



21ST FISHBASE/SEALIFEBASE SYMPOSIUM

**Royal Museum for Central Africa
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21st FishBase/SeaLifeBase Symposium

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Presentation of ichthyological activities at the Royal Museum for
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Heleen Maetens, Arthur Boom, Jos Snoeks, Maarten Van Steenberge
and Nathan Vranken, supplemented by posters with more information
for consultation during the breaks.



Use of FishBase and SeaLifeBase in a new stock assessment tool

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Models for the estimation of productivity and current versus maximum population size, such as needed in fisheries management and conservation, typically need as starting point life history parameters that are not readily available and often difficult to observe. Examples are (1) the maximum rate of population growth, i.e., how long will it take for a population to recovery from depletion; (2) the rate of natural mortality; (3) maximum length or weight; (4) the length where 50% of the individuals mature for the first time; (5) reproductive strategy (one-time-spawning or multiple spawning events); (6) spawning season; (7) fecundity; and (8) longevity. All this information can be found in FishBase or SeaLifeBase, and while it may not be directly applicable to the population in question, it certainly provides a likely range of values from the existing literature for the species, which is exactly what so-called priors are expected to do. In the presentation we show how FishBase/SeaLifeBase is used by a recent stock assessment toolbox (ABC) to provide this crucial information. The ABC toolbox consists of an R shiny interface applications for several stock assessment methods (AMSY, CMSY, BSM, LBB), each one of which follows the Bayesian approach.



Mining the fossil record to reconstruct the diversification of fishes

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Determining the drivers of divergence between species is at the core of evolutionary biology; how these mechanisms scale up to the diversification of major groups (clades) is at the core of macroevolution (evolution at the species level and above). A full picture of diversification requires information from multiple areas of organismal biology (e.g. development, biomechanics, phylogenetics) and ecology (e.g. community dynamics, environmental factors), preferably at multiple scales (e.g. spatial, temporal, molecular, and taxonomic). Fishes can provide essential data on all these aspects. The records of the 34,000 living species of fishes are enhanced by the abundant fish fossil record that stretches back 450 million years and includes the ancestors of all living vertebrate clades. Here, I show how the synthesis of phylogenetics, trait databases, and ecosystem-level investigations of fossil fishes are challenging our views of diversification, as well as mass extinction and the origins of modern marine ecosystems. Quantitative analyses of species-rich fossil clades have revealed unexpected roles for diet, species interactions, habitat choice, and even life histories in determining the fate of nascent radiations, particularly after global environmental events. These discoveries contribute to a new understanding of the drivers determinative of diversification.



Seascape guardians: empowering divers and snorkelers with AI fish identification for conservation

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The world's oceans are teeming with a diverse array of marine life, yet the identification and documentation of these species remain challenging, impeding our understanding of marine ecosystems and hindering conservation efforts. The following idea presents a novel concept that leverages technological innovation and citizen science to address this issue by introducing an app to engage divers and snorkelers in the collection of crucial data for marine conservation through the use of artificial intelligence (AI).

The proposed app seeks to revolutionize underwater exploration by combining AI image recognition technology with the enthusiasm and expertise of recreational divers and snorkelers. By allowing users to easily log and identify fish and other marine species they encounter during their underwater adventures, the app transforms them into active participants in the process of data collection for conservation purposes. This innovative approach not only harnesses the power of citizen science but also provides a valuable resource for researchers and conservationists working to protect fragile marine ecosystems.

In the first place the app will be a digital diver's log book. The app's AI image recognition capability forms the core of its extended functionality. Users can capture images of marine life, which are then processed by the AI to identify the species. This automated identification process reduces the reliance on manual expertise, making it accessible to a broader audience and enabling rapid data collection on a larger scale. Moreover, the app will contribute to the

enrichment of species databases and the development of comprehensive species distribution maps, aiding conservationists in making informed decisions and formulating effective conservation strategies.

The app will be developed by the Germany based company Sunbird Images OHG through collaboration between technology developers, marine scientists, and conservationists, the proposed app aims to bridge the gap between the diving and scientific communities. By making marine data collection engaging, accessible, and impactful, the app transforms everyday divers and snorkelers into crucial contributors to marine conservation efforts. The AI empowers users with accurate species identification promoting a sense of stewardship towards marine environments.

In conclusion, the idea of creating an app for divers and snorkelers to log and identify fish and other marine species with AI has the potential to revolutionize marine data collection for conservation purposes. By leveraging the enthusiasm and expertise of citizen scientists, this app offers a collaborative approach to gathering vital information about marine ecosystems, ultimately contributing to the protection and preservation of the world's oceans.



‘You can’t catch me’: increasingly more non-native freshwater fishes in Flanders (Belgium)

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Considering the recent EU regulation 1143/2014 on the prevention, early detection and rapid eradication, and management of invasive alien species (EC, 2015) it is important that all member states, after non-native organisms have been discovered, follow up the invasive populations. Reporting on non-native species’ presence, spread and also pathways is an important part of the regulation’s obligations. Verreycken et al. (2007) reviewed the non-native freshwater fish species in Flanders (North Belgium) and described the status, pathways and trends of the 14 non-native freshwater fish species present at that time. Now, 16 years onwards, already 29 non-native freshwater fishes have been recorded in this small area (13 522 km²). While certain species, such as *Ictalurus punctatus*, are only known from a singular discovery, others, such as *Neogobius melanostomus*, have proliferated significantly and now exist in great numbers across many areas over the past five years. We will discuss all the non-native freshwater fishes present in Flanders and highlight their distribution, origin and pathways but also their impact and invasiveness. We will also consider non-native fish species that are currently present in nearby regions and expected to migrate to Flanders in the future.



One fish, two fish, red fish, blue fish: how FishBase adds ecological value to video-derived data on diversity, abundance and size

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Species richness, abundance and size are core metrics estimated by ecologists. These metrics provide a common (non)species-specific currency that allows ecologists to explore, amongst other questions, large-scale biogeographical patterns such as those described by the Latitudinal Diversity Gradient and Bergmann's Rule on size. However, there is a host of other species-specific data, curated by FishBase, that augment an understanding otherwise based on just diversity, abundance and size. We deploy baited remote underwater video systems (BRUVS) that specifically capture information on taxonomic identification, abundance and size. These data are expanded, for instance, by incorporating attributes such as trophic level, phylogenetic diversity, fishing vulnerability and IUCN status to characterise fish assemblages from functional and conservation perspectives.



Fishy business: using genetic diversity to hook sustainable fisheries in South China Sea

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The South China Sea is one of the most species-rich marine areas. However, due to severe anthropogenic pressures, the marine life in this region is at risk. In addition, species information is poorly inventoried creating a significant knowledge gap for facilitating marine conservation. To address this gap, FishBase/SeaLifeBase and the Swire Institute of Marine Science (SWIMS) at the University of Hong Kong initiated a collaboration leading to SWIMS becoming the Asian marine node of the FishBase Consortium. Over the course of four years, SWIMS collated and encoded approximately 10,000 records for over 2,000 species in Hong Kong and adjacent regions. This effort is a significant step towards addressing the knowledge gap and facilitating marine conservation in the region. However, there is still much work to be done.

FishBase is constantly being adapted to meet suggestions and new needs. SWIMS is aiming to utilize the wealth of existing, but currently scattered genetic diversity data to develop a simple and easy-to-understand metric – the genetic diversity risk indicator, which can assist in effective fisheries planning with the goal of safeguarding food supply for the future. By identifying the genetic diversity of species in the South China Sea, fishery managers and stakeholders can make informed decisions about sustainable fisheries practices.

Through this presentation, SWIMS seeks to connect with more researchers and fishery management stakeholders to create a collective

effort for a more sustainable future. By working together, we can better understand the marine environment in the South China Sea and take meaningful steps towards conserving it for future generations.



Application of the Gill-Oxygen Limitation Theory to the Elasmobranchs: surprising and beautiful results

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The Gill Oxygen Limitation Theory (GOLT) is a single unifying theory based on the geometric constraints that gills impose on fish to explain their growth, reproduction, and much of their ecology. A major aspect of the GOLT deals with the fact that with growth, relative oxygen supply per unit weight declines, leading to a critical hypercapnic/acidic threshold, which trigger maturation, and explains why the relationship between maximum length (L_{\max}^D) and length at maturity (L_m^D) is similar across evolutionary distinct fishes, with 'D' represents gill growth relative to body weight. While well documented in bony fishes, this relationship was not tested in cartilaginous species. This was addressed by an investigation of chimaera, ray, and shark species in which at least one L_{\max}/L_m data pair could be obtained from the literature; this showed that L_{\max}^D/L_m^D is similarly conserved across marine Chondrichthyes ($L_{\max}^D/L_m^D \approx 1.14$), which is lower than in bony fish ($L_{\max}^D/L_m^D \approx 1.35$), suggesting the cartilaginous species mature at a greater fraction of their maximum size. It was hypothesized that the high concentrations of urea retained by marine Chondrichthyes, which is used for osmoregulation is the likely reason for this difference, and this was tested via comparisons of marine, euryhaline, and freshwater rays which all retain differing concentrations of urea, indicating that decreasing urea retention is correlated to an increase in L_{\max}^D/L_m^D . Overall, this work lends strong to the existence of a critical maturation threshold in fish, while also suggesting a role for urea that was previously unknown.



Alien fish species and mean temperature of the catch in the Aegean Sea

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The Mediterranean Sea, and especially its eastern part (Levantine and Aegean Seas) is considered as one of the most invaded marine regions of the world with more than 1,000 validated non-indigenous species (NIS), most of which are molluscs, fishes, and crustaceans and are regarded established. In the Greek Seas, the vast majority of NIS is being recorded in the Aegean Sea with the latest update estimating the presence of 242 NIS and 64 cryptogenic species, i.e., species of uncertain origin that cannot be demonstrably classified as native or introduced in a particular region. In the southern Aegean Sea, some of those species have established viable populations that are being commercially exploited by the local fishing fleets and widely marketed, often in large quantities. Some of them have been inhabiting the Aegean Sea since the 1940s (such as the dusky spinefoot *Siganus luridus*), some since the 2000s (round herring, *Etrumeus golanii*) and some are very recent (lionfish *Pterois miles*). However, the catch of NIS is not being officially recorded in the catch statistics of Greece or the General Fisheries Commission for the Mediterranean (GFCM); thus, the effects of these populations on ecosystems and fisheries are unknown. The aim of the present work was to update previous studies that used the preferred environmental

temperature of species to examine climate effects by including NIS in the calculations. Here, we calculated the Mean Temperature of the Catch (MTC) index for the Aegean Sea for the period 1982-2021 based on the official catch statistics (without alien species) and by using unofficial catch of NIS locally reported by fishers. The results showed that the – updated with recent catch data – MTC is increasing at higher rates compared to previous studies, which are even higher when NIS are included. This is because the preferred temperature of most NIS exceeds 25°C, which lies at the upper extreme of local species. The increasing trend is expected to persist as the abundances of NIS increase and their geographical expansion continues. We conclude that official catch statistics are not sufficient to describe ecosystem dynamics in the Aegean Sea unless they include NIS and that the effect of species invasion, which is related to sea warming, may currently be masked.



Population genomics of polar cod (*Boreogadus saida*) in a vanishing Arctic seascape

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The Arctic Ocean is experiencing rapid environmental changes, including alterations in sea-ice conditions, that have a direct impact on the organisms living in close association with sea ice. One of those organisms is the polar cod (*Boreogadus saida*), an abundant fish with circumpolar distribution and a key species in the Arctic marine food web. Despite its ecological importance, the spatial genetic population structure and connectivity are not fully understood. We used 812 high-quality single nucleotide polymorphisms (SNPs) obtained through genotyping-by-sequencing to assess the circumpolar population structure as well as local and large-scale connectivity patterns. At a circumpolar scale, four large-scale clusters are differentiated at a low, but significant level (F_{ST} ranging from 0.000 - 0.108): Alaskan Arctic (Beaufort and Chukchi Sea), West Greenland, and major and minor Transpolar Drift and East Arctic (Iceland, Laptev Sea, Central Arctic Ocean, Northeast Canada). The major and minor Transpolar Drift and

East Arctic clusters share the same region but differentiate in their genetic profile and number of individuals assigned. Sub-structuring is detected in all four groups. Connectivity driven by sea-ice drift associated dispersal of larvae and juveniles, as well as active migration by adults, and the potential presence of ecotypes with intrinsic behavioural mechanisms for migration and spawning, might explain the genetic differentiation patterns. Future disruptions in sea-ice pathways due to climate change will likely act as a barrier to gene flow and hamper connectivity of sea-ice associated larvae and juveniles. While adult dispersal may be less affected, ongoing loss of spawning habitat is likely contracting the distribution range and biomass. It will be important to monitor the evolution of the polar cod metapopulation in the future.



Estimating length at first maturity for invertebrates in SeaLifeBase

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Mean age (t_m) or mean length (L_m) at first maturity is an important parameter used in fish life history studies and in fisheries research and management. FishBase has assembled almost 9,500 population records of t_m and/or L_m for 3,185 fish species while SeaLifeBase has about 1,200 records for 468 species. Because t_m is difficult to estimate, notably for invertebrates, and acquires its full importance only when growth parameters are also available, L_m is often used as proxy. Thus, the goal of this study is to provide L_m estimates for invertebrates.

Pauly in 1981 proposed an equation of the form: $D = 0.6742 + 0.03574 \cdot \log W_{\max}$, where W_{\max} is the maximum weight (grams) and D is a parameter of the von Bertalanffy Growth Function that relates body size to fish gill surface area. D is used in the relationship $L_{\max}^D / L_m^D \approx 1.35$ and thus $L_m = L_{\max} / (1.35^{1/D})$, where L_{\max} is the maximum length. The equation applies to most teleostean fishes (except elasmobranchs and coelacanths) and to crustaceans, most mollusks (except very large squids), chaetognaths and probably other phyla. All the exceptions appear to be due to urea being used for osmotic regulation, as in sharks, coelacanths and large squids. We applied this to 120 invertebrate species without t_m or L_m estimates, but with L/W relationships and L_{\max} estimates. W_{\max} values were obtained from length-weight relationships, i.e., $W = aL^b$.

We obtained estimates of D between 0.65 to 0.84 for 63 species of Arthropoda, 0.80-0.82 for 2 species of Cnidaria, 0.74-0.84 for 7 species of Echinodermata and 0.67-0.90 for 48 species of Mollusca. The estimated mean L_{\max}/L_m was 1.48, close to independently derived ratios of 1.46 for lobsters and 1.42 for crabs. Thus, for the time being, in the absence of D estimates from an empirical relationship applying to invertebrates or specific phyla, SeaLifeBase will provide estimates of L_m using the relationship tested for fishes and crustaceans.



FishBase contribution to improve knowledge in data-poor regions: a case study on the Sea of Marmara, Eastern Mediterranean

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The Eastern Mediterranean is a typical data-poor region where it has limited or incomplete information available about various ecological, physical, and chemical parameters that are crucial for understanding and managing marine environments. Turkish waters are particularly challenging for researchers, conservationists, and policymakers because those marine regions hinder our ability to make informed decisions about marine conservation, resource management, and the effects of human activities on marine ecosystems. In this sense, FishBase plays a crucial role in bridging information gaps for researchers from data-poor regions, providing them with access to a wide range of data and knowledge that can contribute to their scientific endeavors and conservation efforts. Turkish researchers frequently use various data provided by FishBase, in which a total of 578 documents including research article, review article, book chapter, conference paper and notes were cited from 2004 to 2023.

Here, FishBase's scientific impact and its importance for data-poor regions are presented via a case study on the status of fishery resources in the Sea of Marmara. It is a semi-enclosed sea that comprises the Turkish Straits System along with the Çanakkale and Istanbul Strait and a transition zone between the Black Sea and Mediterranean Sea. The fisheries characteristic is mainly coastal for benthic/demersal species by beam trawling, and the rest is seasonal pelagic fishery by purse-seines related to seasonal migrations of

pelagic species. The total landed catch has been gradually declining in years, with the lowest catch observed during the last years. If the total catch in the 2000s is 100%, it was about 60% in 2010 and 35% in 2022. Landed catch showed dramatic declines in demersal fishes followed by pelagic fishes while trends were almost stable for small pelagic fish. The mean trophic level of the catch gradually decreased from 2000 to a minimum in the 2022 meaning withdrawal of predatory species such as European hake, turbot, and Atlantic bonito during 2000s, which led to the dominance of prey species such as anchovy, Mediterranean horse mackerel and deep-water pink shrimp in 2010s. Although total vessel number decreased by its 1/4, LPUE values did not show any increase, instead, gradually decreased after 2010, indicating stocks are declining and fishing efforts are no longer sustainable as it is.



Know your fish with FishBase and help protect it. Responding to consumer hopes for sustainable fish food

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There is significant unmet demand for purchasing decisions concerning sustainable fish and at least basic information on marine life in school curricula usually devoid of units related to the ocean and, more generally, for aquatic food production. FishBase offers a massive amount of information by species, but navigating through the plenty is not intuitive enough for many non-specialists. In addition, internet access is increasingly through mobile devices. Here we present the FishBase Guide app, which can be searched with any of the 325,900 common names in 342 languages or the scientific names of all 35,100 fish species in FishBase. Downloading for free from the Google Play Store installs the app. Upon choosing a country all names associated with species recorded for that country will download minimising the need for permanent internet access and large data volumes. The app search will return pictures for all species that contain the name used and upon choosing the fish of interest show its minimum reproductive size, the optimum size for stable maximum catches, and the maximum size recorded. It will also provide the IUCN Red List status, spawning season when available and a broad description of its distribution. Translation is also implemented. We suggest that the app provides a rather easy access to start familiarising with FishBase, particularly in response to frequent consumer demand

for guidance towards purchasing sustainably caught fish. It has also been welcomed by teachers as a ‘modern’ entry to trigger curiosity and serve as a ‘hook’ to encourage broader learning about fish biology, aquatic ecosystems and much needed responsible human stewardship.



15 years of WoRMS - Above and Beyond: completing the World Register of Marine Species

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In 2022, the World Register of Marine Species (WoRMS) celebrated its 15th anniversary. And just one year earlier – in 2021 – WoRMS has been endorsed as a project under the United Nations Decade of Ocean Science for Sustainable Development, entitled ‘Above and Beyond – Completing WoRMS’. During the UN Ocean Decade, WoRMS will continue its endeavors to provide a full taxonomic overview of all marine life, thereby not only supporting scientists, but everyone who makes use of species names, including policy, industry and the public at large. Next to addressing the remaining taxonomic gaps, new challenges in the field of taxonomy will be explored, in addition with a further focus on the documentation of relevant species traits and attributes.

Ever since the start of WoRMS, there has been a strong collaboration with FishBase. WoRMS recognizes FishBase as the key provider of taxonomic and ecological information on fish. Since 2013, WoRMS is investing in the semi-automatic synchronization of its fish-taxonomy with FishBase. This synchronization - performed on a regular basis at the WoRMS side - allows to reflect the FishBase content through WoRMS as closely and up to date as possible. For each FishBase

taxon available through WoRMS, a deep link is created to the related FishBase page and due recognition is provided to FishBase as the information provider. This allows WoRMS users to easily access the source data system, where they can possibly retrieve more information on a taxon.

In 2018, a Memorandum of Understanding was signed between WoRMS, FishBase and SeaLifeBase. This was the result of conversations during the 15th International FishBase Symposium (2017), where it became clear that not only FishBase, but also its sister-database SeaLifeBase could significantly contribute to and benefit from a collaboration with WoRMS. SeaLifeBase is especially rich in life traits data, being e.g. biological, ecological and distributional information. Linking this with WoRMS will provide benefits as well as extra recognition and visibility for both systems. A fundamental basis for this collaboration is to minimize duplication of efforts, by clearly identifying possible overlaps. The actual data flow between SeaLifeBase and WoRMS will be initiated one taxonomic group at the time, to allow the data management teams of both systems to work as efficiently as possible.



Fish-infecting monogenean flatworms: tools, threats, and targets in conservation

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The effects of the introduction of non-native species as one of the major causes of biodiversity decline worldwide are well-established. However, while conservation science increasingly devotes attention to parasites, in terms of information they can provide on their hosts, and of the decline and potential extinction threats parasites face themselves, invasion biology mainly focuses on free-living organisms. Monogenean flatworms are suitable models in the parasitology of introduced fish species. Given their one-host lifecycle (without intermediate hosts) they are more likely to be co-introduced with their hosts, and established in new ecosystems, than parasites with a complex lifecycle. Moreover, their allegedly quite narrow host-specificity ensures tight relationships with their host species, rendering monogeneans “tags” for history and ecology of their host population and host species, without other hosts as confounding factors.

With case studies on Ponto-Caspian invasive gobies in Belgium, and freshwater sardines introduced into several African lakes, we demonstrate how occurrence and identity of monogenean parasites may be informative regarding methods and pathways of fish introduction.

Special attention is devoted to Nile tilapia introduced throughout Africa. Its parasitological impact on indigenous fishes and their ecosystems is hardly studied, especially in Africa. Conservation and management lack understanding of the origin and identity of

introduced Nile tilapia strains, let alone of their parasite fauna. Monitoring only provides partial answers for want of baseline data: native parasite biodiversity is scarcely studied. Focusing again on monogenean flatworms, we investigated whether parasites were co-introduced with their non-native Nile tilapia hosts, and whether they were transmitted between native and introduced cichlids. To this end, a collection-based morphological study enabled establishing pre-introduction baselines, and distinguishing non-native from naturally occurring parasite species. We also discovered that at least one monogenean species may serve as “magnifying glass”: as it shows higher intraspecific genomic differentiation than its tilapia hosts, it can help elucidate the history of tilapia populations.

It can be safely assumed that countless fish parasite species are also of serious conservation concern, for example in view of potential co-extinction with their hosts, or competition with non-native parasites. We therefore also highlight our involvement in the recently established IUCN SSC Parasite Specialist Group.

In summary, we hope to demonstrate how our team’s parasitological work, including approaches hinging on collections and databases, aims to contribute to a better understanding of challenges in the management and conservation of not only parasites, but also their fish hosts.



Diverse linkages between distant water fleet fishing and food security

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There is widespread acknowledgement that industrial, distant water fleets (DWFs) are negatively impacting fishery sustainability and marine ecosystems, but governments have also identified DWFs as a key threat to food security. DWFs may decrease fish availability for small-scale fishers, reduce economic benefits to local fleets, and diminish opportunities for fisheries to address domestic food and nutrition needs. We used a mixed method, synthetic approach to characterize and, where possible, quantify the linkages between DWFs and host country food security with case studies in Peru, Madagascar, the Philippines, and the Pacific Islands. Our results highlight the multi-faceted and context-dependent nature of the DWF-food security relationship and quantify the contributions of four focal stocks to local nutrition needs. We use the results to present case-specific policy recommendations for improving food security and offer key themes related to DWFs, fish availability, access to fish, and aquatic food-based nutrition that can be applied globally.



Why do larvae hatch when they do?

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Hatching corresponds to the moment an individual leaves its egg envelope. Yet, hatching has scarcely aroused the interest of biologists, and the question posed here “why do larvae hatch when they do?” appears to have been rarely asked, except in the obvious context of the temperature-induced acceleration of egg development. Here, we tested the hypothesis that fish larvae hatch when a specific ratio between larval surface area and egg surface area is reached, i.e., when the oxygen supply through the egg surface becomes insufficient to cope with the oxygen requirements of the embryo. We found for 15 species a strong relationship between these two variables, suggesting that larval surface area is in all bony fish species about 2 times equal to the egg surface area. This is currently verified for more species, but if it holds, this implies that dissolved oxygen strongly constrains the incubation of fish eggs irrespective of their size, and also explains why most bony fish species produce many small eggs. We also anticipate that global changes will result in both the acceleration of the embryo development (mainly due to warming) and premature hatching of larvae (mainly due to decrease of dissolved oxygen). Most ecological consequences of these findings are unknown, but can be expected to be relevant to fisheries and aquaculture research.



Development and applications of a global harmonized zooplankton trait database

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Zooplankton research has a rich history of recording trait information. We addressed the call to centralize the previously unlinked datasets into a standardized and harmonized database. The global zooplankton trait database currently contains 56 traits on morphology, biochemical composition, physiological rates, behavior, and life history for 3,535 species encompassing seven marine zooplankton phyla. We aggregated 33 trait datasets and supplemented these with more than 150 references resulting in over 57,000 individual-level trait records which were summarized to about 15,000 trait records at the species-level. The database structure and terminologies followed the ecological trait-data standards and the Darwin Core standards, and the taxonomy was anchored to match the World Register of Marine Species. Ancillary information related to the trait records and data source provenance were retained to facilitate data curation. We assessed the trait and taxonomic coverage of the database and identified key gaps that may guide future efforts in collecting or measuring trait data. We evaluated the relative strength of associations between traits and compared the accuracy of statistical approaches in estimating trait values for species with missing trait information. Our analysis showed that the best methods are trait-specific, taxon-specific, and sensitive to the number of species observations. We will further present examples of ecological applications of the trait

database. Although the current database can be a useful resource for researchers requiring zooplankton trait information, its continued development and expansion is necessary to improve the accuracy of trait value estimates and the coverage of trait information for the diversity of zooplankton organisms. We envision that this database will engage the aquatic sciences community including ecologists, modellers, and future trait data contributors and promote trait-based research, trait data sharing, and FAIR data practices.



FLASH TALK

Provisionally valid species? The case of *Merluccius peruanus* and *Merluccius gayi*

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Ginsburg (1954) described two subspecies of *Merluccius gayi*: *M. g. gayi*, Guichenot 1848 in Chile, and *M. g. peruanus*, Ginsburg 1954, in Peru. They show an allopatric distribution with a geographical separation of ~1,300 km. *Merluccius g. peruanus* is distributed between 6°S and 14°S and *M. g. gayi* between 23°S and 47°S. Morphologically, the number of rays of the second anal and dorsal fins are the traits that separate them. These traits, together with the differences in allozymic allelic frequencies, could be plastic changes and not differences found within the subspecies. At present, the former subspecies *M. g. peruanus* was included in FishBase as *M. peruanus*, as provisional valid species, and by extension, it was accepted as valid species in the World Register of Marine Species (WoRMS). A standardized region of the mitochondrial cytochrome C oxidase subunit I (COX1) gene has been adopted as the “DNA barcode” for molecular identification in most animal groups, including

fishes. The FISH-BOL campaign has produced extensive COX1 sequences available in public databases. Sixteen *M. g. gayi* larvae were collected at 35°S to obtain DNA. A ~650 bp fragment of the COX1 gene was bidirectionally sequenced by Sanger using the COI-3 cocktail from Ivanova *et al.* (2007). They were aligned using MUSCLE v5.1 with sequences from *M. gayi* (*M. g. peruanus*, n=5 and *M. g. gayi*, n=12), *M. angustimanus* (n=9), and *M. productus* (n=49) mined from BOLD Systems and Genbank. *Merluccius angustimanus* and *M. productus* are the phylogenetically closest species to *M. gayi*. Phylogenetic reconstruction was performed with PhyML v3.3.2 plugin in Geneious Prime v2023.2.1. Species delimitation analyses were performed with Assemble Species by Automatic Partitioning (ASAP) and SpeciesIdentifier v1.8 (All Barcodes and Best Close Match methods). ML phylogenetic reconstruction showed two main haplotypes, and both are present in sequences of *M. gayi* from Chile and Peru. ASAP found five best partitions, of which four showed the *M. gayi* sequences belonging to a single group, regardless of their geographic origin (Peru or Chile). SpeciesIdentifier found a similarity threshold value of 0.33% to identify barcodes as conspecific, not being able to separate *M. gayi* (formerly *M. g. gayi*) from *M. peruanus* (formerly *M. g. peruanus*). These results cast doubt on the existence of *M. peruanus* and even the subspecies of *M. gayi*. Therefore, it is necessary to reevaluate the inclusion in FishBase of a new *Merluccius* species from the Southeast Pacific.



FLASH TALK

Assessing the vulnerability and viability in fishing households: evidence from Gulf of Guinea, West-Central Africa

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Fishing is among the most prominent and accessible economic activities for people in inland and coastal fishing communities around the world, but particularly in sub-Saharan Africa, where it provides livelihoods and essential nutrition to over 200 million people. However, there are numerous compounding threats that limit the ecosystem services provided by the ocean in supporting the food security and livelihoods of so many. This research project is part of a larger collaboration that focuses on the Gulf of Guinea along the coast of West-Central Africa (Nigeria and Cameroon), known to be a global hot spot for climate change impacts and IUU fishing, as well as illicit trade in seafood. Here, the combination of Food-Climate-Biodiversity (FCB)-related stressors exacerbates the challenges to the livelihoods, food security, and wellbeing of millions of people. This study will investigate the socio-economic attributes of fishing households with detailed references to their vulnerability to FCB stressors and strategies adopted for resilience to multidimensional poverty to attain sustainable livelihoods. The study aims to enhance the resilience of marine ecosystem services for sustainable livelihoods under climate change scenarios. Data will be sourced utilising a mixed-methods

approach and secondary data, drawing on poverty and sustainable livelihood frameworks. It also employs participatory research approaches to make recommendations for reducing vulnerability. The findings will provide key information for policies and programmes to build resilience in the FCB domain in sub-Saharan Africa, address major challenges, and empower fishing households and communities in Nigeria and Cameroon.



FLASH TALK

Coastal fish biodiversity and habitat use

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The COP15 meeting in 2022 aimed to protect 30% of land and oceans to halt biodiversity loss. For marine protected areas (MPAs), knowledge about biodiversity and habitats will be critical to ensure that they cover the full diversity of marine ecosystems. However, coastal fish biodiversity data is geographically sparse and often focused on commercial fisheries and indicator species. In particular, crypto-benthic fishes, which dominate reef biodiversity, are often excluded. Habitat diversity and fish-habitat associations are even less well documented and currently missing in FishBase.

In 2023 we carried out a 3-month visual survey of coastal fishes in Dauin (Negros Oriental, Philippines), covering seagrass, muddy, sandy, and various reef habitats between 1 and 30m depth. A total of 790 distinct fish species were documented photographically, including multiple range extensions and first records for the Philippines. This data is currently being added to FishBase as an ecosystem entry and, when completed, will be the most species rich survey from the Philippines.

Collecting, encoding and disseminating habitat diversity and fish-habitat association data is a considerably bigger challenge. Yet knowledge about habitat requirements throughout the life stages of fish species is clearly key to biodiversity conservation. It can also contribute to predictive models about the distribution potential of species. Our approach has been to use a modified roving diver survey

method where initially habitats are mapped at different scales, followed by repeat visits to these habitats during subsequent fish surveys. This is a work in progress and both theoretical issues, e.g. what habitat features are important and how to describe them, as well as practical issues regarding data collection, entry and dissemination are yet to be resolved. Input from the FishBase research community is welcome.



FLASH TALK

Taxonomy, morphology and growth pattern of pen shells in northern Iloilo, Philippines

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This study aimed to describe the morphological characteristics and growth pattern of pen shells along the coasts of northern Iloilo, part of Visayan Sea, Philippines. A total of 381 pen shell individuals were taken from the study site using compressor diving. The species were identified based on nine properties of the valve for the genus *Pinna* and eight characters for *Atrina*. These characteristics were then correlated with their adductor muscle morphology to identify species of pen shell using this adductor muscle as identifier. Analysis of variance revealed that *Atrina pectinata*, *A. inflata* and *A. vexillum* were significantly different in eight characters of the valve ($p < 0.05$) whereas *Pinna bicolor*, *P. atropurpurea* and *P. deltodes* were morphologically different on the basis of the dorsal posterior shell margin, shell width, sulcus width and the distance between posterior adductor margin and posterior nacreous margin ($p < 0.05$). The regression equations between the thickness of the adductor muscle in relation to total shell length of *A. inflata* ($r^2 = 0.80$, $p < 0.05$), *A. vexillum* ($r^2 = 0.80$, $p < 0.05$), *P. bicolor* ($r^2 = 0.88$, $p < 0.05$) and *P. deltodes* ($r^2 = 0.84$, $p < 0.05$) showed high correlation. For *A. pectinata*, highest correlation was found between the adductor muscle length and total

shell length (0.70, $p < 0.05$). The high coefficient of determination and significant p values could be a good predictor of growth and contributed to a substantive conclusion that the increase in size of adductor muscle correlates to the increase in size of shell length, and therefore could be used as an index for species identification. The relationships between length and weight of pen shells were estimated using the equation $W = aL^b$. Results showed that the length-weight relationship demonstrated positive allometric growth for *A. pectinata* ($W = 0.00001L^{3.0688}$), *A. inflata* ($0.000002L^{3.5937}$), *A. vexillum* ($0.00004L^{3.0496}$), *P. bicolor* ($0.00001L^{3.1216}$) and *P. atropurpurea* ($0.00000009L^{3.8388}$). The length-length relationships for these five species revealed that the growth of different shell lengths were symmetrical with relationship equations of total shell length to different shell length parameters highly significant ($p < 0.05$) with an r^2 values range of 0.65-0.99. Since there is no previous study of this kind yet in the Philippines, this study will provide relevant information for related biological research on other pen shell species and for the management of pen shell resources in the northern Iloilo and, possibly, other parts of the Philippines.



FLASH TALK

The exception that isn't one? Sexual dimorphism and male parental care in the chocolate gourami *Sphaerichthys osphromenoides* Canestrini, 1860

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The family Osphronemidae (Anabantiformes) consists of 14 genera and about 135 species, all of which show parental care. The extensive literature on these fishes and their reproductive biology describes paternal and sometimes biparental care in this family, with the exception of the chocolate gouramis *Sphaerichthys osphromenoides* Canestrini, 1860, and *Sphaerichthys selatanensis* Vierke, 1979. In these two mouthbrooding species, females were hitherto believed to be caregivers. We tested this assumption in an aquarium experiment and produced filmed evidence of spawning events and brooding fish. For correct fish sex identification, we estimated the cytological state of the gonads after the experiment. Our findings show that sex in *Sphaerichthys osphromenoides* has not correctly been determined so far: according to our data and observations, this species also shows male parental care.

Our findings do not only show that the current state of knowledge on parental care in chocolate gouramis (*Sphaerichthys spp.*) needs revision but also suggest that there are probably no exceptions to the rule of paternal care in Osphronemidae. This corroborates the observation that maternal mouthbrooding is extremely rare in non-

cichlid fishes. We discuss different explanations for the prevalence of male care in mouthbrooding fish species and explore the hypothesis that paternal care may have been selectively advantageous for energetic reasons as it might enable more spawning events within a given period of time. According to our observations, male chocolate gouramis can brood more than three times in a row with only one or two days of feeding in between. Such frequencies would be highly unlikely (if not impossible) in females where sufficient food intake is necessary to produce enough ripe eggs. We compare our findings to studies on other fish taxa for which significant differences in the energetic costs of mouthbrooding between sexes are reported, for example in cichlids with biparental care. While a more comprehensive theorization of the energetic costs of mouthbrooding is still a desideratum, we argue that energetic expenditures may partly explain the strong prevalence of male parental care in Osphronemidae and other fishes.



FLASH TALK

A new species of *Parauchenoglanis* (Claroteidae: Siluriformes) from the Upper Lualaba River (Upper Congo), with further evidence of hidden species diversity within the genus

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The catfish genus *Parauchenoglanis* is present all over the central part of the African continent and comprises nine species. The Congo basin is the most species rich of the continent, with four valid species, and the possible occurrence of a fifth one, *P. pantherinus*. Recent surveys (2012 and 2016) on the Upper Lualaba resulted in the collection of *Parauchenoglanis* specimens that could not readily be attributed to any of the currently known species. Using an integrative approach, combining colour pattern, morphological and molecular evidence, these specimens are being described as a new species endemic to the Lubudi River Upper Lualaba in the Upper Congo Basin. *Parauchenoglanis zebratus* sp. nov. is distinguished from all its congeners known from the Congo Basin and adjacent basins by the presence of (1) distinctive dark brown or black vertical bars on the lateral side of the body, at least for specimens about ≥ 120 mm SL, (2)

a broad and triangular humeral process embedded under the skin and (3) a well-serrated pectoral-fin spine. Genetic analysis based on mtDNA COI sequences confirmed the genetic distinctiveness (2.8–13.6% genetic divergence) of *P. zebratus* sp. nov. from congeners within the Congo and adjacent river basins. The study also revealed additional undocumented diversity within *P. ngamensis*, *P. pantherinus*, *P. punctatus* and *P. balayi*, indicating the need for further in-depth alpha-taxonomic attention to provide more accurate species delimitations for this genus. The discovery of yet another new species endemic to the Upper Lualaba, and this well outside the currently established protected areas, highlights the critical need for further assessments to accurately document the species diversity to guide freshwater conservation prioritisation and biodiversity management in this region.



FLASH TALK

Tubbataha Reefs Natural Park, Philippines in FishBase and SeaLifeBase

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Tubbataha Reefs Natural Park (TRNP) is a marine protected area in the Coral Triangle with a rich biodiversity. It is recognized as a UNESCO Heritage site. FishBase and SeaLifeBase provide marine biodiversity data that might be used to strengthen conservation efforts and promote sustainable management practices in the TRNP. A total of 1,285 marine species were confirmed to occur in the TRNP from 17 publications, with the help of collaborators and experts. This includes 641 species of bony fishes, 22 chondrichthyans (sharks and rays), 64 vertebrates (whales, dolphins, seabirds and sea turtles), and at least 492 invertebrates and 66 plant species.



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Family outlines in SeaLifeBase: Bivalvia

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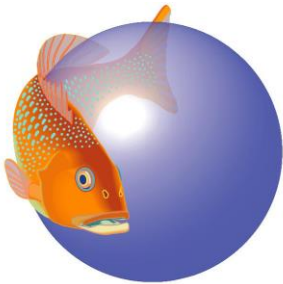
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Outline drawings of the general shape and morphology of representative species of a family is an initial step in species identification. Such outlines are available for commercially exploited species via FAO publications. These were adapted in SeaLifeBase, with priority on Bivalves and Decapods. As FAO publications do not provide all families with outline drawings, SeaLifeBase aims to complete these with hand-drawn outlines from photos of the type species of each Bivalve and Decapod family. The work so far completed for 110 families of marine Bivalvia species is presented here.



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