23rd FISHBASE/SEALIFEBASE SYMPOSIUM

BOOK OF ABSTRACTS

Royal Belgian Institute of Natural Sciences
Brussels, Belgium

2–3 September 2025

FishBase
35TH ANNIVERSARY

SeaLifeBase
20TH ANNIVERSARY

23rd FISHBASE/SEALIFEBASE SYMPOSIUM

Published on 1 September 2025 by: The Royal Belgian Institute of Natural Sciences
Editors: Tobias Musschoot and Maarten Van Steenberge
Cover photo: Royal Belgian Institute of Natural Sciences
Sponsored by: Royal Belgian Institute of Natural Sciences

How to cite this publication:
Musschoot T. & Vansteenberge M. (eds) 2025. *Book of Abstracts of the 23rd Fishbase/SeaLifeBase Symposium, at the Royal Belgian Institute of Natural Sciences, Brussels, 2–3 September 2025*.

CONTRIBUTORS

What are they waiting for? Some thoughts about the timing of reproduction

Tom FROESE [1] & Rainer FROESE [2,*]

[1] Okinawa Institute of Science and Technology OIST, Japan.
[2] Helmholtz Centre for Ocean Research Kiel GEOMAR, Germany.
[*] presenting author

Keywords: generation time, maturation, survival, lifespan, optimal waiting time.

Many organisms, from single-celled to plants, invertebrates, fish, birds and mammals do not start reproduction at the earliest opportunity but rather time reproduction such that the peak of offspring production falls into the lower half of their lifespan, somewhere between ¼ and ½ of maximum age. One of us (RF) noted that maximum age (t_{max}) divided by the age at peak reproductive output, which is a good approximation of generation time (t_{gen}), often approximates Euler's number, with $t_{max}/t_{gen} \approx e$. But why? What does that tell us? The solution was proposed by one of us (TF), namely that this was a case of optimal waiting time before employing a certain decision-making strategy to increase the probability of success beyond the random probability of $1/n$, where n is the number of opportunities for peak reproduction.

The presentation explains the optimal waiting time theorem, checks whether its assumptions are satisfied by biological reproduction, presents preliminary evidence for empirical support, and then dives into population dynamics theory to explore what life history traits have to be aligned to result in the peak of reproductive output overlapping with optimal waiting time. It ends with a closer examination of birds and mammals, which are distinguished from all other species by a combination of homeothermy plus air-breathing plus obligatory parental care plus constant fecundity plus terminate growth and thus constant body size during reproductive age. With negligible growth during reproductive age and constant fecundity, growth and fecundity cannot explain their observed hump-shaped curve of reproductive success. Instead, it is hypothesized that experience determines their reproductive success and that acquisition of experience follows a curve similar to that of somatic growth in other species.

Diversity and multiple origins of Moroccan monogenean parasites and their cyprinid hosts: tracing a complex evolutionary history

Rahmouni I.[1], Berrada Rkhami O.[1] & Pariselle A.[2]

[1] Laboratory of Biodiversity, Ecology and Genome, UM5R, Morocco.
[2] ISEM, Université de Montpellier, CNRS, IRD, 34000 Montpellier, France.

Keywords: Morocco, *Dactylogyrus*, Cyprinidae, biogeography.

The native ichthyofauna of Morocco is dominated by the Cyprinidae family, with 20 valid species, 18 of which being endemic. These species are distributed across freshwater systems from the northern Mediterranean basins to the Drâa River in the south, and from the eastern regions to the Atlantic coastal watersheds. To explore their evolutionary history, we studied their gill monogenean parasites, known for their strict host specificity and value as biogeographic markers.

Examination of over 700 cyprinid specimens led to the identification of 14 species of *Dactylogyrus*, as well as one new species of *Markewitschiana*, reported for the first time outside Asia. Morphological and molecular analyses, using 28S, 18S, and ITS1 markers, revealed high species diversity and the presence of cryptic species of dactylogyrids.

Phylogenetic analyses of the parasites, combined with those of their hosts and supported by character mapping, revealed multiple biogeographic origins for both hosts and associated monogeneans:

- an African origin for *Pterocapoeta* and its specific parasites,
- a European origin for *Luciobarbus*,
- and an Asian origin for *Carasobarbus*, with *Dactylogyrus* lineages related to Eastern species.

These findings indicate that the evolutionary history of Moroccan cyprinids did not result from a single colonization event, but rather from successive and independent episodes of diversification and geographic expansion. This complex pattern is likely shaped by past hydrographic connections and paleogeographic changes linking Africa, Europe, and Asia.

The study of monogeneans, through their tight co-evolution with their hosts, provides critical insights into processes of speciation, historical migration, and host differentiation. It highlights the value of host–parasite systems as robust models for reconstructing the historical structure of freshwater communities, particularly in biogeographic transition zones like Morocco.

By integrating parasitological and genetic approaches, this work contributes to a deeper understanding of both parasite diversity and the evolutionary dynamics of freshwater fish in the Mediterranean region.

AquaX: An enhanced and revised AquaMaps methodology to model marine species distributions and biodiversity

Gabriel REYGONDEAU [1,*], Yulia EGOROVA [1], Kristina BOERDER [2],
Derek P. TITTENSOR [2], Kristin KASCHNER [3], Kathleen KESNER-REYES [4],
Nicolas BAILLY [4,5] & William W.L. CHEUNG [5]

[1] University of Miami. Rosenstiel School of Marine, Atmospheric, and Earth Science. Miami, FL 33149. United States.

[2] Future of Marine Ecosystems Lab. Dalhousie University. Halifax. Canada.

[3] Department of Biometry and Environmental Systems Analysis, Albert-Ludwigs University, Freiburg im Breisgau, Germany.

[4] Quantitative Aquatics, Inc., Los Baños, Laguna, Philippines.

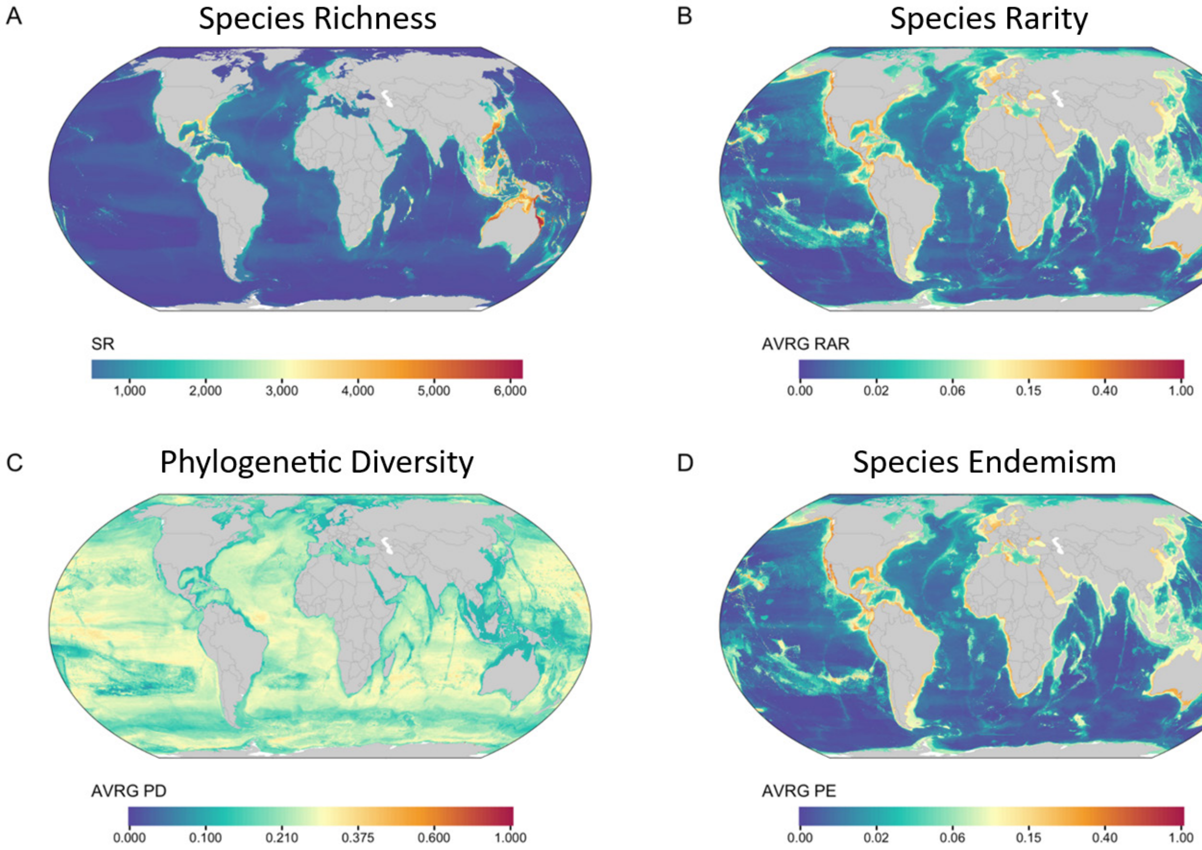
[5] Institute for the Oceans and Fisheries. University of British Columbia. Aquatic Ecosystems Research Lab. 2202 Main Mall. Vancouver. BC V6T 1Z4. Canada.

[*] Corresponding author and author to whom all correspondence and material requests should be addressed: gabriel.reygondeau@gmail.com; tel: +1 778 251 3759.

Keywords: species distribution model, biogeography, machine learning, species richness, biodiversity.

Marine biodiversity underpins ecosystem health and is critical for the provision of essential ecological services. Global efforts to mitigate biodiversity loss are underway but require comprehensive knowledge on the biogeography of species to be effective. However, key challenges limit comprehensive mapping of species distributions, including the complexity of ocean ecosystems and the difficulty of sampling the marine realm. Global initiatives such as AquaMaps pioneered large-scale marine species mapping using species distribution models (SDMs) or Ecological Niche models (ENMs) and provided the knowledge base for effective marine conservation and management. Recently, methodological and data advances have enabled a more modern and robust approach that enables higher resolution outputs more suited to conservation applications at all scales. Here, building on AquaMaps, we develop a next-generation marine species habitat suitability modelling platform called AquaX, providing a suite of advances that include an ensemble of ten machine learning algorithms, enabling spatial uncertainty assessments, validation indices, and ecological niche representation at a ten-fold improved spatial resolution of 0.05°. Furthermore, AquaX integrates (i) accepted taxonomy from the World Register of Marine Species, (ii) species-specific ecological, physiological, and biogeographical information (D3-Ocean system), (iii) updated occurrence records validated through expert input, and (iv) refined species range maps using expert knowledge and biogeographical divisions. AquaX also projects species' habitat suitability for both present and future conditions based on two time periods and three climate scenarios. This work provides species range maps for numerous species compared to previously available datasets and improves the accurate use of observational data. The innovative approaches described here improve predictive accuracy at scales

more relevant to marine biodiversity conservation, and offer an openly accessible tool to support marine biodiversity research and conservation planning under accelerating environmental change. AquaX represents an important step forward in species distribution modeling, enabling researchers and policymakers to better understand marine biodiversity patterns and develop more effective conservation strategies.



Host-symbionts crosstalk in metabolism and inflammation during cavefish evolution

Ana SANTACRUZ [1,2,*], Daniel ACHEAMPONG [2], Melainia MCCLAIN [2] &
Nicolas ROHNER [1,2]

[1] University of Münster, Germany.
[2] Stowers Institute for Medical Research, Kansas City, MO, USA.
[*] Email: ana.santacruz@uni-muenster.de

Animals evolve immersed in constant symbiotic interactions, which may have facilitated the exploitation of new environments for some species over others. For example, symbiosis can expand or constrain the host's metabolic repertoire, shaping its phenotype and influencing its ability to occupy novel ecological niches. Caves are an unreachable niche for most species, requiring highly specialized adaptations to survive in extremely nutrient-deprived conditions, which come with a trade-off: reduced interspecific competition. One such example, the Mexican cavefish *Astyanax mexicanus*, a typical troglobiont fish -eyeless and unpigmented- has repeatedly thrived in cave environments, evolving unique metabolic and immune traits; cavefish can survive starvation for extended periods, accumulating fat reserves when food is available. During its repeated cave adaptation, it has co-colonized together with its symbionts (mutualistic and parasitic), unexpectedly including intestinal trophically-transmitted parasites. This scenario has created an adaptive landscape of host-symbionts interactions across the many extant cavefish populations that likely fluctuates between resistance-tolerance mechanisms to cope with infections. This implies that the intestine simultaneously faces parasites and nutrient deficit that typically compromise intestinal barrier integrity. Surprisingly though, cavefish maintain a functional intestinal barrier under such stressors. Single-cell transcriptomic analyses indicate that the cavefish intestine exhibits an enhanced nutrient absorption capacity during feeding periods. Meanwhile, under food deprivation, protective mechanisms are activated, mediated primarily by adaptive immune responses, autophagy, and tissue regeneration pathways, in concert with a reassembly of its symbiotic interactions. Collectively, we reveal an interplay between host symbionts and intestinal tissue remodeling following cave colonization, highlighting a unique capacity to withstand environmental stressors through finely tuned immune responses. These findings establish the Mexican cavefish as a powerful evolutionary model for exploring how diet and symbiosis together drive metabolic and immune adaptation.

Breeding critically endangered European weatherfish in captivity in Flanders (Belgium): a holistic approach also conserves threatened parasitic flatworms

T.P. Gobbin[1], N. Kmentová[1,2], J. Auwerx[3], A. Martel[4], A. Nelson[5],
N. Terriere[4], J. Van Wichelen[3] & M.P.M. Vanhove[1]

[1] Research Group Zoology: Biodiversity and Toxicology, Centre for Environmental Sciences, Hasselt University, Diepenbeek, Belgium.
[2] Freshwater Biology, Operational Directorate Natural Environment, Royal Belgian Institute of Natural Sciences, Brussels, Belgium.
[3] Research Institute for Nature and Forest, Brussels, Belgium.
[4] Wildlife Health Ghent, Department of Pathobiology, Pharmacology and Zoological Medicine, Faculty of Veterinary Medicine, Ghent University, Merelbeke, Belgium.
[5] North Carolina State University Department of Applied Ecology, Raleigh, North Carolina, United States of America.

Keywords: co-extinction, *Gyrodactylus fossilis*, *Gyrodactylus misgurni*, *Actinocleidus cruciatus*, Monopisthocotyla.

Despite its large Eurasian range and global Red List status of Least Concern, in Flanders (Belgium), European weatherfish *Misgurnus fossilis* (Teleostei, Cobitidae) is a critically endangered freshwater fish. Conservation actions for this species in Flanders include ex-situ captive breeding. The parasite fauna of the European weatherfish in Belgium was never studied. Conservation science often overlooks parasites or sees them as threats to the species targeted by conservation programs. Conversely, not only are parasites conservation-relevant in their own respect, a holistic approach to captive breeding recognises positive contributions of parasites to resilience of their farmed hosts.

With this in mind, we investigated the parasite fauna of European weatherfish in the Flemish captive breeding program, focusing on monopisthocotylan flatworms. These helminths are the dominant ectoparasites of bony fishes, and mainly infest gills and external surfaces. Several species naturally parasitizing on European weatherfish were proposed to be threatened by extinction in Czech Republic and Slovakia following IUCN criteria in 1997. We hypothesized that captive breeding of European weatherfish also allows maintenance of native and potentially threatened species of these flatworms, and that certain artificial conditions may be associated with higher abundances of these parasites and possible fish mortality.

Our parasitological survey, including morphological and genetic characterisation, found three monopisthocotylan species on captive weatherfish: *Actinocleidus cruciatus* (Dactylogyridae) and *Gyrodactylus misgurni* (Gyrodactylidae) on gills, *Gyrodactylus fossilis* on skin. All three are new records for Belgium, and were suggested to be conservation-sensitive in Czech Republic and Slovakia. Scrutinising conspecific hosts from 1932–1973 in the vertebrate collection of the Royal Belgian Institute of Natural Sciences supported the status of the former two species as native to Belgium.

We further provide new molecular resources that can be used for detecting these policy-relevant parasites in captivity and in nature.

In the hatchery, juvenile weatherfish indeed suffered from massive infection by one of these parasites, *G. fossilis*. As adult weatherfish maintained at lower densities still host this parasite without visible harm, this breeding program can be used as a case study to conserve several host-parasite combinations without jeopardising the fish.

In view of the presumed rarity of these parasite species, and of the health benefits that helminths can even have for their hosts (e.g., in development of immunity), we propose conservation efforts to also consider monopisthocotylan flatworms when reintroducing weatherfish in nature, obviously in discussion with stakeholders.

One Health perspectives on marine invasions: the case of *Callinectes sapidus* and parasite transmission in Moroccan lagoons

LAMKHALKHAL A. [1,2], VANHOVE M.P.M. [2], RAHMOUNI I. [1], MACHHOUR K. [1], SELFATI M. [3], BAZAIRI H. [1,4], KMENTOVÁ N. [2,5]

[1] Laboratory of Biodiversity, Ecology and Genome, UM5R, Morocco.
[2] Research Group Zoology: Biodiversity and Toxicology, Centre for Environmental Sciences, Hasselt University, Belgium.
[3] Laboratoire Santé et Environnement, UH2C, Morocco.
[4] Natural Sciences and Environment Research Hub, University of Gibraltar, Gibraltar.
[5] Royal Belgian Institute for Natural Sciences, OD Nature, Freshwater Biology, Brussels, Belgium.

Crustaceans are key components of coastal ecosystems, playing essential roles in benthic regulation, sediment stabilization, and nutrient cycling. In Morocco, native crab species such as *Carcinus maenas* and *Afruca tangeri* contribute to ecological stability, enhance nutrient cycling and support the productivity of local fisheries. However, the introduction of the invasive Atlantic blue crab *Callinectes sapidus*, native to the western Atlantic and established along Moroccan coasts since 2017, presents significant ecological and economic concerns. Invasion biology increasingly recognizes the role of parasites in mediating invasion success and impact. Parasites can influence host population dynamics, facilitate or hinder establishment (via enemy release, spillover, or spillback), and disrupt native host-parasite networks. Understanding parasite-host relationships is thus relevant for predicting invasion outcomes, managing associated risks and safeguarding socio-economic systems under an integrative (One Health) framework.

Our efforts combine multiple approaches to investigate the invasion dynamics of *C. sapidus* and its interactions with the selected native crab species in Moroccan lagoons. A total of 110 *C. sapidus* specimens from four sites (Merja Zerga, Sidi Moussa, Oualidia, and Marchica) were analyzed using a 572 bp fragment of the mitochondrial COI gene. Haplotype network analysis revealed high genetic variation within Moroccan populations and suggest multiple introduction events from the native range along the eastern coast of North America. Comparative analyses with native and other non-native populations highlight complex invasion dynamics. These results provide key insights into introduction pathways and potential sources of parasite co-introduction.

To assess parasite diversity, 165 crab specimens (*C. sapidus*, *C. maenas*, *A. tangeri*) from Merja Zerga were examined through hemolymph and organ analysis. *Hematodinium* sp., a parasitic dinoflagellate of major concern in crustacean health, was detected in all three species. Additionally, *C. sapidus* harbored digenean trematodes and microsporidians; *C. maenas* and *A. tangeri* carried haplosporidians; and amoebae and ciliates were found in *C. maenas*. These findings suggest parasite exchange between native and invasive hosts, raising concerns about spillback events.

By integrating molecular and parasitological data, this study emphasizes the importance of parasite surveillance in invasion biology. Monitoring invasive species like *C. sapidus* and their associated symbionts is essential for evaluating ecological risks, protecting native biodiversity, and informing effective coastal management strategies within a One Health framework.

The missing link in fish records: parasites and why we should care

Miriam I. SHIGOLEY[1,2], Nicolas-Antoine MOUSSIAUX[2] & Maarten P.M. VANHOVE[1]

[1] Research Group Zoology: Biodiversity & Toxicology, Centre for Environmental Sciences, Hasselt University, Agoralaan Gebouw D, 3590 Diepenbeek, Belgium.

[2] Department of Veterinary Management of Animal Resources, Faculty of Veterinary Medicine, Liège University, 4000 Liège, Belgium.

Keywords: fish health, aquaculture, stakeholder engagement, biodiversity databases.

FishBase has made it easier to access information about fish species worldwide. However, a critical part of fish biology is still mostly missing: parasites. These organisms live in or on fish, affecting their health, growth and survival. Most databases and monitoring programs do not include parasite data, creating a gap in scientific understanding and practical decisions in fish farming. Nile tilapia, a globally farmed species, is a case in point. Despite its importance, the parasitological knowledge about this species is limited, fragmented, under-reported and rarely linked to practical decisions on farms. Our research focused on Kenya's Upper Tana River region, where we conducted fish parasite surveys and health assessments. We engaged 48 participants, including 36 fish farmers, 11 fisheries and extension officers and one veterinarian. Preliminary findings show that parasitic infections, including detection of species such as *Clinostomum cutaneum*, *C. phalacrocoracis*, *C. tilapiae*, *Euclinostomum heterostomum*, *Cichlidogyrus halli*, *C. sclerosus*, *C. thurstonae*, *C. mbirizei*, *C. tilapiae*, *Scutogyrus longicornis* and *S. gravivaginus*, are common. Many farmers did not realise these parasites were causing problems like poor growth or fish deaths. This lack of awareness is not due to a lack of concern, but due to limited training, diagnostic tools, and institutional support. The gap is not only technical but also a visibility problem. Parasite knowledge often remains within scientific circles and fails to reach those who need it most. Platforms like FishBase could help change this by including parasite data and linking it to fish health outcomes. This would make fish records more complete and useful for farmers, extension officers and policymakers. Parasites offer more than insight into fish health; they also tell us about the health of aquatic environments. Their presence, abundance and sensitivity to pollution make them effective early-warning indicators of ecological stress. However, this role is often overlooked in environmental assessment and remains untapped in many aquaculture regions. Addressing this challenge requires involving people. Farmers, extension officers, researchers and local institutions must be part of how parasite information is produced, interpreted and applied. When communities see their knowledge reflected in global systems and when these systems help answer their real-world questions, uptake and impact improve. Parasite data should not sit in scientific silos. It should inform farm-level decision making, public health awareness and broader ecosystem management. Recognising parasites in databases like FishBase is not just about completeness, it is about connecting science with society.

Darwin's nightmare revisited: a dual decline of cichlids and their parasites

Laura OBEN[1], Maarten VAN STEENBERGE[2], Maarten P.M. VANHOVE[1] &
Tiziana P. GOBBIN[1]

[1] Research Group Zoology: Biodiversity and Toxicology, Centre for Environmental Sciences, Hasselt University, Diepenbeek, Belgium.
[2] Operational Directorate Taxonomy and Phylogeny, Royal Belgian Institute of Natural Sciences, Brussels, Belgium.

Keywords: Cichlidae, ectoparasites, anthropogenic change, historical ecology.

Lake Victoria (East Africa) earned its nickname – *Darwin's Dreampond* – because of its extraordinary biodiversity and high levels of endemism, particularly among haplochromine cichlids. Since the 1980s, the lake has experienced severe environmental degradation driven by anthropogenic activities (e.g., species introductions, water eutrophication, overfishing, and climate change). This contributed to the rapid decline of haplochromines, with about half of the species becoming extinct or nearly extinct.

Such environmental degradation and decline in cichlid diversity are expected to alter host-parasite interactions and, consequently, impact parasite communities. Because parasites depend both on their host(s) and on environmental conditions, they can serve as bioindicators to detect ecosystem changes.

We used natural history collections to assess parasites infecting the gills of six haplochromine species (*Haplochromis degeni*, *H. heusinkveldi*, *H. laparogramma*, *H. piceatus*, *H. pyrrhocephalus*, *H. tanaos*). These zooplanktivorous fish species are demersal, living on muddy bottoms, and two of them (*H. heusinkveldi*, *H. piceatus*) are listed as threatened on the IUCN Red List. About 300 fish specimens were originally collected between 1978 and 2011 in Lake Victoria. This allowed us to reconstruct temporal changes in ectoparasite communities across three ecological periods: pristine (pre-disturbance), perturbed (during major environmental degradation), and recovery (post-2000 partial rebound).

The studied fish harboured three species of parasitic flatworms (*Cichlidogyrus bifurcatus*, *C. furu*, *C. nyanza*, the two latter endemic to the basin), two copepods (*Ergasilus lamellifer*, *Lamproglena monodi*) and the larval stage of bivalves. We observed a decrease in parasite abundance and in the number of parasite species per host individual during the perturbed period, coinciding with peak environmental stress. Although some recovery was observed after 2000, parasite abundance did not return to pre-disturbance levels.

Our results indicate that parasite communities are negatively impacted by (human-induced) pressures and environmental changes. The timing of parasite decline and partial recovery matches that of ecosystem changes in Lake Victoria, supporting the idea of parasites as indicators of ecosystem status. Our study highlights the value of historical collections for parasitology and emphasizes the need to include parasites in fish monitoring and in conservation strategies. This will enable the preservation of both parasite diversity and the ecosystem services they support (e.g., energy transfer through trophic interactions, regulation of populations, promotion of host immune development).

Morphological and phylogenetic analyses of species of *Bagrobdella* (Monogenea: Dactylogyridae) parasitising African auchenoglanidid catfishes combined with barcoding of *Auchenoglanis occidentalis* provide insight into host taxonomy

Archimède Mushagalusa MULEGA [1,2], Maarten VANHOVE [1] &
Maarten VAN STEENBERGE [1,3]

[1] Research Group Zoology: Biodiversity & Toxicology, Centre for Environmental Sciences, Hasselt University, 3590 Diepenbeek, Belgium.
[2] Département de Biologie, Centre de Recherche en Hydrobiologie, B.P. 73, Uvira 11215, Democratic Republic of the Congo.
[3] OD Taxonomy and Phylogeny, Royal Belgian Institute of Natural Sciences, 1000 Brussels, Belgium.

In this study, we re-examine the taxonomic status of *Auchenoglanis occidentalis*. To do so, we conduct a barcoding analysis of *A. occidentalis* using all 34 sequences currently available on GenBank. We observed that among the analysed sequences, three were misidentified: two belong to *A. biscutatus*, the species most closely related to *A. occidentalis*. The other one is *Chrysichthys auratus*. The remaining 31 sequences clustered into three groups: one confined to the ichthyoprovince of Upper Guinea, another to the Congo province, and the last to the Nilo-Sudan province. Intra-group genetic distances ranged from 0% to 2%, while inter-group distances varied between 6% and 9%. Based on these results, we concluded that each group likely represents a potential species. Distribution data for *A. occidentalis* and *A. biscutatus* were obtained from FishBase. As an additional tool to investigate this taxonomic question, we examined the gills of *A. occidentalis* to identify the monogenean parasites it hosts. These parasitic flatworms are often species-specific to their host. As such, they can be used as an evolutionary magnifying glass. Specimens of *A. occidentalis* were sampled in the Democratic Republic of the Congo and in Uganda. We identified four species of *Bagrobdella* and provided the first molecular data for this genus. The species identified are: *B. vanhovei* and *B. vansteenbergei* were restricted to the Congo province, while *B. anthopenis* and *B. fraudulenta* were confined to the Nilo-Sudan Province. According to literature, *B. auchenoglanii* is restricted to the western edge of the African continent. The three groups formed by the distribution of *Bagrobdella* spp., parasites specific to members of Auchenoglanididae, support the hypothesis of at least three distinct species within what is currently referred to as *A. occidentalis*. A taxonomic revision of *A. occidentalis* and of Auchenoglanididae is therefore needed.

Diversity of fish ectoparasites in a South Carolina estuary, and the role of such data in online databases

Martina TOPIĆ [1,*], Nikol KMENTOVÁ [1,2], Maria TKACHENKO [3] &
Maarten P.M. VANHOVE [1]

[1] Research group Zoology: Biodiversity and Toxicology, Centre for Environmental Sciences, Hasselt University, Agoralaan Gebouw D, 3590 Diepenbeek, Belgium.
[2] OD Natural Environment, Freshwater Biology, Royal Belgian Institute of Natural Sciences, Rue Vautier 29, 1000 Brussels, Belgium.
[3] Institute of Vertebrate Biology of the Czech Academy of Sciences, Květná 8, 603 00 Brno, Czech Republic.
[*] Email: martina.topic@uhasselt.be

Keywords: ParasiteBlitz, Monopisthocotyla, copepods, *Mugil cephalus*.

'BioBlitz' is a term used for projects in which a certain area is intensely researched in a narrow time frame, with the aim of recording all living species present in said area. In 2023, a group of parasitologists conducted a similar project focused on parasites, named 'ParasiteBlitz'. The aim of the project was to describe the diversity of parasites in the Stono Preserve, a protected area in the Stono River estuary, in South Carolina, USA. As a part of this study, estuarine fishes were sampled and screened for the presence of direct-life-cycle ectoparasites. Among 125 fishes of 17 species that were caught and inspected for parasites, nine species were infected: *Anchoa mitchilli*, *Fundulus confluentus*, *Fundulus heteroclitus*, *Fundulus majalis*, *Gambusia holbrooki*, *Gobiosoma bosc*, *Menidia* sp., *Mugil cephalus*, and *Mugil curema*. From these fishes, 130 parasites were collected; based on their morphology and genetic data (sequences of 28S, 18S and ITS rDNA), we identified the parasites as belonging to 15 species, of the following taxa: monopisthocotylan flatworms (*Fundulotrema*, *Gyrodactylus*, *Ligophorus*, *Salsuginus*), polyopisthocotylan flatworms (*Metamicrocotyla*), and copepods (*Bomolochus*, *Caligus*, *Ergasilus*, Lerneapodidae). Results of this project show that among estuarine fishes sampled from the Stono Preserve, *M. cephalus* harbors the highest ectoparasite species richness, with seven species of parasitic flatworms and copepods found. For both flatworms and copepods, we noticed patterns of host-specificity, we recorded new species, and expanded the area of distribution for some previously described species of parasitic flatworms. For *G. bosc*, we recorded an infection with a monopisthocotylan flatworm for the first time. The results of this study help fill the knowledge gap of the diversity of fish ectoparasites in the estuaries of temperate climate zones, and particularly on the Atlantic coast of North America. The research on such diversity on this side of the Atlantic has been 'patchy' so far, with publications focusing on ectoparasitic fauna in specific locations or on particular hosts. For the Stono River estuary, the acquired data about ectoparasites is completely new. Ecological data about fish ectoparasites in estuaries is valuable for different types of research on both parasites and their hosts – from evolutionary studies to ones focused on anthropogenic pressures in estuaries. Incorporating this data in online databases such as FishBase and SeaLifeBase would make this type of data more widely accessible and potentially give a push to new research on aquatic organisms in estuaries.

Parasite biodiversity and trophic dynamics of mangrove fishes in a Senegalese marine protected area

Armando J. CRUZ-LAUFER [1,2], Lucas VAN PASSEL [1], Oumar SADIO [3],
Farid DAHDOUH-GUEBAS [2,4,5], Chelsea L. WOOD [6] & Maarten P.M. VANHOVE [1]

[1] Hasselt University, Centre for Environmental Sciences, Research Group Zoology: Biodiversity & Toxicology, Hasselt, Belgium.
[2] Systems Ecology and Resource Management Research Unit (SERM), Université libre de Bruxelles (ULB), Brussels, Belgium.
[3] IRD, Univ Brest, CNRS, Ifremer, LEMAR, BP 1386 Dakar, Senegal.
[4] bDIV: Ecology, Evolution & Genetics, Biology Department, Vrije Universiteit Brussel (VUB), Brussels, Belgium.
[5] Mangrove Specialist Group (MSG), Species Survival Commission (SSC), International Union for the Conservation of Nature (IUCN), Zoological Society of London, London, UK.
[6] School of Aquatic and Fishery Sciences, University of Washington, Seattle, Washington, USA.

Keywords: parasite communities, gut contents, mangrove fishes, West Africa, overfishing.

Mangrove forests provide important ecosystem services to humans, including protection from flooding and erosion, provision of timber and non-timber forest products, and carbon storage. Fisheries production is perhaps one of the most frequently cited resources. However, fisheries also put substantial pressure on aquatic communities, including fishes and their metazoan parasites. In the present study, we aim to provide the first combined quantitative survey of gut content and parasitic infections of mangrove fishes. To test the effect of fisheries on parasite communities, we sampled the gills ($n = 105$) and guts ($n = 72$) of 22 different fish species in the Saloum Delta in Senegal, both inside and outside of a marine protected area (MPA). The Saloum Delta was selected because fish assemblages and trophic dynamics have been extensively studied in the past both inside and outside the MPA. We mainly targeted seven omnivorous and arthropodivorous host species. More than 4000 parasite specimens were collected, including monopisthocotylans, acanthocephalans, nematodes, copepods, and cestodes – several of which may represent new species. The samples were dominated by monopisthocotylans, acanthocephalans, and trematodes. Due to the currently limited sample sizes per host species, no significant differences in prevalence, infection intensity, or species diversity could be detected. However, this survey provides a first baseline for the parasite biodiversity of West African mangrove fishes and will serve as a reference library for infection, morphological, and molecular data.

Fish and food-borne transmission of disease-causing *Vibrio* spp.

Sofie LEEN [1,2], Maarten VANHOVE [2], Nikol KMENTOVÁ [2,3] & Michiel JORISSEN [1]

[1] Belgian Defence Laboratories, Belgium.
[2] University Hasselt, Belgium.
[3] Royal Belgian Institute of Natural Sciences, Brussels, Belgium.

Keywords: Tanganyika, *Vibrio cholerae*, bioaccumulation.

Lake Tanganyika, the longest freshwater lake in the world, is recognized as the only endemic region for *Vibrio cholerae* outside of its natural range and a true hotspot for the cholera disease. From Lake Tanganyika, outbreaks spread frequently throughout the Congo Basin and to neighboring countries. *Vibrio* spp. are aquatic bacteria naturally found in freshwater, brackish, and marine environments. While several species of *Vibrio* can cause vibriosis, toxigenic *V. cholerae* is the most pathogenic and the causative agent of cholera, a severe diarrheal disease with high mortality if left untreated. *Vibrio cholerae* occurs in close relationship with other aquatic organisms, notably zooplankton through its ability to degrade chitin — a major component of zooplankton exoskeletons. Ingestion of *V. cholerae* may aid fish with zooplankton digestion, as symbiote. More specifically, this bacterium has been identified from copepods and chironomid larvae, which are important food sources for many fish species, including Lake Tanganyika sardines. Furthermore, both toxigenic and non-toxigenic strains of *V. cholerae* have been detected in several fish species across the globe. One study found non-toxigenic *V. cholerae* in six sardines from Lake Tanganyika. There are also a few documented instances of people becoming diseased after handling or consuming fish contaminated with *V. cholerae,* as was the case of a domestic infection of a man in Germany from fish imported from Nigeria.

However, the dynamics of *Vibrio* transmission and possible bioaccumulation through trophic levels remain poorly understood. This study aims to investigate the presence and distribution of species of *Vibrio*—with the focus on *V. cholerae*—in water, phytoplankton, zooplankton and various tissues of the lake's most commercially significant fish species: *Stolothrissa tanganicae*, *Limnothrissa miodon*, and *Lates stappersii*. Understanding these host-pathogen interactions may offer critical insights into the ecology of *Vibrio* and the dynamics of cholera outbreaks. Lastly, the Lake Tanganyika sardines and *Lates* spp. currently lack entries in their 'Diseases & Parasites' tab. Our findings will contribute to the completement of the Fishbase database.

The fish and the whale: exceptional preservation cases from the Miocene of Peru inform on past trophic relationships between cetaceans, clupeoid fish and lamniform sharks

Olivier LAMBERT[1], Giovanni BIANUCCI[2], Alberto COLLARETA[2] & Mario URBINA[3]

[1] Institut royal des Sciences naturelles de Belgique, Brussels, Belgium.
[2] Università di Pisa, Pisa, Italy.
[3] Museo de Historia Natural de la Universidad Nacional Mayor de San Marcos, Lima, Peru.

Keywords: baleen whale, beaked whale, East Pisco Basin, *Carcharocles megalodon*, *Sardinops*.

To investigate ancient food webs, palaeontologists generally rely on indirect evidence, including cranial anatomy, comparisons with modern relatives, and palaeoecological data. Though stable isotope analyses on fossil remains can provide clues on positions in trophic chains and on feeding areas for marine vertebrates, other types of information, like the rarely fossilized digestive tract contents and bite marks, yield invaluable insights on predator-prey relationships.

Located on the southern coast of Peru, the East Pisco Basin and the nearby Sacaco area constitute a key region for the study of Miocene marine ecosystems in the southeastern Pacific. Famous for the quantity and quality of preservation of the remains of marine vertebrates recovered in local layers, this Fossil-Lagerstätte has yielded a few exceptional fossils that allowed for testing hypotheses on the trophic relationships between extinct taxa.

While most extant beaked whales (Ziphiidae) are edentulous and catch their prey via suction at meso- to benthopelagic depths, the Late Miocene species *Messapicetus gregarius* was longirostrine and retained a complete set of teeth. Such a cranial morphology and the many specimens that accumulated in layers of the East Pisco Basin deposited a shallow, coastal setting suggest that *M. gregarius* did not share the ecology and feeding strategy of modern beaked whales. The discovery of an individual of this species associated to tens of skeletons of a close relative of the Pacific sardine *Sardinops sagax* has been interpreted as testifying for a predator-prey relationship between the whale and this epipelagic clupeoid fish.

Cetotheriidae is a family of small to medium-size baleen whales whose fossil remains are frequently found in the East Pisco Basin. The local cetotheriid species are characterized by a narrow, elongated rostrum with the anterior portion devoid of baleen plates. Their feeding technique is debated. Two Late Miocene cetotheriid articulated skeletons revealed an aggregate of fish bones in the stomach region. Most of these bones were also identified as sardine elements.

Finally, the study of serrated bite marks on the bones of various marine mammals from the late Miocene of the Sacaco area indicated that the giant predatory shark *Carcharocles megalodon* at least occasionally fed, among others, upon the diminutive cetotheriid *Piscobalaena nana*.

Though each of these records may sound anecdotal, their combination with other proxies for feeding strategies and prey preferences further improves our knowledge of past food webs in the southeastern Pacific, and allows for comparisons with the modern situation.

A morphospace for all fishes: ecomorphological traits date the assembly of modern fish form diversity to the Paleozoic

Adam ASMAT [1], Jisoo KIM [2], Nanako OKABE [1], Ivan SANSOM [3] & Lauren SALLAN [1,*]

[1] Macroevolution Unit, Okinawa Insitute of Science and Technology (OIST), Onna-son, Okinawa, 904-0495, Japan.
[2] Sewanee: The University of the South, Sewanee, Tennessee, 37383, USA.
[3] University of Birmingham, Birmingham, B15 2TT, UK.
[*] Email: lauren.sallan@oist.jp

Keywords: biodiversity, vertebrates, Actinopterygii, Chondrichthyes, ecology.

The high level of ecomorphological diversity observed among modern fishes has been attributed to events of the last 80–200 million years, such as the development of Mesozoic reef systems and teleost innovations. This assumes that fish form and ecology was more constrained prior to this interval, particularly among now-extinct groups. However, it has been difficult to quantify and compare ecomorphological diversity across most extinct and extant fishes using common approaches that are based on strict homology (e.g. geometric morphometrics) or one-dimensional metrics (body shape, size). Here, we created a new set of discrete traits related to ecological and biomechanical function, and used these to construct the first morphospace that can accommodate fishes from all clades, living and extinct. We coded our traits for marine "fishes" from both the initial phases of vertebrate diversification in the Paleozoic and modern Arctic, temperate, and tropical Large Marine Ecosystems. We find that the breadth of fish ecomorphological diversity has remained largely unchanged for the last 340 million years, following phased expansion over the mid-Paleozoic. Occupancy of specific areas of morphospace is related to habitat preference, ecology, and swimming ability, and we observed clustering in these areas by different groups in different intervals and settings. Initially, jawless stem-gnathostomes (armored agnathans) occupied most of the realized space, excluding early jawed fishes from some trait combinations. After the extinction of the former, jawed fishes expanded to fill the range of ecomorphologies observed among living teleosts in modern ecosystems. These results reinforce that fish ecomorphology is constrained by common demands of aquatic ecosystems and vertebrate ancestry, and suggest the same combinations of traits repeatedly evolved among new groups as they replaced older forms.

Colour patterns and pigments in 350 myr old marine invertebrates from Belgium

Stijn GOOLAERTS[1,*], Christian BURLET[1], Pierre GUERIAU[2,3], Aurore MATHYS[1,4,5], Sebastian SCHOEDER[6], Mathieu THOURY[2] & Bernard MOTTEQUIN[1]

[1] OD Earth & History of Life, Royal Belgian Institute of Natural Sciences, Vautierstraat 29, 1000 Brussels, Belgium.
[2] Institute of Earth Sciences, University of Lausanne, CH-1015 Lausanne, Switzerland.
[3] IPANEMA, site du Synchrotron SOLEIL, BP 48 Saint-Aubin, 91192 Gif-sur-Yvette, France.
[4] Royal Museum for Central Africa, Leuvensesteenweg 13, 3080 Tervuren, Belgium.
[5] Faculty of Architecture, Art, Archaeology and Heritage unit, University of Liège, Boulevard de la Constitution, 4020 Liège, Belgium.
[6] PUMA Beamline, Synchrotron SOLEIL, L'Orme des Merisiers, 91190 Saint-Aubin, France.
[*] Presenting author, email: sgoolaerts@naturalsciences.be

Keywords: evolution, shell, Mollusca, Brachiopoda.

Almost nothing is known about the evolution of shell colour in marine invertebrates. This is largely due to the ultra-rarity of fossils in which colour patterns and pigments are preserved and immediately visible, and therefore easy to identify, especially when these are hundreds of millions of years old. This hampers our understanding of the role and function of colour in extinct animals, their ecology, mode of life, interactions, development, and evolution. A good example of this ultra-rarity is the Palaeozoic of Belgium, world-renowned for its exquisitely preserved marine fossils from the Devonian and Carboniferous, enabling to document major transitions in ecosystem dynamics and the evolution of life on Earth (e.g., nekton revolution, major climate changes, anoxic events, biodiversity crises) but from which only a few cephalopod, bivalve and gastropod mollusc as well as brachiopod shells were historically documented preserving colour traces (mostly by L.-G. de Koninck and P. de Ryckholt, mid to late 19th century). Recent discoveries, however, show that many more specimens, particularly from ~350 myr old shallow marine reef environments, retain such traces. This opens new possibilities to examine colour occurrence across different evolutionary lineages of marine invertebrates during a key period of geologic history.

In Brain project B2/P233/P2 nicknamed COLOURINPALAEO, funded by Belspo (Fig. 1), we gathered all specimens from the main Belgian collections. Using multispectral photogrammetry and spectro-imaging, we try enhancing the visibility of preserved colour patterns and pigments. Additionally, Raman micro-probe spectroscopy, synchrotron radiation trace elemental mapping and absorption spectroscopy, are used to determine pigment chemistry and preservation mechanisms. Cephalopods, in particular, show a remarkable diversity in both pattern and pigment composition.

Figure 1. Project logo, featuring the historical depiction of the bivalve *Entolium coloratum* de Koninck, 1885, a life reconstruction of the cephalopod *Cyrtoceras acus* de Koninck, 1844, and the chemical structure of the pigment melanin.

On the impact of Ypresian warming on marine fish populations in the Paris Basin, France

Johan VELLEKOOP [1,2], Jonas CALLAERTS [3], Inge JELU [1] & Hugo GANTE [3,4]

[1] Department of Earth and Environmental Sciences, KU Leuven, Leuven, 3000, Belgium.
[2] OD Earth and History of Life, Institute of Natural Sciences, Brussels, 1000, Belgium.
[3] Department of Biology, KU Leuven, Leuven, 3000, Belgium.
[4] Section Vertebrates, Royal Museum for Central Africa, Tervuren, 3080, Belgium.

Keywords: otoliths, fish populations, Ypresian, climate change.

Anthropogenically-forced global climate change is expected to have detrimental effects on the functioning of marine fish populations. Global warming events in geological history can provide insights into these responses. A series of rapid global warming events, known as hyperthermals, that occurred during the Ypresian (early Eocene, ~56–47.8 million years ago), a time period in Earth's history with high baseline temperatures and elevated CO_2 levels, may provide such geological analogues. Recently, a rapid warming event of ~4°C was identified in the shallow-marine Ypresian Sables de Pierrefonds at Aizy-Jouy, France, based on Mg/Ca paleothermometry on benthic foraminifera. Here, we study the effects of this warming event on the local subtropical fish population, using stratigraphically collected otolith assemblages from Aizy-Jouy. The otolith record of Aizy-Jouy is dominated by juveniles, suggesting that this locality might have served as a nursery ground. Our findings indicate that Ypresian warming led to a significant turnover in local piscine communities, with stenothermal species being replaced by warm-adapted species. These patterns highlight the heterogeneous nature in which different species respond to factors such as warming, food availability, and competition. Moreover, our results reveal a sharp decline in higher trophic levels, and the rise of opportunistic generalists at the expense of specialist species, indicating a trophic simplification of the community.

The otolith collection of RBINS

Kristiaan HOEDEMAKERS

OD Taxonomy and Phylogeny, Royal Belgian Institute of Natural Sciences, Brussels, Belgium.
Email: khoedemakers@naturalsciences.be

Keywords: otoliths, collection, sagittae.

This collection was amassed by one of our former colleagues, palaeontologist dr Dirk Nolf, over several decades from 1968 up to his retirement in 2011. After 2011, mainly material from Taiwan continued to be added until about 2023. The collection was officially handed over to the division of Vertebrates at RBINS in August 2024. It contains an estimated 30000 otoliths belonging to ca 6000 species, the vast majority being saccular otoliths derived from marine fish; only very limited material on freshwater fish is available. Many specimens have been published as line drawings in the numerous papers published by Dirk Nolf and colleagues (see Nolf 2013 and 2019). An updated inventory of the collection is not yet available.

Part of the material was collected via dissection of formaldehyde-preserved fish in the wet collections of several institutes (among them RBINS, Smithsonian, LACM, CAS, Museum of Comparative Zoology, etc.). The saccular otoliths, often only the left, were removed and stored dry in the collection. Unfortunately, the formaldehyde proved to have a very negative effect on the quality of the otoliths. Many more specimens, however, were dissected from fresh fish collected at fish markets, during marine research cruises, from aquariums or even restaurants.

The collection was built up as comparative material for the identification of otoliths in the geological record. Hence, some families are better represented than others, the focus being on those that are well represented in the fossil record of Europe and North America, e.g., Gadidae, Myctophidae, Sparidae, Gobiidae, Pleuronectiformes, etc. Moreover, in some cases, growth series were established to document the ontogenetic variability within and across species. Almost all ichthyological families are represented (see Nolf 2013).

References

Nolf D. 2013. *The Diversity of Fish Otoliths, Past and Present*. Royal Belgian Institute of Natural Sciences, 222 pp. + 359 plates.

Nolf D. 2019. Otolithes des poissons de la mer du Nord et de la Manche. *Faune de Belgique*, 276 pp. (incl. 107 plates).

A new ‘acanthothoracid’ placoderm from the Arctic Canada (Early Devonian) and its bearing on the evolution of jaws and teeth

Sébastien OLIVE [1,2,3], Ilias KOTOULAS [1,4], Daniel GOUJET [5], Philip C.J. DONOGHUE [6], Federica MARONE [7] & Martin RÜCKLIN [1,8,*]

[1] Naturalis Biodiversity Center, Darwinweg 2, Postbus 9517, 2300 RA Leiden, The Netherlands. Email: martin.rucklin@naturalis.nl
[2] Royal Belgian Institute of Natural Sciences, Directorate Earth and Life History, Rue Vautier 29, 1000 Brussels, Belgium. Email: sebastien.olive@naturalsciences.be
[3] Liège University, Freshwater and Oceanic Science Unit of Research, Laboratory of Ecology and Conservation of Amphibians, Quai Van Beneden 22, 4020 Liège, Belgium.
[4] University of Antwerp, Department of Biology, Universiteitsplein 1, 2610 Wilrijk, Belgium. Email: ilias.kotoulas@uantwerpen.be
[5] Unité mixte de recherche, Centre de recherche en paléontologie, Paris 7207, Muséum national d’Histoire naturelle/Centre National de la Recherche Scientifique/Sorbonne Université, CP 38, 57 rue Cuvier, 75231 Paris Cedex 05, France. Email: daniel.goujet@mnhn.fr
[6] Bristol Palaeobiology Group, School of Earth Sciences, University of Bristol, Life Sciences Building, Tyndall Avenue, Bristol BS 8 1TQ, United Kingdom. Email: phil.donoghue@bristol.ac.uk
[7] Swiss Light Source, Paul Scherrer Institut, Villigen, Switzerland. Email: federica.marone@psi.ch
[8] Institute of Biology, University of Leiden, Sylviusweg 72, 2333 Leiden, The Netherlands.

Keywords: ‘acanthothoracid’, placoderm, Devonian, new species, teeth.

The origin of jaws and teeth represents one of the most formative episodes in our own evolutionary history. However, this event is poorly understood for lack of detailed knowledge of key lineages, including the ‘acanthothoracid’ placoderms, which were among the earliest jawed vertebrates. A new species of ‘acanthothoracid’ from the Early Devonian of Arctic Canada will be described in a forthcoming paper. The new species displays anterior supragnathal plates with teeth that we have characterised using synchrotron tomography. Our study shows that teeth are arranged in a concentric manner and that the pattern of tooth addition is centrifugal, including an anterior addition. Overgrowing odontodes, present on the anterior part of the gnathal plates, are covering teeth that can display an hypermineralised layer (likely reflecting the earliest stage of teeth during the ontogeny) or be partially broken. These overgrowing odontodes develop in successive steps and without obvious organization. The presence of a pair of anterior supragnathal plates on the ethmoid part of the endocranium, as well as the growth process of these plates in the new species, are similar to the conditions seen notably in arthrodiran placoderm arguing for those as the gnathostome ancestral condition.

Fish bone remains as markers of dynamic distribution of fishes over time

Wim WOUTERS

Royal Belgian Institute of Natural History, Brussels, Belgium.

Keywords: fish bone remains, archaeology, palaeontology, dynamic distribution of fish.

The amount of information concerning modern fisheries is overwhelming, with extensive data available for the world's economically most important species. However, as we look back in time, the quantity and quality of information gradually decline to almost zero. Archaeological and palaeontological research provide valuable, supplementary tools for understanding how fish populations respond to changing climatic and environmental conditions.

The Wels catfish (*Silurus glanis*) is a well-known European species that is increasingly adapting to rivers in Western Europe as an exotic presence. Yet, archaeological records show that the species was native to Belgium, the Netherlands, and northern France since the Mesolithic period. Recent palaeontological research indicates that it was present in the Netherlands during the Tiglian, around two million years ago. Bone finds of small individuals demonstrate that the species reproduced in localities of this period. Some other species now known only from eastern Europe are also attested in late Pleistocene–early Holocene contexts within this material. This shows that discussions about native versus exotic status are extremely tricky over long timescales; judging status from short periods can be misleading. The same bones also yield information about historical body sizes, offering insight into past population structure. In short, modern data on fishes are highly valuable, but they often present a relatively static view of species. Fishes are highly adaptable and respond to environmental changes by moving or shifting their distributions. To understand these processes more fully, information from fish remains (including otoliths) from archaeological and palaeontological contexts broadens the picture and reveals dynamic patterns of fish behaviour over time.

Life-history variation in invasive fishes: a Mediterranean FishBase approach

Nazli DEMIREL

Institute of Marine Sciences and Management, Istanbul University, Istanbul, Türkiye.
Email: ndemirel@istanbul.edu.tr

Keywords: marine bioinvasions, life-history traits, Mediterranean Sea.

Marine biological invasions represent one of the most pervasive drivers of ecological change, yet the mechanisms enabling non-indigenous species (NIS) to thrive in novel environments remain insufficiently understood. While trait plasticity has long been recognized in marine invaders, accumulating evidence suggests that post-introduction adaptation, whether through selection or plastic response, can drive substantial shifts in ecological performance. FishBase provides a rich, underutilized resource for testing hypotheses about such adaptive changes in invasive fish species by offering standardized life-history data including growth, maturity, and population parameters.

This study proposes a comparative analysis of invasive marine fish species using FishBase records, with a focus on growth coefficients (K), asymptotic lengths ($L\infty$), reproductive traits (e.g., size at maturity, batch fecundity), and population dynamics across both native and introduced ranges. The analysis is set within a Mediterranean context, where some of the most ecologically and economically damaging invaders, *Siganus luridus*, *Lagocephalus sceleratus*, and *Pterois miles,* have become well-established. These taxa are not only among the most impactful in terms of herbivory, predation, and fisheries disruption, but also possess relatively complete life-history data from both their native Indo-Pacific ranges and their introduced Mediterranean populations. Preliminary screening reveals substantial inter-regional variability in life-history traits for these species, potentially reflecting adaptive responses to novel temperature regimes, altered predation landscapes, and resource availability.

Untangling the loach labyrinth: *Misgurnus* mysteries in Flanders, Belgium

Rhea MAESELE[1], Hugo VERREYCKEN[1] & Jeroen VAN WICHELEN[1]

[1] Research Institute for Nature and Forrest (INBO).

The northern oriental weatherfish (*Misgurnus bipartitus*), a non-native loach of North Asian origin, is currently expanding its range in Flanders and the Netherlands. In this presentation, I will trace its spread, from the first confirmed records in the Netherlands to its recent establishment in Flanders. This species poses a growing threat to the already endangered native weatherfish (*Misgurnus fossilis*), primarily through potential hybridisation and competition.

Its anticipated inclusion on the EU List of Invasive Alien Species of Union Concern underscores the urgency of monitoring and management. However, accurate identification within the *Misgurnus* genus remains challenging due to morphological similarities, historical misclassifications, and a complex taxonomy – issues that continue to complicate field surveys and reporting.

I will also demonstrate how the Research Institute for Nature and Forest (INBO) uses FishBase to access and verify critical species information, and how national data contributions could further enhance the quality and completeness of the database.

Biological diversity on the Beninese continental shelf during the demersal fish stock assessment survey

Zacharie SOHOU[1], O. Victor OKPEITCHA[1] & Yacouba SANKARE[2]

[1] Institut de Recherches Halieutiques et Océanologiques du Bénin (IRHOB) et UAC.
[2] Centre de Recherches Océanologiques, Abidjan, Côte d'Ivoire.

Keywords: continental shelf, biodiversity, demersal, index, stratum.

The overall objective of this survey is to assess the biodiversity composition in the tested trawling areas during the survey period. This study was conducted in the framework of the demersal fish stock assessment survey initiated by the West African Economic and Monetary Union, in the continental shelves of state members and neighboring countries (Cote d'Ivoire, Ghana, Togo and Benin) for the south part of Africa, in order to determine fish populations and abundance. This study cannot take into account all species that can occur in the fishing areas because of the shortness of the survey period. To capture the highest possible number of the species present in the area, the study would ideally have to be conducted during four hydrologic periods (2 hot and 2 cold), however, the work could only be done during the most important cold period (April to July). In the waters of Benin, the survey listed 100 taxa including 68 demersal and 21 pelagic fish species, 3 crabs, 4 cephalopods, 1 shrimp, 1 lobster, 1 sea cucumber and 1 Guinean mantis shrimp. Species richness, according to the reports of the trawling stations, varied between 28 and 7 species. Fish abundance was largest at a depth of 25–50 m. According to the inventory, the species count at station 10 (25-50 m) is 28, or 7% of the total recorded, followed by station 19 (50-100 m) with 26 taxa and station 4 (10-25 m) with 25 species, or 6%. The lowest taxon counts are recorded at stations 8 (10-25 m) and 13 (25-50 m), with 12 species, or 3%, respectively.The Simpson's index is close to 0, varying between 0 and 0.049, demonstrating a great diversity in especially the first stratum of 10-25 m. This study allows to evaluate species diversity in different fishing areas and the consequences of the significant increase of fishing pressure on the community, beyond the usual focus on a few populations of commercially important species.

Artificial intelligence in small-scale fisheries

Alex TILLEY & Hamza ALTARTURI

WorldFish, Penang, Malaysia.

Small-scale fisheries (SSF) support the livelihoods and food security of billions worldwide, yet they remain underrepresented in technological innovation efforts, including Artificial Intelligence (AI). Yet these fisheries face severe pressures stemming from compounding climate impacts, governance challenges, and persistent poverty conditions further exacerbated by inadequate data and limited visibility of their informal nature. While rapid advances in AI, including open-access Generative AI and Large Language Models, hold promise for improving management through complex modelling and innovative applications, the adoption of AI in SSF has lagged behind industrial fisheries and terrestrial agriculture. Using a comprehensive bibliometric and content analysis of 227 publications from the past decade, we evaluate the progress and scope of AI solutions in SSF and assess the constraints to broader uptake. Our findings reveal a lack of targeted research, limited resources, and scarce data, particularly in socio-economic aspects and studies utilising AI. This underscores the need for sustainable, context-sensitive AI tools. Building on these insights, we propose a taxonomy that aligns AI applications with Environmental, Social, Economic, and Governance (ESEG) sustainability dimensions, offering a roadmap for future exploration. This study highlights emergent research trends and provides a best practice framework and practical guidance to policymakers and researchers striving to leverage new digital and data advances to enhance fisheries and environmental sustainability.

Exploring fish in the World Register of Marine Species (WoRMS): how FishBase completes WoRMS and its many sub-registers, providing excellent service to the global marine biodiversity community

Leen VANDEPITTE*, Stefanie DEKEYZER, Mona GOHARIMANESH, Lynn DELGAT,
Ben BOYDENS & Bart VANHOORNE

Flanders Marine Institute (VLIZ), InnovOcean Site, Wandelaarkaai 7, 8400 Oostende, Belgium.
* Email: leen.vandepitte@vliz.be; info@marinespecies.org

Keywords: marine taxonomy, species register, WoRMS, FishBase, SeaLifeBase.

Taxonomy is fundamental to our understanding of marine biodiversity—it underpins research efforts and enables us to track the pace of species discovery and shifts in biodiversity across the world's oceans. At the core of this work is the World Register of Marine Species (WoRMS), a dynamic and authoritative resource that offers a comprehensive list of marine species names, along with synonymy and taxonomic details. Recognized internationally as the standard reference for marine taxonomy, WoRMS offers consistent and reliable knowledge of marine taxon names.

The World Register of Marine Species (WoRMS) was established in 2007 and is a global, open-access inventory of names of marine taxa. WoRMS is managed within Aphia, an infrastructure designed to capture taxonomic and related data as well as information, and includes an online editing environment. Through this editing environment, experts can update and maintain the content of the database in a timely fashion. A network of more than 450 editors across the globe is helping to keep the content of WoRMS up to date.

As long as WoRMS has existed, there has been a collaboration with FishBase, where synchronization is performed on a regular basis, making sure that the FishBase content is represented in WoRMS as accurately as possible. Over the years, a close connection with SeaLifeBase has been developed, also here with the goal of offering rich information but avoiding duplication of efforts between the data systems.

Without a doubt, FishBase (FB) and SeaLifeBase (SLB) have successful platforms, strong user- and expert communities and excellent communication channels. Sharing part of their content through the World Register of Marine Species gives them even a broader impact and visibility, as they become part of an even more global picture. The data and information from FishBase and SeaLifeBase are indispensable: it is part not only of WoRMS, but also of its many related regional and thematic registers. By including FB and SLB, each of these registers becomes more complete and more impactful, all in a spirit of joint, open collaboration.

This talk will not only highlight the overall collaboration between WoRMS, FB and SLB. It will also focus on the impact of their joint efforts, from a WoRMS editor and user perspective.

From research to reef: mobile AI tools for fish identification and citizen science

Kirk LARSEN

Conservation X Labs, Washington DC, USA.

Keywords: fish identification, visual machine learning, FishBase / SeaLifeBase integration, mobile applications, taxonomic classification.

Artificial intelligence offers promising tools to support fish biologists in species identification, biodiversity monitoring, and fisheries management. This talk highlights current and emerging applications of visual machine learning—particularly convolutional neural networks (CNNs) – for identifying fish from images. We examine the opportunities for deploying these models on mobile devices and discuss the challenges of achieving reliable taxonomic classification, translating research results into field-ready tools, and prioritizing more attainable genus- and family-level identifications over species-level precision. Beyond image recognition, we explore how large language models can leverage the ecological and distributional richness of FishBase and SeaLifeBase to provide context-aware identifications. We also consider how geographic range data can enhance location-aware mobile applications for citizen science. Finally, we touch on the potential of acoustic classification as an additional modality. With field-ready applications becoming increasingly feasible, now is the time for fish biologists to shape the development and responsible deployment of these technologies.

The World Archives of Species Perception (WASP) project: what do the public think of fish?

Tuan NGUYEN[1,2], Maarten P.M. VANHOVE[2], Diogo VERÍSSIMO[3], Luc JANSSENS DE BISTHOVEN[2,4] & Robert MALINA[1]

[1] Research Group Environmental Economics, Centre for Environmental Sciences, Hasselt University, Diepenbeek, Belgium.
[2] Research Group Zoology, Biodiversity and Toxicology, Centre for Environmental Sciences, Hasselt University, Diepenbeek, Belgium.
[3] Environmental Change Institute, School of Geography and the Environment, University of Oxford, Oxford, UK.
[4] Capacities for Biodiversity and Sustainable Development (CEBioS), Operational Directorate Natural Environment, Royal Belgian Institute of Natural Sciences, Brussels, Belgium.

Keywords: public perception, biodiversity conservation, human-nature connectedness, human emotion of species.

While public perception strongly influences societal support for species conservation, its underlying mechanisms remain poorly understood. Previous public perception studies are limited to a number of taxa and employed various methods and settings, which makes the current understanding of public perception of species highly fragmented, and any future effort using such an approach would be

resource and time-intensive to reach an understanding of species at large. To help streamline global endeavours to understand public perception of species, the World Archives of Species Perception (WASP) project was established as the first large-scale data collection effort to map the public perception of species across the animal and "plant" kingdoms. The public perception of animal (WASP-A) dataset currently contains nearly 100 000 responses, representing public perception over six public perception dimensions (beauty, cuteness, dangerousness, intelligence, conservation status, and ecological importance) of 1973 animal species. The species were sampled using a stratified randomization protocol from a pool of species that is (1) listed in the IUCN Red List of Threatened Species, and (2) have images available on iNaturalist. The resulting animal species represent 25 classes, 192 orders, 1037 families, and 1705 genera. Here, we present our recent findings, with a focus on the public perception of fish, and reflect on how the WASP project may benefit from and support the FishBase and SeaLifeBase platforms.

infraFADA: Upgrading the taxonomic backbone of global freshwater animal biodiversity research infrastructures

Géraldine MERTENS[1], Astrid SCHMIDT-KLOIBER[2] & Koen MARTENS[3]

[1,3] Royal Belgian Institute of Natural Sciences (RBINS), OD Natural Environments, Freshwater Biology, Vautierstraat 29, 1000 Brussels, Belgium.
[2] Institute of Hydrobiology & Aquatic Ecosystem Management, Department of Ecosystem Management, Climate and Biodiversity, University of Natural Resources & Life Sciences (BOKU Vienna), Gregor-Mendel-Strasse 33, 1180 Vienna, Austria.
[3] Ghent University, Department Biology, K.L. Ledeganckstraat 35, 9000 Gent, Belgium.
[1] Email: gmertens@naturalsciences.be
[2] Email: ask@boku.ac.at
[3] Email: kmartens@naturalsciences.be; darwinula@gmail.com

Keywords: aquatic biodiversity, taxonomy, FAIR principles, interoperability.

The Freshwater Animal Diversity Assessment (FADA) comprises an extensive set of global taxa lists for freshwater animal groups. At present, more than 125 000 described freshwater animal species in more than 11 000 genera have been documented. However, taxonomy is a living scientific discipline, where new taxa are continuously being described, and existing taxa are being placed in new taxonomic positions. Therefore, after a period of relative inactivity, the BELSPO (Belgian Science Policy) project "infraFADA" (2023–2026) re-establishes the global FADA consortium of taxonomic experts, so that all taxa lists will be brought up to date, both technically and in terms of content. infraFADA is developing a living, updated, and global FADA database, fully in open access and according to the FAIR principles. Part of FADA's data originates from existing global resources such as FishBase. In particular, the freshwater fish component of FADA was established in close collaboration with FishBase as a primary reference to ensure taxonomic consistency and completeness of species lists. While FishBase offers authoritative coverage of fish species worldwide – including freshwater fishes – FADA goes further by encompassing all freshwater animal groups, from invertebrates to other vertebrates. SeaLifeBase is likewise relevant, as it includes many non-fish marine taxa with freshwater representatives or life stages, highlighting important connections between these systems. The FADA database is intended for use and consultation by the freshwater scientific community or interested stakeholders, for example, ecosystem managers, biodiversity conservationists, and others. On the other hand it helps the experts to curate their data using FADAtims. Most importantly, FADA will also serve as a taxonomic backbone for other global biodiversity data infrastructures, such as the Catalogue of Life (CoL), the Global Biodiversity Information Facility (GBIF), the Freshwater Information Platform (FIP), and others. As such, FADA will provide a digital and living heritage of freshwater data, building bridges between science and society and helping to sustainably maintain freshwater resources.

Enhancing interoperability to enable broad data reuse: the Belgian Marine Data Centre perspective

Hong Minh LE, Nicolas DE VILLE DE GOYET, Ruth LAGRING, Johnny RYMENANS, Yvan STOJANOV, Thomas VANDENBERGHE, Nils VAN DEN STEEN & Francis STROBBE

Royal Belgian Institute of Natural Sciences, Brussels, Belgium.

Keywords: data stewardship, NODC, interoperability, FAIR, data standardisation.

As part of its mission as Belgium's National Oceanographic Data Centre (NODC), the Belgian Marine Data Centre (BMDC) provides access and stewardship for the national resource of oceanographic data. BMDC gathers, validates, ensures long-term preservation, and disseminates environmental datasets. Its activities are guided by the FAIR principles (Findable, Accessible, Interoperable, Re-usable), ensuring that locally generated data are interoperable with international platforms and available for broader reuse by scientists, policy-makers, and citizens. Following the principle "collect once, use many times," BMDC promotes cost-effective data valorisation by applying standards and protocols that overcome barriers to reuse. Data harmonisation has been, and remains, a key process supporting environmental assessments (e.g. Regional Sea Conventions, EU Marine Directives) and underpinning policy recommendations.

Today, with the development of Digital Twins of the Ocean at regional (EDITO for Europe) and global (DITTO) scales, we are entering a new era in which information is aggregated in meta-platforms designed to move beyond data silos towards integrated and federated infrastructures. Such systems can serve diverse domains, reflecting the complexity of the ocean and its interactions with social and economic activities.

As a long-standing member of IOC-IODE (International Oceanographic Data and Information Exchange), BMDC curates data collected by Belgian and partner scientists (e.g. onboard the RV Belgica) and disseminates them to international platforms. For example, through the SeaDataNet pan-European infrastructure, BMDC data feed EMODnet, the European Marine Observation and Data Network, and further downstream, the EU EDITO Digital Twin, while biodiversity data flow into GBIF. In addition, the RBINS metadata portal, which is INSPIRE compliant, is now connected to ODIS, the UN Global Ocean Data Information System, contributing to the UN Sustainable Development Goals.

BMDC enhances interoperability capabilities by deploying community standards and vocabularies, including those prescribed by EOSC (European Open Science Cloud), while maintaining strong data governance. Looking ahead, new perspectives are opening as multiple domains require expertise in data harmonisation, standardisation, and interoperable network development. Fisheries represent one of these domains, where FishBase provides a cornerstone platform to build interoperable infrastructures that foster broader data reuse and support evidence-based policy decisions.

Updating FishBase with freshwater and marine information from southern Africa and the Western Indian Ocean

Willem COETZER

South African Institute for Aquatic Biodiversity, Makhanda (Grahamstown).

The South African Institute for Aquatic Biodiversity (SAIAB) is a significant regional centre for the study of fish taxonomy and systematics, and related fields. Within South Africa, we play an important role in the community of natural science museums, especially in the area of biodiversity data curation. The quality of biodiversity data is particularly important. An opportunity has presented itself in the form of a collaboration with FishBase, to compare the South Africa country list in FishBase with the SAIAB database, to identify new country records and re-identify incorrectly identified specimens known to be absent from the country. Related database fields that are important include the Darwin Core terms: establishmentMeans (e.g., indigenous or not) and degreeOfEstablishment (e.g., cultivated or naturalised), as well as the waterbody (river names are especially important) and degree of salinity. Other important information will be collected, including images and literature related to endemic species, as well as national status of threat and conservation. These contributions will be discussed in the context of the protocol of 12 activities for FishBase collaborators.

Doubling down on the Gill-Oxygen Limitation Theory

Daniel PAULY

Sea Around Us, University of British Columbia, Vancouver, B.C. Canada.

Keywords: internal hypoxia, outliers, convergence of evidence, glycolytic vs oxidative enzymes.

The Gill-Oxygen Limitation Theory (GOLT), which I developed over the last 45+ years with an increasing number of colleagues, depends crucially on the surface area (S) of the gills, or other respiratory surface of adult fish or other water-breathing ectotherm (WBE), relating to their body weight (W) according to $S = a \cdot W^d$, with d generally ranging from 0.6 to 0.9, but always < 1. So far, critics of the GOLT have failed to identify values of $d \geq 1$ in adult WBE. In connection with linking the GOLT with Fick's law, which postulates that respiration (R) is proportional to respiratory surface ($R \propto S$), we documented (in Pauly & Müller 2025) that (*i*) ontogenetic changes in scaling (OCS) appears to be the rule in fish and other WBE, which implies that d values estimated for adults will be too high (≥ 1) when small (i.e., young) individuals are included in a log(S) or log(R) linear regression vs log(W) and (*ii*) that the gill lamellae of fish become thicker with increasing body size. Item (*i*) fully explains occasional instances of $d \geq 1$ in the literature, while item (*ii*) causes the gills of large (old) fish and WBE (a species each of crab and lobster, from another paper) to become, given Fick's law, less efficient and thus more limiting to adults. These two points strengthen the GOLT, initially formulated without reference to them.

Reference

Pauly D. & Müller J. 2025. Fick's diffusion laws and scaling of the gill surface area and oxygen uptake in fish. *Fishes* 10 (5): 233. https://doi.org/10.3390/Fishes10050233

Integrating FishBase and SeaLifeBase into marine ecosystem models

Léo BARBUT & Geneviève LACROIX

Operational Directorate Natural Environment, Royal Belgian Institute of Natural Sciences, Brussels, Belgium.

Keywords: marine ecosystem modelling, biological parameterization, larval dispersal, fisheries management, flatfish species.

Marine ecosystem models, ranging from simple to complex, all require one essential ingredient: reliable biological and ecological data. This talk explores the integration of FishBase (FB) and SeaLifeBase (SLB) into marine modelling workflows, with a particular focus on larval drift models used to support fisheries management. These models are highly sensitive to parameterization, yet key biological traits—such as spawning periods and pelagic larval duration—are often not well documented or inconsistently available.

We illustrate this with a test case involving six species of flatfish in the North Sea. For each species, we applied a distinct parameterization based on available data from FB, SLB, and supplementary literature sources. The resulting larval dispersal patterns and connectivity maps differed markedly between species, underlining the importance of accurate, species-specific inputs.

In addition to highlighting current uses of the databases, we propose pathways for enhanced integration: (1) model outcomes, such as sensitivity analyses, could inform future database entries and help identify priority traits; and (2) literature-based parameter extraction efforts for modelling could be systematically fed back into FB and SLB to expand trait coverage.

By fostering a bidirectional exchange between models and databases, we aim to create a more dynamic, data-informed foundation for marine biodiversity research and sustainable fisheries management.

A series of fisheries, ecosystem, and bio-economic models in the Aegean Sea

Athanassios C. TSIKLIRAS, Kostantina MICHAILIDOU, Maria LAZARINA,
Sophie MANOUSI & Donna DIMARCHOPOULOU

Laboratory of Ichthyology, Department of Zoology, School of Biology, Aristotle University of Thessaloniki, 54124, Thessaloniki, Greece.

MarinOmics Research Group, Center for Interdisciplinary Research and Innovation (CIRI), Aristotle University of Thessaloniki, 57001, Thessaloniki, Greece.

Keywords: marine fisheries, Mediterranean Sea, socio-ecological systems, model integration, scenario testing.

SURIMI is a European H2020 project aiming to develop a series of interconnected fisheries, ecosystem, social, and economic models for integration into the European Digital Twin of the Ocean (EU DTO). The development of models and scenarios will be done through collaborations with stakeholders from industry, science, policy, and civil society. By utilizing simulated ecological and fisheries data, the project seeks to investigate the impacts of fishing activities on sensitive species, seabed habitats, and biodiversity hotspots. At the same time, it promotes broader participation in ocean sciences by offering user-friendly tools that enhance access to the EU DTO. SURIMI plans to integrate databases and computational models to create a comprehensive socio-ecological layer within the EU DTO, thus strengthening its capacity to support evidence-based decision-making and policy development in marine ecosystem management. As part of the SURIMI project, a series of models will be developed for the Aegean Sea, across three layers (Fisheries – Assessment, Biology – Ecosystem, Economy – Supply Chain). Initially, the CMSY++ fisheries model will be applied to assess the status and exploitation level of fish stocks in the area. This will be followed by the development of a Model of Intermediate Complexity for Ecosystem assessments (MICE), based on the existing, more complex Ecopath with Ecosim (EwE) model. Finally, the EwE value chain flow model will incorporate the economic dimension of fisheries, tracing the supply chain from fishing vessels to consumers. This sequence of SURIMI models, combined with policy and evaluation models, will enable scenario creation and impact analysis across multiple scales. Their integration into the EU Digital Twin of the Ocean will enhance the sustainable management of marine resources, transforming the DTO from a data repository into an advanced decision support tool.

Levels of domestication in fish: update and perspectives for global aquaculture

Fabrice TELETCHEA

Université de Lorraine, CNRS, LIEC, Nancy, France.

Keywords: aquaculture, domestication levels, strain, FAO, FishBase.

Aquaculture has increased tremendously since the early 1950s, so that the volume produced has surpassed the volume of the global capture fisheries in the mid-2010s for the first time ever in human history. For fish, this exponential growth has relied party on the domestication of an increasing number of species, so that today some have been farmed for a couple of centuries while others for only a handful of years. In order to better describe this rapid evolution and be able to compare this diversity of domestication histories between species, we coined a new concept about 15 years ago, the domestication levels. This new classification includes five levels: first trials of farming a new species (level 1), part of the life cycle controlled in captivity (level 2), entire life cycle controlled in captivity but with wild inputs (level 3), entire life cycle controlled in captivity but without wild inputs (level 4), and selective programs applied to improve some traits (level 5). This new concept was applied to all farmed species listed in the FAO database in 2009, highlighting that only one-third had reached level 4 (n = 30) or level 5 (n = 45). Since its publication, over 500 articles have cited it and some colleagues even applied this new concept on various topics and other taxa, such as crustaceans. The aims of the present presentation are to provide an update of the domestication levels and discuss which species may have reached a new level (6), which corresponds to FAO's strain: "a farmed type of aquatic species having homogeneous appearance (phenotype), homogeneous behaviour and/or other characteristics that distinguish it from other organisms of the same species and that can be maintained by propagation". Lastly, we will discuss the potential of including these domestication levels in FishBase.

Documenting the marine biodiversity of the world's archipelagos: practical and theoretical considerations

Anna-Luna ROSSI [1], Fabrice TELETCHEA [2], Nicolas BAILLY [1,3] & Daniel PAULY [1,*]

[1] *Sea Around Us*, University of British Columbia, Vancouver, B.C. Canada.
[2] Université de Lorraine, CNRS, LIEC, Nancy, France.
[3] Biodiversity Centre, University of British Columbia, Vancouver, B.C. Canada.
[*] Presenter.

Keywords: Saint-Pierre and Miquelon, archipelago, shelf area, temperature, biodiversity.

To match the recent completion of a checklist of fishes in the Saint Pierre and Miquelon (SPM) archipelago, an extensive literature review incorporating biodiversity assessments performed in and around SPM was done to identify marine animal species (e.g., marine invertebrates and mammals, seabirds, marine mammals) occurrence in SPM, and update SeaLifeBase with up-to-date information on SPM. The numbers thus obtained for SPM were combined with biodiversity data currently included in both FishBase and SeaLifeBase from 39 other archipelagoes throughout the world, including large ones such as Indonesia. These data were then used, based on multiple regressions applied to different groupings of taxa, to test the applicability of McArthur and Wilson's Theory of Island Biogeography to marine organisms. As expected, this work confirmed that both surface area (here: of the shelf of each archipelago) and temperature (via latitude) largely determine species richness in various taxa. More importantly for us, concerned about the utility of FishBase and SeaLifeBase, the consistency of these results and the relatively low variance of the datapoints representing archipelagoes along the trend lines identified by the multiple regressions, were very encouraging, as they suggested that the current coverage of these two databases, while incomplete – particularly so in the case of SeaLifeBase – still allows broad and insightful marine biodiversity studies.

Beyond diversity, abundance and size: a smorgasbord of applications of video-based methods to marine ecology and conservation

Jessica MEEUWIG

University of Western Australia, Perth, Australia.

When evolution clicks: congruence between phylogeny, morphology and acoustics in Holocentridae

Marine BANSE [1,*], Maarten VAN STEENBERGE [2], Gontran SONET [3], Denisa MAGDA [2],
Yves CORBISIER DE HARBONNIER DE COBREVILLE [1], David LECCHINI [4],
Terry J. DONALDSON [5] & Eric PARMENTIER [1]

[1] Laboratory of Functional and Evolutionary Morphology, University of Liège, 4000 Liège, Belgium.
[2] Operational Directorate Taxonomy and Phylogeny, Royal Belgian Institute of Natural Sciences, Vautierstraat 29, Brussels B-1000, Belgium.
[3] Joint Experimental Molecular Unit (JEMU), Operational Directorate Taxonomy and Phylogeny, Royal Belgian Institute of Natural Sciences, Vautierstraat, 29, 1000 Brussels, Belgium.
[4] Center for Insular Research and Observatory of the Environment (CRIOBE), Moorea, French Polynesia.
[5] University of Guam Marine Laboratory / Guam EPSCoR, UOG Station, Mangilao, Guam 96923, USA.
[*] Corresponding author: mbanse@uliege.be

Keywords: evolution, sound, holocentrid, acoustics, morphology.

Although many fish species are known for their social acoustic communication abilities, few studies have investigated the evolutionary history of this trait. The aim of this study was to tackle this challenging topic by investigating a wide range of holocentrid species using a multidisciplinary approach. We first carried out a comparative analysis of 7662 sounds recorded in the same behavioural context, collected from 388 individuals across 73 populations (Guadeloupe, French Polynesia, Guam, Seychelles, Philippines) representing 33 species. This comparison conclusively demonstrated that sounds can be reliably used to determine taxonomic affiliation across different taxonomic levels. Our new phylogeny reveals that morphological and acoustic data strongly support the existence of two main clades within Holocentridae, corresponding to the subfamilies Myripristinae and Holocentrinae. Minor modifications within these subfamilies facilitated speciation. However, differences in sound features at lower taxonomic levels (such as genera, subgenera, and species) do not always align with morphological differences. This suggests that species may exploit similar mechanisms in distinct neuro-physiological ways. Overall, the interplay between morphology and acoustics highlights the diversification within Holocentridae, showing how subtle modifications in sound production mechanisms reflect phylogenetic divisions and contribute to speciation.

Advancing Southern Ocean fish knowledge: the SCARFISH contribution to FishBase and SeaLifeBase

Anton P. VAN DE PUTTE[1,2], Erica CARLIG[3], William REID[4], Philippe KOUBBI[5], Dale MASCHETTE[6] & the SCARFISH Biology and Life History Working Group

[1] Royal Belgian Institute of Natural Sciences, Vautierstraat 29, 1000 Brussels, Belgium.
[2] Université Libre de Bruxelles, Belgium.
[3] Institute for the study of anthropic impacts and sustainability of the marine environment (IAS), National Research Council (CNR), Genoa, Italy.
[4] Modelling, Evidence and Policy, School of Natural and Environmental Sciences, Newcastle University, NE1 7RU, UK.
[5] LOCEAN-IPSL (Sorbonne Université, CNRS, IRD, MNHN), Laboratoire d'Océanographie et du Climat - Expérimentations et Approches Numériques, Paris, France.
[6] Fisheries and Aquaculture Centre, Institute for Marine and Antarctic Studies (IMAS), University of Tasmania, 20 Castray Esplanade, Battery Point, Tasmania 7001, Australia.

The Southern Ocean is a critical, yet understudied, marine environment, home to a unique and diverse ichthyofauna. Understanding the biology and life histories of Antarctic and Southern Ocean fish species is paramount for effective conservation and ecosystem-based management, particularly in the face of climate change and increasing human activities. FishBase and SeaLifeBase serve as indispensable global repositories of aquatic species data, providing scientifically validated information that supports research, education, and conservation worldwide.

This abstract outlines the significant mutual benefits of the Scientific Committee on Antarctic Research (SCAR) SCARFISH action group's collaboration with and contribution of Southern Ocean fish trait data to FishBase and SeaLifeBase. The SCARFISH working group on Biology and Life Histories is actively engaged in reviewing, estimating, and improving knowledge on key biological and ecological parameters, including reproductive strategies, early life history stages, growth, feeding ecology, natural mortality, and essential habitats (e.g., nesting and nursery grounds).

By systematically collating and integrating this specialised Southern Ocean fish trait data into FishBase and SeaLifeBase, and by extension, linking with the World Register of Marine Species (WoRMS), SCARFISH will:

1. **Enhance Data Accessibility and Comprehensiveness:** Make crucial Southern Ocean fish data more widely available to the global scientific community, filling existing knowledge gaps and enriching the overall datasets of these platforms, ensuring consistency and broader taxonomic integration through WoRMS.
2. **Facilitate Comparative Analyses:** Enable broader comparative studies across different fish species and regions, fostering a deeper understanding of ecological strategies and responses to environmental stressors.

3. **Support Policy and Management:** Provide robust, accessible data to inform international bodies like CCAMLR,BBNJ and IUCN, aiding in the development of science-based conservation measures and Red List assessments.
4. **Promote Collaboration and Capacity Building:** Strengthen the collaborative network between Antarctic researchers and the wider aquatic science community, encouraging further data sharing and research initiatives across interconnected biodiversity databases.

This synergistic relationship will not only bolster the utility and impact of FishBase and SeaLifeBase but also significantly advance our collective knowledge of Southern Ocean fish biology and ecology, ultimately supporting more effective marine life conservation in this vital polar region.

Resource partitioning and dietary shifts in *Oreochromis niloticus* and *Oreochromis leucostictus* in Lake Edward and Lake George (East Africa)

Elysée Rutakaza NZIGIRE [1,2,3,*], Christine COCQUYT [4], Hocein BAZAIRE [1,5] & Maarten VAN STEENBERGE [3,6]

[1] Department de biologie, Centre de Recherche en Hydrobiologie CRH-Uvira, Uvira, Sud-Kivu, DR Congo.
[2] Laboratoire de Biodiversité, Ecologie et Génome, Faculté de Sciences, Université Mohammed V, Rabat, Maroc.
[3] Centre for Environmental Sciences, Hasselt University, Belgium.
[4] Research Department, Meise Botanic Garden, Meise, Belgium.
[5] Natural Sciences and Environment Research Hub, University of Gibraltar, Europa Point Campus, Gibraltar.
[6] OD Taxonomy and Phylogeny, Royal Belgian Institute for Natural Sciences, Brussels, Belgium.
[*] Email: nzigirerutakaza@gmail.com

Keywords: *Oreochromis*, trophic ecology, niche overlap, algal composition, East African lakes.

Oreochromis niloticus (Linnaeus, 1955) and *Oreochromis leucostictus* (Trewavas, 1933) are important food fishes, with *O. niloticus* being one of the most widely cultivated fish worldwide. Both species are native to Lakes Edward and George, two lakes that are connected by the Kazinga Channel. The two species primarily feed on algae but occupy different habitats: *O. leucostictus* is typically found in inshore waters, while *O. niloticus* prefers offshore areas. However, major changes in abundances and therefore also in the composition of catches have been observed in recent years. In both lakes, *Oreochromis leucostictus* is increasingly replacing the larger-bodied *O. niloticus* as the dominant tilapia species, likely due to overfishing of the latter. In this study, we will investigate whether *O. leucostictus* is also replacing *O. niloticus* by feeding on its preferred food. In analyses of 66 gut samples from both recent and historical collections of *Oreochromis*, 128 algal taxa were identified, including diatoms, dinoflagellates, euglenophytes, cyanobacteria, chrysophytes, and chlorophytes. These findings confirm that both *O. leucostictus* and *O. niloticus* primarily feed on algae. The most diverse algal groups found were diatoms (55 taxa) and Chlorophyta (26 taxa).

Our planned work will focus on determining whether the gut contents of the fish can detect differences in algal composition in the diet in the two lakes. We will also assess the degree of overlap in diet (niche overlap) between the two species in both recent and historical samples to investigate possible changes in the diet of these fishes. For this, we will examine the gut of at least 10 specimens per species, per lake, and per time period. The historical samples were collected in 1933 and 1953, while the recent samples were collected between 2016 and 2018.

Geometric morphometric otolith shape analysis of *Labeobarbus* species in Lake Tana, Ethiopia

Felegush ERARTO [1,2], Minwyelet MINGIST [2], Wondie ZELALEM [2], Degsera AMERO [2], Mulugeta KIBRET [3], Enyew ADGO [4], Elie VERLEYEN [5], Kristiaan HOEDEMAKERS [6], Maarten VAN STEENBERGE [1,6] & Alain DE VOCHT [1,7]

[1] UHasselt, Centre for Environmental Sciences, 3590, Diepenbeek, Agoralaan, Belgium.
[2] Department of Fisheries and Aquatic Sciences, Bahir Dar University, Bahir Dar, Ethiopia.
[3] Department of Biology, Bahir Dar University, Bahir Dar, Ethiopia.
[4] Department of Natural Resource Management, Bahir Dar, University, Bahir Dar, Ethiopia.
[5] Department of Biology, Ghent University, Ghent, Belgium.
[6] OD Taxonomy and Phylogeny, Royal Belgian Institute for Natural Sciences, Brussels, Belgium.
[7] PXL University College, Hasselt, Belgium.

Keywords: endemic species, identification, Lake Tana, landmarks, morphometric analysis, otolith shape.

The shape of otoliths may provide an alternative way for delineating the endemic *Labeobarbus* species in Lake Tana (Ethiopia), yet the efficacy of this approach has not been properly assessed. Here we investigated interspecific differences in *Labeobarbus* species using 2D landmark-based geometric morphometric analysis (GMA) of the largest otolith, asteriscus. We evaluated the discriminatory power of 17 otolith characteristics in distinguishing species, to determine which characteristic contributes most to species differentiation using standardized metrics, normalized variability, and pairwise differentiation scores. The results revealed five characteristics exhibiting maximum variability (1.00) and full pairwise discriminatory power (1.00) in successfully differentiating between all possible species pairs, namely anterior rim-rostrum, anterior rim-excisura, dorsal rim-anterior, ventral rim-general, and preventral angle. By contrast, anterior rim-antirostrum, dorsal rim-posterior, postdorsal angle, posterior rim, and postventral angles showed moderate discriminatory power, with variability values ranging from 0.75 to 0.94. The postdorsal angle had the highest contribution (variability = 0.94, pairwise score = 0.89), indicating its relatively strong role in distinguishing between species, while the other characteristics provided partial but still functional differentiation. Principal Component Analysis, Discriminant Function Analysis, and Canonical Variate Analysis were performed using 7 landmarks placed on otolith images of preventral angle (LM1), excisura (LM2), end of the anterior process (LM3), deepest part of anterior rim above anterior process (LM4), predorsal angle (LM5), postdorsal angle (LM6), and postventral angle (LM7). The result of the present study revealed a significant shape variation ($p < 0.001$) among the otoliths of these species. The current pioneering study highlights the potential of otolith-based geometric morphometric analyses to improve identification of *Labeobarbus* species.

The long and winding road towards the List of Available Names in Zoology (LAN), partim genus- and species-group level names in Phylum Rotifera

Hendrik SEGERS[1] & Christian D. JERSABEK[2]

[1] Royal Belgian Institute of Natural Sciences, OD Nature, Brussels, Belgium. hsegers@naturalsciences.be
[2] University of Salzburg, Dept of Environment and Biodiversity, Salzburg, Austria. christian.jersabek@sbg.ac.at

Keywords: rotifers, nomenclature, names standard.

As a contribution to stabilizing zoological nomenclature and establish a standard list of species- and genus-level names for rotifers, we initiated in 2008 a process toward the establishment of a Rotifera Part of the *List of Available Names in Zoology*, as outlined in Art. 79 of the International Code of Zoological Nomenclature. This process was concluded by the official adoption of the Part by the International Commission on Zoological Nomenclature under the plenary power, effective as of 30 April 2019 (ICZN 2019). It was the first, and still is, the only Part of the LAN adopted by the ICZN.

We will provide a short overview of the first Part of the List of Available Names, an outline of our approach to the process, a short summary of the results, and present thoughts on ways to streamline and facilitate the preparation of possible future, additional Parts of the List of Available Names.

References

ICZN (International Commission on Zoological Nomenclature) 2019. Opinion 2430 – Parts of the List of Available Names in Zoology for phylum Rotifera: accepted. *Bulletin of Zoological Nomenclature* 76: 74–76. Available from https://biotaxa.org/bzn/article/view/50666/44015

Jersabek C.D., De Smet W.H., Hinz C., Fontaneto D., Hussey C.G., Michaloudi E., Wallace R.L. & Segers H. 2018a. List of Available Names in Zoology, Candidate Part Phylum Rotifera, genus-group names established before 1 January 2000. [1] + 24 + 9 + [2]. Available from https://archive.org/details/LANCandidatePartGeneraRotifera

Jersabek C.D., De Smet W.H., Hinz C., Fontaneto D., Hussey C.G., Michaloudi E., Wallace R.L. & Segers H. 2018b. List of Available Names in Zoology, Candidate Part Phylum Rotifera, species-group names established before 1 January 2000. [3] + 231 + [1] + 45 + 54 + [2]. Available from https://archive.org/details/LANCandidatePartSpeciesRotifera

Fish without borders: unravelling hidden diversity in sawfin barbs from the Lake Edward system

Heleen MAETENS [1,2,3], Eva DECRU [2], Maarten VAN STEENBERGE [3,4],
Arthur BOOM [1] & Jos SNOEKS [1,2]

[1] Royal Museum for Central Africa, Leuvensesteenweg 13, 3080 Tervuren, Belgium.
[2] University of Leuven, Ch. Deberiotstraat 32, 3000 Leuven, Belgium.
[3] Royal Belgian Institute of Natural Sciences, OD Taxonomy and Phylogeny, Vautierstraat 29, 1000 Brussels, Belgium.
[4] Hasselt University, Agoralaan Building D, 3590 Diepenbeek, Belgium.

Keywords: East Africa, *Enteromius*, biogeography, DNA barcoding, morphology.

The African genus *Enteromius*, comprising the small-sized riverine barbs, is currently ranked as the third most species-rich fish genus in the world and may become the most diverse. The hidden diversity of *Enteromius* has long remained under the radar, as many species are morphologically similar, lack vibrant colour patterns and show little ecomorphological or sexual differentiation. Yet, genetic divergences are high.

Our study investigates the species diversity and evolutionary history of *Enteromius* from the Lake Edward system (LES) and neighbouring regions, using an integrative approach that combines morphology, biogeography, ecology, genetics, and whole-genome sequencing.

Based on morphology and literature, five species of *Enteromius* were initially recognised in the LES: two soft-rayed barbs (with flexible dorsal spines) and three sawfin barbs (with serrated dorsal spines). Genetic analyses revealed that the sawfin species each consist of distinct lineages, forming species complexes. While specimens from different complexes are easily distinguishable, specimens from the different lineages within each complex appear virtually identical to the naked eye, but most of the lineages are distinguishable based on multivariate morphometric analyses.

Within each of these three species complexes, a recurring biogeographical pattern was observed: one lineage was found in the highlands, in the eastern part of LES, while another lineage inhabited the lowlands, near the lakes. When expanding our sampling to Lakes Albert, Victoria, and Kivu, additional lineages were discovered, complicating the biogeographical pattern; specimens from Lake Kivu clustered with either the highland or lowland lineages of the LES. We are currently aiming to link the species diversity to historical hydrological changes in this geologically active region in East Africa.

A morphometric analysis of the pharyngeal jaw showed small differences between species complexes but found no variation within complexes. Similar analyses on the kinethmoid bone, important in jaw protrusion, showed no differences between and within species complexes, indicating the absence of ecomorphological divergence. Preliminary genomic results revealed differences in the genome size among specimens of the same lineage, suggesting possible structural variation within a lineage.

FishBased and “ParasiteBased” education for the digital age: a publicly accessible virtual learning environment

Nathan VRANKEN [1,2,*], Morgane MENTEN [1], Emma VERSCHELDE [1], Patrick SEMAL [2], Jonathan BRECKO [2,3], Maarten VAN STEENBERGE [1,2] & Maarten VANHOVE [1]

[1] Research Group Zoology: Biodiversity and Toxicology, Centre for Environmental Sciences, Hasselt University, Diepenbeek, Belgium.
[2] Belgian Institute for Natural Sciences, Brussels, Belgium.
[3] Biological Collections, Royal Museum for Central Africa, Tervuren, Belgium.
[*] Corresponding author: nathan.vranken@uhasselt.be

The availability of high-quality biological specimens is essential for teaching morphology, anatomy, histology, and parasitology. For this, traditional teaching methods rely on collection specimens and dissections of fresh specimens. These can only be accessed during scheduled practical sessions at universities or museums, which restricts students’ opportunities to repeatedly study specimens in detail. The use of animal specimens for teaching dissection skills and insight also raises ethical concerns regarding animal welfare.

Within an educational innovation project at Hasselt University, in collaboration with the Institute of Natural Sciences in Brussels, we are developing a virtual learning environment to address these challenges. We use various digitalisation techniques, including 3D structured light and µCT scanning and 2D scans of microscope slides.

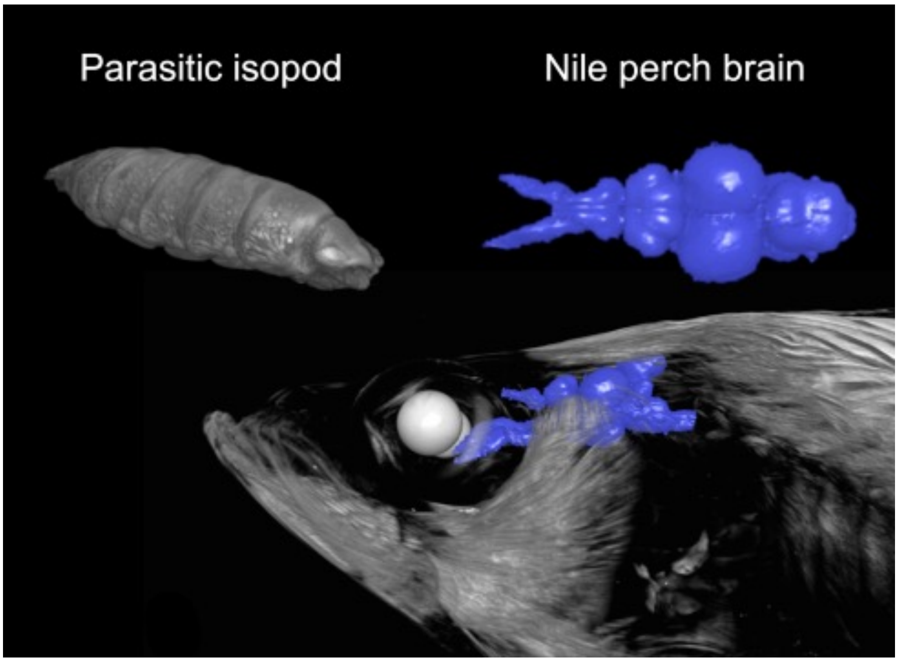


Figure 1. µCT scans of a parasitic isopod and a Nile perch with the brain segmented.

We created 3D surface scans of the dissections of a dogfish, a carp, and a mouse, which are made available through the CANATHIST platform (https://canathist.naturalheritage.be/orthanc). These are being integrated into courses of vertebrate diversity and anatomy at Hasselt University. While student surveys showed that the scans were appreciated as preparation for practical sessions, they do have some limitations, e.g., some structures are poorly visible and the specific position and size of structures and tissues within a living organism can be difficult to grasp. Therefore, we also aim to µCT scan stained museum specimens. As a proof of concept, we scanned a specimen of the Nile perch *Lates niloticus*, an important food fish in tropical Africa, and a parasitic isopod of the European pilchard *Sardina pilchardus* (see Fig. 1). We were successful in segmenting several organs of the Nile perch, while the identification of internal structures proved more difficult for the isopod specimen.

For a parasitology course, we scanned prepared microscope slides with various parasites, which were integrated into an interactive PowerPoint presentation to aid students in their understanding of parasite diversity, ecology, and life cycles. By using resources across different courses and disciplines, we can highlight the integration of different courses and promote interdisciplinary learning.

Beyond its educational value for students, the project supports animal welfare by reducing the need for specimen dissection in teaching. Furthermore, by integrating digital resources in a virtual environment that is publicly accessible, we aim to support collaboration and capacity-building initiatives in the Global South, where access to physical specimens is often limited. In alignment with this aim, we include tropical species, as biology textbooks often use species from temperate zones as models.

Ethnobiological documentation of marine invertebrates in Elmina and Tema fishing communities along the coast of Ghana

Margaret Fafa Awushie AKWETEY [1], Jessica DANSO [1], Paul Kojo MENSAH [1,2], Theodora SAM [3], Oscar GBADAGO [1], Denis Worlanyo AHETO [1,4] & Daniel PAULY [5]

[1] Department of Fisheries and Aquatic Sciences, University of Cape Coast, Ghana.
[2] Institute of Water Resources, Rhodes University, Grahamstown, South Africa.
[3] Independent Researcher, Cape Coast, Ghana.
[4] Africa Centre of Excellence in Coastal Resilience (ACECoR), University of Cape Coast, Ghana.
[5] *SeaAroundUs*, Institute for the Ocean and Fisheries, University of British Columbia, Vancouver, Canada.

Keywords: marine invertebrates, ethnobiology, indigenous knowledge, coastal communities, Ghana.

Marine invertebrates play a vital role in the livelihoods, diets, and traditional knowledge systems of coastal communities, yet they have been largely overlooked in ethnobiological research in Ghana. This study explored the diversity, local nomenclature, and ethnolinguistic and cultural significance of marine invertebrates in Fante and Ga speaking fishing communities in Elmina and Tema respectively using field surveys and photographic documentation. A total of eight (8) species were recorded at Elmina, while twelve (12) species were identified at Tema. *Perna viridis* (Green mussel), *Penaeus monodon* (Black tiger shrimp), *Trona stercoraria* (Droppings cowry), and *Cymbium olla* (Olla volute) were exclusive to the Tema site while *Callinectus sapidus* (Atlantic blue crab), *Calappa rubroguttata* (Spotted box crab), *Goniopsis pelii* (Purple mangrove crab), *Sepia hierredda* (Giant African cuttlefish), *Cymbium glans* (Elephant's snout volute), *Parapenaeus longirostris* (Deepwater rose shrimp), *Panulirus regius* (Royal spiny lobster), and *Hexaplex trunculus* (Trunculus murex snail) were common to both sites. Beyond identification, the study explored the local (Fante and Ga) nomenclature, etymology, and cultural associations of the species. Names were found to reflect species morphology, behaviour, or traditional beliefs. For example, the Fante name *Po snae* ("sea moon") for cuttlefish is based on its morphology, while the Ga term *Kortor fiɔçfiɔç* for the spiny lobster imitates the sound of its tail fan. Shells and body parts of many species were noted for use in food, traditional medicine, ornamentation, and spiritual practices. Some species, such as the purple mangrove crab, were also linked to taboos and ritual significance in certain ethnic groups. Beyond dietary value, the marine invertebrates were found to have significant medicinal, spiritual, and ornamental uses. For instance, cuttlebones are used to treat asthma and skin conditions, while certain mollusc shells are employed in divination. This research underscores the richness of indigenous knowledge systems and their relevance for biodiversity conservation, sustainable fisheries management, and cultural preservation in Ghana's coastal zones.

Towards sustainable shrimp fisheries in West Africa lagoon: stock estimation and gear efficiency in lake Nokoué with its inlet

Sèlomè Wilfried SINTONDJI[1,2,*], Zacharie SOHOU[1,2], Juste Vital VODOUNNOU[1,4],
Yaovi ZOUNON[1,2] & Geneviève LACROIX[3]

[1] Laboratoire de Recherche sur les Zones Humides, Faculté des Sciences et Techniques, Université d'Abomey-Calavi, 01 BP 526 Cotonou, République du Bénin.
[2] Institut de Recherches Halieutiques et Océanologiques du Bénin (IRHOB), 03 BP 1665 Cotonou, République du Bénin.
[3] Royal Belgian Institute of Natural Sciences, Operational Directorate Natural Environment, 29 Rue Vautier, 1000 Brussels, Belgium.
[4] Unité de Recherche en Aquaculture et Gestion des Pêches (URAGeP), Ecole d'Aquaculture, Université Nationale d'Agriculture, BP 55, Porto-Novo, République du Bénin.
[*] Correspondence to: sintondjiwilfried@gmail.com

Keywords: fishing gear, fisheries management, shrimp stock, Palaemonidae, Penaeidae, Lake Nokoué.

The continued use of prohibited fishing gear in Lake Nokoué poses a direct threat to the shrimp industry in Benin. This study aimed to assess the effectiveness of two fishing gears, less destructive than traditional methods, on shrimp catches and to estimate the current shrimp stock in the Lake Nokoué-Cotonou Channel complex as part of a sustainable exploitation strategy. Two different fishing techniques specifically targeting shrimp, namely traps and nets, with identical mesh sizes (0.5 cm), were used simultaneously twice a month over one year to sample shrimp in five stations (North, South, Center, East and West) in the lagoon complex. A total of 1455 shrimp specimens were collected, representing two genera: *Macrobrachium* (*M. macrobrachion*, *M. vollenhovenii*, *M. felicinum*, *M.* cf. *zariquieyi* and *M. equidens*) and *Penaeus* (*P. notialis*, *P. monodon*, *P. kerathurus*). The results revealed that species of the genus *Penaeus* were more abundant from January to August, while *Macrobrachium* species dominated from September to December. Traps showed significantly higher fishing efficiency than nets from August to March (8 months), whereas nets were more efficient from May to July (3 months). In April, both gears performed similarly. A chi-square test indicated no significant difference in the capture of *Penaeus* species (saltwater shrimp) between gear types ($\chi^2 = 6.99$, $P > 5\%$), but traps were significantly more efficient than nets in capturing *Macrobrachium* (freshwater shrimp) ($\chi^2 = 19.77$, $P < 5\%$). ANOVA showed no significant difference in Catch Per Unit Effort (CPUE) between traps (1.51 ± 0.78 g unit^{-1} h^{-1}) and nets (1.36 ± 1.14 g unit^{-1} h^{-1}) at the 5% significance level. Based on these findings, the use of traps is recommended as a priority for shrimp fishing in Lake Nokoué.

Interspecific allometric scaling of home-range size in teleost fishes

Christopher T. MONK [1] & Rodolfo B. REYES Jr. [2]

[1] GEOMAR Helmholtz Centre for Ocean Research Kiel, Kiel, Germany.
[2] Quantitative Aquatics, Los Banos, Philippines.

Keywords: home-range, allometry, acoustic telemetry, meta-analysis.

Home range is the area used in an individual's normal activities of foraging, mating and caring for young, allowing for occasional excursions outside the home-range bounds. Accordingly, home-ranges are formed from an aggregation of behavioural processes, but may be limited by fundamental constraints (e.g. resource availability, or predation risk). Understanding the determinants of home-range size is critical for designing adequate conservation measures, such as protected areas; however, the exact mechanisms driving home-range size are not fully understood. Home-range sizes both within and among species commonly show allometric scaling relationships, hypothesized to relate to the allometric scaling of basal metabolic rate. Home range size has also often been observed to relate to ecosystem productivity and feeding mode, where higher productivity and feeding efficiency enable metabolic needs to be met in a smaller area. It has not yet been tested whether these relationships hold up for a global analysis of teleost fishes. With an increasing capability to track and monitor fish, the number of reported fish home-range sizes is rapidly growing. Based on data from 167 publications and 7313 individual home-range sizes, including fish from rivers, lakes, coasts, coral reefs and the open sea, we indeed observed an allometric scaling relationship with an exponent of 0.79, supporting the idea of metabolic constraints on home-range size. Moreover, for a given body size, home-ranges were largest in the open sea, followed in decreasing order by coral reefs, coastal marine environments, lakes and then rivers, confirming previous literature. This work supports the idea that the space-use required by individual fish to meet their daily needs may be predictable and shaped by general constraints.

FishBase natural sciences .be SeaLifeBase

SeaLifeBase at 20: challenges and opportunities

M.L.D. Palomares[1], L.A. Abucay[2], V.A. Parducho[2],
P.M.S. Yap[2] & D. Pauly[1]

[1] *Sea Around Us*, Institute for the Oceans and Fisheries, University of British Columbia, Vancouver, Canada.
[2] Quantitative Aquatics, Los Baños, Laguna, Philippines.

The idea for a FishBase-like database on other marine animals was conceived in the early 1990s for clams, at the then International Centre for Living Aquatic Resources Management (Makati City, Philippines, now the Malaysia-based WorldFish), by Dr John Munro, who referred to is as ‘ClamBase.’ It wasn’t the first time that this sort of FishBase-like database was developed, as other scientists working on other marine animal groups developed their own databases to help them organize and document the species they were studying (… and then abandoned them). As FishBase became more and more used, however, more queries about a database that united all the different marine animal databases in one place begun to reach the makers of FishBase. Finally, in the early 2000s, Dr Daniel Pauly presented to the Oak Foundation a proposal written by Dr Nicolas Bailly. In 2005, this proposal was approved and SeaLifeBase, led by Dr Maria Lourdes Palomares, was born.

It was an easy birth, as it relied on the FishBase infrastructure and numerous species names were available in the Catalogue of Life, which provided taxonomic information from global species databases worldwide. At about the same time, the World Register of Marine Species (WoRMS) was developed, whose taxonomic editors, through their expertise on the various marine metazoan groups, ensured a high data quality. Thus, it was clear that SeaLifeBase was not going to be a global taxonomic database, like FishBase, because WoRMS filled that niche. Indeed, WoRMS later on became the taxonomic backbone of SeaLifeBase. However, SeaLifeBase, had the comparative advantage of providing ecological and life history traits and focusing on species lists by marine ecosystems, with a view on providing the different food web components required in ecosystem models.

Over these 20 years and with funding from various partners and donors, SeaLifeBase accumulated biogeographic, ecological and life history information for various countries and territories for the coverage of which we received external support (e.g., Australia, The Bahamas, Belize, Crozet Islands, French Polynesia, Hong Kong, Kerguelen Islands, New Caledonia, Oman, Pitcairn Island), as well as large marine ecosystems (e.g., Arctic and Antarctic Seas, Baltic Sea, Mediterranean Sea, North Sea, Salish Sea, South China Sea). This led to a global coverage of about 3500 marine vertebrate and about 68 400 invertebrate species with varying coverage of nomenclature (taxonomy, common names), distribution, ecology and life history traits (maximum size, growth parameters, length-weight relationships, food items, diet composition, reproduction, fecundity, maturity, spawning). In parallel to the ecosystem focus, SeaLifeBase also prioritized charismatic species, along with exploited, threatened, endemic and keystone species.

As with FishBase and the *Sea Around Us*’ fisheries catch database, the main challenge is sustainability and continued funding stream. Because we were focusing on ecosystems, we were able to generate interest from donors with specific geographic interests (as opposed to global) and for which, species lists were available for the priority groups.

Also, as with FishBase, SeaLifeBase encodes data from published literature, preferably from scientific journals. Thus, availability of published data became the second challenge. By focusing on biological traits that are used in assessments of extinction risk and of stock status, we were able to channel our research to information that would most likely be available in scientific publications.

Given that funding was and is tight, our team has remained small, and we have not been able to increase the number of researchers to perform the overwhelming amount of encoding work to be done. We were able to generate interest from graduate students (notably Dr Pauly's students at UBC) to lead the documentation for some important groups, e.g., jellyfishes (Dr Lucas Brotz). In addition, we initiated an undergraduate internship program between SeaLifeBase and the University of the Philippines (in Los Baños, Laguna) to generate interest among BS Biology or Zoology students who were eyeing research careers and as such get exposed to a research work environment. This also helped us increase our work force while training student workers. As SeaLifeBase grew in content and usage, interest in its use as a repository of small datasets that would otherwise become forgotten or even lost to science also grew. For instance, 'CephBase,' a database on cephalopod species and their traits (including occurrences) available online but which was abandoned by its U.S. developers, was adopted by SeaLifeBase. Recent interest by a network of zooplankton scientists and the creator of a zooplankton traits database to include this database in SeaLifeBase opened an opportunity for submitting a proposal to a call emphasizing database sharing. While we are still waiting for news on this, we have already made plans on how to integrate this database into SeaLifeBase. Additionally, there is growing interest by parasitologists to include data on invertebrate fish parasites in SeaLifeBase.

Finally, in the longer term, we plan to merge SeaLifeBase with FishBase such that ecosystem-based biodiversity lists with life history traits can be provided to users, notably to ecosystem modelers.

FishBase and other stories at UNOC3

Cornelia E. NAUEN

Mundus maris asbl and Quantitative Aquatics, Inc.

Keywords: FishBase, SeaLifeBase, UNOC3, implementation gap, science-emotions nexus.

The first UN Ocean Conference (UNOC) took place 5 to 7 June 2017 in NY co-hosted by Fiji and Sweden. It sought to mobilize action for the conservation and sustainable use of the ocean and marine resources and breathe life into the hard-won SDG 14 'Life under water' in Agenda 2030 adopted two years earlier. This year's UNOC3 in Nice was co-hosted by France and Costa Rica with the explicit aim to place the ocean at the center of the global political agenda and accelerate action-oriented commitments from governments, companies, civil society and philanthropy for more investment into SDG14 goals. Two new treaties, the High Seas (or BBNJ) Treaty under the Law of the Sea agreed in 2023 and the Global Biodiversity Framework (GBF) under the Convention for Biological Diversity adopted at the end of 2022 put a spotlight on biodiversity. Entry into force of the BBNJ was a strong focus of UNOC3, with ratifications coming close but not completely in time. In the 35th year of FishBase and the 20th year of SeaLifeBase this can kindle fresh interest into these information systems. Our main focus at UNOC3 was in the public spaces to help visitors to connect global issues to local context. We encouraged them to sense they had agency and could use existing tools, including FishBase and the FishBase Guide app, most effectively in collaborations and through amplification wherever they were in the education system. Pointing to examples of possible change we strove to counter the widespread feeling of impotence without denying the many challenges. We found that listening and a combination of scientific information with an emotionally touching narrative or artistic expression connected more easily to visitors' ground realities, with the highest potential for any follow-up. As many voices of other organisations pointed broadly into similar directions this likely amplified effects, whether for a ban of bottom trawling particularly in marine protected areas, protecting juveniles of fish and invertebrate species, promoting low impact gears, or more emphasis on observation and healing rather than extraction for ocean protection and viable livelihoods. Such 'translations' help garner more public uptake for narrowing the implementation gap of existing laws and regulations.

Science behind the trade: safeguarding vulnerable fish species through CITES

Kelle MOREAU[1] & Christiaan CEUSTERS[2]

[1] Operational Directorate Natural Environment, Royal Belgian Institute of Natural Sciences, Belgium.
[2] CITES Scientific Advisor, FPS Public Health, Food Chain Safety and Environment, Belgium.

Keywords: life-history traits, overexploitation, species protection, CITES, policy advice.

CITES – the Convention on International Trade in Endangered Species of Wild Fauna and Flora – is an international agreement between governments, aimed at ensuring that international trade in wild animal and plant specimens does not threaten the survival of the species. Within this framework, the Royal Belgian Institute of Natural Sciences (RBINS) contributes to regulating the international trade of endangered fish species through its involvement in the Belgian Scientific CITES Committee and the EU Working Group on Sharks and Rays, the latter focusing on reconciliating views of EU Member States in a common point of view, enabling the Union to make strong cases in international discussions.

To evaluate import and export permit applications, analyse trade and exploitation trends, and assess or draft proposals for CITES listings, FishBase is routinely used to obtain life-history traits relevant for assessing species' vulnerability to overexploitation and their recovery potential, as well as for taxonomic and biogeographic reference.

Notably, we provided critical input to the successful listing of all requiem sharks on CITES Appendix II, requiring proof of legal origin for all transactions within the EU and permits for international trade as of 25 November 2023. Ongoing advisory work also includes a wide range of sharks, rays, sturgeons, eels, and species involved in the aquarium trade, such as tropical reef fish, seahorses, and freshwater stingrays. These activities illustrate the importance of science-based decision-making in the implementation of international wildlife trade regulations.

Twenty-five years of FishBase consortium membership and twenty years of capacity building in the Africa Museum: the good, the bad and the ugly

Jos SNOEKS [1,2], Gert BODEN [1] & Tobias MUSSCHOOT [1,3]

[1] Section Vertebrates, Royal Museum for Central Africa, Tervuren, Belgium.
[2] Diversity and Conservation of fishes, Department of Biology, KU Leuven (Leuven University), Leuven, Belgium.
[3] Belgian Biodiversity Platform, Royal Belgian Institute of Natural Sciences, Brussels, Belgium.

Keywords: Africa, fishes, ichthyology, database, FishBase.

In 2000, the Royal Museum for Central Africa (RMCA) became one of the seven founding members of the FishBase Consortium and assumed responsibility for African fish data.

As the updating got up to speed, the African continent emerged as probably the best-covered major region in FishBase, a far from trivial achievement, underappreciated outside of the FishBase community, because of the obvious lack of immediate groundbreaking effects.

A second corner stone of the FishBase-for-Africa project was capacity building. Each year a three-month intensive training in FishBase and Fish Taxonomy was held, resulting in nearly 90 trained African ichthyologists from 21 countries. Many of these trainees are now leading ichthyologists in their national research communities. The programme was reinforced through return study visits and four local training sessions.

We tested the Aquamaps tool, designed to model and predict occurrences of marine species, on African freshwater systems. A directly related innovation was the development of AfriBasins and its implementation in the ecosystems classification in FishBase. AfriBasins is a standardised delineation and classification framework for African inland waters, which facilitates the analysis of fish distributions by mapping river and lake (sub-)basins consistently across the continent. The team embarked in collaborative programmes with IUCN and FAO and, with the Los Baños FishBase team, produced a FishBase DVD version, improving access to the data in areas with limited internet connectivity. Joint research efforts led to numerous co-authored publications, often with former trainees, including a major identification guide to the African fresh and brackish water sardines, herrings and anchovies, a group of large economic importance.

From 2013, FishBase days were organised during the five-yearly Pan-African Fish and Fisheries Association (PAFFA) meetings. Each time, fifteen former trainees were funded to attend the meeting. At these conferences, roughly one-third of the presentations were (co)authored by African scientists trained by or collaborating with the ichthyology team of the RMCA. The RMCA also hosted the annual FishBase consortium meeting and symposium four times.

More recently, the team produced fact sheets on 20 economically important African fish species, and drafted a guide to Mozambique's freshwater fishes. A major milestone was the PhD of Laban Musinguzi (Uganda), who applied data-poor assessment methods for the first time to African inland fisheries. Just as the FishBase-for-Africa project was turning towards further pioneering studies on African inland fisheries, administrative and funding issues brought the whole initiative with this promising new trajectory to an abrupt halt.

Building capacities on taxonomy, ecosystem monitoring and science-based decision-making for sustainable fisheries in Africa and Asia

Anne-Julie ROCHETTE[1], Thomas WOUTERS[1], Pierre HUYBRECHTS[1],
Geneviève LACROIX[2], Alice VANDOMMELE[1], Tania D'HAIJÈRE[1],
Han DE KOEIJER[1] & Luc JANSSENS DE BISTHOVEN[1]

[1] Capacities for Biodiversity and Sustainable Development (CEBioS programme), Institute of Natural Sciences, Rue Vautier 29, 1000 Brussels, Belgium.
[2] Ecosystem Modelling (ECOMOD), Institute of Natural Sciences, Rue Vautier 29, 1000 Brussels, Belgium.

Keywords: capacity building, science-policy interface, sustainable fisheries, marine modelling, international cooperation.

The CEBioS programme of the Institute of Natural Sciences, funded by the Belgian Development Cooperation, aims to strengthen scientific and institutional capacities in its African and Asian partner countries. It supports capacity-building in taxonomic research, ecosystem monitoring, policy support and awareness raising, including in fish ecology and systematics, fisheries management and marine modelling. CEBioS promotes inclusive participation, with particular attention to engaging women scientists.

Data quality, availability and accessibility remain key challenges in CEBioS' partner countries, and online data portals are often underused due to limited infrastructure and capacities. CEBioS addresses this challenge through training workshops for scientists, decision-makers and managers.

In Benin, Democratic Republic of the Congo (DRC) and Vietnam, institutional collaboration on marine ecosystem modelling informs sustainable management of shrimp and oyster fisheries and water quality.

CEBioS helps reinforcing the science-policy interface through workshops gathering scientists and decision-makers that help translating scientific data into policy-relevant biodiversity indicators and recommendations. The workshops are followed by calls for projects to mobilise biodiversity data for sustainable management and informed decision-making and red list assessments. Some projects focus on data mobilisation and fisheries-related indicators in DRC and Uganda, supporting sustainable fisheries management and feeding freshwater data portals and policies. In DRC, follow-up projects awareness led to the creation of a commission to accelerate the adaptation of fishing regulations, to reduce overfishing and illegal practices. In Uganda, a project improved access to freshwater biodiversity data in the Lake Edward by mobilising datasets and developing indicator modules.

CEBioS promotes taxonomic research by funding scholarships in Belgium, where Belgian experts tutor students and researchers from partner countries. They learn and strengthen their capacities in the identification of freshwater and marine fish species, specimen preparation and conservation, use of taxonomic keys and data publication through platforms such as GBIF and FishBase. In-country projects are also supported, with tutors delivering local training, leading to the creation or strengthening of fish collections in universities.

CEBioS also supports Protected Areas (PA) management teams and their research partners to improve sustainable management in and around PAs, and human use of natural resources (ecosystem services) to conserve biodiversity. In Senegal, one project selected through a call will be focusing on the spatio-temporal monitoring of the bioecology of *Mugilidae* and *Cichlidae* for sustainable ecosystem management of the Gandoule Marine Protected Area.

These efforts demonstrate how cooperation fosters science-based decision-making, sustainable fisheries, and biodiversity conservation in African and Asian partner countries.

The Series *Abc Taxa* as a capacity building initiative & tool to advance taxonomy and collection management

Yves SAMYN

Conservator-in-Chief, Recent Invertebrate Collections and Editor-in-Chief *Abc Taxa*, Royal Belgian Institute of Natural Sciences, Brussels, Belgium.

Keywords: taxonomy, collection management, capacity building.

In 2006, the capacity building series *Abc Taxa* was established under the program of the Belgian Global Taxonomy Initiative and this with funding from the Belgian Development Cooperation. The aim of this new series was to establish a toll-free information highway for taxonomic and curatorial capacity and this to advance taxonomic research and collection management in developing countries. The series was conceived as a joint effort of Belgium's three most important natural history collections, being the (i) Royal Belgian Institute of Natural Sciences in Brussels, (ii) the Royal Museum for Central Africa in Tervuren and (iii) the National Botanic Garden in Meise. So far 24 volumes have been released, ranging in taxon from echinoderms to poriferans and from mushrooms to algae with an extensive special edition on field recording techniques for All Taxa Biodiversity Inventories and Monitoring protocols. This contribution highlights the need for this series, introduces its contents and at the same time serves as an invitation for eventual future contributions through the SeaLifeBase and FishBase platforms.

The integration of FishBase into decision support tools for the conservation of fishes of Uganda

Laban MUSINGUZI[1] & Vianny NATUGONZA[2]

[1]National Fisheries Resources research Institute, P.O. Box, 343, Jinja Uganda.
[2]Maritime Institute, Busitema University, Tororo, Uganda.

Limitations on data and information to support conservation decisions at local levels make the conservation of freshwater taxa to lag behind terrestrial and marine biodiversity. This presentation will demonstrate how information on fishes of Uganda available through FishBase is being integrated into decision support tools to guide freshwater conservation research and decision making. The conservation tools developed include species distribution maps scaled down to Uganda, a national red list for the fishes of Uganda, and a digital platform for dissemination and information sharing. The national red list was the first for the fishes of the country, enabling the species to catch up with terrestrial taxa with national red lists. With increasing evidence on the use of the generated conservation tools in research, capacity building, and advocacy, the integration of Fishbase into data and information products has potential to facilitate local conservation and research actions.

North-South collaboration for research using relatively unexplored approaches at the local level for the benefit of freshwater and brackish water fish biodiversity in Benin: achievements, challenges and prospects

Rodrigue Orobiyi Edéya PELEBE [1,2,*], I. IMOROU TOKO [1] &
Maarten VAN STEENBERGE [3]

[1] Research Laboratory in Aquaculture and Aquatic Ecotoxicology, Faculty of Agronomy, University of Parakou, Parakou, Benin.
[2] Centre for Coastal Management, University of Cape Coast, Cape Coast, Ghana.
[3] Operational Directorate Taxonomy and Phylogeny, Institute of Natural Sciences, Brussels, Belgium.
[*] Correspondence: peleberodrigue@yahoo.fr; tel. 00229 (01 96 97 57 62)

Keywords: ichthyofauna, DNA barcoding, fish collection, capacity building, Benin.

The fresh and brackish waters of Benin are home to a rich biodiversity of 221 fish species. Since 2019, the Research Laboratory in Aquaculture and Aquatic Ecotoxicology (LaRAEAq) at the University of Parakou in Benin, in collaboration with the Molecular Systematics Laboratory of the Institute of Natural Sciences in Belgium, has initiated a research programme on integrative taxonomy and genetics of freshwater and brackish water fish populations in Benin, with the support of the CEBioS (Capacities for Biodiversity and Sustainable Development) programme. In this context, three training and laboratory facility utilisation visits to Belgium and two visits for data collection and local capacity building in Benin have been carried out. A unit for basic molecular work was also set up at LaRAEAq. DNA barcoding research confirmed in a scientific publication the identity of an invasive fish species that had dominated the native species in a water reservoir in Savè and identified its affinities with several other natural populations within the Ouémé River basin. COI sequences are generated for nearly 90 freshwater and brackish water species. A physical collection of fish with which these sequences can be linked has been set up at LaRAEAq and constitutes the University's very first fish collection. To assess the impacts of habitat changes linked to historical human interventions such as the creation of the port, the digging of the Cotonou channel, increasing pollution, and increased fishing pressure on fish biodiversity in the Lake Nokoué-Porto-Novo Lagoon complex in southern Benin, a comparative analysis of recent data collected as part of our collaboration is being carried out with data from the 1960s available at the Institute. In addition, Belgian and Beninese students are supervised for their theses on research issues related to fish biodiversity in Benin. The main challenge remains the mobilization of long-term funds to continue the research. Looking ahead, our priority is to sequence all 221 species, place their specimens in the local collection at the University of Parakou, and publish several other scientific articles from currently existing and future data.

FishBase
natural
sciences
.be
SeaLifeBase

Fishy business: using genetic diversity to hook sustainable fisheries

Cheuk-Ho WU [1,*], Timonthy PARAKIKAY [2] & Celia SCHUNTER [1]

[1] The Swire Institute of Marine Science, The University of Hong Kong, Hong Kong, China.
[2] Quantitative Aquatics, Laguna, Philippines.
[*] Email: wcheukho@hku.hk

Keywords: genetic diversity, fisheries management, food security, Indo-Pacific.

Global fisheries face escalating challenges, with marine biodiversity in decline and coastal communities increasingly vulnerable. Science-based tools are urgently required to support sustainable management, particularly in regions affected by overfishing and weak governance. Genetic diversity is a key indicator of species resilience, as greater diversity is often associated with increased adaptability to environmental changes. However, overfishing and other anthropogenic pressures erode genetic diversity, leaving species more susceptible to collapse and underscoring the need for targeted interventions.

These challenges are particularly acute in the Indo-Pacific region, a biodiversity hotspot under severe anthropogenic pressure, where species information remains poorly catalogued, and genetic data—though available—is fragmented and often inaccessible due to the lack of a unified platform for consolidation and dissemination.

To address this gap, FishBase—one of the world's most comprehensive finfish databases—has partnered with the Swire Institute of Marine Science (SWIMS) at the University of Hong Kong to develop a genetic diversity risk indicator. This simple, user-friendly metric harnesses existing genetic data to support fisheries planning and safeguard future food security.

By consolidating genetic data and fostering collaboration among researchers and stakeholders, this initiative seeks to bridge knowledge gaps and improve our understanding of marine biodiversity. These efforts aim to contribute to sustainable fisheries management, helping to ensure the long-term health of vital ecosystems and the livelihoods of communities across the Indo-Pacific and beyond.

From species lists to sequences: building regional genetic databases by leveraging FishBase and SeaLifeBase

Nergiz DUKAN [1,*], Isolde CORNELIS [1] & Sofie DERYCKE [1]

[1] Flanders Research Institute for Agriculture, Fisheries and Food (ILVO), Jacobsenstraat 1, Oostende, Belgium.
[*] Email: nergiz.dukan@ilvo.vlaanderen.be

Keywords: eDNA metabarcoding, reference sequence database, biodiversity monitoring, fish, benthos.

Environmental DNA (eDNA) metabarcoding has revolutionized biodiversity and impact assessments in marine ecosystems. Its non-invasive and cost-effective nature led to its increasing adoption by both research institutions and private companies, particularly those required to comply with EU environmental monitoring directives. eDNA monitoring simplifies the sampling process and improves the sampling capacity by enabling sample collection across a large geographical scale, as well as in areas inaccessible to traditional methods such as trawling.

However, the accuracy of species detection in eDNA analyses critically depends on the quality of the reference sequence database. In region-specific monitoring, the presence of non-native species in the reference database can lead to false positives, while the absence of locally occurring species may result in false negatives. To minimize these errors and improve both the reliability and regional relevance of eDNA analyses, it is essential to construct accurate, FAIR (Findable, Accessible, Interoperable, Reusable), and comprehensive reference databases.

We address this challenge by leveraging FishBase and SeaLifeBase to construct curated reference databases for fish and macrobenthos in the BPNS. Country-specific occurrence data were used to generate targeted species lists that reflect local biodiversity. These lists then guide the extraction of genetic marker sequences from public repositories such as NCBI and BOLD, enabling the construction of regionally tailored reference databases. This approach ensures that the resulting reference sequence databases are geographically grounded and leads to more accurate, reproducible and eDNA-based monitoring in marine ecosystems.

High expectation, low implementation: perceptions of African fish and fisheries experts on genetic indicators in fisheries management

Leona J.M. MILEC[1,2,3], Maarten VAN STEENBERGE[1,4], Jean HUGÉ[1,5,6,7],
Joost A.M. RAEYMAEKERS[2], Sophie VAN SCHOUBROECK[8] &
Maarten P.M. VANHOVE[1]

[1] Research Group Zoology: Biodiversity and Toxicology, Centre for Environmental Sciences, Hasselt University, Agoralaan Gebouw D, B-3590 Diepenbeek, Belgium.
[2] Faculty of Biosciences and Aquaculture, Nord University, Universitetsalléen 11, 8026 Bodø, Norway.
[3] PXL BIO-Research, Hogeschool PXL, Agoralaan Gebouw H, B-3590 Diepenbeek, Belgium.
[4] Operational Directorate Taxonomy and Phylogeny, Royal Belgian Institute of Natural Sciences, Vautierstraat 29, B-1000 Brussels, Belgium.
[5] Laboratory of Systems Ecology and Resource Management Research Unit, Department of Organism Biology, Université Libre de Bruxelles - ULB, Av. F.D. Roosevelt 50, CPi 264/1, Brussels, 1050, Belgium.
[6] Ecology and Biodiversity, Laboratory of Plant Biology and Nature Management, Biology Department, Vrije Universiteit Brussel - VUB, Pleinlaan 2, VUB-APNA-WE, Brussels, 1050, Belgium.
[7] Department of Environmental Sciences, Open University of the Netherlands, Valkenburgerweg 177, Heerlen, 6419AT, the Netherlands.
[8] University of Antwerp, Department of Engineering Management, Prinsstraat 13, 2000 Antwerpen, Belgium.

Genetic indicators are valuable tools for monitoring the resilience and distinctiveness of fish populations. Despite their growing relevance in sustainable fisheries management, the adoption of these indicators remains limited on a global level, particularly in regions like Africa where genetic infrastructure and training are less developed. To better understand global perspectives on genetic indicators, we conducted an online survey of 122 fish and fisheries professionals spanning both African and non-African countries, gathering insights on their awareness, usage, and perceptions of genetic and non-genetic indicators. Our findings show broad awareness and support for genetic tools, with African respondents expressing especially high willingness to implement them. However, actual implementation lags behind, primarily due to resource and capacity constraints.

Our study highlights the need for acknowledging regional differences, lifelong training, centralized genetic services, and better utilization of existing data infrastructures. Addressing regional disparities and fostering collaborations through shared databases like FishBase will be critical for inclusive, effective fisheries management on a global level. We discuss how genetic indicators can be integrated with existing biodiversity and fisheries databases and how established frameworks can be leveraged.

Reconstructing freshwater biogeography using catfish genomes

Julien GASPARD[1], Archimède MULEGA[1,2,3], Jos SNOEKS[4,5] &
Maarten VAN STEENBERGE[1,2]

[1] Operational Directorate Taxonomy and Phylogeny, Royal Belgian Institute for Natural Sciences, Vautierstraat 29, 1000 Brussels, Belgium.
[2] Research Group Zoology: Biodiversity and Toxicology, Centre for Environmental Sciences, Hasselt University, Diepenbeek, Belgium.
[3] Département de Biologie, Centre de Recherche en Hydrobiologie, B.P. 73, Uvira 11215, Democratic Republic of the Congo.
[4] Vertebrates Service, Royal Museum for Central Africa, Leuvensesteenweg 17, 3080 Tervuren.
[5] Fish Diversity and Conservation, Biology Department, KU Leuven, Belgium.

Keywords: biogeography, phylogenomics, Africa, whole genome analyses, barcoding.

Africa has a complex hydrology that was shaped by geological events such as the East African rifting and the Kalahari uplift. Additionally, historical climate fluctuations also altered drainage patterns, with profound impacts on aquatic organisms such as freshwater fishes. As such changes influenced the population dynamics of freshwater fishes, they also left their mark in their genomes. Hence, genetic and genomic analyses can be used to date and describe hydrological changes. However, many freshwater species have restricted distributions or speciated only recently, hindering their use in such an approach.

Here, we propose a model species for the use of genetic and genomic data in freshwater biogeography: the African sharptooth catfish, *Clarias gariepinus*. This is the tropical freshwater fish species with the largest distribution range, encompassing most of Africa and the Levant. As an opportunistic predator that possesses the ability to breath atmospheric oxygen and to move over land, it can withstand adverse ecological conditions. Genomic data, combined with fossil calibrations, revealed the species to be at least 4 myr old.

A study of mitochondrial markers from over 400 individuals from 97 localities suggested the origin of the species to lie in lakes Kivu and Edward. Although currently disconnected and draining towards the Congo and the Nile, respectively, these lakes used to be part of the drainage basin of a single paleolake: Lake Obweruka, before its drainage was severed due to the uplift of the Virunga mountains. Mitochondrial markers also revealed a small degree of variation within North and West Africa, within the central part of the Congo basin, and across southern Africa. High levels of differentiation are, however, found between these regions, giving support for some, but not all of the ichthyofaunal provinces in which Africa is traditionally divided.

Whole genome analyses based on 137 catfish genomes and following two approaches, using ultra conserved elements (UCE) as well as single nucleotide polymorphisms (SNPs), also revealed the centre of origin of the species to lie in East Africa. These analyses also showed a high level of homogeneity within the Congo Basin and within southern Africa. However, contrary to the mitochondrial data, they revealed a complex pattern of hybridisation with a closely related species, *C. anguillaris* in North and West Africa: the region where the two species co-occur. This suggests that the taxonomic status of the two species might need to be re-evaluated.

Connectivity of coral reefs and mangroves in the Indian Ocean

Marc KOCHZIUS[1,*], Debora Mussa BENJAMEN[1], Axel DE PAUW[1], Kushlani DISSANAYAKE[1,2], Min HUI[3], Filip HUYGHE[1], Winnie A. NG'ENDO IKINYA[1,4], Agus NURYANTO[5], Levy OTWOMA[1,4], Hajaniaina A. RATSIMBAZAFY[1,6], Rosa VAN DER VEN[1,7] & Annelore VAN NIEUWENHOVE[1]

[1] Marine Biology – Ecology, Evolution & Genetics, Biology Department, Vrije Universiteit Brussel (VUB), Brussels, Belgium.
[2] Faculty of Fisheries and Marine Sciences & Technology, University of Ruhuna, Sri Lanka.
[3] Key Laboratory of Experimental Marine Biology, Institute of Oceanology, Chinese Academy of Sciences, Qingdao, China.
[4] Kenya Marine and Fisheries Research Institute (KMFRI), Mombasa, Kenya.
[5] Faculty of Biology, Jenderal Soedirman University, Purwokerto, Indonesia.
[6] Institut Halieutiques et des Sciences Marines, University of Toliara, Toliara, Madagascar.
[7] Marine Animal Ecology Group, Wageningen University, Wageningen, The Netherlands.
[*] Email: marc.kochzius@vub.be

All co-authors are in alphabetic order.

So far, connectivity of populations in the Indian Ocean (IO) was rather understudied and no comprehensive picture could be drawn based on the available data. However, this has changed in recent years and meanwhile a growing number of connectivity studies based on genetic data (mtDNA, microsatellites and genome wide SNPs) are published or under way. Even though there are differences in spatial scale, study region and genetic marker used, some general patterns of gene flow are emerging from these different studies on a growing number of coral reef and mangrove dwelling animals. On the large scale of the IO and adjacent seas, the following genetically differentiated regions can be observed: (1) Western Indian Ocean (WIO), (2) Red Sea (RS), (3) Persian Gulf (PG), (4) South Indian Shelf and Bay of Bengal (BoB), and (5) Eastern Indian Ocean (EIO). This genetic structure is congruent with large-scale oceanographic patterns, such as the narrow connections of the RS and PG to the IO, the gyre in the BoB and the large stretches of open ocean between the WIO and EIO. Prevailing currents, gyres and isolation-by-distance are apparently shaping the genetic structure of all these different taxa in the same way. The emerging pattern of a common genetic structure in coral reef and mangrove fauna of the WIO could be summarised as follows: (1) North/East Madagascar, (2) South/Southwest Madagascar, (3) Southwest Madagascar and northern Mozambique Channel, (4) South Mozambique and (5) Tanzania and Kenya.

Future studies utilising genome-wide SNPs analysed by Next-Generation-Sequencing are needed to receive a comprehensive picture of connectivity in the IO. This is needed for a proper spatial arrangement of marine protected areas in a IO-wide network that matches the general connectivity pattern. This will enable sustainable management of marine living resources in the IO in order to reach SDG 14 (life below water).

Fish community structure and diversity in the Tampolo Lagoon, Madagascar: an integrative ichthyological inventory

Martin VAN YPERSELE [1,2,*] , Léa FOURCHAULT [2,3], Brigitte SEGERS [4], Julien GASPAR [2],
Harold TODIZARA [5], Maarten VAN STEENBERGE [2,†], Gaëtan TSIRESY [5,†] &
Bruno FRÉDÉRICH [1,†]

[1] Laboratory of Evolutionary Ecology (FOCUS), University of Liège, Building B6C – Evolutionary Ecology, Quartier Agora, 11 Allée du Six Août, 4000 Liège, Belgium.
[2] OD Taxonomy and Phylogeny, Royal Belgian Institute of Natural Sciences, 29 Vautierstraat, Brussels-1000, Belgium.
[3] Systems Ecology and Resource Management, Université Libre de Bruxelles, La Plaine, 2 Boulevard du Triomphe, Ixelles-1050, Belgium.
[4] BopCo, Royal Belgian Institute of Natural Sciences, 29 Vautierstraat, Brussels-1000, Belgium.
[5] Analanjirofo University, Route de Mananara, Fénérive Est, Analajirofo, Madagascar.
[†] These authors provided equal supervision.
[*] Corresponding author: Martin.VanYperseleDeStrihou@student.uliege.be

Transitional ecosystems such as coastal lagoons, floodplains, and mangroves play a crucial socio-ecological role, but remain largely under-protected. Madagascar, isolated from mainland Africa for approximately 88 million years, is recognized as a global aquatic biodiversity hotspot, with a high degree of endemism. The eastern coast of Madagascar harbours many of these transitional ecosystems, which are exploited as fishing grounds. The current lack of data hinders policy recommendations to preserve these ecosystems. In this context, the Tampolo Lagoon was investigated to better understand its fish community structure. Specifically, this study aimed at (i) conducting an integrative fish inventory combining morphological identification using FishBase, and DNA-barcoding, and (ii) assessing species diversity, community composition, and demographic structure. Standardized fish sampling was complemented by purchases from local fishers. All fishes were measured, weighed, and their tissue were sampled for genetic analyses. Twelve eDNA water samples were also collected, to verify the presence of relict populations of *Paretroplus polyactis* (analysis in progress). A total of 12 morphospecies was captured in experimental nets, representing 364 individuals and ~2.19 kg of biomass. Including fisher catches and pseudo-cryptic species identified through DNA-barcoding (e.g., *Gerres filamentosus* and *Gerres methueni*, indistinctively referred to as 'Fiampotsy' by local fisherpeople), 17 species were recorded. The universal barcoding COI fragment was adequate to identify most species, but the endemic *Sauvagella madagascariensis* could only be identified through 12S barcoding. This study enriched GenBank by generating novel sequences for the following species: *Ambassis ambassis*, *Leiognathus equula*, and *Gerres methueni* (12S), *Sauvagella madagascariensis* (COI), *Scatophagus tetracanthus* (COI and 12S). Among the recorded species, 14 are native to Madagascar, and two are strict endemics: *Ptychochromis grandidieri* and *Sauvagella madagascariensis*. The presence of the invasive *Oreochromis mossambicus* was also confirmed, suggesting anthropogenic introduction and potential ecological risk. Community composition was heavily dominated by *Ambassis ambassis*, accounting for over 87% of total abundance and up to 83%

of biomass. A comparison with FishBase’s theoretical lengths and lengths at sexual maturity revealed that most of sampled fishes were juveniles or sub-adults, with adults representing < 2%. These findings underscore the biological richness and ecological vulnerability of the Tampolo Lagoon. Two priority management actions are proposed: protecting large carnivorous species through minimum catch size regulations, and establishing no-fishing zones or seasonal closures to enhance ecosystem resilience.

Fish n’ Ships Aegean Sea - a tabletop dive into marine conservation

Donna DIMARCHOPOULOU, Ioannis KERAMIDAS & Athanassios C. TSIKLIRAS

Laboratory of Ichthyology, Department of Zoology, School of Biology, Aristotle University of Thessaloniki, 54124, Thessaloniki, Greece.
MarinOmics Research Group, Center for Interdisciplinary Research and Innovation (CIRI), Aristotle University of Thessaloniki, 57001, Thessaloniki, Greece.

Keywords: food webs, sustainability, marine fisheries, Aegean Sea, gamification.

Teaching marine sustainability and ecosystem dynamics in an engaging yet scientifically robust way remains a challenge. *Fish n’ Ships* addresses this need through an educational tabletop game designed for 2–4 players that was initially developed by the National Institute of Oceanography and Applied Geophysics (OGS). The *Aegean Sea* version simulates the management of fisheries and marine ecosystems in the Aegean Sea, Greece. Players compete to manage their “slice” of the sea while navigating the complex trade-offs between sustainable fishing, biodiversity conservation, and climate-driven changes in warming waters. Designed to be both engaging and educational, the game invites players to build and protect their marine food webs using real-world ecological relationships. As they fish, apply management tools like marine protected areas, and deal with adverse environmental pressures like climate change, players quickly learn how fragile marine ecosystems can be – and how strategic choices can lead to profit or losses, resilience or collapse. The game is tailored to the unique species, fisheries, and challenges of the Aegean Sea, featuring region-specific species like sardines, red mullet, and dusky groupers, alongside real-world fishing gear used in local waters like purse seines. Players take on the role of fishers, scientists, or policymakers, balancing environmental, social, and economic factors to build thriving fisheries. In doing so, they face the same kinds of trade-offs that shape marine policy today. Grounded in current ecological and fisheries science, the game introduces concepts such as ecosystem-based management, food webs, fishing impacts, and climate adaptation strategies in an accessible, interactive format. The gameplay is grounded in the ECOPATH food web model that was developed for the Aegean Sea (Keramidas *et al*. 2022) bringing real ecological data to life through interactive play. This tool aims to support experiential learning for students, stakeholders, and the general public, fostering a deeper understanding of sustainability challenges and decision-making in marine systems. It is more than just entertainment, it is a learning tool that promotes curiosity, systems thinking, and dialogue about the future of our oceans.

Reference

Keramidas I., Dimarchopoulou D. & Tsikliras A.C. 2022. Modelling and assessing the ecosystem of the Aegean Sea, a major hub of the eastern Mediterranean at the intersection of Europe and Asia. *Regional Studies in Marine Science* 56: 102704. https://doi.org/10.1016/j.rsma.2022.102704

FishBase

natural
sciences
.be

SeaLifeBase