishes, which resulted in a very large database of fishes stored in the Image Database of Fishes in the Kanagawa Prefectural Museum of Natural History (KPM). The number of photographs in this database has recently exceeded 80,000. The KPM and the National Museum of Nature and Science (NSMT) joined forces to make 55,000 images in the database available on the website of the NSMT. This image database enabled us to make a zoogeographical analysis on coastal fishes of areas in Japan influenced by the Kuroshio. We compared the fish faunas of the following 12 sites under the influence of the Kuroshio Current by using large-scale data of fish image database: 1) Sagami Bay, 2) Osezaki (Suruga Bay), 3) Kushimoto (Kii Peninsula), 4) Kashiwa-jima Island (Shikoku), 5) Yaku-shima Island, 6) Okinawa-jima Island, 7) Ie-shima Island, 8) Miyako Islands, 9) Ishigaki-jima Island, 10) Iriomote-jima Island, 11) Hachijo-jima Island, and 12) Ogasawara Islands. Our zoogeographical analysis indicated that the 12 sites were divided into two groups, one including the five sites in the Ryukyu Islands and the other including the remaining seven sites. The latter group was subdivided into the Ogasawara Islands and the other six sites. The analysis strongly demonstrates a close relationship between fish faunas of Sagami Bay and Osezaki (Suruga Bay). Our data indicate that the fish fauna of the Ogasawara Islands is more similar to those of the sites in the Pacific side of central Honshu and Shikoku, and Yaku-shima Island immediately south of Kyushu, although the Ogasawara Islands and the Ryukyu Islands are located in the same latitudinal zone. This suggests that the Kuroshio Current plays an important role not only in transporting coral-reef fishes from south to north but also forms a barrier for temperate fishes when they migrate south toward the Ryukyu Islands. In addition to the Japanese fish fauna, we analyzed fish faunas of various regions in Micronesia by using data collected from literature. Our preliminary analysis suggests that the fish fauna of the Palau Islands is clearly separated from that of the other island groups.

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12:00–12:30 (Monday)

## **Migratory behavior has driven the evolution in anguillid eels**

Katsumi Tsukamoto

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Evolution of anguillid eels has been closely linked to their unique catadromous migratory behavior. Two major characteristics of their migration are large-scale dispersion of leptocephali and pinpoint spawning of adults at offshore waters. Anguillid eels appeared to originate in the sea from mesopelagic anguilliformes fishes. They migrated to coastal waters, and eventually escaped out of marine habitat to enter freshwater, which appeared to be an origin of their catadromous migration (Random Escapement Theory). Molecular phylogeny of all 18 species+subspecies in the world suggested that the leptocephali of ancestral *Anguilla borneensis*, an endemic species in the Borneo Island in the present day, dispersed westward along paleo-circum equatorial current in the ancient Tethys Sea during the cretaceous age to in-

vade into the eastern coast of Africa and North Atlantic Ocean, which caused speciation of two Atlantic eels and African species (Tethys Sea Hypothesis). Oceanic surveys revealed that the more ancestral tropical eels spawned near their freshwater growth habitats showing a short-distance migration of tens/hundreds kilometers, while temperate species presented typical large-scale migration of thousands kilometers. Long-distance migration of anguillid eels appeared to have evolved from a local migration of tropical eels by obtaining a slower growth rate of leptocephali, a delayed metamorphosis and large leptocephalus size, all of which characters prolonged transportation duration by currents (Migration Expansion Model). Unlike tunas or mackerels, anguillid eels are poor at schooling and males and females appeared to become solitary when they arrive at their spawning area, even if they leave estuaries together towards offshore spawning area forming a big school. Therefore, they need to have a “promised” pinpoint area in a vast ocean to meet each other for fertilization, i.e. seamounts for *Anguilla japonica* (Seamount Hypothesis). Spawning of adults at pinpoint site offshore would enhance fertilization success of eggs, but cause migration failure because of high requirement of accurate navigation mechanism to destination. Such isolated spawning site offshore would facilitate differentiation of population and cause speciation. Thus, it can be concluded that evolution of anguillid eels have been driven by behavioral characteristics of their catadromous migration.

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14:00–14:30 (Monday)

### **Ask not what evolution can do for *Trimma*—Ask what *Trimma* can do for evolution**

Richard Winterbottom

*Department of Natural History, Royal Ontario Museum*  
*E-mail: rickw@rom.on.ca*

Recent research results based on a variety of studies of *Trimma*, a genus of small Indo-Pacific reef gobies, are explored in the context of the interplay between deductive and inductive reasoning. Studies of the transition between abdominal and caudal vertebrae highlight trends in homoplasy, apparently strong selective forces, and character weighting. Age and growth results from a schooling, outer-reef, planktivorous species, *Trimma nasa*, suggest incredibly rapid population turnover with very high daily mortality rates, and development of an associated new reproductive strategy. The evidence suggests an important, yet largely overlooked, role in energy flow on coral reefs which may, in turn, significantly affect conservation strategies.

Analyses for the Fish BarCode of Life Project, based on about 450 base pairs of the mitochondrial cytochrome oxidase 1 gene (CO1), suggest the existence of several “mitochondrial” species in the genus, some of which are at least syntopic, if not truly sympatric. Such ‘species’ are rare—at least among vertebrates—and suggestive of rapid mitochondrial evolution with strong morphological selection pressures. Examples of the opposite regime of selection pressure are also evident, where the ‘species’ are clearly distinguishable morphologically but have much less divergence in the CO1 gene than expected.

These research projects illustrate the reciprocal illumination principle that drives scientific progress. The results are interpreted in the light of evolutionary theory, yet feed back into the body of that theory by providing new or additional examples of the almost limitless ways in which the consequences of that process are expressed.

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14:30–15:00 (Monday)

### **Gobioid genera need re-examination: A case study of *Gobiopsis***

Naomi Delventhal<sup>1</sup> & Randall D. Mooi<sup>2</sup>

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Over 250 genera of gobioids are recognized yet many of these have not been diagnosed by unique characters and fewer still have been examined in a cladistic framework. This is demonstrated by the difficulty of placing new species of gobies within existing genera and the plethora of monotypic genera. *Gobiopsis* Steindachner includes 13 nominal species and several undescribed species. Previous workers have recognized this group based on the presence of both longitudinal ridges of neuromasts and barbels, but our preliminary examination led us to doubt the homology of these characters among different species groups within *Gobiopsis*. We tested their homology by searching for congruence in a wider number of characters in external morphology and osteology. Osteological examination revealed remarkable variation of characters in the cranium (shape and size of vomer, frontals, mesethmoid, lateral ethmoid, pterotic, sphenotic), suspensorium (shape and processes on hyomandibular, preoperculum, metapterygoid, maxilla, premaxilla, dentary, and arrangement of teeth), as well as the gill arches (shape and arrangement of interarcual cartilage, pharyngobranchials and hypobranchials) and axial skeleton (shape of parapophyses and association of epineural ribs). We present synapomorphies that lend strong support to the monophyly of 10 species (*Gobiopsis sensu stricto*), however the placement of the remaining three species (*G. atrata*, *G. exigua*, and *G. springeri*) within *Gobiopsis* is not supported. An examination of previously suspected and potentially related taxa (*Platygobiopsis*, *Barbuligobius*, *Mangarinus*, *Callogobius*, and *Feia*) did not favour any one genus as sister taxon to *Gobiopsis sensu stricto* nor did it suggest appropriate placement for the remaining three taxa. Thus we are expanding taxonomic coverage to include representatives of all gobiid genera. Our study is revealing a wealth of variable characters in the osteology of gobies that may be used to test monophyly and hypothesize relationships at the intra- and intergeneric level.

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15:00–15:30 (Monday)

## Radiation of *Glossogobius* in freshwaters of the Indo-west Pacific

Douglass F. Hoese

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The genus *Glossogobius* is a complex and diverse genus of gobiid fish predominately found in freshwaters of the Indo-west Pacific region. Currently over 50 species are known, but additional sampling and studies may double that figure. The genus apparently is most closely related to *Psammogobius*, *Afurcagobius*, and *Bathygobius*. Three major radiations within the genus *Glossogobius* are known. The *Glossogobius giuris* complex is most speciose in the Indian Ocean. The *Glossogobius circumspectus* complex contains a single widely distributed mangrove inhabiting species and several species in lakes in Sulawesi. The *Glossogobius celebius* complex is the largest with parallel radiations in New Guinea and the Philippines. Most of the species in this complex are small sized, reaching a maximum size of 100 mm SL and confined to mountain ranges above 100 m elevation.

Species show considerable diversity in size and habitat associations. The largest species (*Glossogobius giuris*) reaches a length of 400 mm SL and the smallest about 30 mm SL. Many of the lowland species are widely distributed. Studies are showing that many of the previously recognised widely distributed species are highly variable and show considerable geographical variation. In many cases these are being found to be complexes of two or more often sympatric species. For example two large sized species are going under the name *Glossogobius giuris* in India. The lowland species *Glossogobius celebius* is now known to be a complex of 5 species, which are largely allopatric. Most of the species common to Australia and New Guinea show color and morphological differences between the two areas and some show considerable geographical within Australia and New Guinea. Because of the high variability and apparent convergence in high altitude species, separation of species is, in many cases, highly subjective.

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16:00–16:30 (Monday)

## **The goby genus *Redigobius* and its relationships—A work in progress**

Helen K. Larson

*Museum and Art Gallery of the Northern Territory*

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The gobiid fish genus *Redigobius*, with 44 nominal species, is being revised, and so far includes 12 species and probably more (depending on how *R. bikolanus* is split). Two new species, one from Fiji and one from northern Australia, are being described. *Redigobius* belongs to the subfamily Gobionellinae, and is one of the most plesiomorphic genera of that subfamily. Preliminary genetic analyses seem to confirm Larson's 2001 hypothesis, based on morphology and osteology, that *Redigobius* is most closely related to *Pseudogobiopsis*. *Redigobius* can be distinguished from other genera in the subfamily by a combination of characters, and occurs throughout the Indo-west Pacific, in estuarine to fresh water habitats, with the species-complex *R. bikolanus* being the most widespread group.

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16:30–17:00 (Monday)

## **Phylogenetics of the gobioid fishes: Diversity, taxonomy, and ecology**

Christine Thacker

*Natural History Museum of Los Angeles County*

*E-mail: thacker@nhm.org*

The gobioid fishes are common inhabitants of streams, estuaries, and nearshore marine habitats throughout the world. They are very diverse and usually of small size, making understanding of their taxonomy, phylogeny and evolution particularly difficult. The use of DNA sequence data has allowed resolution of many aspects of gobioid phylogeny, complementing several comprehensive morphological character surveys. The history of gobioid classification is similar to that for the Acanthomorpha as a whole: small, distinct groups have been elevated taxonomically, leaving behind larger, more poorly defined assemblages. In this presentation, a new molecular phylogeny including samples of all gobioid clades is presented, along with explorations of morphological and ecological data in the context of the phylogeny. The phylogeny indicates that the smaller gobioid families and subfamilies are nested within the larger ones (Gobiidae and Eleotridae) and that a new classification is needed in order to associate names with monophyletic groups. This new classification preserves traditional names as much as possible, and reduces the recognized gobioid families from nine to six. Distinctive groups of species that have been subdivided from the remainder are in fact part of the spectrum of diversity seen within the larger gobioid groups. Gobiioidei is shown to be part of a clade that also includes Kurtidae, Apogonidae, Pemppheridae, and Leiognathidae, and characters common to these groups include aspects of the skeleton, soft tissues, and reproductive ecology. The clade that includes Gobiioidei is part of a deep basal split within Perciformes, outside the bulk of perciform diversity. Selected skeletal characters are reinterpreted in light of the phylogeny, and their utility in diagnosing clades is reviewed. The significantly greater diversification found in gobiine gobiids relative to gobionellines is hypothesized to be linked to invasion of marine habitats. Analysis of gobiid diversification indicates that diversification is not significantly elevated at the clade's origin, but appears to have been consistently high throughout the group's history.

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09:00–09:30 (Tuesday)

## Windows into the architecture of fishes

Paula Mabee

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Comparative anatomical studies done by systematists have provided a solid foundation for our understanding of fish evolution. We now seek to understand the explanations for these patterns of variation. I suggest that several new windows of understanding have opened to us through studies from developmental genetic, evo-devo and informatics approaches. First, the developmental basis of fish body plan construction is increasingly well understood through studies of model organisms (zebrafish, medaka, Fugu) and their mutants by molecular geneticists. Though the explosion in knowledge from these molecular approaches and model organisms has to date been poorly related to patterns of variation in fish evolution, it is integral to our understanding. I will give examples here from gill arch development and evolution of cypriniform fishes. Second, the “evo-devo” perspective of modularity provides a way of understanding constraints on body plan. I will illustrate this with examples from fin development and evolution. Third, adopting an ontology-based informatics approach facilitates the integration of genetic data from mutant and wild-type fish phenotypes with patterns of evolutionary variation in fish morphology. To date, these have been poorly integrated. I will give examples from the new “Phenoscape” approach using ostariophysan fishes as a prototype. The sum of these three perspectives yields fresh insights into the constraints on fish morphology and evolution.

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09:30–10:00 (Tuesday)

## Evolutionary history of modern ray-finned fishes: An overview based on 327 whole mitogenome sequences

Masaki Miya<sup>1</sup> & Mutsumi Nishida<sup>2</sup>

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Since divergence from an ancestral osteichthyan (a common ancestor of bony fishes and tetrapods) in the late Silurian about 420 Mya (million years ago), actinopterygians (ray-finned fishes) have attained current diversity of 27,580 species, about a half of all vertebrates, and occupied nearly all aquatic ecosystems. Despite such remarkable diversity and ubiquity, patterns and processes of modern ray-finned fish diversification remain largely unknown owing to incomplete fossil record and a lack of robust phylogenetic framework for extant species.

To provide a comprehensive overview of the history of modern ray-finned fish diversification, 1) we analyzed the ray-finned fish phylogeny using whole mitochondrial genome sequences from 327 species; 2) we constructed evolutionary timetree using a relaxed molecular-clock Bayesian method; and 3) we analyzed clade-specific and global patterns of diversification rates using the timetree.

Based on unambiguously aligned whole mitogenome sequences (10,046 bp excluding entire 3rd codon positions) from 327 species, we conducted partitioned maximum likelihood analyses using RaxML and obtained a single fully bifurcating tree. More than 70% of internal branches were supported by moderate to high bootstrap probabilities of  $\geq 70\%$ .

Divergence time estimation using Multidivetime suggested that a crown group of Teleostei originated 317 Mya in the late Carboniferous. This dating doubles the oldest fossil record of the extant family (151 Mya), although it is more congruent with the estimations based on multiple duplicated genes from nuclear genomes (320–350 Mya).

We found that a global turning point of the actinopterygian diversification was survival of the two ancestral lineages

from the end-Permian mass extinction, which led to the rise of the two extant lineages called Otocephala and Euteleostei. The two lineages have accelerated diversification rates toward the present and undergone remarkable radiations into fresh- and salt water environments, respectively, comprising >95% of the extant species. In both lineages, mass extinction (and the resulting vacant niches) plus continental breakups (and the resulting habitat diversification) are putative causal agents for such acceleration. Rise of the photosymbiotic scleractinian coral reefs during the late Early Jurassic seems to be critical for the explosive radiation within the percomorphs, a crown clade of the Euteleostei.

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10:00–10:30 (Tuesday)

## **The evolution of fish diversity: Lessons from large-scale comparative analysis**

Judith E. Mank<sup>1</sup> & John C. Avise<sup>2</sup>

<sup>1</sup>*Department of Evolutionary Biology, Evolutionary Biology Centre, Uppsala University*  
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<sup>2</sup>*Department of Ecology and Evolutionary Biology, University of California*

Ray-finned fishes have an unusually wide variety of reproductive traits, including spawning tactics, mating systems, sexually selected traits, and parental care strategies. The diversity in these many traits makes these fish an ideal for comparative phylogenetic studies aimed at understanding the pattern and process of reproductive evolution, as well as the relationship between sexual selection and various reproductive adaptations. Toward this goal, we constructed a first draft supertree for the ray-finned fishes, based on numerous overlapping morphological and molecular source phylogenies, and resolving more than 200 actinopterygian families. We then used the resulting cladogenetic structure to study how reproductive traits evolve over time, as well as test several current hypotheses of correlated evolution.

Comparative phylogenetic studies revealed that similar reproductive behaviors have evolved many independent times in the ray-finned fishes, and that there is a clear evolutionary pattern in the progression among behavioral adaptations over hundreds of millions of years. Specifically, male mating strategies evolve in a progression from male mate monopolization, with subsequent alternative strategies evolving to circumvent the costly investment of sexually selected male traits. Similarly, parental care adaptations evolve in a stepping-stone-like fashion for species with external fertilization, with male parental care, which is correlated with sexually selected traits such as dichromatism, progressing to biparental care and terminating in maternal care. The evolution of internal fertilization alters this pathway, and leads directly to maternal care with no paternal intermediate.

Sexually selected male ornaments are also widely dispersed across the Actinopterygii, creating opportunities to test several models of the evolution of these traits. Many sexually selected traits in males are controlled by testosterone, and the increase of male sexually selected traits as a result of female preference leads to increased testosterone levels in both males and females. Over time, there is evidence that selection acts to reduce female testosterone production relative to specific males, suggesting that testosterone is sexually antagonistic in fishes. Finally, despite widespread theoretical predictions, sexually selected male ornaments are not associated with female heterogametic sex chromosomes, suggesting that the evolution of sexually selected traits is a complex process, and needs more complete modeling.

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10:45–11:15 (Tuesday)

## **Refining our understanding of the limits and relationships of Percomorpha: Discovering large clades and the taxonomic challenges they present**

Wm. Leo Smith

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Since the advent of cladistics, the higher-level taxonomy of non-percomorphs has been continually refined. With each step, the existing poly- or paraphyletic taxonomy has been updated and rendered monophyletic (even if the taxonomic

changes were transient). Whereas non-percomorph taxonomy was advanced using studies from the base to the family-level tips and the tips back to the base, the limited resolution of percomorph intrarelationships has proceeded solely from the tips to the base. Attempts to resolve the percomorph problem from the base up inevitably ended with compositional refinements and virtually no resolution of percomorph intrarelationships. Recently, large-scale molecular analyses have begun to address the limits and relationships of percomorphs. These studies have refuted many recently recognized groups and have hypothesized novel groupings that subsequently are corroborated by morphological investigation. Despite the advances brought on by these explicit molecular analyses, there has been a tremendous reluctance to suggest, let alone adopt, taxonomic changes based on their results. Instead, authors have used awkward alphanumeric names (e.g., clade X) or informal names for these suprafamilial clades. Subsequent discussions of these findings are forced to use these obscure alphanumeric names, provide long lists of included families, or enumerate compositional amendments to standard references. While the promotion of scores of new names is not ideal or recommended, the formal recognition of continually recovered or well-supported monophyletic groups is necessary for effective communication among scientists and the advancement of our field. Given modern efforts from DNA barcoding to PhyloCode, it is critical that systematists continue to be at the forefront and promote taxonomy. Otherwise, ecologists and evolutionary biologists who embrace the comparative method, and are less versed in taxonomy, are likely to make classificatory changes, intentionally or inadvertently. Using a combination of published and recently completed phylogenetic studies, these issues will be highlighted and discussed.

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11:15–11:45 (Tuesday)

## **Evolutionary origin and phylogenetic relationships of the Cypriniformes: A multi-gene approach to resolving the evolution of the world's most diverse group of freshwater fishes**

Richard Mayden

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The order Cypriniformes is the largest clade of freshwater fishes in the world with over 3400 described species. Our investigation into the evolutionary history of these fishes involves biogeological, morphological and molecular character variation, with the latter including both mitochondrial and nuclear genes. The current analyses use DNA sequences from seven nuclear genes—Growth Hormone (GH) (ca. 633 bp), Recombination Activating Gene 1 (RAG1) (ca. 1497 bp), Rhodopsin (ca. 831 bp), Interphotoreceptor Retinoid-Binding Protein gene (IRBP) (ca. 849 bp), Early Growth Response (EGR) 1 Gene (ca. 885 bp), EGR 2B gene (ca. 831 bp), and EGR 3 gene (ca. 936 bp). We present three interrelated investigations with different sets of taxonomic coverage particular to the questions we wish to address in cypriniform systematics. First, sampled outgroups (characin, catfish, and gonorynchiforms) and 50 ingroup taxa comprising all cypriniform family and subfamily groups to assess the phylogenetic relationships among the major lineages of cypriniforms. For this analysis we sampled four nuclear genes (GH, RAG1, Rhodopsin, and IRBP) and the published data from whole mitochondrial genomes of the Cypriniformes (Saitoh et al., 2006). Second, we focus on resolving the phylogenetic position of the mysterious genera, *Gyrinocheilus* and *Psilorhynchus* within the Cypriniformes based on multi-locus analysis of all described nuclear loci, excluding GH. Finally, the relationships of the Cypriniformes within the Otophysi, and relationships of the Otocephala was examined in a larger-scale analysis of the Actinopterygii using sequences from mitochondrial gene 12S and 16S and 5 nuclear genes (RAG1, Rhodopsin, IRBP, EGR1, EGR2B and EGR3). From all studies, we will compare the resulting molecular phylogenies derived from both nuclear and mitochondrial genes with total evidence analyses, as well as with the current classification and/or previous hypotheses of relationships of these fishes.

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11:45–12:15 (Tuesday)

### ***Paedocypris*—A developmentally truncated miniature cyprinid with astonishingly complex novel structures**

Ralf Britz

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In the last 15 years, a growing number of miniature cyprinids with extremely small adult maximum sizes of only 10–25 mm standard length has been discovered in Southeast Asia. One of the most unusual is *Paedocypris*, a new genus with two species, comprising some of the smallest fishes and vertebrates. As in other vertebrates that have undergone extreme miniaturization, *Paedocypris* exhibits a number of simplifications of its anatomical structure, but at the same time has evolved several unique morphological specializations, most of which are sexually dimorphic.

The skeleton of *Paedocypris* is characterized by reduction and loss and resembles in many aspects that of a larval/early juvenile stage of its close relatives. More than 50 skeletal components in *Paedocypris* have been affected by developmental truncation. A comparison with the skeletal development of a close relative, the zebrafish *Danio rerio*, demonstrates that the majority of the absent bones or skeletal structures in *Paedocypris* are those that appear in the late phase of ossification in the zebrafish. Their absence in *Paedocypris* thus seems due to simple developmental truncation of terminal stages in the ossification sequence.

The present study of the sexually dimorphic structures in *Paedocypris* demonstrates that predominantly the male exhibits the more complex state: (1) a cleithrum with a pointed posterior process that covers the scapula laterally, (2) a massive, heavily ossified upper most pectoral radial; (3) thickened and enlarged three upper most pectoral fin rays; (4) a large triangular, dorsal process on the massive os suspensorium; (5) an enlarged and shovel-like basipterygium; (6) a hypertrophied 1st pelvic fin ray that supports keratinized pads of skin. Female *Paedocypris* only show a single structure that is better developed than in males: the first proximal-middle radial and the anterior most fin ray of the dorsal fin are more massive and more heavily ossified.

Although the biological role of these dimorphisms is still unknown, they are most likely related to a special reproductive behavior. *Paedocypris* is thus a prime example for the recent claim that among cyprinids miniaturization is associated with evolutionary novelty only in developmentally truncated miniatures and not in proportioned dwarfs. In addition, *Paedocypris* offers a true challenge to *Schindleria* as the most extreme example of progenetic developmental truncation known among fishes.

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14:15–14:45 (Tuesday)

### **Phylogeny of the Medaka and relatives: Molecules versus morphology**

Lynne R. Parenti

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Ricefishes, known best by the model organism, the Medaka, *Oryzias latipes*, comprise the atherinomorph family Adrianichthyidae which ranges broadly throughout fresh and brackish waters of Central, South and Southeast Asia and the Indo-Malay-Philippines Archipelago as far east as Timor. Twenty-eight Recent species are recognized in a monograph in press in the *Zoological Journal of the Linnean Society*. Adrianichthyid monophyly and the sister group relationship of adrianichthyids and exocoetoids is supported by both morphological and molecular data. *Oryzias latipes* is in a species complex that includes *O. luzonensis*, *O. curvinotus* and the miniatures *O. sinensis* and *O. mekongensis*. Species groups within *Oryzias* are diagnosed as monophyletic in the morphology monograph largely by osteology, colour pattern and meristic variation. Species groups and their relationships as inferred from morphology correspond only in part with those groups previously recognized based on chromosome constitution: monoarmed, biarmed, and fused. In con-

trast, these three groups have been recovered in recent molecular analyses. Differences between the morphological and molecular analyses that will be discussed include taxon sampling, character analysis and outgroup comparison. The fused chromosome group, also known as the *celebensis* species group, is paraphyletic in the morphological analysis and includes species with some of the most divergent morphologies, including: lunate versus truncate caudal fin, bifid versus single head of the hyomandibula, high versus low number of vertebrae, and high versus low number of scales in a lateral series.

Despite the utility of morphology as advocated for here, it has not been able to resolve relationships of ricefish species at lower levels with unambiguous synapomorphies. Additional data, from both molecules and morphology, are needed to provide a robust hypothesis of relationships among all ricefish down to the species level. Further, new species remain to be described and added to both analyses. Recent, exciting discoveries include remarkably colourful species from Indonesia, the description and analysis of which will inform both phylogenetic and biogeographic analyses.

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14:45–15:15 (Tuesday)

## **“Scorpaeniform” phylogeny: Morphological approach to a question of its monophyly**

Hisashi Imamura

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The “order Scorpaeniformes” had been recognized as a monophyletic group by having a suborbital stay, a projection extending from the third infraorbital. In addition, two characters, the sensory canal on the parietal and extrinsic swimbladder muscle, were also regarded as synapomorphy of the “order.” Although several authors doubted its monophyly (e.g., Quast, 1965; Nelson, 1994), the strong evidences showing its polyphyly had not been demonstrated until Imamura and Yabe (2002).

Among “Scorpaeniformes,” two major monophyletic lineages, “scorpaenoid lineage” (including scorpaenids and related taxa) and “cottoid lineage” (containing cottids and related taxa), were recognized. The extrinsic swimbladder muscle in the scorpaenoid lineage was inferred being derived from the obliquus superioris and that in the cottoid lineage from the epaxialis; and thus, they are not homologous. The osteological developments of the sensory canal on the parietal in these lineages fundamentally differed and this character cannot strongly support the monophyly of the “order.” Therefore, the “scorpaeniform” monophyly was recognized in dependence on only the suborbital stay.

The family Dactylopteridae also has a suborbital stay. It had been treated as a “scorpaeniform” member or included in distinct order, Dactylopteriformes. However, it was revealed that Dactylopteridae has a non-homologous suborbital stay, extending from the second infraorbital. This fact suggested that the suborbital stay is independently obtainable.

The synapomorphies of the scorpaenoid lineage and those of the cottoid lineage were compared with the characters found in Percomorpha, especially Perciformes. As the result, it was recognized that the scorpaenoid lineage and Serranidae commonly have two derived characters, including a backwardly-directed opercular spine, and the cottoid lineage and Zoarcoidei commonly possess 13 derived characters, containing the parietal sensory canal without spines. It is more parsimonious recognizing a close relationship of the scorpaenoid lineage and Serranidae and that of the cottoid lineage and Zoarcoidei than retaining “scorpaeniform” monophyly based on a single character, suborbital stay. It was concluded that “Scorpaeniformes” should be treated as polyphyletic group, and the classification recognizing the perciform Scorpaenoidei (including scorpaenoid lineage and Serranidae) and Cottoidei (containing cottoid lineage) was proposed.

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15:30–16:00 (Tuesday)

## **Tigerfishes, Tripletails, and Velvetfishes form a clade: Morphological evidence from adults and larvae**

Jeffrey M. Leis<sup>1</sup> & Anthony C. Gill<sup>2</sup>

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The percoid genera *Lobotes* Cuvier (Tripletails), *Datnioides* Bleeker (Tigerperches), and *Hapalogenys* Richardson (Velvetfishes) have long perplexed ichthyologists. *Lobotes* (2 species) are relatively large fishes (ca. 1 m) found worldwide in warm mostly coastal waters, but they are also found in oceanic waters around floating objects. *Datnioides* (5 species) are moderate-sized fishes (ca. 30 cm) of estuaries and freshwaters from India and southeast Asia to New Guinea. Finally, *Hapalogenys* (7 species) are moderate-sized (ca. 30 cm) fishes of coastal waters from Japan and the central Indian Ocean to northwestern Australia. Traditional classifications often placed *Lobotes* and *Datnioides* as the sole members of the family Lobotidae. Because character evidence for a close relationship has been scant, some classifications place *Datnioides* outside the Lobotidae, without specified relationship to other percoids. Traditionally, *Hapalogenys* has been placed in the family Haemulidae, a placement not supported by characters used to define that family or to associate it with other families. Although sometimes placed in a separate family, *Hapalogenys* is provisionally retained in the Haemulidae in most recent classifications, perhaps for the lack of any clear relationship with other taxa. Although no previous classifications have proposed a relationship between *Hapalogenys*, *Lobotes* and *Datnioides*, Leis and Carson-Ewart (2000) noted remarkable similarity in larval morphology of the three genera, particularly in head spination, pigmentation, early development of the posteriorly-placed pelvic fins and general body shape, and placed them together in an informal grouping “*Lobotes*-like.” We examined this hypothesis using both adult and larval morphology. Here, we provide additional evidence that supports the hypothesis of a monophyletic Lobotidae composed of the three genera: in larvae, most convincingly, sculpting on the skull; in adults, tooth replacement mode (Hilton and Beemis, 2005), tooth arrangement and dorsal gill-arch morphology. We are now assessing the relationships of the revised Lobotidae, and a close relationship to acanthuroid fishes looks promising.

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16:00–16:30 (Tuesday)

## **The cetomimoid conundrum resolved—Whalefishes (Cetomimidae), Tapetails (Mirapinnidae), and Bignose fishes (Megalomycteridae): Amazing larval transformations and striking sexual dimorphism**

John R. Paxton<sup>1</sup> & G. David Johnson<sup>2</sup>

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Relationships between cetomimids, mirapinnids, and megalomycterids have been questionable since the latter two families were described in the 1950s and 1960s. A close relationship among the three was suggested by Gosline (1971) and a few others, and convincing evidence for monophyly of such a group was presented by Bertelsen and Marshall (1984). The three families share unique features in the axial skeleton and some species pairs/‘triads’ show striking meristic concordance. Because mirapinnids are known only from larval/ juvenile forms and larval cetomimids are unknown, there has been speculation that mirapinnids are larval cetomimids. Lending credence to this hypothesis is the report of Miya et al. (2003) that a larval mirapinnid has virtually the same total mitochondrial genome (7 base pair differ-

ences of 16,000+) as the cetomimid *Cetostoma regani*. Still puzzling, however, are the existence of mirapinnid juveniles to 65 mm sl and 25 mm sl cetomimids, and the fact that mirapinnids have pelvic fins and short, oblique jaws, whereas cetomimids have no pelvic fins and long, horizontal jaws. Following the molecular analysis, we examined the osteology of the three families in detail. The extraordinary transformations required in the skull, jaws, gill arches, anterior vertebrae, pectoral, and pelvic girdles left us sceptical about the mirapinnid—cetomimid transition, but we concluded that a mirapinnid—megalomycterid transition is possible (Paxton and Johnson, 2005). Our more recent studies have confirmed the latter and we have recognised that type specimens from the original descriptions of each family are transitional between the two, leaving only the mirapinnid—cetomimid conundrum. Fortunately, what we believe to be a transforming specimen of *Cetostoma regani* with two remaining pelvic-fin rays was collected in November 2007. The synonymy of the three families is confirmed. Miya and colleagues concurrently are sequencing additional tissues, including the first ‘megalomycterid.’ Our presentation will detail osteological transformations, aspects of male and female biology, summarise DNA results, and describe first attempts to match ‘species’ of the three life stages. Based on meristics, the unique hairy fish, *Mirapinna esau*, is the juvenile (and senior synonym) of the most generalised cetomimid *Proctichthys krefftii*, while *Parataeniophorus gulosus* and *Cetomimoides parri* are respectively larvae/juveniles and males (and junior synonyms) of *Cetostoma regani*. Matching ‘triads’ of other genera and species will be more difficult.

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16:30–17:00 (Tuesday)

### **Rare, interesting, and scientifically valuable larval fish specimens from the collections of the Far Seas Fisheries Research Laboratory, now housed at the National Museum of Nature and Science**

G. David Johnson

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From the 1950's through the 1980's, the Japanese research vessel Shoyo-maru and others collected larval fish specimens from warm seas worldwide. The major purpose of that project was to search for and collect larval tunas, billfishes and commercially important relatives, but, of course, a myriad of other larval fishes were collected incidentally. Fortunately, two larval fish specialists working on the project at the Far Seas Fisheries Research Laboratory in Shimizu, Drs. Shoji Ueyanagi and Yasuo Nishikawa recognized the importance of these specimens and wisely decided to keep all collected specimens at their laboratory. Their successor, Dr. Shoko Tsuji, made another important decision to transfer the non-scombroid larvae from Shimizu to Tokyo upon the request of Dr. Keiichi Matsuura, Collection Director and Curator of Fishes at the National Museum of Nature and Science. Thus, in July 2001, the entire collection of non-scombroid larval fishes was brought to the NMNS, where the approximately 8,000 lots of unsorted samples, now stored in 70% ethanol, are available for study by the ichthyological community at large. In the winter of 2005, I spent seven weeks exploring these unsorted collections, identified specimens representing more than 130 families of marine fishes, and found them to be rich with rare and interesting specimens. Among these are a preflexion larva of the ateleopid, *Ateleopus*, undescribed larvae and prejuveniles of the veliferid lampridiforms, *Velifer* and *Metavelifer*, and several larvae of the rare stephanoberycids, *Acanthochaenus* and *Malacosarcus*, the latter of which was otherwise known only from disintegrated type specimens. I was also able to assemble a developmental series of echeneids which has made it possible to resolve the long-standing problem of homology of the bony elements of the sucking disc. Particularly noteworthy is the fact that, despite storage for extended periods in formalin, many of the specimens from these collections clear and stain for bone and cartilage quite well and thus offer a potentially valuable resource for developmental osteological studies, as is the case for the echeneids and a series of the moonfish, *Mene maculata*, in which we are studying the development of a unique rib/swimbladder association. In addition to the rare and anatomically valuable specimens, I selected pristine specimens of more common taxa and have begun photographing the best of these for a planned book on larvae of marine fishes to be co-authored with Ralf Britz.

# Titles and Authors of Poster Presentations

Asterisks indicate the presenting authors who will be available during the Poster Session on Monday (odd-numbered posters) or Tuesday (even-numbered posters).

- [01] **A strategy for exhaustive phylogeographic analyses of Japanese freshwater fishes, using GEDIMAP, a database for mtDNA genetic diversity**  
*Katsutoshi Watanabe\** (Kyoto University; [watanak@terra.zool.kyoto-u.ac.jp](mailto:watanak@terra.zool.kyoto-u.ac.jp)), *Yuichi Kano* (Kyushu University), *Hiroshi Takahashi* (National Fisheries University) & *Ryo Kakioka* (Kyoto University)
- [02] **Effects of coral and seagrass habitat loss on spatial distribution patterns of coral reef fishes at the Ryukyu Islands, Japan**  
*Yohei Nakamura\** (University of Tokyo; [ynakamura@ori.u-tokyo.ac.jp](mailto:ynakamura@ori.u-tokyo.ac.jp)), *Masahiro Horinouchi* (Shimane University), *Mitsuhiko Sano* (University of Tokyo) & *Takuro Shibuno* (Seikai National Fisheries Research Institute)
- [03] **Miocene marine fishes from Tottori, Japan, with comments on the origin of some coastal fishes of the western Pacific**  
*Teruya Uyeno\** (National Museum of Nature and Science; [uyeno@kahaku.go.jp](mailto:uyeno@kahaku.go.jp)), *Yoshitaka Yabumoto* (Kitakyushu Museum of Natural History and Human History), *Kazuo Sakamoto* (University Museum, University of Tokyo), *Yusuke Suda* (National Fisheries University) & *Yoichi Sato* (Tokushima Prefectural Museum)
- [04] **The process of a pictorial book of fishes as an educational tool in the Keihin Canal Watershed, inner part of Tokyo Bay**  
*Yusuke Miyazaki\** & *Tsuyoshi Sasaki* (Tokyo University of Marine Science and Technology; [yukke@ayu.ne.jp](mailto:yukke@ayu.ne.jp))
- [05] **Freshwater ichthyofauna in Kagoshima Prefecture, southern Japan, with comments on zoogeography**  
*Mizuki Matsunuma\**, *Hiroshi Suzuki* (Kagoshima University; [bf104108@ms.kagoshima-u.ac.jp](mailto:bf104108@ms.kagoshima-u.ac.jp)) & *Hiroyuki Motomura* (Kagoshima University Museum)
- [06] **Freshwater fish diversity in Cambodia**  
*Hiroyuki Motomura\** (Kagoshima University Museum; [motomura@kaum.kagoshima-u.ac.jp](mailto:motomura@kaum.kagoshima-u.ac.jp)), *Takahiko Mukai* (Gifu University) & *Shinji Tsukawaki* (Kanazawa University)
- [07] **The fishes observed around 200 m depth in the north of Sulawesi waters, Indonesia**  
*Masamitsu Iwata\**, *Shinya Yamauchi*, *Kotaro Yoshimura*, *Yoshitaka Abe* (Aquamarine Fukushima; [m-iwata@marine.fks.ed.jp](mailto:m-iwata@marine.fks.ed.jp)), *M. Kasim Moosa*, *Augy Shahailatua*, *Djoko Hadi Kunarso* (Research

*Center for Oceanography, Indonesian Institute for Science) & Kawilarang W.A. Masengi (Sam Ratulangi University)*

- [08] **Variation in vertebral number in freshwater eels, genus *Anguilla* (Teleostei: Anguillidae): A legacy of life history, migration, and selection**  
*Shun Watanabe\**, Akira Shinoda, Jun Aoyama & Katsumi Tsukamoto (Ocean Research Institute, University of Tokyo; [shunwata@ori.u-tokyo.ac.jp](mailto:shunwata@ori.u-tokyo.ac.jp))
- [09] **Non-native freshwater eels in Japan: Present status and future perspectives**  
*Akihiro Okamura\** (IRAGO Institute; [aokamura@irago.co.jp](mailto:aokamura@irago.co.jp)), Huan Zhang (University of Connecticut), Naomi Mikawa (IRAGO Institute), Aya Kotake (Ocean Research Institute, University of Tokyo), Yoshiaki Yamada, Tomoko Utoh, Noriyuki Horie, Satoru Tanaka, Hideo P. Oka (IRAGO Institute) & Katsumi Tsukamoto (Ocean Research Institute, University of Tokyo)
- [10] **Diversity and evolution of larval migration patterns in the anguillid eels**  
*Mari Kuroki\**, Jun Aoyama & Katsumi Tsukamoto (Ocean Research Institute, University of Tokyo; [mari@ori.u-tokyo.ac.jp](mailto:mari@ori.u-tokyo.ac.jp))
- [11] **Anguilliform leptocephali: remarkable fish larvae of the ocean surface layer**  
*Michael J. Miller\** & Katsumi Tsukamoto (Ocean Research Institute, University of Tokyo; [miller@ori.u-tokyo.ac.jp](mailto:miller@ori.u-tokyo.ac.jp))
- [12] **Morphology, metamorphosis, and identification of leptocephalus of the moray eel, *Gymnothorax minor***  
*Atsushi Tawa\** & Noritaka Mochioka (Kyushu University; [a-tawa@agr.kyushu-u.ac.jp](mailto:a-tawa@agr.kyushu-u.ac.jp))
- [13] **Genetic and morphological identification of larval clupeoid fishes from the Ryukyu Islands**  
*Hiro Ishimori\** & Tetsuo Yoshino (University of the Ryukyus; [hiro@stoneforest.info](mailto:hiro@stoneforest.info))
- [14] **Higher-level relationships of the Otocephala (Teleostei) inferred from whole mitogenome sequences**  
*Sébastien Lavoué\** (Ocean Research Institute, University of Tokyo; [lavoue@ori.u-tokyo.ac.jp](mailto:lavoue@ori.u-tokyo.ac.jp)), Masaki Miya (Natural History Museum and Institute, Chiba) & Mutsumi Nishida (Ocean Research Institute, University of Tokyo)
- [15] **Egg shape evolution in the spawning symbiosis of bitterling with freshwater mussels**  
*Jyun-ichi Kitamura\**, Teiji Sota (Kyoto University; [kitamura@terra.zool.kyoto-u.ac.jp](mailto:kitamura@terra.zool.kyoto-u.ac.jp)) & Jyun Nakajima (Kyushu University)

- [16] **Evolutionary history of endemic *Sarcocheilichthys* fishes (Cyprinidae) in Lake Biwa: An example of ecological divergence and speciation associated with novel environments in the growing lake**  
*Takefumi Komiya\**, Katsutoshi Watanabe & Michio Hori (Kyoto University; [komiya@terra.zool.kyoto-u.ac.jp](mailto:komiya@terra.zool.kyoto-u.ac.jp))
- [17] **Genetic and morphological variation of *Squalidus chankaensis* (Cyprinidae) between lacustrine and fluvial populations around Lake Biwa**  
*Ryo Kakioka\**, Takefumi Komiya & Katsutoshi Watanabe (Kyoto University; [kakioka@terra.zool.kyoto-u.ac.jp](mailto:kakioka@terra.zool.kyoto-u.ac.jp))
- [18] **Relationships among egg size, life history, and phylogenetic positions of Japanese *Cobitis* species**  
*Jun Nakajima\** & Norio Onikura (Kyushu University; [cyprin@kyudai.jp](mailto:cyprin@kyudai.jp))
- [19] **Pelagic eggs and larvae of *Caelorinchus kishinouyei* (Gadiformes: Macrouridae) collected from Suruga Bay, Japan**  
*Atsushi Fukui\**, Munehiro Takami, Takao Tsuchiya, Keiji Sezaki (Tokai University; [afukui@scc.u-tokai.ac.jp](mailto:afukui@scc.u-tokai.ac.jp)) & Shugo Watabe (University of Tokyo)
- [20] **Shedding light on the urban legend of the abyss—Are male ceratioid anglerfishes really parasites?**  
*Toshiro Saruwatari* (Ocean Research Institute, University of Tokyo; [tsaruwat@ori.u-tokyo.ac.jp](mailto:tsaruwat@ori.u-tokyo.ac.jp))
- [21] **Sex chromosome evolution in the Medaka fishes**  
*Yusuke Takehana\** (Niigata University; [yusuke@env.sc.niigata-u.ac.jp](mailto:yusuke@env.sc.niigata-u.ac.jp)), Kiyoshi Naruse (National Institute for Basic Biology), Satoshi Hamaguchi & Mitsuru Sakaizumi (Niigata University)
- [22] **Phylogeny of the family Peristediidae**  
*Toshio Kawai* (National Museum of Nature and Science; [kawai@kahaku.go.jp](mailto:kawai@kahaku.go.jp))
- [23] **Revision of the cottid genus *Astrocottus* Bolin (Perciformes: Cottoidei)**  
*Osamu Tsuruoka\** (Hokkaido University; [tsuru@fish.hokudai.ac.jp](mailto:tsuru@fish.hokudai.ac.jp)), Shuka Maruyama (Hokkaido Kushiro Fisheries Experimental Station) & Mamoru Yabe (Hokkaido University)
- [24] **Low genetic variation of *Cottus kazika* based on mitochondrial ND4 gene sequences**  
*Naoya Ishiguro\** & Hiroyuki Komoto (Fukui University of Technology; [ishiguro@fukui-ut.ac.jp](mailto:ishiguro@fukui-ut.ac.jp))
- [25] **Cryptic diversity in the *Careproctus rastrinus* species complex (Liparidae) from the North Pacific as inferred from molecular and morphological analyses**  
*Yoshiaki Kai\** (Kyoto University; [mebaru@kais.kyoto-u.ac.jp](mailto:mebaru@kais.kyoto-u.ac.jp)), James W. Orr (NOAA), Keiichi Sakai

(Noto Marine Center) & Tetsuji Nakabo (Kyoto University Museum)

- [26] **A peculiar fish collected from southern Okhotsk Sea off the Shiretoko Peninsula: Is it a new family?**  
*Mamoru Yabe\** (Hokkaido University; [myabe@fish.hokudai.ac.jp](mailto:myabe@fish.hokudai.ac.jp)) & *Takahiro Nobetsu* (Shiretoko Nature Foundation)
- [27] **Genetic population structure of the Blacktip Grouper, *Epinephelus fasciatus*, in Japan**  
*Kaoru Kuriwa\** (National Museum of Nature and Science; [kuriwa@kahaku.go.jp](mailto:kuriwa@kahaku.go.jp)), *Satoru N. Chiba* (Yamagata University) & *Hiroyuki Motomura* (Kagoshima University Museum)
- [28] **Review of the genus *Banjos* (Perciformes: Banjosidae)**  
*Gouta Ogihara\**, *Akihiko Shinomiya* (Kagoshima University; [fisheries-gemini@sunny.ocn.ne.jp](mailto:fisheries-gemini@sunny.ocn.ne.jp)), *Yukio Iwatsuki* (University of Miyazaki) & *Hiroyuki Motomura* (Kagoshima University Museum)
- [29] **Genera and species of the family Leiognathidae**  
*Seishi Kimura\** (Fisheries Research Laboratory, Mie University; [kimura-s@bio.mie-u.ac.jp](mailto:kimura-s@bio.mie-u.ac.jp)) & *Yukio Iwatsuki* (University of Miyazaki)
- [30] **Molecular phylogeny and evolutionary features of sparid fishes**  
*Satoru N. Chiba\** (Yamagata University; [satolu@rf6.so-net.ne.jp](mailto:satolu@rf6.so-net.ne.jp)), *Tetsuo Yoshino* (University of the Ryukyus), *Yukio Iwatsuki* (University of Miyazaki) & *Naoto Hanzawa* (Yamagata University)
- [31] **Settlement pattern and habitat selection of chaetodontid juveniles in Tosa Bay, western Japan**  
*Sosuke Oguri* (Kochi University), *Tomonori Hirata*, *Shiori Hirata* (Uwajima City), *Yasuyuki Ichiba* (Kochi University), *Hideaki Yamada* (Seikai National Fisheries Research Institute) & *Kosaku Yamaoka\** (Kochi University; [yamaoka@kochi-u.ac.jp](mailto:yamaoka@kochi-u.ac.jp))
- [32] **Developmental osteology of *Elassoma zonatum* (Elassomatidae)**  
*Yohko Takata* (National Museum of Nature and Science; [takatay@kahaku.go.jp](mailto:takatay@kahaku.go.jp))
- [33] **Cultivation of specific cyanobacteria by a territorial cichlid, *Variabilichromis moorii*, in Lake Tanganyika**  
*Hiroki Hata\**, *Satoshi Ohkubo*, *Hideaki Miyashita*, *Katsutoshi Watanabe*, *Makoto Kato* & *Michio Hori* (Kyoto University; [hata@d01.mbox.media.kyoto-u.ac.jp](mailto:hata@d01.mbox.media.kyoto-u.ac.jp))
- [34] **Systematic review of the genus *Bothrocara* Bean, 1890 (Teleostei: Zoarcidae)**  
*M. Eric Anderson* (South African Institute for Aquatic Biodiversity), *Duane E. Stevenson* (National Marine Fisheries Service) & *Gento Shinohara\** (National Museum of Nature and Science; [s-gento@kahaku.go.jp](mailto:s-gento@kahaku.go.jp))

- [35] **Review of the *Trichonotus setiger* group (Perciformes: Trichonotidae) from the Western Pacific**  
*Eri Katayama\* & Hiromitsu Endo (Kochi University; sandiver@cc.kochi-u.ac.jp)*
- [36] **Phylogenetic systematics of the family Percophidae (order Perciformes)**  
*Kenji Odani\* (Hokkaido University; daniokun@fish.hokudai.ac.jp), Hisashi Imamura (Hokkaido University Museum) & Kazuhiro Nakaya (Hokkaido University)*
- [37] **Structure of feeding territory in an herbivorous blenny, *Istiblennius enosimae* (Perciformes: Blenniidae), inhabiting rock pool at Tateyama Bay, central Japan**  
*Atsunobu Murase\* & Tomoki Sunobe (Tokyo University of Marine Science and Technology; atsunobum@yahoo.co.jp)*
- [38] **Exploring gobioid phylogeny using morphology—Not a lost cause**  
*Randall D. Mooi\* (Manitoba Museum; rmooi@manitobamuseum.ca) & Anthony C. Gill (Arizona State University)*
- [39] **Racial analyses of morphological variations in genera *Acanthogobius* and *Tridentiger***  
*Natascha Miljkovic (University of Vienna; Natascha.Miljkovic@gmx.at)*
- [40] **Origin of non-indigenous populations of 3 *Tridentiger* gobies in North America inferred from mtDNA sequences**  
*Takahiko Mukai\* & Kana Sekiyama (Gifu University; tmukai@gifu-u.ac.jp)*
- [41] **Life history traits of *Sicyopterus japonicus* in comparison with tropical and subtropical sicydiine gobies**  
*Midori Iida\*, Shun Watanabe & Katsumi Tsukamoto (Ocean Research Institute, University of Tokyo; midori@ori.u-tokyo.ac.jp)*
- [42] **Diversity of dispersal strategy of gobioid larvae on the Ryukyu Archipelago**  
*Ken Maeda\*, Nozomi Yamasaki & Katsunori Tachihara (University of the Ryukyus; k058560@eve.u-ryukyu.ac.jp)*
- [43] **Occurrence and pelagic larval duration of gobiid species in the coral lagoons of Okinawa-jima Island**  
*Taiki Ishihara\* & Katsunori Tachihara (University of the Ryukyus; pipefish@mail.goo.ne.jp)*
- [44] **Interrelationships of tetraodontiform families based on the neuroanatomy and myology— Present situation and future perspective—**  
*Masanori Nakae\* (National Museum of Nature and Science; nakae@kahaku.go.jp) & Kunio Sasaki (Kochi University)*

[45] **Rapid radiation and speciation of *Takifugu* species in marine waters of East Asia: Another use of the fugu, *Takifugu rubripes* as a model**

*Yusuke Yamanoue\** (University of Tokyo; [yamanouey@yahoo.co.jp](mailto:yamanouey@yahoo.co.jp)), *Masaki Miya* (Natural History Museum and Institute, Chiba), *Harumi Sakai* (National Fisheries University), *Keiichi Matsuura* (National Museum of Nature and Science), *Seita Miyazawa*, *Naofumi Miyamoto* (Nagoya University), *Hiroshi Takahashi* (National Fisheries University), *Hiroyuki Doi* (Shimonoseki Marine Science Museum) & *Mutsumi Nishida* (Ocean Research Institute, University of Tokyo)

[46] **On the latimeroid coelacanth with an inference about the origin of extant species**

*Yoshitaka Yabumoto\** (Kitakyushu Museum of Natural History and Human History; [yabumoto@kmnh.jp](mailto:yabumoto@kmnh.jp)) & *Teruya Uyeno* (National Museum of Nature and Science)

## Invited Speakers

Bellwood, David R. (James Cook University)  
Britz, Ralf (The Natural History Museum)  
Delventhal, Naomi (University of Manitoba)  
Gomon, Martin F. (Museum Victoria)  
Hoese, Douglass F. (Australian Museum)  
Imamura, Hisashi (Hokkaido University Museum)  
Johnson, G. David (National Museum of Natural History)  
Larson, Helen K. (Museum and Art Gallery of the Northern Territory)  
Leis, Jeffrey M. (Australian Museum)  
Mabee, Paula (University of South Dakota)  
Mank, Judith E. (Uppsala University)  
Masuda, Reiji (Kyoto University)  
Matsuura, Keiichi (National Museum of Nature and Science)

Mayden, Richard (Saint Louis University)  
Miya, Masaki (Natural History Museum and Institute, Chiba)  
Nishida, Mutsumi (Ocean Research Institute, University of Tokyo)  
Parenti, Lynne R. (National Museum of Natural History)  
Paxton, John R. (Australian Museum)  
Senou, Hiroshi (Kanagawa Prefectural Museum of Natural History)  
Smith, Wm. Leo (Field Museum of Natural History)  
Thacker, Christine (Natural History Museum of Los Angeles County)  
Tsukamoto, Katsumi (Ocean Research Institute, University of Tokyo)  
Winterbottom, Richard (Royal Ontario Museum)

## Participants

Aizawa, Masahiro (Biological Laboratory, Imperial Household)  
Amaoka, Kunio (Hokkaido University)  
Chiba, Satoru N. (Yamagata University)  
Doiuchi, Ryu (Wakayama Research Center of Agriculture, Forestry, and Fisheries)  
Endo, Hiromitsu (Kochi University)  
Fukui, Atsushi (Tokai University)  
Hagiwara, Kiyoshi (Yokosuka City Museum)  
Hata, Hiroki (Kyoto University)  
Hatooka, Kiyotaka (Osaka Museum of Natural History)  
Hayashi, Masayoshi (Yokosuka City Museum)  
Hori, Masato (University of the Ryukyus)  
Hoshino, Kouichi (Seikai National Fisheries Research Institute)  
Ikeda, Yuji (Biological Laboratory, Imperial Household)  
Ishiguro, Naoya (Fukui University of Technology)  
Ishihara, Taiki (University of the Ryukyus)  
Ishimori, Hiro (University of the Ryukyus)  
Isokawa, Keitaro (Nihon University)  
Iwata, Masamitsu (Aquamarine Fukushima)  
Kaga, Tatsuya (Hokkaido University)

Kai, Yoshiaki (Kyoto University)  
Kakioka, Ryo (Kyoto University)  
Katayama, Eri (Kochi University)  
Kawahara, Ryouka (Ocean Research Institute, University of Tokyo)  
Kawai, Toshio (National Museum of Nature and Science)  
Kim, Ik-Soo (Chonbuk National University)  
Kimura, Seishi (Mie University)  
Kitamura, Jyun-ichi (Kyoto University)  
Kobayakawa, Midori (Kyushu University)  
Kobayashi, Keisuke (M.P.J.)  
Komiya, Takefumi (Kyoto University)  
Kon, Takeshi (Ocean Research Institute, University of Tokyo)  
Konishi, Yoshinobu (Seikai National Fisheries Research Institute)  
Kuriwa, Kaoru (National Museum of Nature and Science)  
Kuroki, Mari (Ocean Research Institute, University of Tokyo)  
Lavoué, Sébastien (Ocean Research, University of

Tokyo)  
Mabuchi, Kohji (Ocean Research Institute, University of Tokyo)  
Maeda, Ken (University of the Ryukyus)  
Matsunuma, Mizuki (Kagoshima University)  
Meguro, Katsusuke (Biological Laboratory, Imperial Household)  
Meguro, Masatoshi (Kagoshima University)  
Iida, Midori (Ocean Research Institute, University of Tokyo)  
Miljkovic, Natascha (University of Vienna)  
Miller, Michael J. (Ocean Research Institute, University of Tokyo)  
Miyazaki, Yusuke (Tokyo University of Marine Science and Technology)  
Mochioka, Noritaka (Kyushu University)  
Mooi, Randall D. (Manitoba Museum)  
Motomura, Hiroyuki (Kagoshima University Museum)  
Mukai, Takahiko (Gifu University)  
Murase, Atsunobu (Tokyo University of Marine Science and Technology)  
Musikasinthorn, Prachya (Kasetsart University)  
Nakabo, Tetsuji (Kyoto University Museum)  
Nakae, Masanori (National Museum of Nature and Science)  
Nakajima, Jun (Kyushu University)  
Nakamura, Tsuyoshi (M.P.J.)  
Nakamura, Yohei (Ocean Research Institute, University of Tokyo)  
Odani, Kenji (Hokkaido University)  
Ogihara, Gouta (Kagoshima University)  
Okamura, Akihiro (IRAGO Institute)  
Okiyama, Muneo (Marine Ecology Research Institute)  
Sado, Tetsuya (Natural History Museum and Institute, Chiba)  
Saitoh, Kenji (Tohoku National Fisheries Research Institute)  
Sakai, Keiichi (Noto Marine Center)  
Sakamoto, Katsuichi (Biological Laboratory, Imperial Household)  
Sakurai, Hiroshi (Tokyo Zoological Park Society)  
Saruwatari, Toshiro (Ocean Research Institute, University of Tokyo)  
Sasaki, Tsuyoshi (Tokyo University of Marine Science and Technology)  
Sato, Takashi (Ocean Research Institute, University of Tokyo)  
Shimose, Tamaki (National Research Institute of Far Seas Fisheries)  
Shinohara, Gento (National Museum of Nature and Science)  
Sunobe, Tomoki (Tokyo University of Marine Science and Technology)  
Tachihara, Katsunori (University of the Ryukyu)  
Takagi, Kazunori  
Takami, Munehiro (Tokai University)  
Takata, Yohko (National Museum of Nature and Science)  
Takegaki, Takeshi (Nagasaki University)  
Takehana, Yusuke (Niigata University)  
Tawa, Atsushi (Kyushu University)  
Tokunaga, Koutarou (Oarai Aquarium)  
Tominaga, Koji (Kyoto University)  
Tsuruoka, Osamu (Hokkaido University)  
Uyeno, Teruya (National Museum of Nature and Science)  
Watanabe, Shun (Ocean Research Institute, University of Tokyo)  
Watanabe, Katsutoshi (Kyoto University)  
Yabe, Mamoru (Hokkaido University)  
Yabumoto, Yoshitaka (Kitakyushu Museum of Natural History and Human History)  
Yamaguchi, Shogo (M.P.J.)  
Yamamoto, Mitsumi (Hokkaido University)  
Yamanaka, Tomoyuki (Hokkaido University)  
Yamanoue, Yusuke (University of Tokyo)  
Yamaoka, Kosaku (Kochi University)  
Yamauchi, Shinya (Aquamarine Fukushima)  
Yokoo, Toshihiro (Tokyo University of Marine Science and Technology)  
Yonezawa, Toshihiko (Kagoshima Environmental Research and Service)

