



12th FishBase Symposium

**Big Old Data and Shiny New Insights:
Using FishBase for Research**

Book of Abstracts

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Big Old Data and Shiny New Insights: Using FishBase for Research

Book of Abstracts

12th FishBase Symposium
Beaty Museum of Biodiversity
University of British Columbia, Vancouver, Canada

M.L.D. Palomares, E. Taylor and D. Pauly (editors)

A report prepared by the *Sea Around Us*
for the Paul G. Allen Family Foundation, the Pew Charitable Trusts
and the Consulate General of France in Vancouver

8 September 2014



12th FishBase Symposium
Big Old Data and Shiny New Insights: Using FishBase for Research

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PROGRAM

Time	Title of talk	Name of speaker	Affiliation	Email
9:00 – 9:10	Welcome address	John W. Hepburn	Vice President Research & International, UBC, Vancouver, Canada	
9:10 – 9:20	Welcome address	Ted Schmitt	Head, Technology Projects, Vulcan and Paul G. Allen Family Foundation	
9:20 – 9:40	Welcome address	Rick Taylor	Professor of Zoology, Director and Curator of Fishes, Beaty Museum of Biodiversity, UBC, Vancouver, Canada	etaylor@zoology.ubc.ca
9:40 – 10:00	Symposium rationale	Daniel Pauly	Principal Investigator, <i>Sea Around Us</i> , Fisheries Centre, UBC, Vancouver Canada	d.pauly@fisheries.ubc.ca
10:00 – 10:30	Coffee break			
10:30 – 10:50	From data to best available knowledge: recent developments in FishBase	Rainer Froese	FishBase Consortium Coordinator, GEOMAR Helmholtz-Centre for Ocean Research, Kiel, Germany	rfroese@geomar.de
10:50 – 11:10	Catalog of Fishes: the global nomenclator and taxonomic authority for fishes	William N. Eschmeyer	Curator Emeritus, Ichthyology, Academy of Science, San Francisco, California, USA	b.eschmeyer@calacademy.org
11:10 – 11:30	New classification of bony fishes in FishBase?	Nicolas Bailly	FishBase Project Manager, WorldFish and FishBase Information and Research Group, Los Baños, Philippines	n.bailly@cgiar.org
11:30 – 11:50	OsteoBase: an online interactive tool for osteological knowledge and identification	Sandrine Tercerie	Chargée de mission Référentiel taxonomique, Service du Patrimoine Naturel, Muséum national d'Histoire naturelle	tercerie@mnhn.fr
11:50-12:10	FISH-BoL: the global barcoding initiative for all fishes of the world	Robert Hanner	Associate Director, Canadian Barcode of Life Network, Biodiversity Institute of Ontario, University of Guelph, Canada	rhanner@uoguelph.ca
12:10 – 13:30	Lunch break			

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PROGRAM

13:30 – 13:50	Multi-model ensemble projections of climate change effects on global marine biodiversity	William Cheung	Associate Professor, Changing Oceans Research Unit, Fisheries Centre, UBC	w.cheung@fisheries.ubc.ca
13:50 – 14:10	The role of FishBase in trophic ecosystem modelling	Francisco Arreguin-Sanchez (presented by Manuel Zetina-Réjon)	Professor, Centro Interdisciplinario de Ciencias Marinas del IPN, Mexico	farregui@ipn.mx
14:10 – 14:30	NF-UBC Nereus Program: to advance our understanding of the future of fisheries	Yoshitaka Ota	Co-Director Nereus Program, Fisheries Centre, UBC	y.ota@fisheries.ubc.ca
14:30-14:50	Making big data available: the University of British Columbia Institute of Fisheries field record lab notebooks experience	Robert Stibravy	Digital Projects Librarian, Digital Initiatives Irving K. Barber Learning Centre, UBC	robert.stibravy@ubc.ca
14:50-15:10	Spaceship Earth - summary of an unusual international roundtable	Cornelia Nauen (presented by Rashid Sumaila)	Mundus Maris, Brussels, Belgium	info@mundusmaris.org
15:10 – 15:40	Coffee break			
15:40 – 16:00	IsotopeBase: a new stable isotope-based trophic addition to FishBase and SeaLifeBase	Todd Miller (presented by ML Deng Palomares)	Head of Fisheries, Division of Fish and Wildlife, Commonwealth of the Northern Mariana Islands, Saipan, Marianas Protectorate	tmiller.dfw@gmail.com
16:00 – 16:20	Problems in capture fisheries in the Philippines: costs of inaction	Vincent Hilomen	Executive Director for Priority Programmes, Biodiversity Management Bureau, Department of Environment and Natural Resources, Republic of the Philippines	vvhilomen@up.edu.ph
16:20 – 16:40	Estimation of mean trophic level of the bottom trawl fishery in the North-eastern Aegean Sea (Eastern Mediterranean)	Çetin Keskin	Professor, Istanbul University, Faculty of Fisheries, Istanbul, Turkey	seahorse@istanbul.edu.tr
16:40-17:00	Occurrence of Brazilian freshwater fish species by state	Kátia Freire	Professora Adjunta, Centro de Ciências Biológicas e da Saúde Núcleo de Engenharia de Pesca, Universidade Federal de Sergipe, Sergipe, Brazil and CAPES/Brazil	kfreire2006@yahoo.com.br
17:00-17:20	Summary and closing	Kostas Stergiou	Chair, FishBase Consortium, Aristotle University of Thessaloniki, Greece	kstergio@bio.auth.gr

BACKGROUND

The FishBase Symposium, held in tandem with the FishBase Consortium Annual Meeting, is usually a local event, emphasizing the contributions of the Vice Chair's institution to FishBase (www.fishbase.org), an online information system on all fishes of the world. The FishBase Consortium is made up of 9 international members, i.e., three European natural history museums, three universities (Fisheries Centre, UBC included), and 3 non-government organisations (details at www.fishbase.org/home).

The FishBase Symposium comes to Vancouver in September 2014 with its theme being embodied in the title, "Big Old Data and Shiny New Insights: Using FishBase for Research" in line with the growing use of "big" data in research meta-analyses.

FishBase is used in research. Google Scholar indicates an h-index=10 for 5,217 citations since its first CD-ROM version was released in 1995. Google Web Analytics run on all of the 9 FishBase mirror sites indicates an average of 0.4M unique visits and about 45M hits a month globally. About 21% of this usage is coming from Canada, and about 3% specific to Vancouver (with a browsing average of 9 pages per visit). The UBC community registers a monthly usage average of 3,500 visitors with a browsing average of 11 pages per visit. From a collection of 227 peer-reviewed articles citing or using FishBase data, 39 are from Canadian institutions, the Sea Around Us research group being one of them.

FishBase's coverage is global, and not only specific to fisheries. A recent Web of Science citation analysis, for instance, shows that parasitologists, among others, cite FishBase the most.

Its long history (25 years since inception) permitted an evolution from a global species database geared for use by fisheries scientists to an information system that offers, in addition to scientific and common names, distribution, ecological and biological data, and research tools for a wide range of fish-related disciplines. The Sea Around Us, the Beaty Museum, and a few other Canadian institutions in collaboration with the FishBase Information and Research Group (FIN) contributed to this evolution.

The Symposium scheduled for 8 September 2014 at the Beaty Museum Auditorium, UBC, Vancouver, Canada is a joint event between the Sea Around Us and the Beaty Museum with funding support from the Consulate General of France in Vancouver, the Nereus Program of the Fisheries Centre and the FishBase Information and Research Group, Los Baños, Laguna, Philippines.

BACKGROUND

FishBase Symposia are traditionally geared towards the local research community of the organizer's institution. This year however, we endeavour to extend our reach to collaborators from within Canada, the USA, Brazil, Turkey, the Philippines and Europe. The invited speakers are either FishBase users, collaborators, educators with the aim of teaching FishBase as a research tool or researchers with the aim of linking their research or projects with FishBase. They will talk about the importance of FishBase in "big" data research meta-analyses from taxonomy and nomenclature (William Eschmeyer, California Academy of Science; Nicolas Bailly, WorldFish), to Bayesian predictions of life history parameters (Rainer Froese, GEOMAR, Kiel, Germany) and applications to country-specific fisheries-related case studies (Vincent Hilomen, Department of Environment and Natural Resources, Philippines; Çetin Késkin, Istanbul University, Turkey; Kátia Freire, Universidade Federal de Sergipe, Brazil). Studies in global climate change (William Cheung, Changing Oceans Research Unit, Fisheries Centre), ecosystem-based management (Francisco Arreguin Sanchez, Centro Interdisciplinario de Ciencias Marinas del IPN, Mexico), socio-economics (Yoshitaka Ota, Nereus Program, Fisheries Centre) and links with other fish-related projects (Sandrine Terceirie, OsteoBase Muséum National d'Histoire Naturelle, France; Robert Hanner, Fish-BoL, University of Guelph, Canada; Todd Miller, IsotopeBase, Division of Fish and Wildlife, Saipan, Marianas) will complete the gamut of research applications for which FishBase is used.

With the agreement of the invited speakers, the Symposium proceedings will be published in the FishBase section of the journal *ACTA Ichthyologica et Piscatoria*.

It is also hoped that the Symposium will generate more active collaborations between the Fisheries Centre (Sea Around Us in particular) and the representatives of other institutions, and in particular with the Beaty Museum.

SPONSORS

The Sea Around Us, Fisheries Centre, UBC



The Beaty Museum of Biodiversity, UBC



The Consulate General of France in Vancouver



The Nereus Program, Fisheries Centre, UBC



The FishBase Information and Research Group



HOSTS

Maria Lourdes ‘Deng’ PALOMARES

Senior Research Associate, Sea Around Us, Fisheries Centre, UBC;
and Vice-Chair, the FishBase Consortium

Maria Lourdes ‘Deng’ Palomares is in charge of issues related to FishBase (www.fishbase.org), a scientific database for the world’s fishes and Coordinator for SeaLifeBase (www.sealifebase.org), a database patterned after FishBase for all marine organisms other than fish. Deng was appointed by the Board of the FishBase Information and Research Group (FIN, a Philippine NGO acting as the administrator of FishBase and SeaLifeBase) as Associate Scientific Director in September 2012. Originally from the Philippines, Deng obtained her Ph.D. from the Ecole Nationale Supérieure Agronomique de Toulouse (France) in 1991 and worked with the FishBase Project at the International Center for Living Aquatic Resources Management (Manila, Philippines) for 10 years before joining the *Sea Around Us* in 2001. Deng was the FishBase Consortium Vice-Chair in 2006, Chair Elect in 2007, and accepted another appointment as Vice-Chair in 2014. Deng is a marine biologist with an extensive background in software development, which was instrumental in her path towards fisheries science, trophic ecology and eventually biodiversity information systems.



Eric TAYLOR

Professor of Zoology, Director and Curator of Fishes,
Beaty Museum of Biodiversity, UBC

Freshwater fishes represent a spectacular adaptive radiation; about 40% of all fishes (which constitute more than 50% of all vertebrates) are found in freshwater habitats which comprise only 0.8% of the Earth's surface area! I am a Professor in the Department of Zoology and my research focuses on understanding patterns of genetic variation within and between natural populations of fishes, the processes that promote and organize such variation, and their relevance to the origins and conservation of biodiversity. In particular, I am interested in population structure and the historical and contemporary processes that influence population structure, speciation and hybridization (both ecological and genetic mechanisms of divergence and persistence in the face of gene flow), and the implications of these processes to biodiversity conservation. We develop and apply techniques in molecular biology to address questions in the evolution and ecology of natural populations. Molecular genetic (utilizing mitochondrial and microsatellite DNA markers, mtDNA and intron sequencing and RFLP analyses), morphological, and ecological, studies are conducted in the general fields of population genetics, molecular ecology and systematics, and conservation genetics and biodiversity. I am also the Director of the Beaty Biodiversity Museum (BBM), the curator of the Fish Collection at the BBM and a member of Biodiversity Research Centre at UBC. I also teach undergraduate courses in Honour's Research (Biology 447) and Diversity and Evolution of Fishes (Biology 465).



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WELCOME ADDRESSES

Ladies and gentlemen,

It is my pleasure to open, on behalf of UBC, this Symposium, which I understand is the 12th in the 20 year existence of the FishBase Consortium, with its predecessors having been held in cities as diverse as Thessaloniki in Greece, Tervuren in Belgium, Qingdao in China and Vancouver in 2006. I hope that those of you who have been here in 2006 will appreciate all the changes that happened in the UBC campus, notably in the facility we are presently are which is now one of our gems.

UBC is a research university and in 1994, when its newly established Fisheries Centre acquired Dr. Daniel Pauly as a newly minted professor of fisheries, we knew that we would have in him a person who would concentrate on international fisheries with emphasis in the tropics. However, we didn't know that we would, through him, also acquire a stake in FishBase.

This is understandable because FishBase, at the time, was only a little fish biodiversity project in the Philippines competing against lots of little projects of this type, a small fish in a large pool. It is only in 1996 that FishBase went online and begun an ascent which is nothing if not extraordinary, regularly reaching over half a million unique users a month, who might get carpal tunnel syndrome from the 40-50 million times they click on of the multiple pages of FishBase every month.

Though FishBase was initially conceived for use by a few hundred fisheries managers in the tropics, the number of its users grew enormously as its content increased in species coverage and depth and now the majority of its users originate from North America, including Canada with 21% of the global usage, of which about 3% is from Vancouver mostly from UBC. At UBC, the major user of FishBase is the Fisheries Centre whose students and researchers all use it routinely; however, other students and researchers throughout UBC also use FishBase. Much of this use goes through the Canadian mirror site www.fishbase.ca, hosted at the UBC IT department, and one of 8 mirror sites throughout the world.

Thus, FishBase is used at UBC much more than most of the scientific journals we subscribe to. In recognition of this fact, I suggest that the FishBase Consortium enter with the UBC library in a dialog about ways it could collaborate with FishBase, such that some of the library holding related to fish would be available through FishBase, and a dedicated version of 'FishBase-at UBC' created to which the library could subscribe. If an arrangement of this sort can be negotiated, you may then turn to other universities in Canada and the USA to propose similar arrangements which could help address the perennial funding problem which, I am told, besets FishBase, as it does many of similar ventures, such as Wikipedia.

I make this suggestion because FishBase represents the best of scientific cooperation. It is international, with over 2,000 formal collaborators in essentially all countries of the world. It is run by a non-profit international consortium that is diverse and based in three continents. And it maintains and deepens a scientific tool that is of universal appeal, used in virtually every university of the world and everywhere else where people work on fish, from the fishing and processing industry to the governments of various countries and back to the tourism industry, not to speak of thousands of kids who used it for their homework. Also, it is an international product with a strong Canadian component. Indeed, I am told that the UBC fish collection that was then housed in the bowels of the Zoology Building, and now part of

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the Beaty Biodiversity Museum collection, is one of the first museum collections integrated into FishBase, through an agreement between our Professor Don McPhail, now retired, and Daniel Pauly. This gave FishBase the credibility to talk with curators of other collections in North America, thus giving FishBase in the mid-1990s a boost that it needed to get into the big league.

I hope that the collaboration with the UBC library, will give FishBase another similar boost, at least in North America, so that universities and libraries which make wide use of FishBase can do their share in the support of this wonderful tool, and deepen its coverage in the process.

I wish you good luck in your deliberations and good luck to the future of FishBase.

John W. HEPBURN

Vice President Research and International,
University of British Columbia

John Hepburn was born in Hamilton, Ontario, and was educated at the University of Waterloo (BSc, 1976), University of Toronto (PhD, 1980), and University of California Berkeley (NATO Postdoctoral Fellow, 1980-82). He began his academic career back at the University of Waterloo, where he was appointed an Assistant Professor of Chemistry and Physics in 1982, and ultimately Chair of Chemistry in 1998. In 2001, he moved to the University of British Columbia as a Professor of Chemistry and Physics & Astronomy, and Head of Chemistry. He became Dean of Science in 2003, and Vice President, Research in 2005. The international portfolio was added to John's list of responsibilities in August 2009. He has been a Fellow of the A.P. Sloan Foundation, a Foreign Research Fellow of the CNRS (France), and a Canada Council Killam Fellow. He has been awarded the Rutherford Medal and the Noranda Prize and is a Fellow of the Royal Society of Canada, the American Physical Society, and the Canadian Institute for Chemistry. In addition to his work at UBC, John Hepburn currently serves as a Board member for numerous organizations.



WELCOME ADDRESSES

Ted SCHMITT

Head, Technology Projects,
Vulcan and Paul G. Allen Family Foundation

Ted Schmitt leads technology projects for philanthropic initiatives at Vulcan and the Paul Allen Family Foundation. Prior to joining Vulcan, Ted was a Senior Program Officer for the Computer Science and Telecommunications Board at the National Academies of Science, where he directed studies on topics ranging from disaster communications, healthcare IT, to broadband policy. He served as Technical Director at several technology start-ups in Germany, Sweden, and the United States, leading projects applying technology for impact on a range of issues. He started his career in 1984 as a software engineer for IBM, earning patents and several technical achievement awards. Ted holds an MA in International Science and Technology Policy from George Washington University, a BS in Electrical Engineering, and a BA in German from Purdue University. He also studied at Universität Hamburg, Germany.



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WELCOME ADDRESSES

I am very pleased to welcome all to the Twelfth Annual FishBase Symposium: *Big Old Data and Shiny new Insights: Using FishBase for Research* (FishBase 2014) being held at the Beaty Biodiversity Museum (BBM) at the University of British Columbia (UBC, Vancouver).

By way of introduction, the BBM is Vancouver's natural history museum and has been open since October of 2010. The BBM consists of more than two million biological specimens, from fossils to fishes, arranged in six major collections: the Spencer Entomology Collection, the UBC Fish Collection, the UBC Herbarium, the Cowan Tetrapod Collection, the Marine Invertebrate Collection, and the Fossil Collection (which is also a part of the Pacific Museum of the Earth at UBC). These collections (or about 99.9% of them) are housed in state-of-the-art archival units that are arranged in such a way as to provide access to the public in an engaging and educational manner to promote a better understanding of the importance of biodiversity and collections-based research.

The BBM has been very successful since its 2010 opening; we have welcomed over 100,000 visitors from around the world, including literally hundreds of school groups, hosted other symposia and scientific talks, held biodiversity-themed art exhibitions, and engaged in many aspects of biodiversity research.

The vision of the BBM is a world where biodiversity, and its importance to humans, is better understood, valued, and protected. We strive towards this vision by engaging in collections-based research, education, and public outreach.

As the director of the BBM, the curator of fishes, and a professor of zoology, I am particularly pleased that FishBase 2014 is being held at the BBM. First, I encourage any meeting that explores the wonderful world of the biology of fishes and helps us to protect them. Second, FishBase 2014 allows us to showcase the BBM and its tremendous legacy of biological collections from BC, Canada and the world. Finally (and please excuse the boast here), but it is great to have FishBase 2014 at the BBM. The importance of a globally accessible database on fishes that included access to biological collections for research and education was recognized very early on with a partnership between my colleagues Drs. Don McPhail (professor and curator emeritus) and Daniel Pauly who entered into a partnership in 1995 that resulted in the UBC Fish Collection being the **first** to be indexed and accessible through FishBase. This novel partnership grew to 40 collections in FishBase.

Finally, I want to thank our sponsors, the Consulate General of France in Vancouver via Mr Mathieu Leporini, The Nereus Program of the Fisheries Centre via Dr Yoshitaka Ota and The FishBase Information and Research Group via Dr Mary Ann Bimbao.

I also thank Dr. Deng Palomares who, despite my co-chairmanship of this meeting, actually did all the work! I also appreciate the invitation from Deng and Daniel to participate in the meeting, and Deng and I thank the team at the BBM for assisting with meeting logistics. I look forward to an interesting set of talks and discussions.

Eric B. (Rick) TAYLOR

Professor of Zoology

Director and Curator of Fishes

Beaty Biodiversity Museum

SYMPOSIUM RATIONALE

Welcome and please note that I have no PowerPoint presentation – look mommy, no hands...!

One could argue that no symposium, i.e., ‘drinking together’, needs a rationale; drinking together needs none but then, I don’t drink. It could also be argued that doing the 12th of anything needs no rationale – you just do it because you have done it 11 times before. This is also not good. The real rationale is that we are constantly challenged to restate and reaffirm what is behind FishBase and how it can be enhanced and used to best effect by a wide range of people from all walks of life.

The original reason for FishBase was to provide key data for managing fisheries in developing countries in Africa, the Caribbean and the Pacific (ACP) countries, i.e., the former colonies of countries of the European Union, which initially funded FishBase. Its growth was extraordinarily rapid because of an emphasis on content, not design, and because it was opportunity driven, i.e., concentrated on encoding existing data sets. However, FishBase was soon found to be a useful source of data outside of the intended clients, e.g., diving resorts, the Dutch custom office, aquarium shops, and ultimately US high school students working on science projects – all attracted by the content of FishBase.

But new science based on the ‘old data’ in FishBase took a while to emerge. One major initiative in this will be presented to you by Rainer Froese – the use of FishBase to estimate prior distributions for parameters to be used in Bayesian stock assessments. In a sense, FishBase is now was initially designed for, but for developing and developed countries, which is neat.

This builds on a principle we noted earlier, that ‘quantity leads to quality’. Thus, a set of growth parameters, for example is ‘validated’ if it is within a cloud of other such parameters, in doubt when not, whatever its source - *Nature* or the Tuvalu Department of Fisheries – which brings us to ‘Big Science’.

The earliest examples of big science were astronomy, then geography and oceanography. I don’t know which precise data are transferred in astronomy, but I know that major discoveries were made by Johannes Kepler and later Nicolaus Copernicus on the basis of painstaking observational data collected by Tycho Brahe by watching the Danish sky for decades with the naked eye. Similarly, Geography built on the knowledge encoded in early maps, which are ancient communication tools. Here knowledge could be accrued cumulatively; Geography was a big science from the onset.

Meteorology and physical oceanography built on this model. Thus, Matthew Maury of the US Navy traded local knowledge about currents, winds and depth soundings against maps generalizing the observations of hundreds of cooperating mariners in the North Atlantic. This established a pattern for these disciplines, which additionally, deal with easy-to-encode numerical observations.

SYMPOSIUM RATIONALE

But biology, before the advent of DNA sequences, did not seem to have ‘encodable’ knowledge outside of nomenclatural and distributional data. The literature seemed too disparate. What was required, thus, was a re-definition of all aspects of ichthyology in form of multiple choice and numeric fields. This is what allowed for scattered information on fishes to become encodable. This is what permits FishBase, via the power of relational databases, to contribute to science. Because doing science, to a large extent, is establishing relationships between things that were thought to be unrelated. This is FishBase!

Daniel PAULY

Principal Investigator, the Sea Around Us, Fisheries Centre
and Professor of Zoology, University of British Columbia

Born in France and raised in Switzerland, Daniel Pauly studied in Germany, where he acquired a doctorate in fisheries biology in 1979, from the University of Kiel. He did his first intercontinental travel in 1971 (from Germany to Ghana for field work related to his Masters) and has since experienced a multitude of countries, cultures, and modes of exploiting aquatic ecosystems in Africa, Asia, Oceania and the Americas. This perspective allowed him to develop tools for managing data-sparse fisheries, as prevailed for example in the Philippines, where Dr. Pauly worked through the 1980s and early 1990s. In 1994, Dr. Pauly became a Professor at the University of British Columbia Fisheries Centre, and was its Director from 2003 to 2008. In 1999, Daniel Pauly founded, and since leads, a large research project devoted to identifying and quantifying global fisheries trends, funded by the Pew Charitable Trusts and called The Sea Around Us after Rachel Carson’s 1951 bestselling book. Daniel Pauly is also co-founder of FishBase (www.fishbase.org), the online encyclopedia of more than 30,000 fish species, and he has helped develop the widely-used Ecopath modeling software. He is the author or co-author of more than 500 scientific and other articles, books and book chapters on fish, fisheries and related topics. Two of news books, reflecting his current interests were published in 2010: “Five Easy Pieces: Reporting on the Global Impact of Fisheries” and “Gasping Fish and Panting Squids: Oxygen, Temperature and the Growth of Water-Breathing Animals”.



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Big Old Data and Shiny New Insights: Using FishBase for Research

From data to best available knowledge, Froese, R.

FROM DATA TO BEST AVAILABLE KNOWLEDGE:
RECENT DEVELOPMENTS IN FISHBASE¹

Rainer FROESE, GEOMAR, Kiel, Germany; rfroese@geomar.de

In most fields, the number of annually published studies far exceeds the ability of specialists to absorb or even read them. Over the past 24 years, FishBase has selected studies with key information on growth, maturity, mortality, reproduction and diet of fishes and has encoded these data in a standardized form. Yet, this leads to four questions: (1) For a species with many studies on a topic, how can this information be best summarized? (2) For a species with only one available study, how representative is it? (3) For a species with no dedicated study, how can information from related species be used? (4) How can existing information inform a new study? The answer to all of these questions is provided by Bayesian hierarchical inference, where prior and related knowledge is combined with the analysis of new data to provide posterior "best" knowledge with indication of uncertainty. In this example, a certain piece of knowledge, which was available for only a few thousand species, is spread to all 32,000 species of fishes in FishBase. This approach will be expanded stepwise, with the goal to have an estimate of resilience for all fish species in about two years from now.

¹ Cite as: Froese, R. 2014. From data to best available knowledge: new developments in FishBase, p. 13-18. In: Palomares, MLD, Taylor, E, Pauly, D (eds.), 12th FishBase Symposium, Big Old Data and Shiny New Insights: Using FishBase for Research. September 8, 2014, Beatty Museum of Biodiversity, University of British Columbia, Vancouver, Canada. A report prepared by the *Sea Around Us* to the Paul G Allen Family Foundation and the Pew Charitable Trusts.

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From data to best available knowledge, Froese, R.

From Data to Best Available Knowledge New Developments in FishBase

Rainer Froese, GEOMAR, rfroese@geomar.de
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Beatty Museum of Biodiversity, UBC, Vancouver, 09.09.2014

Overview

- Data in FishBase as of August 2014
- From Data to Insights
- Example of Qualifying, Summarizing and Spreading Existing Knowledge
- The Most Important Number
- Ongoing Research Towards that Number
- Discussion



Data in FishBase

Cyclopterus lumpus Linnaeus, 1758
Lumpfish

Upload your photos and videos

All content Google Image - Photos



Cyclopterus lumpus
Photo by Aquaricus Kati

Add your observation in Fish Watcher



This map has images provided within but has no metadata.
Latitude: 50.000000 Longitude: -100.000000

Classification / Names
Actinopterygii (ray-finned fishes) > Scorpaeniformes (Scorpaeniformes and Seaheads) > Cyclopteroidei (Lumpfishes)
Erythrinidae: Cyclopterus: Genus, kyllis = round + Genus, pinn = fin (Ref. #1111), name on author: Linnaeus.
Common names | Synonyms | Catalog of Fishes (Gen., sp.) | ITIS | CoL.

Environment / Climate / Range
Marine, benthopelagic, circumtropical (Ref. 22191), depth range 0- 800 m (Ref. 10190), usually 50 - 100m (Ref. 4191) Polar: 80°N - 32°N, 80°W - 40°E

Size / Weight / Age
Maturity: L_∞ = 1, range 1 - 1.100
Max length: 41.6 cm TL, unsexed (Ref. 10190), 42.9 cm SL (female); max. published weight: 9.5 kg (Ref. 4191); max. published weight: 9.5 kg; max. reported age: 13 years (Ref. 14307)

Short description
Demersal species (depth: 3 - 8, depth with eyes (depth): 9 - 11, head up (depth): 9 - 10, vertical: 28 - 28). Firm dorsal fin present but covered by thick layer of skin forming a characteristic high cover with scudged spines. Bony scutes present, arranged in 3 widely separated rows of large dorsal scutes on each side of body. Gill openings large, round, extending below level of upper pectoral fin ray. Pyloric process 36-76. Visual working distance based by the scudged pelvic fin (Ref. 253).

Distribution
Western Atlantic, Western Indian Ocy to Japan Bay and Labrador to Canada to New Jersey in USA, mostly in Chesapeake Bay in USA and Bermuda, Eastern Atlantic, Western Sea, Iceland and Greenland to Spain (Ref. 4191).

Biology
Demersal, solitary rather than schooling fish. Exhibits a larval period (Ref. 9717). Adults mostly bottom feeders but may occur during breeding season. Migrations considerable. Immature in an annual cycle between deeper waters in winter and shallower waters in summer (Ref. 23115). Maximum depth reported at 800 m (Ref. 19124). Epilimnetic pelagic (Ref. 19470). During the spawning season the male becomes reddish in color on the underside, whereas the female is blue-green. Feeds on amphipods, molluscs, small crustaceans, polychaetes, jelly fish and squid tubes. Visited by their eggs, which make an unproductive ovary (Ref. 19115). Grows in Arctic, temperate, equatorial fresh or brackish. Male fish is more muscular and has a solid body (Ref. 19116).

Available Data

More information

Countries	Common names	Age/Size	Partners	Collaborators
FAO areas	Synonyms	Growth	Aggregates	Photos
Ecosystems	Metabolism	Length-weight	Aggregates profile	Stomach
Occurrences	Predators	Length-length	Sexual	Sounds
Interactions	Systematics	Length-frequency	Genetics	Ciguatera
Stocks	Reproduction	Morphometrics	Adult frequency	Spine
Ecology	Maturity	Morphology	Heritability	Spec. type
Diet	Spawning	Larvae	Diversity	Gill area
Food intake	Feasibility	Larval dynamics	Processing	Otoliths
Food consumption	Eggs	Recruitment	Mass conversion	Brain
Routes	Egg development	Abundance	Vision	

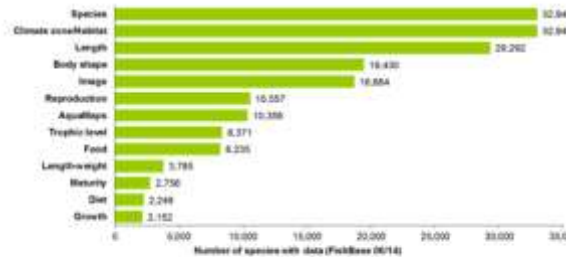
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From data to best available knowledge, Froese, R.

Available Data for Growth



Data in FishBase



From Data to Insights

FishBase has compiled thousands of studies on growth, maturity, reproduction, diet, etc

- How can the information be summarized?
- How good is a single study?
- How can new studies be informed?
- How can best estimates for species without studies be derived?

From Data to Insights

- Assemble all relevant facts, with probability distributions
- Establish their correlations, with probability distributions
- Select suitable models to explain data and predict key parameters
- Let the computer test all possible combinations and select those with highest overall probability



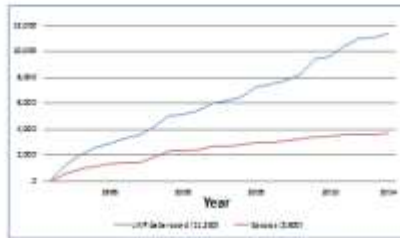
Bayesian Inference in a Nutshell

- Prior: express existing knowledge (textbook, common sense, logic, best guess, previous studies) with a central value (such as a mean) and a distribution around it (such as a normal distribution and a standard deviation).
- Likelihood function: analyze new data, get the mean and distribution
- Posterior: Combine prior and likelihood into a new, intermediate mean and distribution

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Accumulation of LWR and species with LWR



- 3,600 species have LWR; 28,400 do not
- 284 families do not have a single LWR
- Search for refs showed this as a knowledge gap

Length Weight Relationships

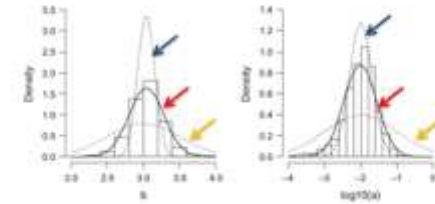


A Bayesian approach for estimating length-weight relationships in fishes

By R. Froese¹, J. T. Thorson² and R. B. Reyes A³

¹GEOMAR Helmholtz Centre for Ocean Research, Kiel, Germany; ²Physical Science Institute and Monitoring Station, Northwest Fisheries Science Center, National Marine Fisheries Service, National Oceanic and Atmospheric Administration, Seattle, Washington, DC, USA; ³FAO, U.S. Asia Ref. JRC, Los Baños, Laguna, Philippines

LWR Across All Studies

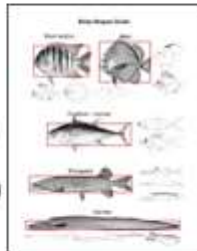


Weighted distribution of parameters b and $\log_{10}(a)$ in 5150 studies for 1821 species.

- from mean and standard deviation of the data
- from overall priors derived from the literature
- predictive posterior distribution

Body shape priors

- Eel-like (1,700 species)
- Elongated (7,300 species)
- Fusiform (7,100 species)
- Short and /or deep (2,600 species)
- Other (700 species; e.g., seahorses)



LWR Priors

Body shape	Mean $\log_{10}(a)$	SD $\log_{10}(a)$	Geom. mean a	95% range a	Mean b	SD b	95% range b	n
eel-like	-2.99	0.175	0.0110	0.000444 - 0.00223	2.06	0.696	1.68 - 3.24	142
elongated	-2.41	0.171	0.00369	0.00130 - 0.0042	3.12	0.890	2.94 - 3.30	712
fusiform	-2.50	0.173	0.0112	0.00314 - 0.0245	3.04	0.857	2.67 - 3.21	2478
short & deep	-1.76	0.175	0.0260	0.0182 - 0.0218	3.01	0.893	2.83 - 3.19	798
all	-2.08	0.313	0.0109	0.00244 - 0.0411	3.04	0.119	2.81 - 3.27	5150

Weighted means and standard deviations of parameters a and b from 5150 studies for 1821 species of fishes, by body shape. Geom. mean = geometric mean and 95% range includes about 95% of observations.

LWR for all species Example: *Cyclopterus lumpus*

Estimates of some properties based on models

Phylogenetic diversity index (Ref. 1913): $PD_{sp} = 1.0000$ (Uncertainty: $95\% \text{ CI } = 0.9 - 1.0$)

Bayesian length-weight: $a = 0.02144$ (0.00028 - 0.04188), $b = 3.02$ (2.79 - 3.25), based on LWR estimates for this Subfamily-body shape (Ref. 95245).

Trophic Level (Ref. 69272): 3.5 ± 0.1 yr. Based on diet studies.

Resilience (Ref. 69278): Low; minimum population doubling time 4.5 - 14 years ($K = 0.12$; $m = 3.5$; $\text{mean} = 13$; $\text{FW} = 100,000$).

Vulnerability (Ref. 88132): High vulnerability (67 of 300).

Price category (Ref. 88786): Low.

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Self-Learning Database

- When Daniel and Rainer first discussed about FishBase, they envisioned an artificial intelligence system
- Some years (decades) later, we are getting there:
 the addition of LWRs for 16 species improved LWR quality for over 400 species

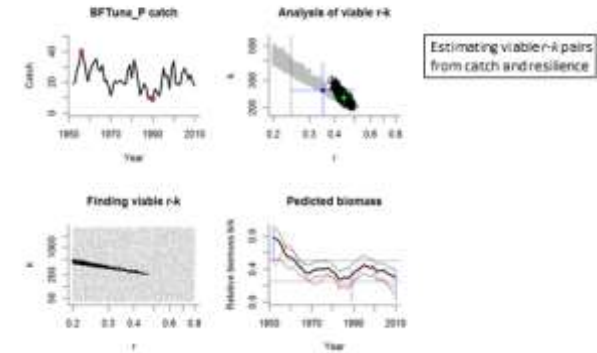
The Most Important Number

r_{max}
 maximum intrinsic rate of population increase

Determines:

- productivity (F_{msy})
- population recovery time
- resilience
- vulnerability

The Most Important Number

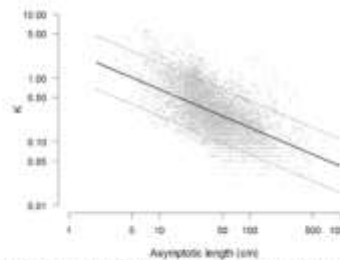


The Most Important Number

r_{max}
 is highly correlated with

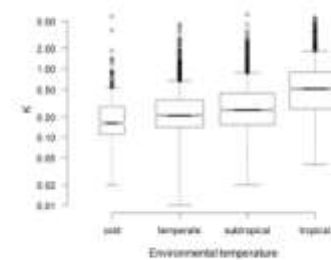
- age at maturity / generation time
- body size
- natural mortality
- somatic growth rate
- metabolism/temperature
- life style / activity

Ongoing Research



Growth parameter K plotted over asymptotic length, based on 7,275 growth studies for 1,863 species, with the bold line representing the mean for demersal subtropical species and with dashed lines indicating the 95% high density interval. Note that these lines would shift upward for tropical species and downward for temperate and cold species, with the same slope.

Ongoing Research

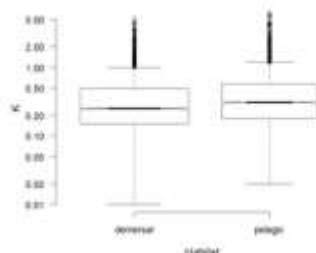


Box plots of growth parameter K for different environmental temperatures, based on 7,275 growth studies for 1,863 species. The width of the boxes is proportional to the square root of the number of observations.

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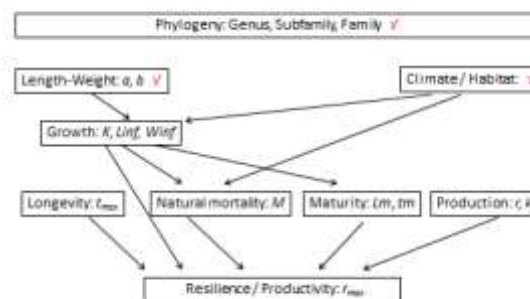
From data to best available knowledge, Froese, R.

Ongoing Research



Box plots of growth parameter K for different habitat uses, based on 7,275 growth studies for 1,863 species. The width of the boxes is proportional to the square root of the number of observations.

Ongoing Research for all Species



Resilience for all species, to be replaced by rmax with confidence limits

Estimates of some properties based on models

Phylogenetic diversity index (Ref. 3230): $PD_{sp} = 1.0000$ (Uniqueness, from 0.5 = low to 2.0 = high)
 Bayesian length-weight: $a = 0.02144$ (0.00000 - 0.04100), $b = 3.02$ (2.70 - 3.25), based on LWR estimates for this Subfamily-body shape (Ref. 95245)
 Trophic Level (iter: 00276): $TL = 3.9$ ± 0.1 se: Based on diet studies
 Resilience (Ref. 60176): Low, minimum population doubling time 4.5 - 14 years ($R = 0.12$; $m = 3.5$; $ms = 13$; $Z_{95} = 100,000$)
 Vulnerability (Ref. 38157): High vulnerability (63 of 100)
 Price category (Ref. 89766): Low

Rainer Froese is senior scientist at the GEOMAR Helmholtz Centre for Ocean Research in Kiel, Germany. Together with Daniel Pauly he ‘invented’ FishBase (www.fishbase.org) and since 1990 he is FishBase Project Leader and Coordinator. FishBase is the most widely used biological information system with over half a million visitors per month. Froese is author of over 100 scientific publications with over 2,000 citations in the primary literature. His research interests range from fish biology, population dynamics, aquatic biodiversity and biogeography to improved fisheries management. He was also a founding member of Species 2000, an initiative to compile scientific names of all organisms on Earth, and of the Ocean Biogeographic Information System (OBIS), the information component of the Census of Marine Life program. In addition to FishBase, Froese coordinates the AquaMaps project, which has created the first global atlas of the living ocean (www.aquamaps.org). This ‘largest-ever’ atlas is now in its third edition, with digital distribution maps for over 17,000 species, including all marine mammals, about half of all marine fishes and several thousand invertebrates such as cephalopods or crustaceans. The atlas shows which of these species occur at any given spot in the Oceans, and also where these species may occur by 2100, given predicted climate change. Froese is fisheries biologist by training and has published numerous papers documenting the worrisome state of global and European fish stocks. Currently he is working on innovative methods to estimate the status of fish stocks for which only limited data are available, i.e., the majority of European as well as global fish stocks. More information and a full list of publications are available on Froese’s personal page at <http://www.fishbase.de/rfroese>.



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Catalog of Fishes, Eschmeyer, W.

CATALOG OF FISHES: THE GLOBAL NOMENCLATOR
AND TAXONOMIC AUTHORITY FOR FISHES²

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b.eschmeyer@calacademy.org

The Catalog of Fishes database (<http://research.calacademy.org/ichthyology/catalog>) is the nomenclator for fishes, recording their original names, type information and nomenclature issues from the original descriptions of genera and species. It is also the global taxonomic authority file as it gives the current valid name for all original names. It records the intermediary name and taxon assessments and statuses from the primary taxonomic literature since it started in the mid-1980s. It has been maintained for 30 years and includes information on about 55,000 available species and 11,000 genera. About 33,500 species are valid.

New species are being described at an average rate of one species per day for the past 20 years (17 years if only valid species are retained) with a noticeable acceleration at the turn of the millennium (ca. 385/year in the period [1999-2013] against ca. 285/year [1984-1998]). More freshwater species than marine are described constantly since 1955 (between min. 56% in 1984 and max. 65% in 2013 in the past 30 years [1984-2013]). More recently, the list of family names was compiled, and the status of the current list will be presented. The Catalog of Fishes and FishBase share a long history of collaboration since the mid-1990s, and are still cross-checking and synchronizing their data entries. In a way the benefits of the well-known double-entry procedure for database quality control has been rediscovered on the ground. Anyhow, a number of problems regularly emerged from that collaboration, recurrent issues that are undermining rapid progress in data sharing in biodiversity informatics, such as the proper data re-use and citation from third parties in aggregators, and discrepancies between two databases due to different goals and uses, database structure, update frequency, etc. In addition to names, a number of other datasets were collated with the help of a number of ichthyologist colleagues: references, journals, fish collections, and webpage browsing tools were developed to navigate in the classification and to check taxon statistics at one glance. As a recommendation, when colleagues cite fish numbers (total or per family or genus or else), they should rather refer to the Catalog of Fishes that is the most updated, and not anymore to J.S. Nelson's *Fishes of the World*: since the latest edition in 2006, ca. 3,300 valid spp. were described (10% of all valid species!) in 229 families (41%) in 1,050 genera (21%).

² Cite as: Eschmeyer, W. 2014. Catalog of fishes: the global nomenclator and taxonomic authority for fishes, p. 19-23. In: Palomares, MLD, Taylor, E, Pauly, D (eds.), 12th FishBase Symposium, Big Old Data and Shiny New Insights: Using FishBase for Research. September 8, 2014, Beaty Museum of Biodiversity, University of British Columbia, Vancouver, Canada. A report prepared by the *Sea Around Us* to the Paul G Allen Family Foundation and the Pew Charitable Trusts.

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Catalog of Fishes, Eschmeyer, W.

Catalog of Fishes

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 Curator Emeritus
 Department of Ichthyology
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 Catalog of Fishes Project

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In the Beginning
 (Circa 1965-1970)

No PCs
 No Google
 No internet
 No email
 No databases
 No scanners
 No Xerox machines
 No word processors
 No gps
 No trees

15 year later (ca 1985)

- PCs (slow)
- Copy machines
- Database software (primitive)

"My 10-year project"

All genera and species of fishes, all original descriptions, location of types, etc., in a database.

After 1990
 What Happened

More workers
 Scuba, then rebreathers
 New techniques (submersibles, etc.)
 More survey work/conservation
 Molecular studies/bar coding/gen bank
 Better communication (literature, types, etc.)
 Xerox machines, then scanners, pdfs
 Team approach
 Digital photography
 Species concepts changed some
 Catalog of Fishes/FishBase
 Online literature
 More journals
 More exploration (esp. freshwater)
 Difficulty collecting (due to restrictions)

Species per Author (Top 9)

Author	Valid	Syn.	Undoc.	Total	% valid
Bleeker	820	794	324	1928	43
Valenciennes	960	956	231	2150	36
Günther	919	582	153	1634	56
Fowler	572	892	181	1648	40
Jordan	687	943	107	1737	51
Boulenger	789	309	36	1134	70
Cuvier	419	513	125	1057	40
Steindachner	630	298	210	1138	52
Regan	566	281	87	934	61

Rhinopias argoliba



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Catalog of Fishes, Eschmeyer, W.

Where are the new species?

A. Few new Taxa:

- North America freshwater.
- Europe freshwater.
- Most of Australia.
- North Pacific, most of Atlantic.
- Antarctica (shallow).
- Shallow reefs.
- Africa freshwaters (except Rift Lakes).
- Mediterranean, Red Sea, Caribbean Sea, Arctic.
- (Large species, pelagic species, commercial species).

"It is now difficult to find new shallow water reef species" (J. E. Randall)

"There are many new deep reef species but few new genera" (R. Pyle)

Where are the new species?

B. Most New Taxa

- South America freshwater
- Asia freshwater
- Indonesia freshwater
- Indian Ocean
- SW. Pacific
- Certain deep-sea depths
- Deep reefs
- African Rift lakes, Congo basin
- Specialized habitats: seamounts, rises, deep rocky areas (Small fishes)

**SPECIES AND SUBSPECIES VS. TIME
 (ROUNDED AVERAGES)**

Period	Species	Subsp.	% Subsp.	Total
1950-59	166	26	13.4	192
1960-69	179	19	9.4	198
1970-79	196	22	10.2	219
1980-89	269	14	5.0	282
1990-99	253	5	2.0	258
2000-08	399	4	1.0	403

- Total taxa per year increased over the last 50 years
- Use of subspecies in fishes has declined substantially

Conclusions

Species/subspecies

- Decline in new subspecies from about 20% to 1%
- Average per year max about 350-400
- % valid/described – about 50% valid as species, now about 90+ percent.
- Describers – about 50 until late 1800s, great increase since 1950
- Molecular – few new species taxa so far, useful for relationships/higher categories
- Estimates: 2000. Maximum, 25000 valid (too low).
- HOW MANY VALID – 32,400 (now); 40,000 by 2050

Catalog of Fishes - 1990



**Catalog of Fishes – 1998
 One of Three**



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Catalog of Fishes, Eschmeyer, W.

Marine Fish Diversity

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Marine fish diversity: history of knowledge and discovery (Pisces)

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Corresponding author: E-mail: weschmeyer@calacademy.org

Number of Species

Year	New species described
1995	249
1996	186
1997	267
1998	314
1999	228
2000	304
2001	440
2002	299
2003	312
2004	421
2005	452
2006	397
2007	408
2008	322
2009	293
2010	287
2011	366
2012	403
2013	439
2014	248
2015	1076

Citing the Catalog of Fishes

Eschmeyer, W. N. (ed). CATALOG OF FISHES: GENERAL SPECIES REFERENCES. <http://www.catalogoffishes.org/2015/05/01/catalog-offishes-general-species-references/>. Electronic version accessed 08 June 2014. [This section was added by Don Diamond.]

Frick, R. (ed). REFERENCES. <http://www.catalogoffishes.org/2015/05/01/catalog-offishes-references/>. Electronic version accessed 08 June 2014.

van der Laan, R., Eschmeyer, W. N., Frick, R. FAMILY-GROUP NAMES. <http://www.catalogoffishes.org/2015/05/01/catalog-offishes-family-group-names/>. Electronic version accessed 08 June 2014.

Frick, R. & Eschmeyer, W. N. JOURNALS. <http://www.catalogoffishes.org/2015/05/01/catalog-offishes-journals/>. Electronic version accessed 08 June 2014. [Includes all journals appearing in the Catalog, including publication information and ISSN numbers.]

Frick, R. & Eschmeyer, W. N. GUIDE TO FISH COLLECTIONS. <http://www.catalogoffishes.org/2015/05/01/catalog-offishes-guide-to-fish-collections/>. Electronic version accessed 08 June 2014. [Arranged by museum abbreviation and by country; includes type catalogs and historical publications and also sites where available.]

Eschmeyer, W. N. & Fong, J. D. SPECIES BY FAMILY/SUBFAMILY. <http://www.catalogoffishes.org/2015/05/01/catalog-offishes-species-by-family-subfamily/>. Electronic version accessed 08 June 2014. [Reorganized with 6400 new entries, based on current literature, this provides all available species names, used species, and species described in the last 10 years by family/subfamily.]

Search Results from the Catalog of Fishes

Select the database to search:

[GENERA](#) [SPECIES](#) [REFERENCES](#)

Include unavailable names

Comments: [William Eschmeyer](#)

Species that contain: *albifimbria* (not including unavailable names) [1] records

albifimbria, *Scorpaena* Evermann [E. W.] & Marsh [M. C.] 1900:275, Fig. 82 [Bulletin of the U. S. Fish Commission v. 20 (pt 1) [for 1900]; ref. 14833] Off Culebra Island, 5.25 miles southwest of Culebras Light-house, Puerto Rico, Fish Hawk station 6093, depth 15 fathoms. Holotype (unique) USNM 49532. -Valid as *Scorpaena albifimbria* Evermann & Marsh 1900. -[Eschmeyer 1965:115 [ref. 3211], Eschmeyer 1969:58 [ref. 3274], Robins & Ray 1986:273 [ref. 24100], Acero-P. & Navas S. 1987:04 [ref. 26470], Smith-Vaniz et al. 1999:197 [ref. 30034], Collette et al. 2003:166 [ref. 30334], Foss & Eschmeyer 2003:1261 [ref. 32043], Smith et al. 2003:19 [ref. 32033], Nelson et al. 2004:113 [ref. 32032], McGuckin & Fockelmeier 2007:39 [ref. 33810], Page et al. 2013:116 [ref. 32320], Victor 2012:30 [ref. 32343].] Current status: Valid as *Scorpaena albifimbria* Evermann & Marsh 1900. Scorpaenidae: Scorpaeninae. Distribution: Western-Atlantic. Habitat: marine.

Table 1. Species of Fishes by Family/Subfamily

Class	Order	Family	Subfamily	Available	Valid	Last Ten Years
Muraeniformes						
Muraenidae						
		Muraenidae		67	73	17
		Muraenidae		33	36	4
		Eptatretidae		35	47	13
Cathaloidei						
Petromachoninae						
		Petromachonidae		115	41	0
		Petromachonidae		36	37	0
		Gedoniidae		15	1	0
		Mordaciidae		4	3	0
Placodiformes						
Hexanchiformes						
		Hexanchidae		30	4	0
		Chalybiodontidae		1	1	0
Neoselachiformes						
Heterodontiformes						
		Heterodontidae		19	8	1
Carangiformes						
		Rhinodontoideae		5	1	0
		Percypteroideae		10	8	2
		Brachaelonidae		4	2	0
		Oreochromidae		17	11	5

Genera Results from the Catalog of Fishes

Select the database to search:

[GENERA](#) [SPECIES](#) [REFERENCES](#)

Include unavailable names

Comments: [William Eschmeyer](#)

Genera that contain: *scorpaena* (not including unavailable names) [31] records

Buffeithys (subgenus of *Syngnathus*) Swainson [W.] 1839:268 [ref. 4303]. Maso. *Scorpaena formida* Linnaeus 1766. Type by subsequent designation. Not p. 181, where *Buffeithys* is a misprint for *Syngnathus* = *Esox* (see Eschmeyer & Rams-Rac 1973:343 [ref. 4381]). Replaced by *Phrymichthys* Agassiz 1848. Type designated by Swain 1882:277 [ref. 5900]. -Synonym of *Syngnathus* Bloch & Schneider 1801. -[Eschmeyer & Rams-Rac 1973:341, 363 [ref. 4381], Mandryka 2001:264 [ref. 30030].] Current status: Synonym of *Syngnathus* Bloch & Schneider 1801. Syngnathidae: Syngnathinae.

Centrogenys Richardson [J.] 1842:190 [20] [ref. 32345]. Fem. *Centropomus scorpaenoides* Cuvier 1829 in *Scorpaena vaigiensis* Cuvier & Gaimard 1824). Type by monotypy. Original not examined. The correct spelling of the family is *Centrogenyidae*. -Valid as *Centrogenys* Richardson 1842. -[Moozbach in Masuda et al. 1984:124 [ref. 6447], Paston et al. 1989:490 [ref. 32443], Lee & Truiki 1999:413 [ref. 34201].] GR 1999:2549 [ref. 44917], Hoese 2006:1036 [ref. 28283]. Current status: Valid as *Centrogenys* Richardson 1842. Centrogenyidae.

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References Results from the Catalog of Fishes

Select the database to search:

[GENERA](#) [SPECIES](#) [REFERENCES](#)

Include unavailable names

Comments: [William Eschmeyer](#)

References that contain: 33222 [1] records

Andrews, J. R. H. 2012 (June) [ref. 33222] The East Coast of the North Island—zoologica collections of the Endeavour voyage. *Journal of the Royal Society of New Zealand* v. 42 (no. 2): 135-144.



In the early years, my research was in traditional taxonomy - revisions and new taxa primarily of scorpionfishes, stonefishes and their allies. These revisions continued while I spent about 8 years in administration, ending as Director of Research. In the early 1980s, I decided to “organize the information of ichthyology” as I called it. The importance can be summarized in that I did a “little bit of every ichthyologist’s research” - tracking down nearly all original descriptions, building a database of all available names in fishes, going to many collections gathering information on types, solving nomenclatural issues and assisting ichthyologists with inquiries. The first volume of the *Catalog of Fishes*, treating the genera, was published in 1990. This was followed in 1998 by publication of all genera, species, and original literature. Regular online editions have been posted continuously. New species in 2008 numbered over 500. Into the early 1900s, the number of authors describing new species in a year was about 50; now hundreds of enthusiastic workers per year have the experience of describing new fish taxa and contributing to our knowledge of fishes. It is an interesting time for us all, and I look forward to receiving pdfs weekly. My health is good, and I am as enthusiastic as ever to continue the *Catalog of Fishes* project.



12th FishBase Symposium
Big Old Data and Shiny New Insights: Using FishBase for Research

New classification of bony fishes, Bailly, N. et al.

NEW CLASSIFICATION OF BONY FISHES IN FISHBASE?³

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Since its creation in 1990, FishBase, a global Biodiversity Information System on all finfishes of the World (ca. 33,000 species) has used a mix of the classifications from the four editions of J.S. Nelson's *Fishes of the World* (FoW 1976, 1984, 1994, 2006) and the intermediary improvements endorsed by W.N. Eschmeyer's in the regular updates of his *Catalog of Fishes* (CofF). For a longer time, the irresolution of the Acanthomorpha clade was described by G. Nelson (1989) as "the bush at the top of the teleostean tree". Indeed the Perciformes, the most speciose order of that clade (a third of all finfishes), was known to be polyphyletic as early as the 1930s. Although a number of suborders were well defined, their interrelationships were not established even with the starting molecular phylogenetic methods in the 1980s: depending on the gene and taxonomic sampling, the results were contradictory. More recently, the Scorpaeniformes were clearly dismantled by such studies, but in 2006, J.S. Nelson did not endorse the changes yet because he correctly pointed out that without the resolution of Perciformes, nobody would be able to place the suborders that were separated from the Scorpaeniformes new definition!

In 2010, Wiley and Johnson published a new classification of the Teleostei on the basis of evidenced and published morpho-anatomical synapomorphies, addressing J.S. Nelson's issue. In 2013, Betancur-R. et al. published a new phylogeny of the Osteichthyes (bony fishes) on the basis of 21 molecular markers (one mitochondrial and 20 nuclear genes) for 1,410 bony fish taxa from 1,093 genera in 369 families, and all traditionally 49 recognized orders. Besides the resolution of new clades, this analysis confirmed many proposals by Wiley and Johnson. A second iteration was published on the web (www.deepfin.org/Classification_v2.htm) with 1,591 bony fish taxa in total incl. additional 165 genera (total 1,258 over ca. 4,900 valid ones) and 25 families (total 394 over ca. 520 valid ones), taking into account the results of Near et al. (2013) and remarks from other colleagues. The combination of the extensive sampling in genes and taxonomy correlated with the morpho-anatomic synapomorphies makes the classification based on this phylogeny

³ Cite as: Bailly, N., Betancur, R.R., Wiley, E., Miya, M., Lecointre, G., Ortí, G. 2014. New classification of bony fishes in FishBase?, p. 24-30. In: Palomares, MLD, Taylor, E, Pauly, D (eds.), 12th FishBase Symposium, Big Old Data and Shiny New Insights: Using FishBase for Research. September 8, 2014, Beaty Museum of Biodiversity, University of British Columbia, Vancouver, Canada. A report prepared by the *Sea Around Us* to the Paul G Allen Family Foundation and the Pew Charitable Trusts.

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an important milestone in Ichthyology that should be endorsed by many global initiatives and information systems around the world.

FishBase helped to cross-checked the classifications in Coff, FoW2006, and FishBase, and for nomenclature issues: discrepancies are available in a downloadable MS-Excel file in the DeepFin webpage, as well as the list of families not yet examined with a call to ichthyologist colleagues to provide with tissues or already published results that would have been overlooked. On the web, the DeepFin classification webpage and the FishBase family summary pages are already cross-linked.

Can FishBase endorse that new classification at that point? As far as possible, we would like that other initiatives move as well in a short time-span to avoid the confusion for users. Indeed, some intermediary ranks established by that classification are still debatable (and debated!). But the orders and families that are confirmed or newly established will be without doubt the framework for further research in the next 50 years just like the revolutionary classification of Greenwood et al. (1966) has been up to now. As FishBase and Coff do not use the intermediary ranks, the changes incurred should not be a complicated task, but certainly tedious. However, the 9 series strongly supported in Percomorpha could be included because they will help to clarify the overall biological, ecological, biogeographical, exploitation and conservation understanding of that clade using information stored in FishBase. Another novelty is the elevation of polypters at Class rank. Incidentally, the international community through the Catalogue of Life is currently addressing the issues raised at that taxonomic Class level where FoW and Coff were different (6 classes in Coff that were subclasses in FoW): if the DeepFin classification is endorsed as such then amphibians, birds, mammals cannot be classes, which might be a change hardly acceptable by the rest of the society, at least not without a long educational process. Solutions are under study.

Such a classification must be the result of an international collaborative work, just like is FishBase. It is also important that the interoperability between global (Coff, FishBase, ASFIS, CoL, Fish-BoL, IUCN, CITES, WoRMS, FADA, EoL, ...), regional (ITIS, ERMS, FaEU, STEP, ...), and national (ALA, CaRMS, INPN, ...) initiatives is conserved for the convenience of users of one finfish classification. It must not prevent that alternative classifications are confronted within the taxonomic ichthyology community as its scientific work. Such a classification could also be seen as a recognized consensus and a management hierarchy helpful to manage knowledge about finfish. Already a third iteration is planned before the summer so the oral presentation will be based on the new results.

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New classification of bony fishes in FishBase?

08 September 2014
Beatty Museum of Biodiversity
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Version 3, 30th July 2014

- Version 2 (27 Nov. 2013) and 3 on the web

Phylogenetic Classification of Bony Fishes
Based mostly on Molecular Data — Version 2

Version Date: 30 July 2014
Contributors to this version: [Francis Delfino-Fr. De Witte](#), [Nicolas Bailly](#), [Masaki Miya](#), [Guillaume Lecointre](#), [Guillermo Ortí](#)

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Betancur-R. R., S. Wiley, N. Bailly, M. Miya, G. Lecointre, and G. Ortí. 2014. Phylogenetic Classification of Bony Fishes -Version 3 (http://www.deepfin.org/Classification_3.html)

Betancur-R. R., R.F. Sraughon, R.O. Wiley, K. Capetian, J.A. Lopez, C. Li, H. Hareff, D. Arida, M. Sanjangan, J. Claret, F. Zhang, T. Duser, M. Campbell, T. Rowley, J.A. Balazs, G. Li, T. Grande, G. Arida & G. Ortí. 2013. The tree of life and a new classification of bony fishes. [PLOS Currents Tree of Life](#) 2013 Apr 16.

Download useful resources:
[SpeciesList](#) with complete classification scheme; [taxonomic phylogeny](#) used as basis for classification (from version 2, needs to be updated to reflect the current classification scheme); [summary files](#) with all major groups.

A new classification of bony fishes published in 2013

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The Tree of Life and a New Classification of Bony Fishes

APRIL 16, 2013 · TREE OF LIFE

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REVISIONS
This article is either a revised version of its previous revisions or a new article.
Edition 1 - April 16, 2013

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Integrate the DeepFin classification in FishBase? Challenges

- **Socio-psychological:**
- Resistance to changes, even when well documented (remember Greenwood et al. 1966)
- Competition, recognition, career ...

Material and method (v1 & v3)

- DNA sequence data for **21 molecular markers** (one mitochondrial and 20 nuclear genes)
- 1410 bony fish species (5%) **1596 (4%)**
- 1093 genera (22%)
- 369 families (75%) **394 (79%)**
- 49 orders (100%) **67 (100%)**
- Names up family level checked against Coff
- Names above from Wiley & Johnson 2010
Wiley, E.O., and G.D. Johnson. 2010. A teleost classification based on monophyletic groups, p. 123-182. In: Origin and Phylogenetic Interrelationships of Teleosts. J. S. Nelson, H. P. Schultze, and M. V. H. Wilson (eds.). Verlag Dr. Friedrich Pfeil, München, Germany.

Integrate the DeepFin classification in FishBase? Challenges

- **Technical:**
- Reassign species though genera and families, included those missing in the analysis
- Multiclassifications?

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**Integrate the DeepFin classification in FishBase?
 Challenges**

- **Networking:**
- Importance to keep interoperability between information systems:
 Global (Coff, Fow, FishBase, ASFIS, CoL, Fish-BoL, IUCN, CITES, WoRMS, FADA, EoL, ...);
 Regional (ITIS, ERMS, FaEU, STEP, ...), and
 National (ALA, CaRMS, INPN, ...)...

**Integrate the DeepFin classification in FishBase?
 Challenges**

- **Users:**
- Avoid confusion in the front-end for end-users
- Keeping a back-end dedicated to specialists.

What changes are we talking about?

- Two frameworks of reading:
 What matters for Coff and FB:
 The main level point of view:
 (Kingdom, Phylum,
 Class, Order, Family, Genus, Species)
- All intermediary ranks
 What is reported in Coff and DF:
 (Almost) all phylogenetic nodes with given
 intermediary ranks

20 ranks in DF classification

Megaclass	Section
Superclass	Subsection
Class	Division
Subclass	Subdivision
Infraclass	Series
Megacohort	Superorder
Supercohort	Order
Cohort	Suborder
Subcohort	Infraorder
Infracohort	Family

Pholidichthyiformes with Cichlidiformes?



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What changes are we talking about?

Families "new" 17 (6 really new)
 168 spp. + ca. 18 = ca. 200 spp (0.6%)

Bembropidae	(SF)	Scorpaenichthyidae
Botiidae	(SF)	Diplophidae
Congrogadidae	(SF)	Horabagridae
Gaidropsaridae	(SF)	Jordaniidae
Girellidae	(SF)	Siniperidae
Niphonidae	(Tribe)	Sudidae
Paralichthodidae	(SF)	
Poecilopsettidae	(SF)	
Rhombosoleidae	(SF)	
Steindachneriidae	(SF)	
Zaniolepididae	(SF)	

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What changes are we talking about?

Families "lost" 19 (124 spp 0.4%)

Centracanthidae	Sparidae	Comephoridae	Cottidae
Phractolaemidae	Kneriidae	Cottocomephoridae	Cottidae
Scaridae	Labridae	Hemitripterae	Agonidae
Caesionidae	Lutjanidae	Latidae	Centropomidae
Abyssocottidae	Cottidae	Microdesmidae	Gobiidae
Achiropsettidae	Rhombosoleidae	Olyridae	Bagridae
Anopteroideae	Alepisauridae	Omosudidae	Alepisauridae
Arapaimidae	Osteoglossidae	Percillidae	Percichthyidae
Bathylutichthyidae	Psychrolutidae	Scomberesocidae	Belonidae
		Sundasalangidae	Clupeidae

What changes are we talking about?

- 36 families affected over 502 7% → 496 (330 spp. 1%)
- Number of non-monophyletic families: 41 in version 2
30 in version 3

Non-monophyletic families: Issues to be solved

30 (1258 spp 4%)

Acropomatidae	Macrouridae
Agonidae	Nototheniidae
Alepocephalidae	Ophidiidae
Bathydraconidae	Paralepididae
Bathymasteridae	Paralichthyidae
Bythitidae	Phosichthyidae
Chlorophthalmidae	Polyprionidae
Clupeidae	Scombridae
Cottidae	Scopelarchidae
Gempylidae	Scorpaenidae
Grammatidae	Sternopygidae
Gymnotidae	Stichaeidae
Hemiramphidae	Synodontidae
Ipnopidae	Trachichthyidae
Labrisomidae	Zenarchopteridae

Attempt to define criteria

Within and constrained by an established phylogeny

- **Morphologic:** The more taxa look alike the more and at higher rank they should be classified together
- **Ecologic:** in particular the life zone (salt or fresh waters)
- **Ontogenic:** about the morphology/anatomy of larvae.
- **Practical:** split speciose taxa vs not multiplying monotypic families

What changes are we talking about?

Orders "new"

- Previously as suborders of Perciformes: 9
Acanthuriformes
Anabantiformes
Blenniiformes
Gobiiformes
Istiophoriformes (as Xiphioidel)
Kurtiformes
Labriformes
Pholidichthyiformes
Scombriformes

What changes are we talking about?

Orders "new"

- Previously as families (sometimes suborders in FoW) of Osmeriformes (number of families): 4
Alepocephaliformes (3)
Argentiniformes (4)
Galaxiiformes (1)
Lepidogalaxiiformes (1)

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**What changes are we talking about?
Orders "new"**

- **Previously as families in Perciformes in various suborders (number of families): 9**
Ehippiformes from Acanthuroidei (2)
Chaetodontiformes from Percoidei (2)
Cichliformes from Labroidei (1)
Carangiformes from Percoidei (5)
Centrarchiformes from Percoidei (2)
Lobotiformes from Percoidei (2)
Pempheriformes from Percoidei (13)
Spariformes from Percoidei (4)
Uranoscopiformes from Trachinoidei (4)

**What changes are we talking about?
Orders "new"**

- **Previously as families in various orders (number of families): 3**
Hiodontiformes (1) from Osteoglossiformes
Holocentriformes (1) from Beryciformes
Stylephoriformes (1) from Lampriformes

**What changes are we talking about?
Orders**

- **From 49 to 67 orders**
- **15 as changed ranks from suborders or families**
- **13 with family re-arrangements**

**What changes are we talking about?
Orders "lost" 8**

- **Orders in Coff/FB are not any more in DF: 8**
- Gasterosteiformes:
 In Zoarciformes (Cottoidei:Gasterosteales)
- Gobiesociformes: In Blenniiformes (Gobiesocoidei)
- Lepidosireniformes:
 In Ceratodontiformes (Lepidosirenoidei)
- Saccopharyngiformes: In Anguilliformes
- Scorpaeniformes: In Perciformes (Scorpaenoidei but restricted circumscription)
- Cetomimiformes: In Beryciformes
- Stephanoberyciformes: In Beryciformes
- Incertae sedis Elasmobranchii (In Perciformes in FB):
 In Centrarchiformes

**What changes are we talking about?
Orders "lost" 8**

- 9 suborder
- Infrastructure internal access
- What about external dissemination?
- Importance of policies, even for internal uses, for users' information and proper management by the infrastructure

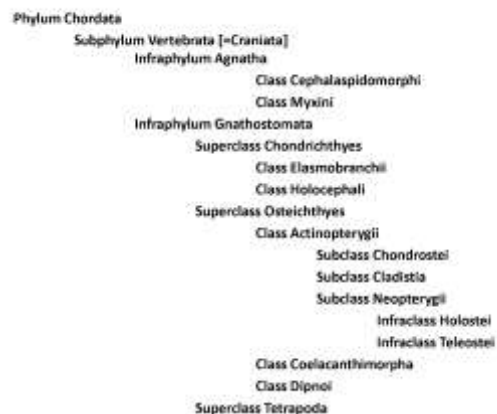
Higher classification

A Higher Level Classification of All Living Organisms, submitted to PloS One
Michael A. **Ruggiero**,
Dennis P. **Gordon**,
Nicolas **Bailly**,
Thierry **Bourgoin**,
Richard C. **Brusca**,
Thomas C. **Cavalier-Smith**,
Michael D. **Guiry**,
Paul M. **Kirk**,
Thomas M. **Orrell**

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Higher classification



Conclusions

- In FishBase, implementation of family changes asap in coordination with Coff
- Changes in orders after 2nd assessment but Perciformes suborders could be done asap
- Implement higher classification
- Coordinate with other initiatives in particular Coff and FoW

Maraming Salamat Po

The Consulate General of France in Vancouver



Nicolas Bailly (PhD) is an ichthyologist who specializes in Biodiversity Informatics since 1983, mainly on the database structures for taxonomy and systematics. He is currently the FishBase Project Manager in the Philippines (since 2005). After being the Head of the Philippine Office of the WorldFish Center (now WorldFish) for 5 years (2005-2010), he is now acting as the FIN Scientific Director (FishBase Information and Research Group, 2011-present). He participated to the creation of the FishBase Consortium of which he was the head for one year. He is a scientific advisor for SeaLifeBase. He participated to the following projects under the European EC-FP5, FP6 and FP7, all related to biodiversity informatics: ERMS, ENHSIN, Fauna Europaea, BioCase, ENBI, D4Science (I and II), HighARCS, BioFresh, iMarine, and EU-BON. He organized the 3rd GBIF Governing Board meeting in Paris (2001). He participated in many initiatives on biodiversity information systems at the French national level during his employment at the Muséum National d'Histoire Naturelle in Paris (1992-2005). He is currently the chair of the Taxonomic Group (since 2007) and the vice-chair of the Global Team of the Catalogue of Life (since 2013). He is a co-author of the second iteration of the new classification of bony fishes published on the web on 27 November 2013 (http://www.deepfin.org/Classification_v2.htm).



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OsteoBase, Tercerie, S. *et al.*

OSTEOBASE: AN ONLINE INTERACTIVE TOOL FOR
OSTEOLOGICAL KNOWLEDGE AND IDENTIFICATION⁴

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Bones constitute the essential research material of several fields in biology. To ensure the reliability of osteological identifications, researchers need reference collections for comparison purposes. OsteoBase is an interdisciplinary project that aims to develop an online interactive tool for osteological identification, fish osteology learning and comparative anatomy practice. One of the main originalities of OsteoBase is the navigation through the pictures: the entire osteology can be explored just by hovering and clicking on pictures, and can therefore be used as an educational tool to learn osteology. This bilingual website (English/French) provides a double access to pictures, either by bone or by taxon, which can be sorted by geographical zones. Additional ways to sort and to filter the data will be added when the number of taxa will increase significantly. OsteoBase also manages osteometric data which can be downloaded. This prototype is hosted in the Muséum national d'Histoire naturelle (MNHN, Paris: <http://osteobase.mnhn.fr>). For the time being, it includes parts of the cranial and post-cranial skeleton of 57 fish species (Actinopterygii) representing 46 families and 18 orders. All the specimens illustrated are housed in the MNHN fishbone collection. A unique link exists between FishBase and OsteoBase species (link 1-1 between both databases) so that users can benefit from the complementary of both tools. This work began with a master training course and then it was supported by different initiatives/programs within the MNHN (ATM Form, e-muséum).

⁴ Cite as: Tercerie, S., Béarez, P., Vigne-Lebbe, R., Pruvost, P., Valderrama, I., Bailly, N., Lecointre, G. (2014) OsteoBase, an online interactive tool for osteological knowledge and identification, p. 31-38. In: Palomares, MLD, Taylor, E, Pauly, D (eds.), 12th FishBase Symposium, Big Old Data and Shiny New Insights: Using FishBase for Research. September 8, 2014, Beaty Museum of Biodiversity, University of British Columbia, Vancouver, Canada. A report prepared by the *Sea Around Us* to the Paul G Allen Family Foundation and the Pew Charitable Trusts.

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12th FishBase Symposium
Big Old Data and Shiny New Insights: Using FishBase for Research

2 September 2014
10h-12h (open access)
University of British Columbia, 1021 Malaspina
Vancouver, BC V6T 1Z4, Canada



OsteoBase

an online interactive tool
for osteological knowledge & identification

S. Tercerie, P. Báñez, R. Vignes-Lebbe,
P. Pruvost, N. Bailly & G. Lecointre



- One observation:
need of reference collections of bones for comparison purposes
- OsteoBase complementary to FishBase
- Interdisciplinary project (zoarchaeology, ichthyology, comparative anatomy, informatics)
⇒ Identification tool
⇒ Pedagogical tool
- Development of a database and a dynamic web interface
- Photographic acquisition of osteological material




OsteoBase
Web interactive exploration for osteology

Let's get started!
Welcome on OsteoBase website!
Color code of the site
Get on the website

OsteoBase is an interactive website designed for osteological exploration. From the initial selection to concluding bones, the reference specimens are in presence at a collection of osteological traits, organized to compare these osteological traits in different taxa. This OsteoBase interface is an osteological identification tool providing the steps to compare.

Users can either select a label to make comparisons across several taxa (navigation by osteological specimens) or select a group to study (by taxon / navigation by taxon). Tax can be sorted by geographical zones.

One of the main objectives of OsteoBase is the navigation through the platform: the online navigation can be explored just by hovering and clicking on buttons, without a need to know the name of bones. OsteoBase can therefore be used as an educational tool to learn osteology to include users like students or biologists not specialized in this field (for reference materials, who wish to identify any remains).

About OsteoBase

OsteoBase receives support from:
 - Muséum national d'Histoire naturelle, Paris
 - Centre National de la Recherche Scientifique
 - CNRS
 - UPMC
 - Université de Bordeaux
 - Université de La Rochelle
 - Université de La Réunion
 - Université de La Martinique
 - Université de La Guyane
 - Université de La Nouvelle-Calédonie
 - Université de La Polynésie Française
 - Université de La Réunion
 - Université de La Martinique
 - Université de La Guyane
 - Université de La Nouvelle-Calédonie
 - Université de La Polynésie Française

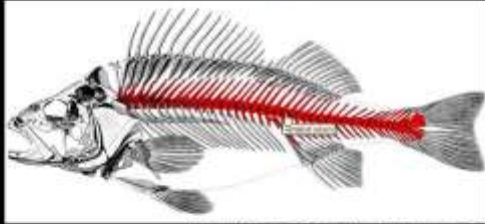


OsteoBase
Web interactive exploration for osteology

Osteology of Actinopterygii

Skeleton of *Perca fluviatilis* (Perch). Source: Carlin & Mansueti, 1983.

To explore more in depth the osteology of this group, select an osteological area - as for the previous menu - or on the drawing by hovering over the skeleton with your mouse, the selectable osteological area become red, click to access.



OsteoBase
Web interactive exploration for osteology

Osteology of Actinopterygii

Skeleton of *Perca fluviatilis* (Perch). Source: Carlin & Mansueti, 1983.

To explore more in depth the osteology of this group, select an osteological area - as for the previous menu - or on the drawing by hovering over the skeleton with your mouse, the selectable osteological area become red, click to access.



OsteoBase
Web interactive exploration for osteology

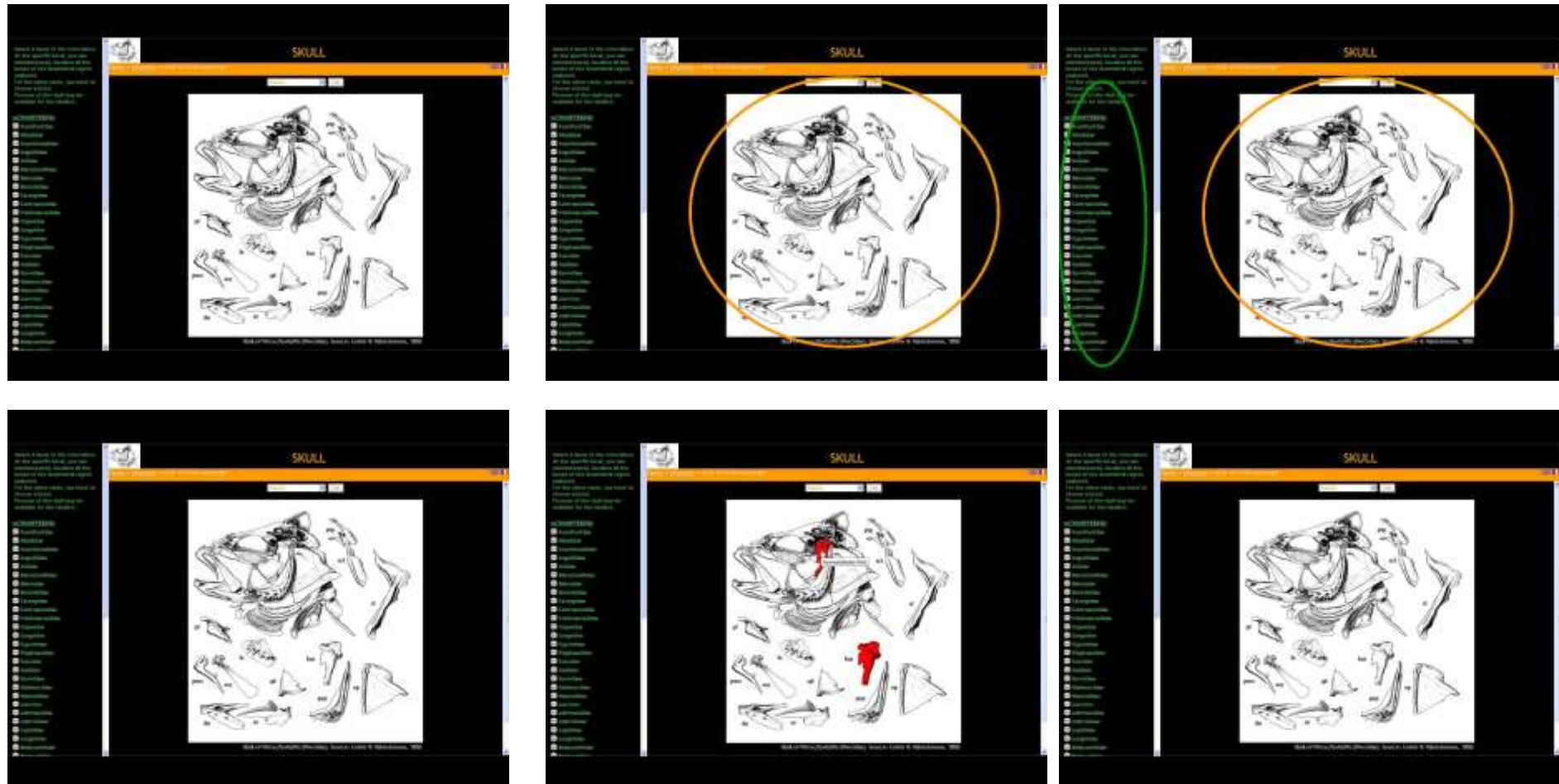
Osteology of Actinopterygii

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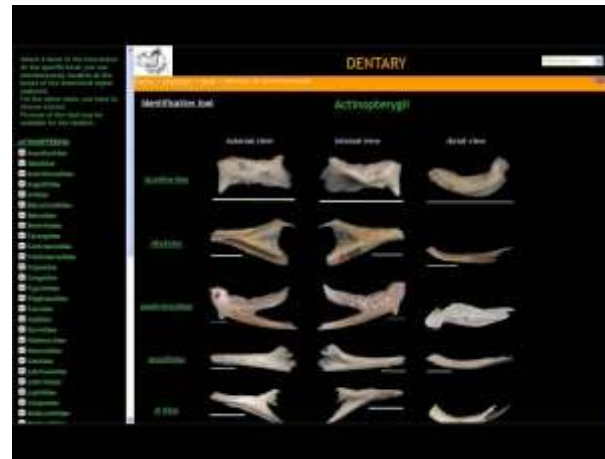
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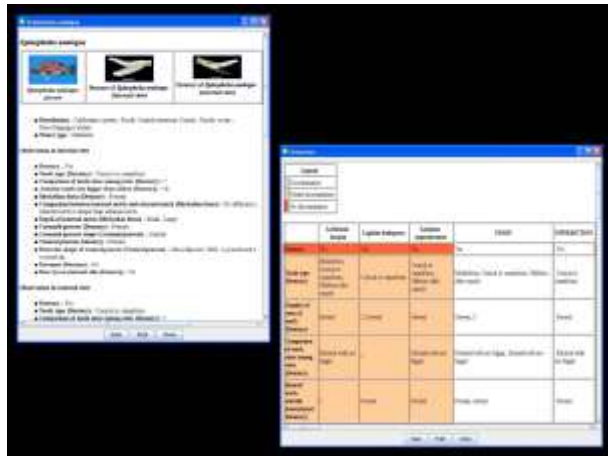
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OsteoBase, Terceire, S. et al.



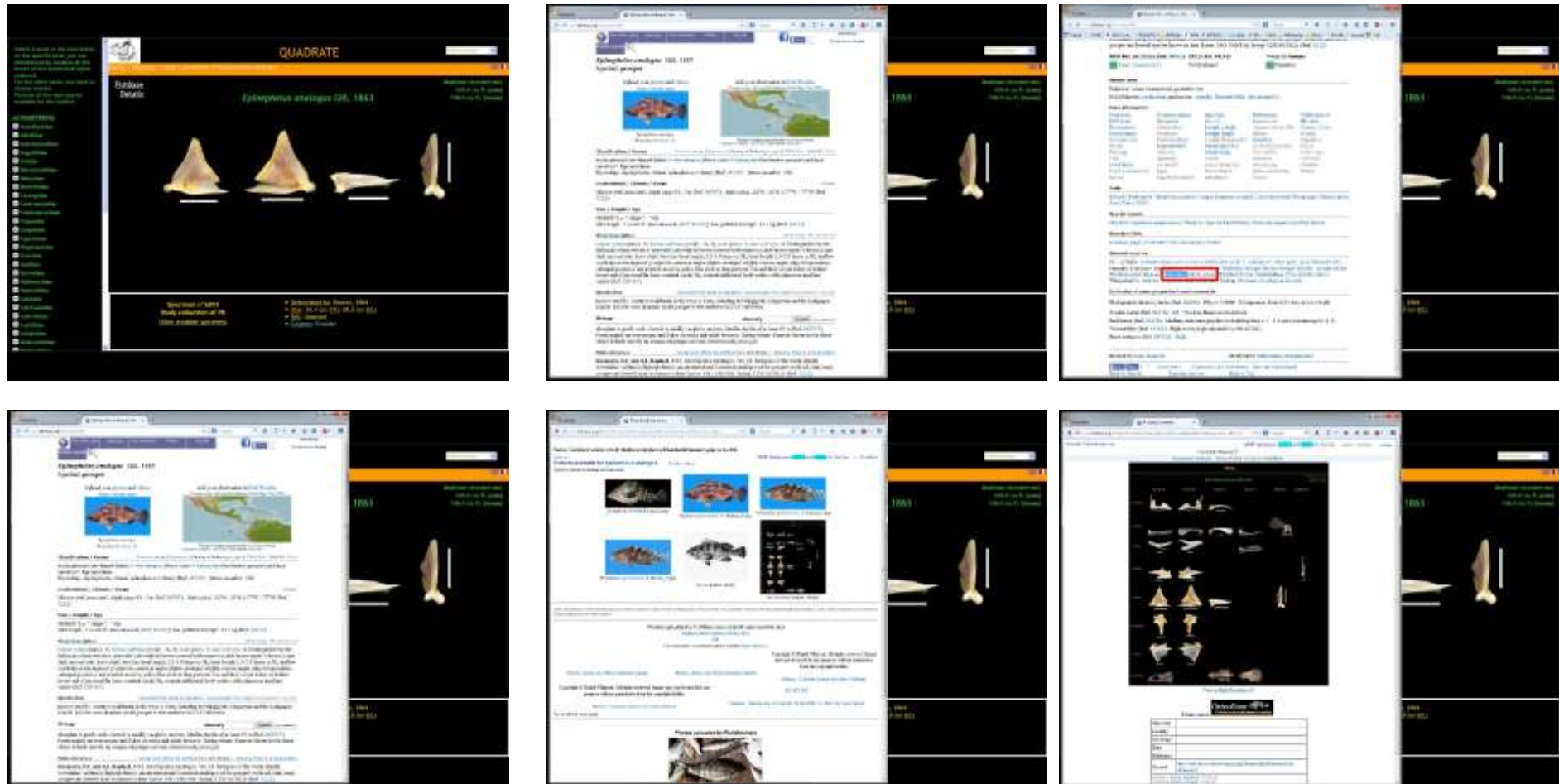
12th FishBase Symposium Big Old Data and Shiny New Insights: Using FishBase for Research

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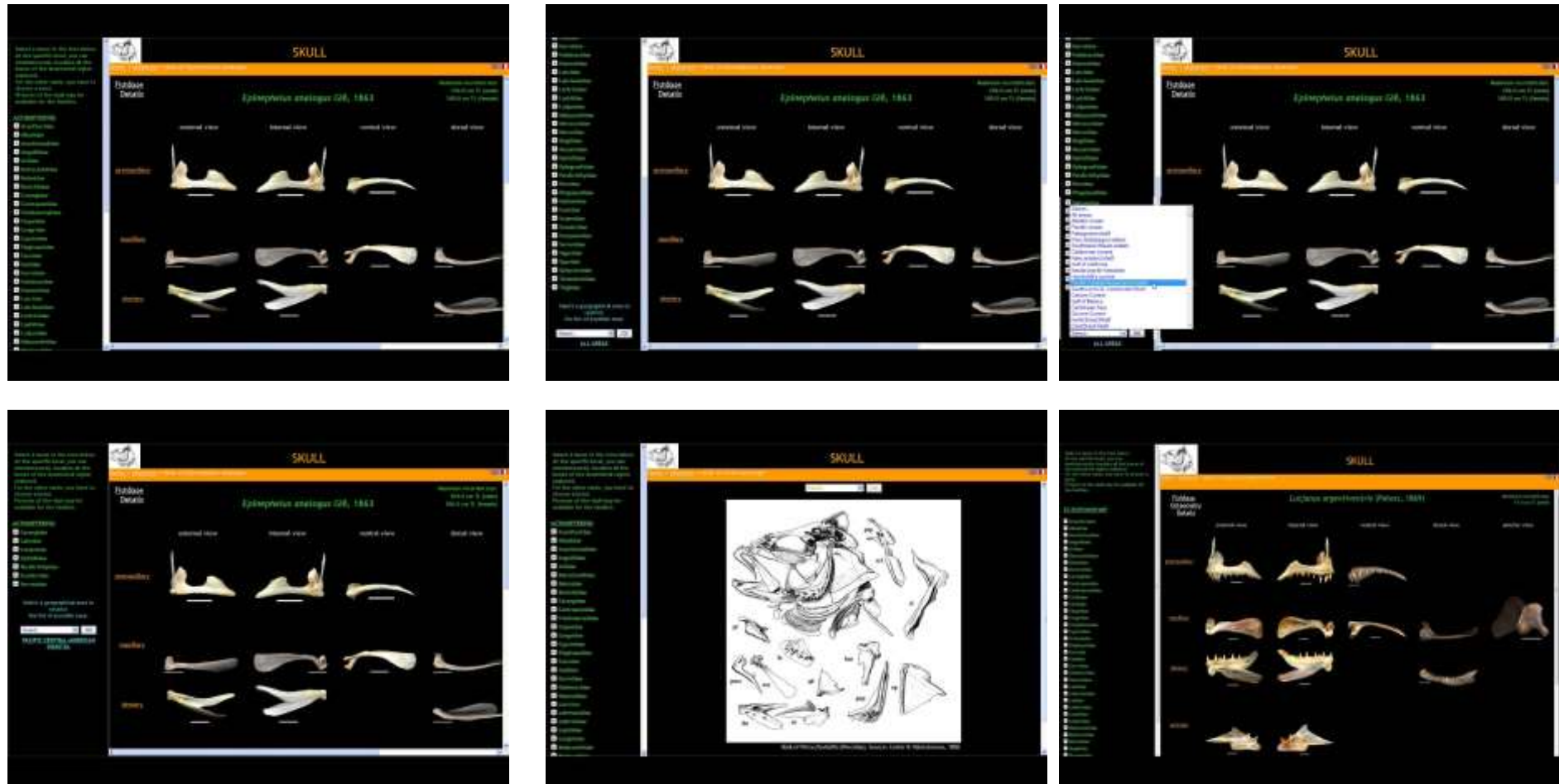
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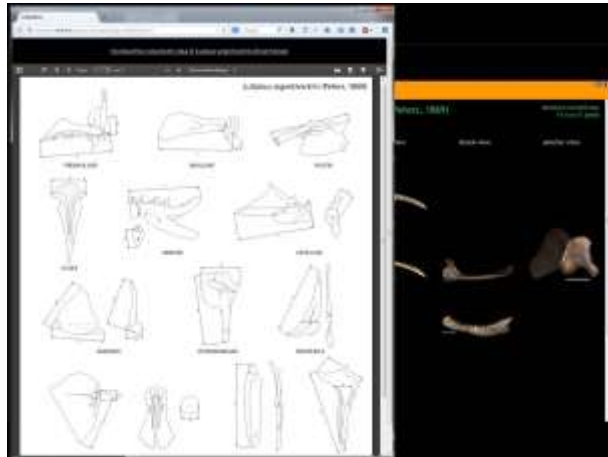
12th FishBase Symposium
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Species	Bone number	Preparation	Length (mm)	Width (mm)	Height (mm)	Area (mm²)	Volume (mm³)	Weight (mg)	Color	Material	Year	Sex	Age	Size (mm)	Locality	Collector	Notes
Labeo gibelus	1001	1001	10.0	1.0	1.0	10.0	1.0	1.0	10.0	1001	2010	♂	10.0	France	S. Tercerie		
Labeo gibelus	1002	1002	10.0	1.0	1.0	10.0	1.0	1.0	10.0	1002	2010	♀	10.0	France	S. Tercerie		

OsteoBase osteobase.mnhn.fr
Web interactive explorations for osteology

- Prototype hosted in the National Museum of Paris (MNHN)
- Total of ~2500 photos for more than 70 species and 13 bones
- Project still in development and improvement

Perspectives

- Keep increasing the number of species and bones
- Improve the interface
- Develop knowledge bases on bones (Xper²)
- Reinforce et develop links with the ontologies of Phenoscape

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27 September 2016
Muséum national d'Histoire naturelle, 1282 MUSEUM
Symposium 06: 047-054, Paris, France

osteobase.mnhn.fr **Thank you!**

S. Tercerie, P. Báarez, R. Vignes-Lebbe,
P. Pruvost, N. Bailly & G. Lecointre

MUSEUM NATIONAL D'HISTOIRE NATURELLE
fishbase
ciprs
UPMC

Sandrine Tercerie is currently one of the assignment managers of the French taxonomic register for mainland and overseas, at the Natural Heritage Department, Muséum national d'Histoire naturelle (MNHN), Paris. She has also worked on ontologies and their use in bioinformatics tools to manage morphological data, as a member of a research team focused on acanthomorph systematics (UMR 7138, Systematics and Evolution Department, MNHN). She designed the OsteoBase project during her master's studies at the Université Pierre et Marie Curie (Paris VI) and since then she goes on developing this online interactive tool designed for osteological knowledge and identification.



12th FishBase Symposium
Big Old Data and Shiny New Insights: Using FishBase for Research

FISH-BoL, Hanner, R.

FISH-BoL: THE GLOBAL BARCODING INITIATIVE FOR ALL FISHES OF THE WORLD⁵

Robert HANNER

University of Guelph, Centre for Biodiversity Genomics,
Guelph, Ontario, Canada; rhanner@uoguelph.ca

The Fish Barcode of Life Initiative (FISH-BoL) is a global effort to coordinate an assembly of a standardized reference DNA sequence library for all finfish species, one that is derived from voucher specimens with authoritative taxonomic identifications. The benefits of barcoding fishes include facilitating species identification for all potential users, including taxonomists; highlighting specimens that represent a range expansion of known species; flagging previously unrecognized species; and perhaps most importantly, enabling identifications where traditional methods are not applicable, in particular linking eggs and larval stages to the adult forms. About 30% of the 33,000 valid fish species have at least one barcode (more than 10,000), a result stemming from the about 100,000 specimens barcoded since the start of the initiative. Interestingly, more than 2,000 barcode clusters could not be identified: 2,000 over 12,000 in total which may represent the rate of cryptic diversity in fishes (15%). More species remain to be described and named. At the early stages of FISH-BoL, FishBase provided the complete list of names, as well as regional lists for the system information management purposes, broadly based on the FAO fisheries statistics areas. New updates are difficult to integrate though, and FishBase needs to develop the relevant web services to facilitate data exchange. This is also the case with Coff from where the type information, in particular on the type locality, is crucial for the barcoding exercise (having at least one barcode from the type locality to fix the name-barcode links).

Not all groups of fishes respond satisfactorily to barcode identification (e.g., sturgeons, cichlids in East African lakes), and some additional markers remain to be found and experimented. Also data sharing issues may hide the actual barcode coverage of finfishes. Misidentifications of the voucher specimens are also a difficult issue, generating unnecessary questions about species validity, or genus or even family monophyly. The involvement of specialists is highly appreciated there. However, over the last 9 years the Fish Barcode of Life effort has been creating a valuable public resource in the form of an electronic database containing DNA barcodes, images, and geospatial coordinates of examined specimens. The database contains linkages to voucher specimens, information on species distributions, nomenclature, authoritative taxonomic information, collateral natural history information and literature citations. FISHBoL thus complements and enhances existing information resources, including the Catalog of Fishes, FishBase and various genomics databases. The current status of the initiative will be presented as well as some hints for a future strategy to complete the FISH-BoL catalogue.

⁵ Cite as: Hanner, R. (2014) FISH-BoL: the global barcoding initiative for all fishes of the world, p. 39-52. In: Palomares, MLD, Taylor, E, Pauly, D (eds.), 12th FishBase Symposium, Big Old Data and Shiny New Insights: Using FishBase for Research. September 8, 2014, Beaty Museum of Biodiversity, University of British Columbia, Vancouver, Canada. A report prepared by the *Sea Around Us* to the Paul G Allen Family Foundation and the Pew Charitable Trusts.

12th FishBase Symposium
 Big Old Data and Shiny New Insights: Using FishBase for Research

FISH-BoL, Hanner, R.

FishBase Symposium, UBC 8 September 2014

FISH-BoL: the global barcoding initiative for all fishes of the world

Robert Hanner, PhD
 Associate Professor
 Centre for Biodiversity Genomics,
 University of Guelph, Ontario, Canada

1758 - Linnaeus (& Artedii)

1859 - Charles Darwin

Biological specimens: come in many forms

Identifiable adults

Juvenile stages

Processed products

DNA-based Identification works on all forms

e.g. Bartlett & Davidson, 1992. FINS (Forensically important nucleotide sequences): A procedure for identifying the animal origin of biological specimens. *Biotechniques*, 12(3), 408-411.

What is DNA Barcoding

A method of species identification based on DNA sequences derived from standard marker genes for animals (COI), plants (rbcL and matK) and fungi (ITS).

The hypothesis is that, for that gene segment, every species will have a unique sequence (or a unique assemblage of closely related sequences).

This sequence is termed a 'barcode'. For example:

Species A:	CCTAAGCTTACGTTTCC	
Species B:	CCTAAGCTTACGTTACC	

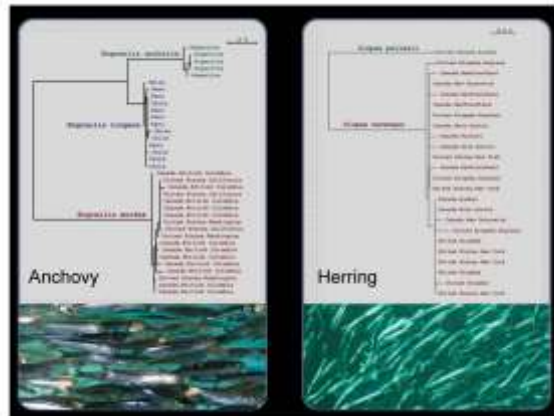
Low Interspecific Divergences are rare...

White-headed Gulls

Cichlids

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FISH-BoL, Hanner, R.



GenBank is based on Inference

>JNAP069-08Myoxocephalus scorpiusCOI-5PUN027322
 CCTATATCTAGTATTGGTGCCTGAGCCGGAAATAGTAGGCACAGCTCTAAAGCCCTCTA

Species name and FASTA file are Inferred

Specimens and raw data not accessible for inspection...
 and records cannot be annotated by 3rd parties.

Abstract: Phylogenetic and Evolutionary
 104 (1) 16, 1 January 2008 1688
 doi:10.1093/iob/obp017 Available online at <http://www.oxfordjournals.org/doi/10.1093/iob/obp017>

COMMENTARY

The Importance of Being Earnest: What, if Anything, Constitutes a "Specimen Examined?"

Luis A. Ruedas,¹ Jorge Salazar-Bravo,¹ Jerry W. Drago, and Terry L. Yates
¹Museum of Southwestern Biology, University of New Mexico, Albuquerque, New Mexico 87131-5006
 Received June 14, 2008

In the publishing literature upon "earnest" use of the specimens examined by phylogeneticists. This Request (2008) asks the question "Is L1?" The question is then placed in the context of the request. Because it is not clear what would constitute an examination of a specimen in the context of a phylogenetic study, we argue that in no way do we wish to suggest the strict interpretation or consequences of any of the labels used herein in the other years' volume and think that a legitimate question remains (especially) open for a clear and consistent interpretation for all papers published in the journal. We are sure that all the authors of the journal will agree that the requirements for all papers published in the journal should be consistent with the requirements for all papers published in the journal.

"Only [27%] of papers had a legitimate specimens examined section, with museum numbers for each voucher, and names of the museums where the specimens used in the study could be examined"

Barcoding is based on Evidence

>JNAP069-08Myoxocephalus scorpiusCOI-5PUN027322
 CCTATATCTAGTATTGGTGCCTGAGCCGGAAATAGTAGGCACAGCTCTAAAGCCCTCTA

{ Evidence }

Voucher Specimens are Critical !!!

Needed for re-examination and taxonomic validation

"DNA barcode" labels on vouchers are important for bidirectional linkage between barcode records & museum collections.

Phred: log scale probability of base-call accuracy

Phred Score	Error	Accuracy
10	1 in 10	90%
20	1 in 100	99%
30	1 in 1,000	99.9%
40	1 in 10,000	99.99%
50	1 in 100,000	99.999%

The Barcode Data Standard

Controlled annotation with the reserved **keyword BARCODE** in DDBJ/EMBL/GenBank:

1. Minimum 500bp, <1% ambiguous base calls
2. Double stranded sequence (e.g. 2X coverage)
3. Trace files and associated quality scores
4. Primers used to generate sequence
5. Linkages to:
 1. A morphological voucher specimen
 2. Structured reference to collections
 3. Geospatial reference information
 4. Valid species name
 5. Who performed the identification
 6. Literature citations

Rationale for Defining "BARCODE" keyword in GenBank

- ✓ Provides the community with reference records with verifiable and retrievable data:
 - ✓ Associated with retrievable voucher specimens (including tissue, DNA, etc.)
 - ✓ Linked to on-line metadata
 - ✓ Meet an agreed upon standard of taxonomic identification
 - ✓ Provide an assured level of data completeness
 - ✓ On an agreed upon gene region
 - ✓ Recommended for use in identifying unknowns



First BARCODE Compliant Publication

Identifying Canadian Freshwater Fishes through DNA Barcodes

Wesley Hesse, Robert Hoover, Sidney Miller, Nicholas S. Mendel, Eric Taylor, Mary Burchette, Douglas Robinson, Chuan Chuan, Alan Gony, Paul Kesteven, Junliang Zhang, John Agri, Leah Berveniche

ABSTRACT

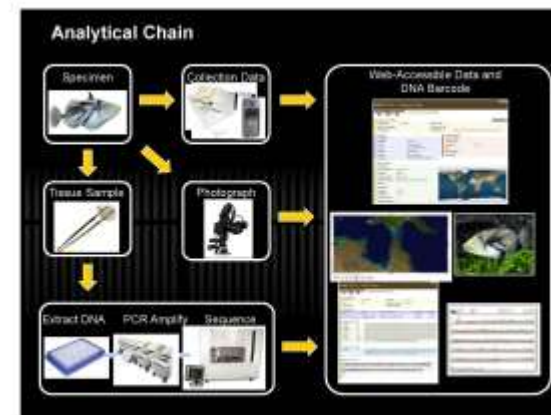
Background: DNA barcoding refers to the use of a short section of DNA to identify species. In this study, we use a short section of the mitochondrial cytochrome b gene to identify 100 fish species from the Great Lakes region. The cytochrome b gene is a highly conserved region of the genome that is present in all vertebrates. This makes it an ideal target for DNA barcoding. We used a highly sensitive PCR protocol to amplify the cytochrome b gene from tissue samples of 100 fish species. The resulting PCR products were sequenced and compared to the GenBank database to identify the species. This study demonstrates the power of DNA barcoding to identify fish species, even in the case of poorly preserved specimens.

Informatics Platform for Barcode Data - BOLD

BOLD SYSTEMS

Advancing species identification and discovery by providing an integrated environment for the assembly and application of DNA barcodes.

Public Data Portal | BOLD Taxonomy | BOLD Identifications



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BOLD Workbench

BOLD provides community with:

- Support for BARCODE data standard
- Secure data storage & Online access
- Permission based sharing
- Taxonomy progress reports
- Built-in quality control checks
- Analysis tools on BOLD compute cluster
- Barcode Index Numbers (BINs)
- DOIs for data sets
- Community Annotation tags

Barcode Gap

- Tabular Format
- Requires low level taxonomy
- Highlights:
 - ✓ Low Divergence compared to nearest neighbour
 - ✓ Divergence that is less than the intra-specific



Barcode Gap Analysis


Identification

- COI for Animals
 - 4 databases for different needs
 - BLAST, HMM and linear search
- matK/rbcL for Plants
 - BLAST algorithms
- ITS for Fungi
 - BLAST algorithms
- Batch or single FASTA identifications



Batch Identification Engine

Example from the Holocentrids




Molecular phylogenetics of squirrelfishes and soldierfishes (Teleostei: Serraniformes: Holocentridae): Rectifying more than 100 years of taxonomic confusion

Key Denliker^{1,2}, Jan A. Moore^{1,3}, Galen Webster¹, Dan J. Ravasi⁴, Matthew C. Stanley¹, Scott E. Stepien¹, Peter L. Manooch¹, Thomas J. May^{1,4}


¹Neoniphon inaequalis GenBank accession numbers: JX390738 JX390779 JX390817 JX390857 JX390893 JX390926 JX390964

²Neoniphon opercularis GenBank accession numbers: JX390740 JX390769 JX390806 JX390848 JX390818 JX390965

Example from the Holocentrids



Sargocentron inaequalis (expected species)



Neoniphon argenteus (actual species)

BOLD features for correct species IDs
 The BIN system



Flagging records

- BIN consistency system for samples
- Report a missing image of the specimen
- The number of images present for the sample
- Sequence is Barcode Complete
- Specimens present in JGI/GenBank
- Checksums present or missing
- Flagged records: Masked from the BIN system

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Barcode Index Numbers (BINs)

- COI sequences clustered algorithmically
- Aggregation of data from clusters presented in BIN pages
- Annotation framework – researchers can review and critique elements of BINs: rapid validation
- Accessible in Public Data Portal



BIN Page

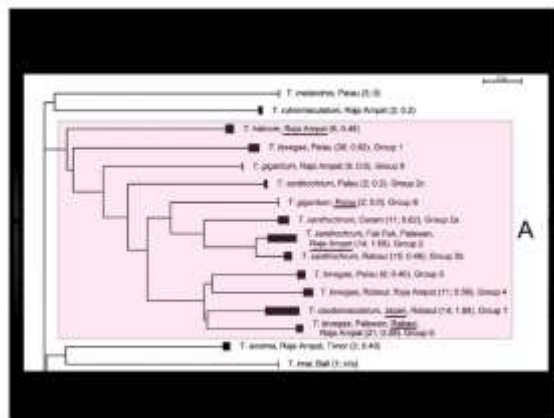
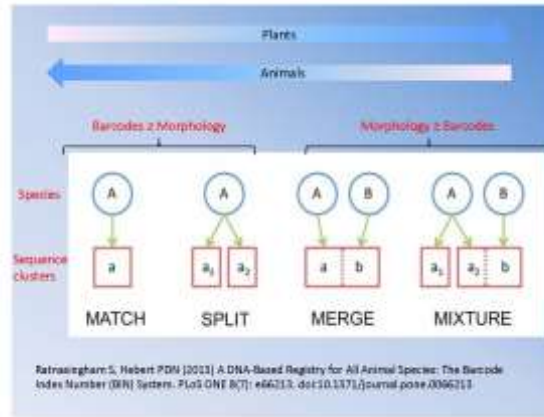
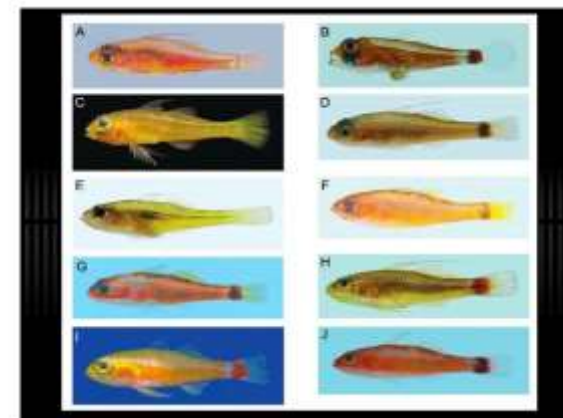


Table 1. Results from a barcode analysis of 142 specimens of *Tristramia* *tristrami*.

Group #	Locality	n	Var.	Minimum distance between groups									
				1	2a	2b	2c	4	5	6	7	8	9
1 (as <i>T. tristrami</i>)	Palau	28	0.6	17.7	21.3	19.3	16.7	21.5	21.3	22.4	20.8	21.6	18.1
2 (as <i>T. sandelwoodi</i>)	FFI/IRA	14	1.6	—	7.7	3.5	16.1	14.7	14.8	14.2	11.8	10.7	15.2
2a (as <i>T. sandelwoodi</i>)	Cerua	11	0.6	—	7.8	16.3	15.8	14.8	16.2	13.9	12.0	17.3	
2b (as <i>T. sandelwoodi</i>)	Bahau	15	0.5	—	16.7	16.2	14.6	15.1	14.4	10.3	14.6		
2c (as <i>T. sandelwoodi</i>)	Palau	3	0.0	—	15.8	14.9	15.2	14.6	15.6	15.9			
4 (as <i>T. tristrami</i>)	RA/RA	11	0.6	—	—	9.2	9.5	9.1	15.1	17.0			
5 (as <i>T. tristrami</i>)	Palau	8	0.5	—	—	—	9.5	9.1	14.7	18.5			
6 (as <i>T. tristrami</i>)	FFI/IRA	23	0.4	—	—	—	—	7.8	14.5	16.8			
7 (as <i>T. tristrami</i>)	Japan/RA	14	1.7	—	—	—	—	—	14.1	16.8			
8 (as <i>T. tristrami</i>)	Palau	2	0.0	—	—	—	—	—	—	16.7			
9 (as <i>T. tristrami</i>)	RA	6	0.0	—	—	—	—	—	—	—			



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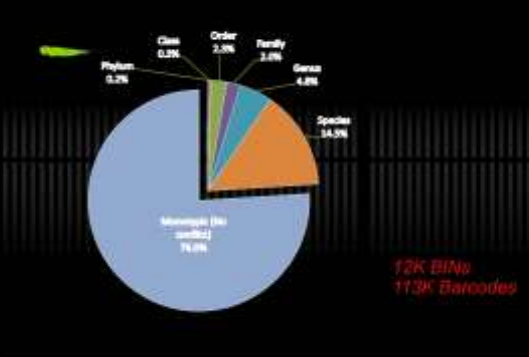
Summary:

73 valid described species currently recognized

Increase from 52 to 94 potential species (e.g. BINs) in our sampling

Raises the predicted total number of species in this genus from about 110 to nearly 200

Taxonomic Conflict Revealed with BINS



Reasons for Discordance

- Morphological misidentification
- Taxonomic uncertainty, revision needed
- Barcode sequence sharing
- Flaws in sample processing

At Issue (for fishes):

- BOLD taxonomy Browser lists ~12,500 species and 113,000 specimens barcoded (including GenBank data) with 2K un-named BIN clusters
- An unacceptable proportion of "barcoding" papers using outmoded approaches, lacking reference to vouchers and trace files
- Community annotation of BARCODE records on BOLD needed, especially to highlight topotypic material, questionable IDs, etc.
- New descriptions need accompanying barcodes!

Species description

Identification (ID) confidence annotation

- Level 1: Highly reliable identification by expert
- Level 2: Reliable identification using literature
- Level 3: Reliable to genus level
- Level 4: Limited confidence (e.g. Family)
- Level 5: Superficial or unknown (e.g. GenBank)

*Use Extra Info field on BOLD (e.g. ID-L#) for annotation so confidence level can be printed on NJ trees.

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A Ranking System for Reference Libraries of DNA Barcodes: Application to Marine Fish Species from Portugal

Filipe D. Costa¹, Mariana Louf², Ângela Martins³, Maria M. Costa⁴, Maria S. Costa⁵, Miguel Carvalho⁶, Maria J. Alves⁷, Dêb Stelbrink⁸, Gery R. Carvalho⁹

Abstract
Background: The increasing availability of reference libraries of DNA barcodes (BOLD) offers the opportunity to the user the level of concordance of DNA barcode data among libraries, in order to detect possible discrepancies generated from taxonomic uncertainty or operational shortcomings. We propose a ranking system to all those a confidence level in species identification associated with DNA barcode records from a BOLD, here we apply the proposed ranking system to a newly generated BOLD for marine fish of Portugal.

Methodology/Principal Findings: Approaches to BOLD representing 32 marine fish species were collected along the continental shelf of Portugal, morphological identified and processed in a minimum confidence. Samples were deposited at the Barcode of Life System (BOLD) and a new BOLD was created. BOLD barcodes had average 98% similarity and interspecific distance (p-distance) 0.026 and 0.046, respectively within the same locality observed for marine fish. 20 specimens were noted in their different works (100% according to the assignment of the nearest barcode data species identification and the respective fragments DNA barcodes). Grades A to E were attributed upon identification of individual specimen assignments to BOLD BOLD and comparison of the clustering pattern in the 50 base generated. Overall similarity resulted in 71.9% of assignments correct (in species), 1.8% approximately consistent barcode versus actual and 23.3%, but leading external concordance (grade A), and 18.1% of species identification with lower levels of reliability (grades C-E).

Conclusions/Significance: We highlight the importance of implementing a system to link barcode records in BOLD, in order to help user in level of taxonomic resolution, to reduce ambiguity of database data. With increasing BOLD barcode records publicly available, this cross-validation system could provide a means of quality control of barcodes, while providing the centralized register and annotation required in taxonomic work.

Cross-Library Concordance:

- Grade A: External concordance with other published data
- Grade B: multiple specimens with Internal concordance (no match on BOLD)
- Grade C: Sub-optimal concordance (internal genetic structure)
- Grade D: Insufficient data (no match on BOLD)
- Grade E: Discordant species assignment

Data sharing is necessary

Barcodeing has advanced a standard marker enabling broad comparison of sequences, but now we need to solve the data silo problem...

BOLD supports BARCODE Standard and provides an efficient platform for disambiguating and reconciling the application of names across projects, facilitates submission of BARCODE records to GenBank, provides attribution to collections, links to publications, improves the efficiency of integrative taxonomy and supports the user community with high quality data records.

Database linkages needed

Accessing names and type localities from, and providing Barcode and BIN information to Catalog of Fishes could aid taxonomic calibration

Providing locality and Barcode data to FishBase could extend knowledge of species ranges and aid fish identification, while extracting range data from FishBase could aid identification of outliers in BOLD

FISHMONGERS

Species Summary for *Paralichthys lethostigma* (Red snapper)

Barcode of Life System (BOLD) interface showing a phylogenetic tree and a list of species with their corresponding barcode data.

DNA Barcoding Investigations Bring Biology to Life

When you're in the market, you know you're looking for the best. But what if you could find the best fish? DNA barcoding can help you do that.

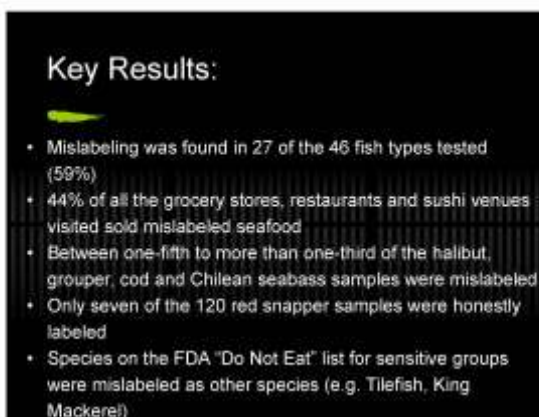
Fish Tale Has DNA Hook: Students Find Bad Labels

Gene Smelling Fishes: Students Find Bad Labels

PHOTO: J. HANNER

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California Enacts New Legislation:

PADILLA LEGISLATION TARGETS MISLABELED SEAFOOD
August 2014

SACRAMENTO – Senator Alex Padilla held a press conference today at Taylor’s Market in Sacramento to announce Senate Bill 1130 which addresses the growing problem of seafood mislabeling and its effects on public health, consumer choice, and sustainable fishing practices.

Joining Senator Padilla was Dennis Johnson from Taylor’s Market who conducted a seafood identification demonstration highlighting how easy it is to mislabel seafood. Also attending was Geoffrey G. Chesser, Ph.D., the California Director of Oceans, the largest international organization focused solely on ocean conservation.

“SB 1130 would mean it’s unlawful for any person to knowingly sell mislabeled seafood. While spending on seafood in the United States has grown to more than \$90 billion annually, state law does not provide clear guidance regarding accurate labeling of seafood. The lack of standards has led to high rates of mislabeling throughout our state. In a recent survey by Clooney, Rife & Southern, California seafood samples were mislabeled and 85% of restaurants visited in Northern California mislabeled their fish offerings. SB 1130 is modeled after similar legislation passed in the state of Washington. The bill is scheduled to be heard by the Senate Health Committee on Wednesday, April 9, at 11:30 a.m. in House-6200 of the State Capitol.”

“SB 1130 will address the growing problem of seafood mislabeling. To protect our health, economy and oceans it is essential that seafood be labeled accurately,” said Senator Alex Padilla. “Honesty is always the best policy,” added Padilla.

US Task Force Announced

148 White House
Office of the Press Secretary
For Immediate Release June 17, 2014

Presidential Memorandum – Comprehensive Framework to Combat Illegal, Unreported, and Unregulated Fishing and Seafood Fraud

MEMORANDUM FOR THE HEADS OF EXECUTIVE DEPARTMENTS AND AGENCIES
SUBJECT: Establishing a Comprehensive Framework to Combat Illegal, Unreported, and Unregulated Fishing and Seafood Fraud

The United States is a global leader in sustainable seafood. Over the course of the last 8 years, the United States has largely avoided overfishing in federally managed waters and successfully rebuilt a record number of stocks depleted by the stresses of the past. At the same time, effective domestic management and enforcement of fishing regulations have supported near record highs in fish landings and revenue for our domestic fishing industry. As a result, the U.S. management scheme is recognized internationally as a model for other countries as they work to end overfishing.

THE UNITED STATES ATTORNEY'S OFFICE
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NEWS

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Miami Seafood Firm Pleads Guilty And Is Sentenced For Imported Seafood Labelling Fraud

FOR IMMEDIATE RELEASE August 5, 2014

Wafiro A. Ferrer, United States Attorney for the Southern District of Florida, and Tracy Duan, Special Agent in Charge, National Oceanic and Atmospheric Administration (NOAA), Office of Law Enforcement, announce that the Miami-based seafood company True Nature Seafood, LLC (TNS), was sentenced in Miami on a plea of guilty to knowingly making and submitting a false record, account, or label for fish which had been or was intended to be imported, exported, transported, sold, purchased, in violation of the Lacey Act, Title 16, United States Code, Sections 3372(a)(1) and (2), 3373(a)(1)(A), and Title 18, United States Code, Section 2.

Public now has access to testing

1 Collect a Sample
2 Scan & Document It
3 Submit Your Bill
4 View Your Results

Example user interface for a mobile app. The app is designed for users to collect a sample, scan it, and submit it for testing. The interface is simple and user-friendly, with clear instructions and a QR code for scanning.

TRU-ID

United Nations' Agreement on Food & Fisheries Products

TRU-ID Vision & Mission

"Our vision is to provide consumers confidence in the authenticity of food & seafood products."

"Our mission is to advance TRU-ID based applications designed for testing and to make it possible for clients and their customers to view the authenticity of mislabeled or misrepresented ingredients in their products. Authenticity is consumer product confidence."

Product Differentiation

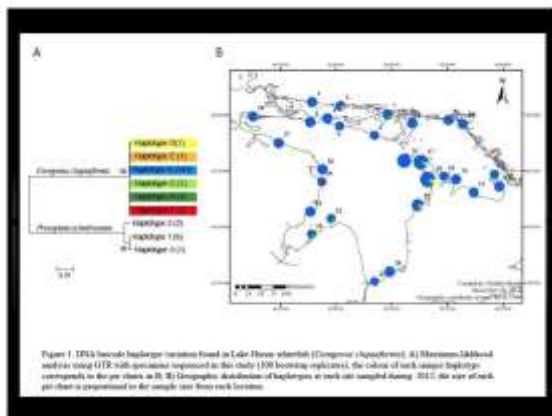
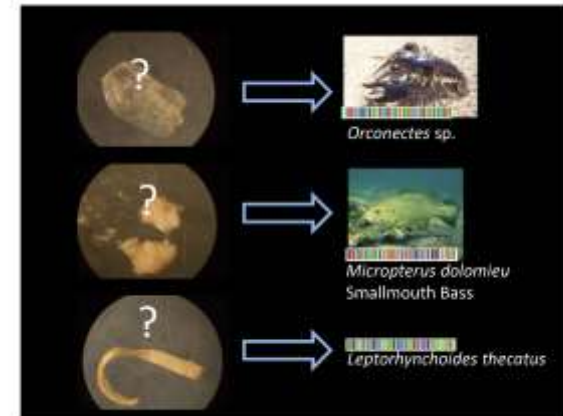
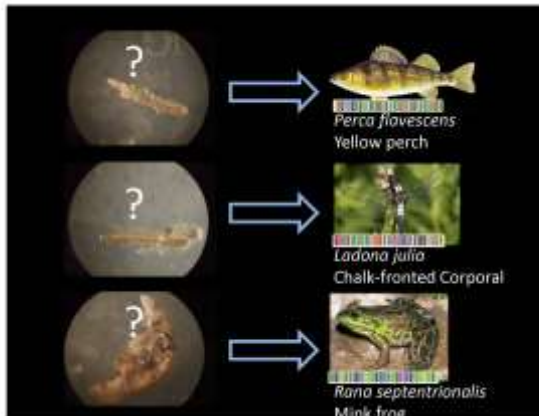
12th World Fisheries Symposium

12th World Fisheries Symposium
12-14 October 2014
Ljubljana, Slovenia

Great Lakes Fishery Commission

12th FishBase Symposium Big Old Data and Shiny New Insights: Using FishBase for Research

FISH-BoL, Hanner, R.



biology letters
Population genetics

Species detection using environmental DNA from water samples

Gaëlle Francour Florestal^{1,2*}, Claude Miaud¹, François Poupardin¹ and Pierre Taberlet¹

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²Laboratoire d'Ecologie Evolutive et Fonctionnelle, CNRS, UMR 5175, Université de Montpellier, 34293 Montpellier Cedex 05, France

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The assessment of species distribution is a first critical phase of biodiversity studies and is necessary in many disciplines such as biogeography, conservation biology and ecology. However, several species are difficult to detect, especially during particular time periods or developmental stages, particularly during early instars. Here we present a novel approach, based on the limited persistence of DNA in the environment, to detect the presence of a species in fresh water. We used specific primers that amplify short mitochondrial DNA sequences to track the presence of a frog (*Musca autosheloni*) in controlled environments and natural wetlands. A multi-sampling approach allowed the species detection in all environments where it was present, even at low densities. The

long time periods, as shown by the studies on old sediments, peatbogs and ice cores (Hydroise et al. 2003; Wilbur et al. 2003, 2007). While short DNA sequences may be present at high density in the environment, their potential for the study of present-day communities of macro-organisms remains schematically unexplored. Here we present a novel approach, based on the persistence of DNA in the environment, to detect the presence of a species in fresh water. We examined whether DNA signatures are preserved in the aquatic environment and whether they can be used for a reliable assessment of current species presence. We first used the method in controlled environments and then evaluated whether it could be applied under natural field conditions. The model species was the American bullfrog (*Rana catesbeiana*) (= *Lithobates catesbeiana*), an invasive amphibian for which high-quality genetic data exist (Stuart et al. 2007a,b). This allowed reliable field validation. The American bullfrog is native to western North America, but has been introduced into ecosystems around the globe. It is considered one of the world's most harmful invasive species, since it is responsible for the decline of native amphibians by direct predation, competition, diffusion of disease and complex biotic interactions (Stuart & Knouffer 2003; Ken & Feyer 2005; Haver et al. 2006).

2. MATERIALS AND METHODS

We performed experiments to test potential conditions and natural wetlands. Bullfrogs were found in naturalized sites of 10 or more, collected in a natural water spring or 10000 above sea level and at 1000 m from the nearest building road. We used 5, 1, 1 and 10 samples per apartment, each sample was obtained on three dates: after 24 hours, we collected a 10 ml water sample from each apartment.

The success of Barcoding is...

Chiefly due to the fact that its data standards enhance current practices in Molecular ID

Standardization, large-scale collaboration, compulsory deposition of voucher specimens and active curation of the resulting database supports diverse applications, highlighting the importance of taxonomists and collections

12th FishBase Symposium
 Big Old Data and Shiny New Insights: Using FishBase for Research

FISH-BoL, Hanner, R.

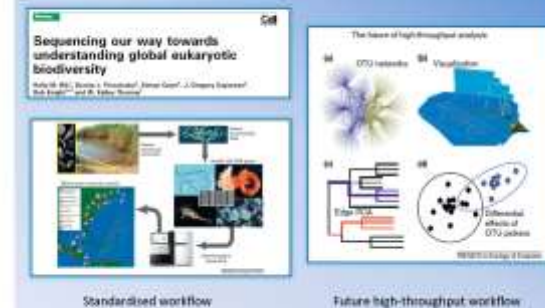
Expected Benefits:

- Standardize the application of names.
- Facilitate species identification for all users, particularly in cases where traditional methods are not applicable.
- Highlight specimens that represent a range expansion of known species.
- Flag unrecognized or cryptic diversity.
- Demonstrate the value of collections and taxonomists contributing to the campaign.

Need for a Taxonomic Revolution?



Future of Taxonomy?



International Barcode of Life Project

Imagine...
 a world in which you can know the name of

5 Years
5M Specimens
500K Species

This is the world that iBOL will build

DNA- A Digital Future for Biodiversity

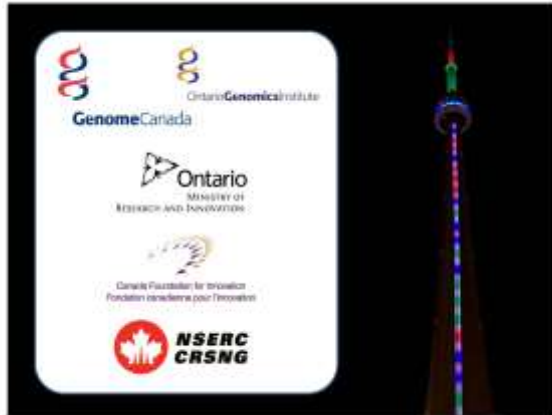
Core Facilities Mass Analyses Handheld Devices

Acknowledgments:

- Members of the Hanner lab (past & present)
- Paul Hebert & the Biodiversity Institute of Ontario (BIO) staff
- Royal Ontario Museum
- Jon Deeds and Haile Yancy, US FDA
- Participants of the FISH-BOL Campaign
- The International Barcode of Life Project (iBOL.org)

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FISH-BoL, Hanner, R.



Molecular Ecology (2010) 19(1), 1–12 © 2009 The Authors
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BARCODING VERTEBRATES Identifying sharks with DNA barcodes: assessing the utility of a nucleotide diagnostic approach

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Abstract
Shark detection molecules are widely commercialized, but the fragmenting shark fin industry in the last few decades has made monitoring such and trade of these animals critical. As a tool for molecular species identification, DNA barcoding offers significant potential. However, the genetic distance-based approach towards species identification employed by the Barcode of Life Data System may compromise both the specificity needed for regulatory or legal applications that require nonambiguous identification results. This is because such specificity is not typically achieved by anything less than a 100% match at the query sequence to an entry in the reference database using genetic distance. Although various divergence thresholds have been proposed to define acceptable levels of interspecific variation, enough exceptions exist to cast reasonable doubt on any less than such a match when using a distance-based approach for the identification of unknowns. An alternative approach aims at the identification of discrete nucleotide characters that can be used to unambiguously diagnose species. The objective of this study was to assess the performance differences between these competing approaches by examining more than 1000 DNA barcodes representing nearly 20% of all known elasmobranch species. Our results demonstrate that a character-based, nucleotide diagnostic (ND) approach to barcode identification is feasible and also provides novel insights into the structure of haplotype diversity among closely related species of sharks. Considerations for the use of NDs in applied fields are also explored. **Keywords:** DNA barcoding, sharks, single nucleotide diagnostic

Table 3. Statistical parsimony networks that contain multiple species, with at least one that is distinguishable with an ND.

Species	Statistical parsimony network	Character between species
1) <i>Carcharias taurus</i> 2) <i>Megalodon</i> (old)		3
1) <i>Carcharias taurus</i> 2) <i>Carcharias brydensayi</i>		4
1) <i>Carcharias mackinacensis</i> 2) <i>Carcharias acronotus</i>		8 or 11
1) <i>Megachasma pelagios</i> 2) <i>Megachasma</i> (old)		10
1) <i>Carcharias glaucus</i> 2) <i>Carcharias acronotus</i> (see Fig. 4) 3) <i>Carcharias longimanus</i>		10

Each node and circle represent a unique haplotype, and is numbered to correspond with the species names in column 1. The third column shows the number of character changes between each species. The shaded circle represents the *Carcharias glaucus*/*Carcharias acronotus* pair shown in Fig. 4.

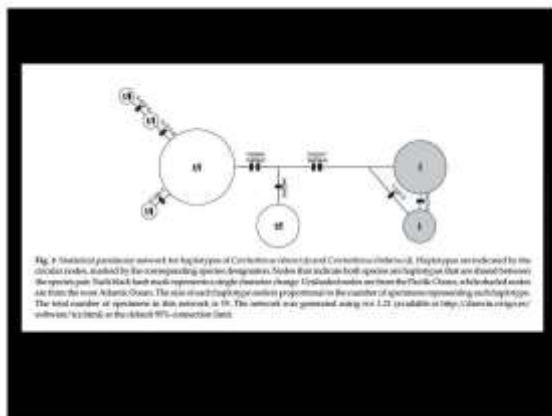
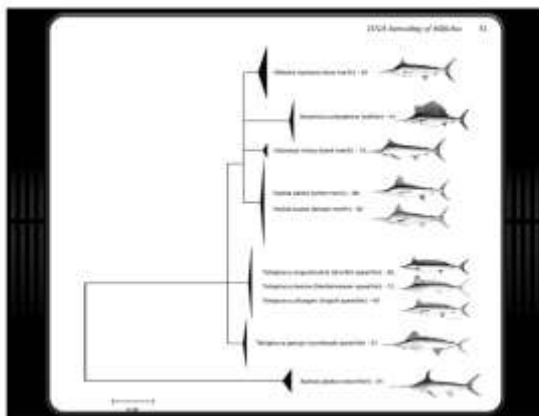


Fig. 3. Statistical parsimony network for haplotypes of *Carcharias taurus* (1) and *Carcharias brydensayi* (2). Haplotypes are indicated by the circled nodes, numbered by the corresponding species designation. Shaded circles indicate both species and haplotypes that are shared between the species pair. Node 11 has a small representation (single character change). Unshaded nodes are those that differ from the *Carcharias taurus* haplotype. The size of each node is proportional to the number of specimens representing each haplotype. The total number of specimens in this network is 10. The network was generated using vst 1.2.2, available at <http://bioinformatics.org/~delwiche/vst1.2.2/>, or the R package SPS (available at <http://www.ropensci.org>).



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Glacial cycles as an allopatric speciation pump in north-eastern American freshwater fishes

JULIEN APRIL*, ROBERT H. HANNER†, ANNE-MARIE DUIN-CÔTÉ* and LOUIS BURNATCHEZ*

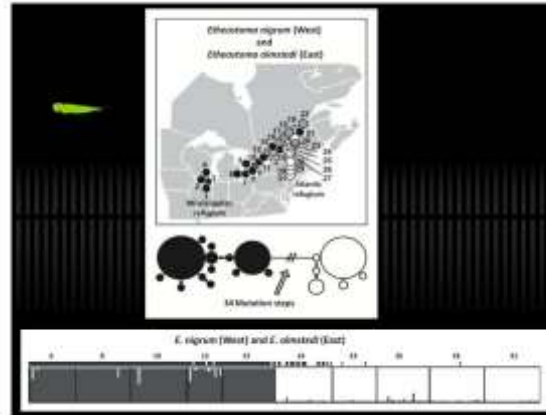
*Chaire de Biodiversité et de Gestion (CBG), Département de Biologie, Université Laval, Québec, QC, Canada G1V 0A2; †Biodiversity Institute of Ontario, University of Guelph, Guelph, ON, Canada N1G 2W1

Abstract
Allopatric speciation may be the principal mechanism generating new species. Yet, it remains difficult to judge the generality of this process because few studies have provided evidence that geographic isolation has triggered the development of reproductive isolation over multiple species of a regional fauna. Here, we first combine results from new mitochondrial *Ade* and published literature *H* loci to show that the eastern Great Lakes drainage represents a multidispersive refugia zone for glacial lineages of freshwater fishes with variable levels of genetic divergence. Second, we performed amplified fragment length polymorphism analyses among four pairs of *Trageogomphus* species that diverged with relatively deep levels of mtDNA *rbcL* divergence (median divergence: 6.2%) developed along reproductive barriers, while lineages with lower levels of divergence show weaker reproductive isolation when tested in *mtDNA*. This suggests that a threshold of 2% sequence divergence of mtDNA could be used as a first step to flag cryptic species in North American freshwater fishes. By describing different levels of divergence and reproductive isolation in different coexisting fishes, we offer strong evidence that allopatric speciation has contributed significantly to the diversification of north-eastern American freshwater fishes and confirm that Pleistocene glacial cycles can be viewed as a 'speciation pump' that played a predominant role in generating biodiversity.

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FISH-BoL, Hanner, R.

- Map of samples' localities & mtDNA haplotype network
- Taxa characterized by two distinct mtDNA clades, black and white circles were used to distinguish them. Sample sites where haplotypes from both mtDNA clades were found are filled in grey.
- Bar plot showing the admixture proportion of each specimen based on AFLP data (calculated using STRUCTURE).
- Sampling site numbers are given above bar plots.
- Each individual corresponds to a vertical bar, and the proportion of the genome from each of the genetic groups is represented by its corresponding colour (black = west and white = east). Individuals possessing mtDNA haplotypes from the western genetic group are marked with a black line above bar plots.



Further considerations for using barcodes

- Proportion of species with barcode coverage relative to known species in the genus
- Proportion of unidentified or conflicting BINs relative to well characterized barcoded species
- The level of precision required...

Robert Hanner is the Associate Director for the Canadian Barcode of Life Network, headquartered at the Biodiversity Institute of Ontario, University of Guelph. He currently chairs the Database Working Group of the Consortium for the Barcode of Life (CBOL) and also serves as Campaign Coordinator for the Fish Barcode of Life (FISH-BOL) initiative, a project of global scale that aims to assemble a standard reference sequence library for the molecular identification of all fishes. Dr. Hanner is a Past President of the International Society for Biological and Environmental Repositories (ISBER). Prior to his arrival in Guelph (August of 2005), he served as the Scientific Program Director for the Coriell Cell Repositories (at the Coriell Institute for Medical Research) and prior to that, he was a Curatorial Associate at the American Museum of Natural History where he spearheaded the establishment of the Ambrose Monell Collection for Molecular and Microbial Research.



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Multi-model ensemble projections on climate change, Cheung, W.

MULTI-MODEL ENSEMBLE PROJECTIONS OF CLIMATE CHANGE
EFFECTS ON GLOBAL MARINE BIODIVERSITY⁶

William CHEUNG

Assistant Professor, Fisheries Centre, University of British Columbia,
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Species Distribution Models (SDMs) are important tools to explore the effects of future global changes in biodiversity. Previous studies show that variability is introduced into projected distributions through alternative datasets and modelling procedures. However, a multi-model approach to assess biogeographic shifts at the global scale is still rarely applied, particularly in the marine environment. Here we apply three SDMs to assess the global patterns of change in species richness, invasion and extinction intensity in the world's oceans. Specifically, AquaMaps, Maxent and the Dynamic Bioclimate Envelope Model are three commonly applied approaches in the marine environment and have been evaluated and validated in previous studies. We make species-specific projections of distribution shift using each SDM, subsequently aggregating them to calculate indices of change across a set of 802 species of exploited marine fishes and invertebrates. Results indicate an average poleward latitudinal shift across species and SDMs at a rate of 15.5 and 25.6 km per decade for a low and high emissions climate change scenario respectively. Predicted distribution shifts result in hotspots of local invasion intensity in high latitude regions while local extinctions were concentrated near the equator. Specifically, between 10°N and 10°S, we predicted that, on average, 6.5 species would become locally extinct per 0.5° latitude under the climate change emissions scenario RCP (Representative Concentration Pathway) 8.5. Average invasions were predicted to be 2.0 species per 0.5° latitude in the Arctic Ocean and 1.5 species per 0.5° latitude in the Southern Ocean. These averaged global hotspots of invasion and local extinction intensity are robust to the different SDM used and coincide with high levels of agreement.

⁶ Cite as: Cheung, W. (2014) Multi-model ensemble projections of climate change effects on global marine biodiversity, p. 53-57. In: Palomares, MLD, Taylor, E, Pauly, D (eds.), 12th FishBase Symposium, Big Old Data and Shiny New Insights: Using FishBase for Research. September 8, 2014, Beaty Museum of Biodiversity, University of British Columbia, Vancouver, Canada. A report prepared by the *Sea Around Us* to the Paul G Allen Family Foundation and the Pew Charitable Trusts.

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Multi-model ensemble projections on climate change, Cheung, W.

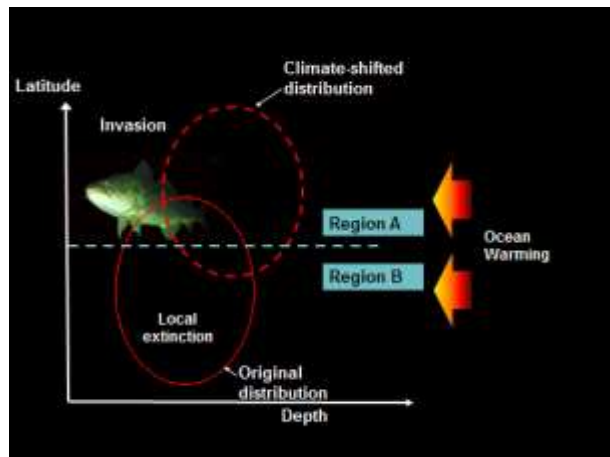
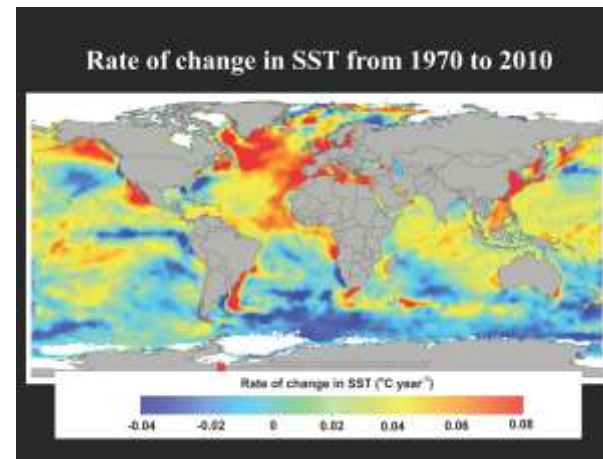
Multi-model ensemble projections of climate change effects on global marine biodiversity

William Cheung & Miranda Jones

Nereus Program
 Changing Ocean Research Unit
 The University of British Columbia
 FishBase Symposium, 8 Sept 2014

Contributors

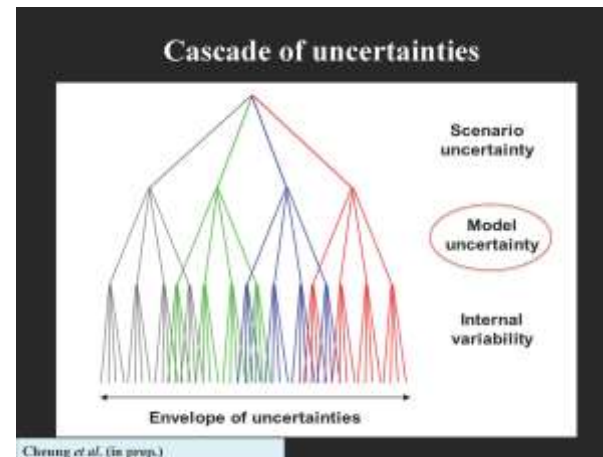
- Charlie Stock (GFDL)
- Daniel Pauly (UBC)
- Deng Palomares (UBC)
- Jorge Sarmiento (Princeton)
- Thomas Frölicher (ETH Zurich)



Species Distribution Modelling

- Predict the range of a species as a manifestation of habitat characteristics that limit or support the organism of interest.
- Evaluate the movement of distribution in time and space, with consideration of population dynamics and dispersal under climate change – Dynamic bioclimate envelope model

Cheung *et al.* (2009) Fish and Fisheries



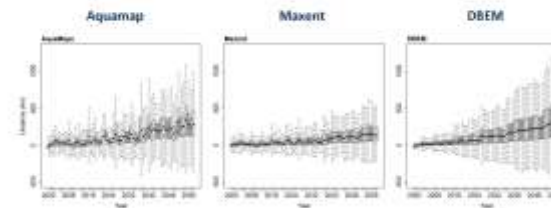
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Multi-model ensemble projections on climate change, Cheung, W.

The Models

- **AquaMaps** (Kaschner *et al.* 2006; 2008) (in FishBase)
 - Simple, trapezoidal response curve
- **Maxent** (Phillips *et al.* 2004; 2006)
 - Complex Bayesian approach
- **Dynamic Bioclimate Envelope Model (DBEM)** (Cheung *et al.* 2008; 2011)
 - Delimiting approach, incorporating logistic population growth model, ecophysiology and dispersal

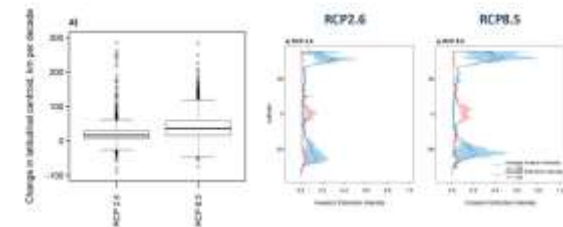
Projected Distribution Shifts (RCP8.5)



- 900 species of exploited fishes and invertebrates globally;
- Year: 2000 to 2050, RCP 2.6 and RCP 8.5;
- Driven by outputs from GFDL ESM2M.

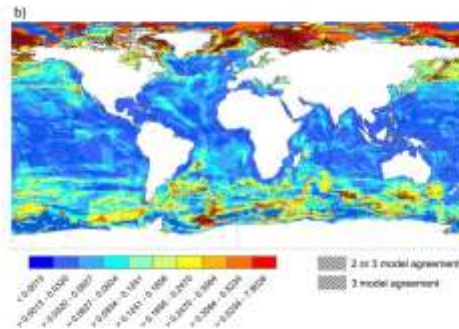
Jones and Cheung (in press) ICES Journal of Marine Science

Projected Invasion and local extinction

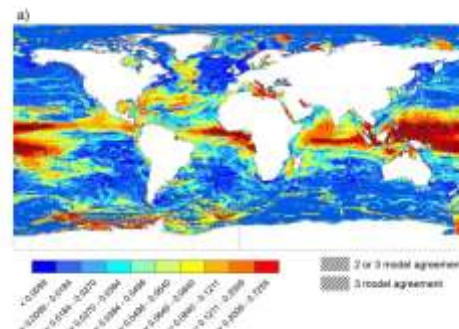


Jones and Cheung (in press) ICES Journal of Marine Science

Invasion intensity (RCP 8.5)



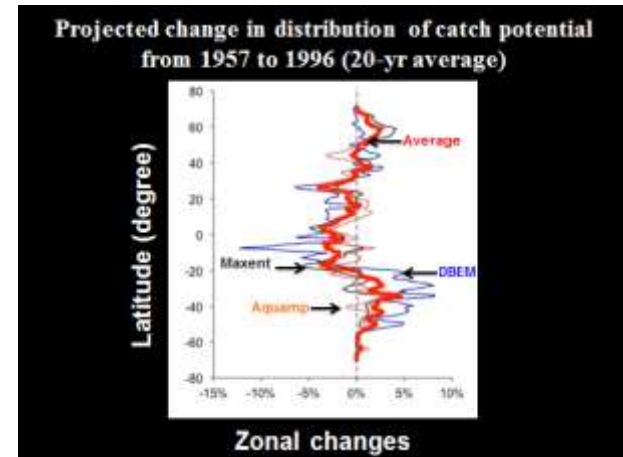
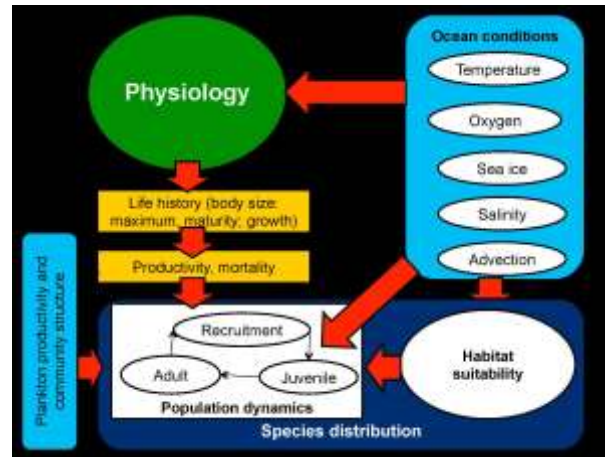
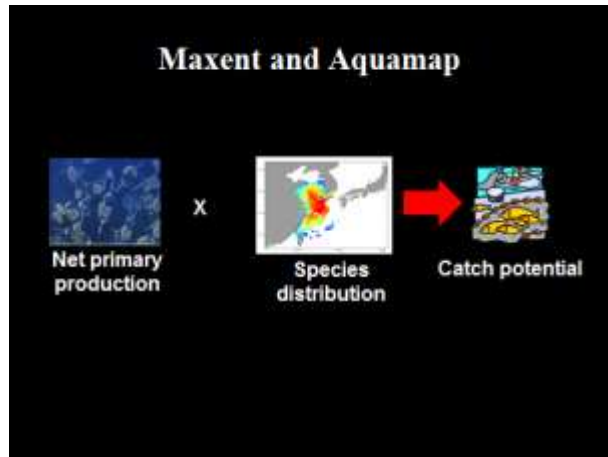
Extinction intensity (RCP 8.5)



How projections of catch potential differ between species distribution models?

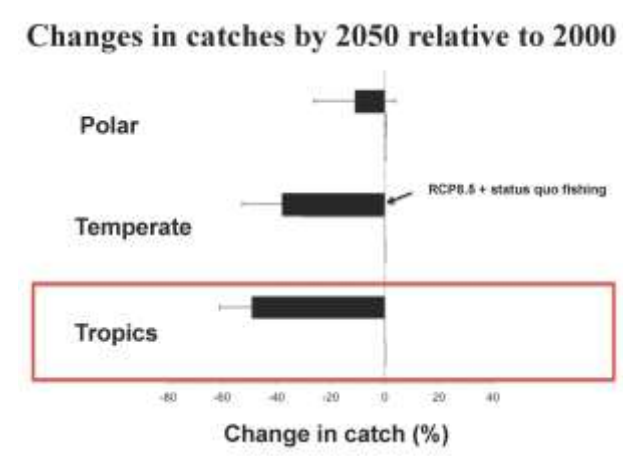
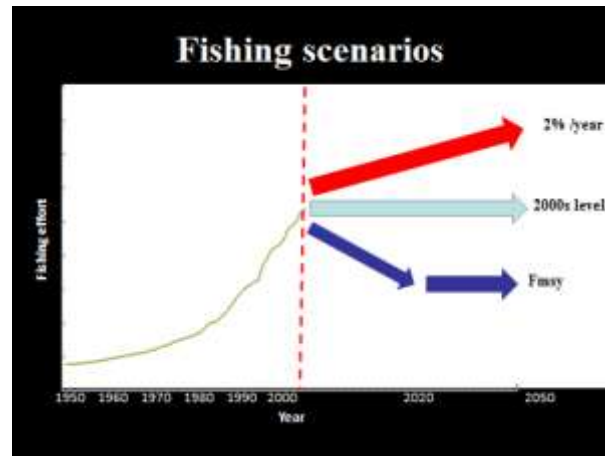
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Multi-model ensemble projections on climate change, Cheung, W.



Effects of fishing and climate

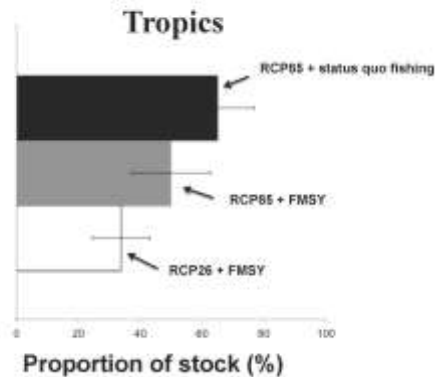
- Combine species distribution models with Catch-MSY model (Martell and Froese 2013);
- Divided into stocks (Large Marine Ecosystems and species);
- Catches and proportion of stocks with high risk of large decrease in abundance.



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Multi-model ensemble projections on climate change, Cheung, W.

Risk of large population decline by 2050



Summary

- Large-scale patterns of species turn-over under climate change are robust to structural model uncertainty;
- With continuing climate change, improving fisheries management can help reduce the risks on global-scale effects on marine biodiversity and fisheries;
- To assess climate risk on biodiversity, we need to systematically explore the envelope of uncertainties, with the use of global databases such as FishBase.

Acknowledgement

- National Geographic Society;
- Nippon Foundation-Nereus Program;
- Natural Sciences and Engineering Research Council of Canada.

William Cheung is an Assistant Professor at the [UBC Fisheries Centre](#) since 2011, and is head of the [Changing Ocean Research Unit \(CORU\)](#). William obtained a BSc. (Biology) in 1998, and subsequently a M.Phil. in 2001 from the University of Hong Kong. After working in WWF Hong Kong for two years, he moved to Vancouver and completed his PhD in Resource Management and Environmental Studies in the UBC Fisheries Centre in 2007. He then worked as a postdoctoral fellow in the *Sea Around Us* project for two years. From 2009 to 2011, he was Lecturer in Marine Ecosystem Services in the [School of Environmental Sciences, University of East Anglia](#) in the UK. Currently, his main research area is on assessing impacts of fishing and climate change on marine ecosystems and their goods and services, and studying ways to reconcile trade-offs in their management. Specifically, he develops empirical and numerical simulation models to examine the impacts of climate change on marine biodiversity and fisheries, globally and in various regional seas. He applies interdisciplinary approaches to evaluate the trade-offs between ecological, economic and social objectives in managing coastal social-ecological systems. Moreover, his research involves the development and application of original approaches to study historical changes in fish stocks and ecosystems. He works on various interdisciplinary research projects with global collaboration networks in the UK, China, Australia, Africa, USA and Canada. He has been a member of the [IUCN Groupers and Wrasses Species Specialist Group](#) since 2005 and serves on the editorial board of *Fish and Fisheries* and *International Journal of Sustainable Society*.



12th FishBase Symposium
Big Old Data and Shiny New Insights: Using FishBase for Research

FishBase in trophic ecosystem modelling, Arreguin-Sanchez, F. et al.

THE ROLE OF FISHBASE IN TROPHIC ECOSYSTEM MODELLING⁷

Francisco ARREGUIN-SANCHEZ, Instituto Politécnico Nacional, Centro Interdisciplinario de Ciencias Marinas (CICIMAR), Apartado Postal 592, La Paz, 23090, Baja California Sur, México; farregui@ipn.mx and Gustavo de la Cruz Aqüero, **Manuel J. Zetina-Réjon (presenter)**, Pablo del Monte-Luna, Mirtha Albañez-Lucero, Arturo Tripp-Quezada, José de la Cruz Agüero; CICIMAR

In 1995, Dr Rainer Froese invited Mexican scientists to join FishBase. At that time, ichthyologists responsible for collections and fish ecologists were not fully convinced of the benefits of sharing data at a global level. Fisheries biologists were more open to FishBase because they recognized the value of easily accessible data for modelling as a base tool for natural resources management. The FishBase module in Mexico began in 1996 with a small grant from CONABIO (National Commission of Biodiversity) to contribute to a database of Mexican fishes using FishBase as a bridge. A strong link between FishBase and trophic ecosystem modelling began, which we assume has a parallel history in other parts of the world. Today, the role of FishBase in trophic ecosystem modelling is more than indubitable; it is almost inseparable. Take the input scheme of the software Ecopath with Ecosim (EwE) as an example. FishBase contributes with both, inputs and/or confirmation-validity of model parametrization. Primary information, such as species distribution, habitat, occurrence and depth ranges help in constructing the components of an ecosystem. Once an ecosystem is constructed, modelers turn to FishBase to assemble Ecopath input parameters (P/B, Q/B, diets, food items, predators, trophic levels, etc.). Once an Ecopath model is balanced, modelers may proceed to time-dynamic modelling of the ecosystem using Ecosim. For this, FishBase links from species groups to catch time series (to FAO catch statistics via ISCAAP codes, or to the *Sea Around Us* reconstructed catches database), recruitment time series, or specific information to identify environmental variables that force a species' production. The next step, time-space modelling with Ecospace, is also facilitated with the relevant FishBase data on fish habitats, occurrences, ecology, swimming speed, among others. Globally, FishBase provides a powerful base that supports interpretations of EwE outputs, to create realistic scenarios of ecosystem management or to test theoretical hypotheses. Last but not the least, FishBase plays a relevant role in teaching the practice of ecosystem modelling. CICIMAR, for instance, offers an Ecopath course each semester since mid 1996. FishBase is used throughout this course as a basic tool to obtain information on and thus construct an ecosystem model, and in addition, to learn about fish around the world. In this contribution, we show some examples where FishBase and EwE interact in the process of constructing trophic ecosystem models.

⁷ Cite as: Arreguin-Sanchez, F, de la Cruz Aqüero, G, Zetina-Réjon, MJ, del Monte-Luna, P, Albañez-Lucero, M, Tripp-Quezada, A, de la Cruz Agüero, J (2014) The role of FishBase in trophic ecosystem modelling, p. 58-64. In: Palomares, MLD, Taylor, E, Pauly, D (eds.), 12th FishBase Symposium, Big Old Data and Shiny New Insights: Using FishBase for Research. September 8, 2014, Beaty Museum of Biodiversity, University of British Columbia, Vancouver, Canada. A report prepared by the *Sea Around Us* to the Paul G Allen Family Foundation and the Pew Charitable Trusts.

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FishBase in trophic ecosystem modelling, Arreguin-Sanchez, F. et al.



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Selection of functional groups:

- Occurrence
- Distribution
- Habitat

Group name	Habitat area (ha)	Biomass (t)	Production (t/yr)	Consumption (t/yr)
1. Fish	10000	0.1000	0.1000	0.1000
2. Squid	10000	0.0500	0.0500	0.0500
3. Crustaceans	10000	0.0500	0.0500	0.0500
4. Plankton	10000	0.0500	0.0500	0.0500
5. Detritus	10000	0.0500	0.0500	0.0500
6. Unassimilated	10000	0.0500	0.0500	0.0500
7. Unassimilated	10000	0.0500	0.0500	0.0500
8. Unassimilated	10000	0.0500	0.0500	0.0500

P/B, Q/B, ... or parameters to estimate them

Human uses

Fisheries: commercial; gamefish: yes
FAO fisheries: production; publication: search | FisheriesWiki | Sci Animal 11

More information

- Common names: **Snapper**
- Synonyms: **Long-neck**
- Production: **Abundance**
- Reproduction: **Abundance**
- Abundance: **Abundance**
- Genetics: **Abundance**
- Alloch. specimens: **Abundance**
- Identification: **Abundance**
- Images: **Abundance**
- Strains: **Abundance**
- Genetics: **Abundance**
- Alloch. specimens: **Abundance**
- Identification: **Abundance**
- Images: **Abundance**
- Strains: **Abundance**
- Genetics: **Abundance**
- Alloch. specimens: **Abundance**
- Identification: **Abundance**
- Images: **Abundance**
- Strains: **Abundance**

Life History Data on *Lutjanus campechanus* Northern red snapper

Family: Lutjanidae Snappers

Max. length (L_∞): 180.0 cm TL

Length (L₀): = 0.07 * (TL - 1.0) + 0.0

K: 0.18 /year RT = 5.18
Median RT value with related L_∞ and K.

M: -4.77 years Estimated from L_∞ and K.

Harvest mortality (M): 0.11 s.e. 0.01 0.42 /year
Estimated from L_∞, K and annual mean temp. = 24.2 °C

Life span: 12.0 years Estimated from L_∞, K and M.

Main food: mainly animals (trophs 2.0 and up)

Trophic level: 4.0 +/- s.e. 0.50 Estimated from food data.

Food consumption (FCM): 5.24 times the body weight per year

Note: The estimates are derived from default values taken from FishBase and will thus not be appropriate for every population. You can change these values and recalculate the life history parameters.

Diets...

Food and Feeding Habits: Diet Composition, Navikaige sggz

Main Food	Prey	Trophic Level (TL)	Prey's Life Stage	Country	Locality	Ref.
fish	62	2.4	juv-adult	Peru	Chicama, 1000-1300	41-63
crustaceans	75	3.1	juv-adult	Peru	Miraflores coast 9° 20' S, 78° 10' W	41-60
crustaceans	82	3.1	larvae	Peru	Miraflores coast	302-6
crustaceans	84	3.2	larvae	Peru	Miraflores coast	302-6
crustaceans	87	3.1	juv-adult	Japan	125 km S of the Pacific coast of Japan	171-3
crustaceans	88	3.0	larvae	Peru	Miraflores coast	302-6
crustaceans	89	3.0	larvae	Peru	Miraflores coast	302-6

after the Balancing process ...

... the Consistency test

FishBase Offers a number of values of P/B (non-exploited) and for Q/B for the species (or functional groups) to check or provide inputs,

... but also to test estimated outputs as result of model parametrization (by observing ranges).

testing consistency of



using FishBase

- Omnivory
- Predation rates
- Respiration
- Prey overlap
- Predator overlap

Other parameters estimated by the model can also be used for the consistency test

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FishBase in trophic ecosystem modelling, Arreguin-Sanchez, F. et al.



... about Ecosim input data

Group name	Max. rel. P/B	Max. rel. feeding time	Feeding time actual rate (%)	Fraction of other mortality due to changes in feeding time	Proportion effect on feeding time (S.T.)	Density (mg. availability) Group (a) (n=1)	Optimal (Q10) for feeding time (n=1)	Swimming cover parameter (S-Z)
1: Dolphins	3.0000	-0.5000	1.0000	0.0000	1.0000	1.0000	1.0000	0.0000
2: Seals/leopard	2.0000	-0.5000	1.0000	0.0000	0.0000	1.0000	1.0000	0.0000
3: Sea turtles	2.0000	-0.5000	1.0000	0.0000	0.0000	1.0000	1.0000	0.0000
4: LT-Pseudorasbora	0.0000	-0.5000	1.0000	0.0000	0.0000	1.0000	1.0000	0.0000
5: LT-Jaculus	2.0000	-0.5000	1.0000	0.0000	0.0000	1.0000	1.0000	0.0000
6: LT-Cetorhinus	2.0000	-0.5000	1.0000	0.0000	0.0000	1.0000	1.0000	0.0000
7: LT-Thrasops	2.0000	-0.5000	1.0000	0.0000	0.0000	1.0000	1.0000	0.0000
8: LT-Hippocampus	2.0000	-0.5000	1.0000	0.0000	0.0000	1.0000	1.0000	0.0000

Optimum salinity (x/0)	Salinity tolerance below optimum (x/0)	Salinity tolerance above optimum (x/0)	Optimum temperature (x/0)	Temperature tolerance below optimum (x/0)	Temperature tolerance above optimum (x/0)
35.000	1300.000	1000.000	10.0000	1000.000	1000.000
35.000	1300.000	1000.000	10.0000	1000.000	1000.000
35.000	1300.000	1000.000	10.0000	1000.000	1000.000
35.000	1300.000	1000.000	10.0000	1000.000	1000.000
35.000	1300.000	1000.000	10.0000	1000.000	1000.000
35.000	1300.000	1000.000	10.0000	1000.000	1000.000

FishBase support

... time series of catch found in FishBase help to calibrate time dynamics model

FAO – Sea Around Us – recruitment

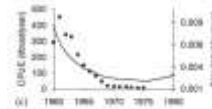
Fitting time series in Northern Gulf of California
(Lereari & Arreguin-Sánchez 2008)

Fitting time series for Campeche Bank model

... in addition to other local or global sources

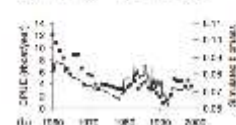
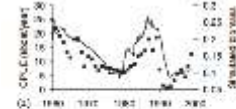
time series of local abundance (biomass, cpue...), primary production, forcing environmental variables

Totoaba (*Totoaba macdonaldi*)

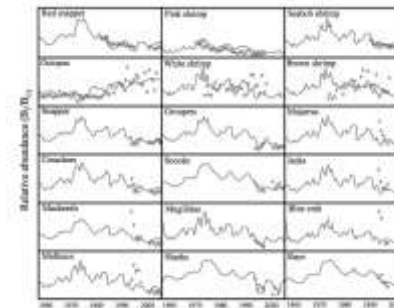


Sea lion (*Zalophus californianus*)

Blue shrimp (*Litopenaeus stylirostris*)



Brown shrimp (*Farfantepenaeus californiensis*)



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FishBase in trophic ecosystem modelling, Arreguin-Sanchez, F. et al.



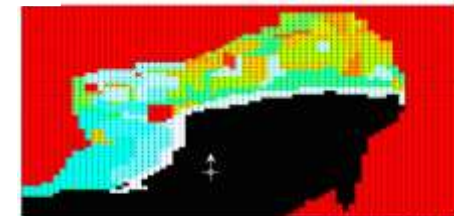
... about Ecospace
input data

Fishbase provides inputs like...

- Geo-referenced maps
- Occurrence
- Species distribution
- Habitat
- Depth ranges

Map constructed with Ecospace showing habitats in the Campeche Bank, México.

Color / numbers indicates habitat



- 1 Coastal water - Campeche
- 2 Coastal zone - Yucatan
- 3 Sand/Inshore - Yucatan shelf
- 4 Sand/Inshore - Yucatan slope
- 5 Sandy beach - Campeche
- 6 Sandy beach - Yucatan
- 7 Reef - Campeche
- 8 Reef - Campeche
- 9 Reef - Campeche
- 10 Reef - Campeche
- 11 Reef - Campeche
- 12 Reef - Campeche
- 13 Reef - Campeche
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- 98 Reef - Campeche
- 99 Reef - Campeche
- 100 Reef - Campeche

Map constructed with Ecospace showing habitats and distribution of fishing fleets in the Northern Gulf of California, México.

Color / numbers indicates habitat

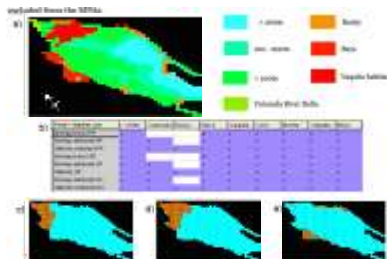
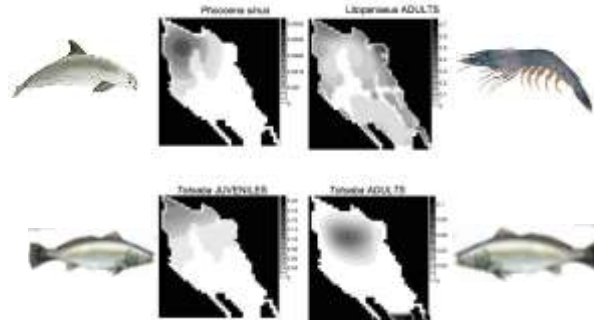


Figure 6. Distribution of fishing fleets in the Northern Gulf of California, México. The map shows the distribution of fishing fleets in the Northern Gulf of California, México. The map shows the distribution of fishing fleets in the Northern Gulf of California, México. The map shows the distribution of fishing fleets in the Northern Gulf of California, México.



Ecospace outputs for the Northern Gulf of California showing species distribution

At this step we have a (consistent) model, as a tool to test hypotheses

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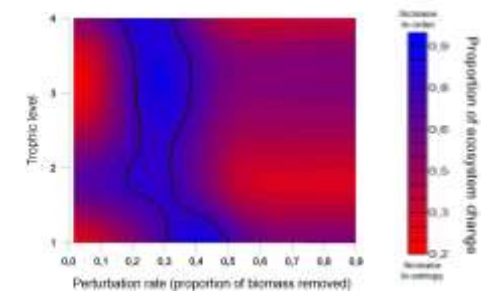
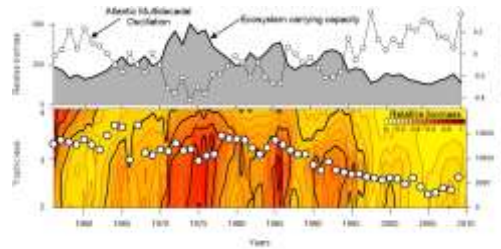
FishBase in trophic ecosystem modelling, Arreguin-Sanchez, F. et al.



ecosystem evolution

“ecosystem limit reference level” concept

Next two slides show briefly an application towards an ...
“ecosystem approach to fisheries management and sustainability”



(taken from Arreguin-Sánchez et al. 2014. Fisheries, AFS, accepted)

(taken from Arreguin-Sánchez et al. 2014. Fisheries, AFS, accepted)

... this is an example of how we can link FishBase to ecosystem modeling, in our case “Ecopath with Ecosim”, using outputs to advice directly fisheries management.

...so, we can identify limits of fishing of fish stocks in an ecosystem, derived from the holistic concept of *“ecosystem limit reference level”*.



The Role of FishBase in Trophic Ecosystem Modelling

Francisco Arreguin-Sánchez, Gustavo de la Cruz Agüero, **MANUEL J. ZETINA-REJÓN**, Pablo del Monte-Luna, María O. Albañez-Lucero, Arturo Tripp-Valdez, José de la Cruz-Agüero



Instituto Politécnico Nacional, Centro Interdisciplinario de Ciencias Marinas farregui@ipn.mx

thanks

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FishBase in trophic ecosystem modelling, Arreguin-Sanchez, F. et al.

Francisco Arreguín-Sánchez is Professor at the National Polytechnic Institute at the Interdisciplinary Center of Marine Sciences (CICIMAR), in La Paz, Baja California Sur, Mexico. His research is focused on fish population dynamics, stock assessment and management; and since 1991 strongly involved in dynamics of exploited ecosystems, with emphasis on fisheries management. As FishBase Mexico coordinator (1995) he organizes the collection of data from the literature and internal research reports, and to convince Mexican ichthyologists to collaborate with FishBase, especially those holding scientific collections. He was director of CICIMAR (2001-2004), is member of the Mexican Academy of Sciences, and of the National System of Researchers. At the present he leads the Laboratory of Dynamics and Management of Aquatic Ecosystems and, through the active projects, his group maintain direct collaboration with more than 10 international scientific institutions and 15 at national level, as well as a strong and permanent linkage with governmental entities involved in management and conservation of living marine resources.



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NF-UBC Nereus Program, Ota, Y.

NF-UBC NEREUS PROGRAM:
TO ADVANCE OUR UNDERSTANDING OF THE FUTURE OF FISHERIES⁸

Yoshitaka OTA

Nereus Program Co-Director and Nippon Foundation Senior Research Fellow,
Fisheries Centre, UBC; y.ota@fisheries.ubc.ca

The NF-UBC Nereus Program is an international marine science initiative aiming to advance our understanding of the future of fisheries at the global scale. By forming a collaborative research network of 7 research institutes—including UBC, Princeton University, Duke University, the University of Cambridge, the World Conservation Monitoring Centre, Stockholm Resilience Centre, and Utrecht University—we account for the complex socio-ecological systems of global fisheries and ocean governance in our projections regarding the future of fisheries and the world's oceans.

With an interdisciplinary approach that addresses climate change, marine biodiversity, coastal systems, fisheries economics, ocean governance, and marine anthropology, our assessments of the mechanistic dynamics that guide future ecological changes and corresponding impacts to fisheries are supported by international datasets. In particular, FishBase has provided essential data required for projections regarding changes in species distributions and abundances at various scales.

These collaborative initiatives provide vital opportunities to explore analytical gaps, combine interdisciplinary research perspectives, and create new datasets. However, it is important to acknowledge the full 'supply chain' required to produce these datasets, and to ensure that those who have gathered the data are not alienated from the final product. I argue that there is a need not only to promote meaningful academic interaction between data collectors and end users, but also to advance new ideas and support collective creativity above pragmatism.

⁸ Cite as: Ota, Y (2014) NF-UBC Nereus Program: to advance our understanding of the future of fisheries, p. 65-69. In: Palomares, MLD, Taylor, E, Pauly, D (eds.), 12th FishBase Symposium, Big Old Data and Shiny New Insights: Using FishBase for Research. September 8, 2014, Beaty Museum of Biodiversity, University of British Columbia, Vancouver, Canada. A report prepared by the *Sea Around Us* to the Paul G Allen Family Foundation and the Pew Charitable Trusts.

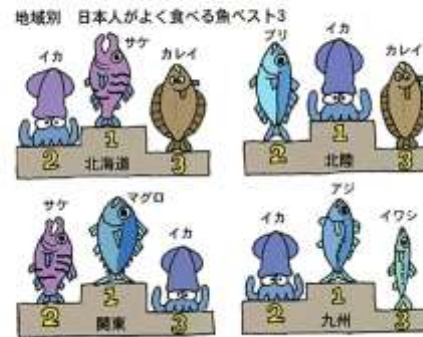
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NF-UBC Nereus Program, Ota, Y.

Fish Base in Japanese



Fish Base in Japanese



Receiving Feedbacks from Japanese Users



The partners



- Sits at science-policy interface
- Develop Capacity building of Marine Science and Ocean Governance



- Big-picture fisheries science, importance of interdisciplinary network
- Developing new tools for global outlook



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NF-UBC Nereus Program, Ota, Y.

Participating Researchers

Participants: 15 researchers (6 Professors, 3 Assistant Professors, 5 Research Associates)
Disciplines: 11 Natural Scientists, 4 Social Scientists

UBC: Fisheries Centre



Yoshitaka Ota William Cheung Daniel Pauly

Piscataway University Duke University University of Cambridge Stockholm University Utrecht University



Jorge Sarmiento Patrick Halpin Tom Spencer Carl Folke Alex Ouzis Elferink

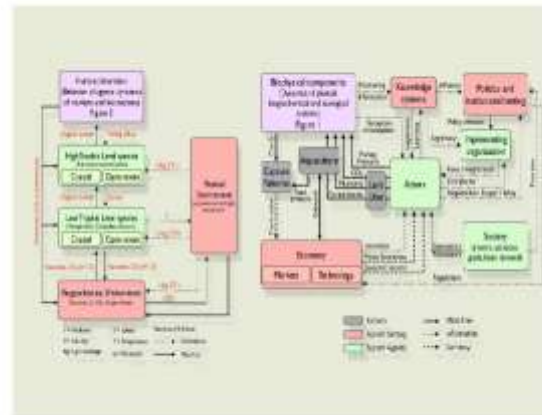
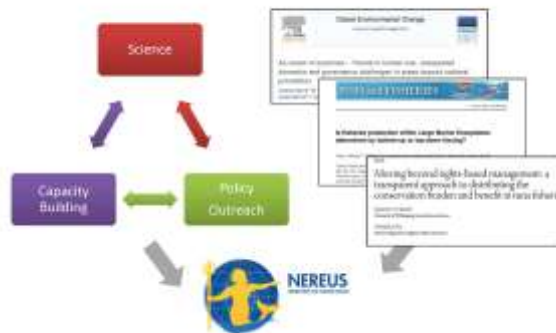
Why: Uncertainty of the future fisheries



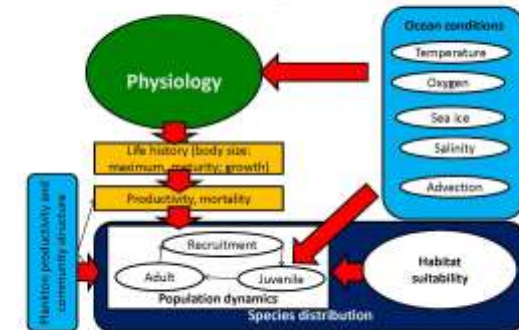
Why: new networks

- Mechanistic climate models exist: why not integrated with fisheries model (Cheung+)?
- Cumulative effects of manifold anthropogenic impacts
- Projecting the socio-ecological-governance system
- Community development of adaptive capacity

How?



Climate change and fisheries



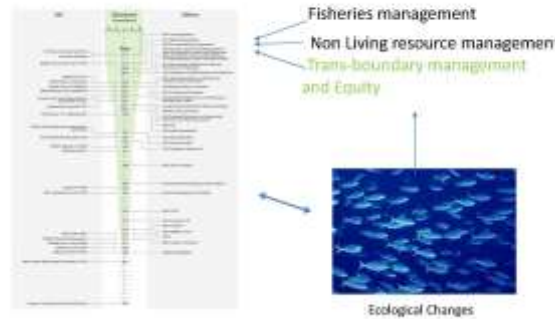
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Collaboration research approach

Key Questions	Thematic Topics	Local/Scale	Regional/Scale	Global scale
How will the ocean capacity support fisheries change in the future?	<ul style="list-style-type: none"> Temperature Oxygen Acidification Phytoplankton production 	<ul style="list-style-type: none"> Oxygen effect on fish distribution in the CCS Ocean Acidification in the CCS 	<ul style="list-style-type: none"> Changes of Oxygen distribution in the WBC Ocean Ocean Acidification in the WBC Ocean Regional differences in local fishery 	<ul style="list-style-type: none"> Oxygen variability FAO and national changes Climate-induced sea-level rise
How will the distribution of key fisheries change in the future?	<ul style="list-style-type: none"> Distribution Food Web Genetics Habitat Types 		<ul style="list-style-type: none"> Key fish species Phylog. habitat change 	<ul style="list-style-type: none"> Trade-offs between Deep-Phylog. biogeography
How will fisheries management and governance adapt to deal with "ecosystem transitions" in the future?	<ul style="list-style-type: none"> Ecological-based research Open governance 	<ul style="list-style-type: none"> Co-management to catch Oceans Pacific Blue Fin Tuna juvenile fishing 	<ul style="list-style-type: none"> Conservation based of migratory stock WFO governance 	<ul style="list-style-type: none"> High sea governance Fisheries industry changes Data boundary management
Market Transition	<ul style="list-style-type: none"> Fisheries Economics Socio-economic change of coastal communities Development of aquaculture 	<ul style="list-style-type: none"> Climate change impact on BC indigenous fisheries 	<ul style="list-style-type: none"> Fisheries business model Key of volatile social responsibility Use of global indigenous fisheries 	<ul style="list-style-type: none"> Apperthure and industry of global food per wide Industry in evolution

Governance and Legal context



How:

- Investigation of ecological mechanism
- prediction and scenarios (simulating impact)
- Perturbations, resilience, and ecosystem collapse
- Communication and policy

Prediction and Scenario:

United Nations : Informal Consultative Process on Ocean and Law of the sea



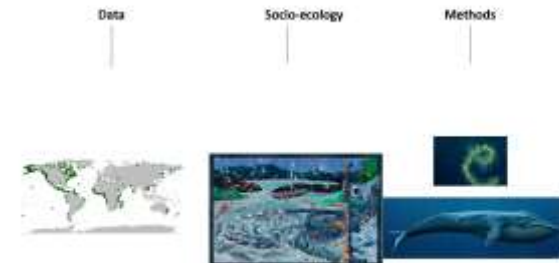
Investigation of ecological mechanism:

Elucidating the drivers of global fisheries production



Moore et al (2014): Is fisheries production within LME determined by Bottom up or top-down forcing, Fish and Fisheries

Improvements



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NF-UBC Nereus Program, Ota, Y.



Summary so far...

We are developing a model for integrated fisheries study:

- Potentially extremely valuable to policymakers/conservation practitioners:
 - Individual-based so capable of calculating a range of metrics.
 - Applicable across a range of spatial and temporal scales from global to local (eg farm-scale)
 - Applicable to real, complex scenarios – providing rich information
- Potentially extremely valuable for unifying fisheries studies and ocean governance:
 - Systems ecology, tests how theory/research fits into the bigger system
 - Identification of gaps in our understanding/predictive ability
 - Could enable a needs-based data collection strategy



Yoshitaka Ota received his PhD in anthropology from University College London in 2006. As a social anthropologist, he specializes in fishing practices, including the economics, social organization and lifestyles attached to this activity. For 18 months, he lived in Palau, Micronesia, learning fishing as an apprentice of a famous spear-fisherman in town. Through fieldwork, he became interested in socio-cultural aspects of fisheries, particularly how social changes reflect upon the value and materiality of fish and how they create a new social dynamic in the human-ecosystem relationship. While conducting post-doctoral research in the UK, he worked at the University of Kent (Department of Anthropology and Durrel Institute of Conservation and Ecology) for an ethnographic project on English small-scale fisheries and the CHARM Project, an interdisciplinary fisheries management research initiative developed for the Eastern English Channel. He has worked on field-based research projects in various locations—Palau (Micronesia, 2000-2001), the English Channel (UK and France, 2003-2009 for ESRC Funded project on European small-scale fisheries), Ache (Indonesia, 2007, for the post-tsunami assessment of local fisheries), Victoria (Australia, 2007, for BA-funded research)—all of which developed his interest in theoretical and methodological perspectives on marine, environmental and socio-economic issues affecting coastal communities. In 2008, he returned to Japan to join a policy think-tank in Tokyo—the Ocean Policy Research Foundation — which specializes in research and policy suggestions for both international and domestic marine management and ocean governance. At the foundation, Dr Ota worked on issues concerning community-based management, coastal habitat reconstruction (Sato-Umi) and Marine Spatial Planning. In 2011, Yoshitaka joined UBC's Fisheries Centre as the Co-Director of the NF-UBC Nereus program, a partnership between the Nippon Foundation and UBC dedicated to developing an interdisciplinary approach towards the promotion of sustainable fisheries. He is also passionate about supporting the post-tsunami relief for the northern Japanese fisheries communities. He conducted his first research on fisheries communities affected by the disaster in summer 2011.



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Making big data available, Stibravy, R.

MAKING BIG DATA AVAILABLE: THE UNIVERSITY OF BRITISH COLUMBIA
INSTITUTE OF FISHERIES FIELD RECORD LAB NOTEBOOKS EXPERIENCE⁹

Robert STIBRAVY

Librarian, Digital Projects, Digital Initiatives,
Irving K. Barber Learning Centre, UBC; robert.stibravy@ubc.ca

From May 2013 through June of 2014 Rick Taylor, Director and Curator of Fishes, Beaty Museum of Biodiversity and Rob Stibravy, Digital Projects Librarian at the the University of British Columbia Library's Digitisation Centre collaborated on the conversion of 11,200 pages of field records from the Museum's collection from analogue to digital format. Find out how this was accomplished, what the challenges were and how these data will be accessible to researchers and the world at large.

⁹ Cite as: Stibravy, R (2014) Making big data available: the University Of British Columbia Institute of Fisheries Field Record Lab notebooks experience, p. 70-73. In: Palomares, MLD, Taylor, E, Pauly, D (eds.), 12th FishBase Symposium, Big Old Data and Shiny New Insights: Using FishBase for Research. September 8, 2014, Beaty Museum of Biodiversity, University of British Columbia, Vancouver, Canada. A report prepared by the *Sea Around Us* to the Paul G Allen Family Foundation and the Pew Charitable Trusts.

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Making big data available, Stibravy, R.

The UBC Library Digitization Centre

Making Big Data Available:
The University of British
Columbia Institute of Fisheries
Field Record Lab Notebooks
Experience

Robert Stibravy, Digital Projects Librarian

A "Solution"

- Call Rick Taylor at UBC and get him to...
 - Look for the data
 - Photocopy the relevant pages
 - Mail or fax or email those pages to you
- Let us just hope that you only have one of these data requests in your career! (Rick is a nice guy, but come on!)
- Or...

The Problem

- What do you do when you have 11035 pages of this...



The Problem (cont.)

- ...and you want to find all 311 occurrences of this species in the UBC Institute of Fisheries Field Record collection?



Obigocottus maculiflavus

- Or some other salient data from the collection?
- You could...

The Solution!

- Digitize the collection and make it full-text searchable
- Put it in a content management system (CMS) and allow (encourage!) global access and linking to the data (and the original images of the notebooks)
- Hook the data in to the FishBase database so that users will see these in their search results

The Work

- Digitize all 11035 pages
- Post-process these to correct for brightness, contrast, sharpness, etc.
- Optical character recognition (OCR) for the parts of each notebook page that are amenable to OCR, transcribe the rest by hand
- Load in to the CMS
- Export metadata to allow linking with FishBase

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Big Old Data and Shiny New Insights: Using FishBase for Research

Making big data available, Stibravy, R.



Fujitsu fi-6670A

High speed document scanner – this is what we scan large document collection with

Results

- 11035 pages of difficult-to-access data available to the world
- A proof of concept for future endeavours of this nature and the realization that "it can be done!"
- Cost: approximately \$22K CAD (not including existing infrastructure)
- Nice to have: domain expertise for better quality control and possibly faster work

The Work (cont.)

- The scanning and the post-processing go well – we have done this before
- But (there is always a "but") the OCR is a washout – and that leaves us with a single choice
- Full Hand Transcription!
- Uh oh!

The (New) Solution

- Hand transcription – at first look this does not seem to be practical
- Sampling various pages, however, and testing these with several different people doing the transcription gives us a result of 12-15 months with two students working on it and my project management
- In the end it takes about 14 months

Q & A

- Questions or Comments?
- Thank you/Maraming salamat/
Dankeschön/Arigatō/Merci/Gracias/
Dankjewel/Teşekkür ederim/Obrigado!



Work With Us!

- Interested in working with us on a project and are UBC affiliated or have a collaborator who is?
- Visit digitze.library.ubc.ca or contact me to discuss your idea
- Thanks again!

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Big Old Data and Shiny New Insights: Using FishBase for Research

Making big data available, Stibravy, R.

Rob Stibravy is a Digital Projects Librarian at the University of British Columbia Library's Digitisation Centre. He has an undergraduate degree in Integrative Biology from the University of California, Berkeley and a Master of Library and Information Science from the University of British Columbia School of Library, Archival and Information Science. He manages digital projects for the Library and oversees the Digitisation Centre's infrastructure.



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Spaceship Earth, Nauen, C.

SPACESHIP EARTH - SUMMARY OF AN UNUSUAL INTERNATIONAL ROUNDTABLE¹⁰

Cornelia E. NAUEN

Mundus maris – Sciences and Arts for Sustainability, Brussels, Belgium;
ce.nauen@mundusmaris.org – www.mundusmaris.org

The diversified uses and users of FishBase are a good illustration of making the hidden potential of data and information visible, once they become available in the public domain and can be used in both planned and unexpected ways. Using FishBase for art work was certainly not in the original intentions, but has become yet another one of the unexpected uses. It opens up opportunities for storytelling and listening to stories as an exploration of what lies hidden between the data and disciplines and what new insights and action opportunities we gain from the confrontation of diverse expertise and experiences.

Concern for the gravity of threats to the ocean was the motivation to host the international roundtable “Spaceship Earth” at the Peter Wall Institute for Advanced Studies in Vancouver in an unconventional format. Blending science, arts, diverse disciplines, cultures and practices, the roundtable created the conditions to discover rich trajectories to our individual and collective sustainability in relation to maritime and coastal sub-systems. Methods of action research combined with art of hosting approaches created the conditions for new collective intelligence and new storylines to emerge. The individual and group learning journeys of participants embarked on led to a host of action lines. Several projects aiming to bring about change are already underway or even accomplished. The greatest challenge is to keep the energy and motivation to act during the roundtable alive once participants have returned to their respective working environments. But the format has certainly potential to bridge the well-known gap between knowledge and action.

¹⁰ Cite as: Nauen, C (2014) Spaceship Earth - summary of an unusual international roundtable, p. 74-77. In: Palomares, MLD, Taylor, E, Pauly, D (eds.), 12th FishBase Symposium, Big Old Data and Shiny New Insights: Using FishBase for Research. September 8, 2014, Beaty Museum of Biodiversity, University of British Columbia, Vancouver, Canada. A report prepared by the *Sea Around Us* to the Paul G Allen Family Foundation and the Pew Charitable Trusts.

12th FishBase Symposium
Big Old Data and Shiny New Insights: Using FishBase for Research

Spaceship Earth, Nauen, C.



Spaceship Earth - Summary of an
Unusual International Roundtable

Cornelia E. Nauen (1)
presented by **U. Rashid Sumaila** (2)

(1) Mundus maris
Sciences and Arts for Sustainability asbl
(2) Fisheries Economics Unit
University of British Columbia

FishBase Symposium, Vancouver, 08/09/2014

Glocal

The tyranny of small decisions is at least partially to blame for the sorry state of affairs of the ocean and its inhabitants

- sector and disciplinary perspectives prevail
- most individuals and companies optimise their decision for local conditions only.

Yet the ocean is a global system and interconnected not only hydrologically, biologically, but economically, socially and in so many other dimensions.

But, many are not engaged or even aware...

Unexpected Consequences

Public EU funding for FishBase was justified in the 1990s as support to fisheries sector administrations in developing countries. Through the FB guest book we found users and uses in:

- Fisheries Departments
- Students in school and higher education
- Recreational fishers and angling trip organisers
- Artists
- Customs Services...

Source: Nauen, C.E., 2006. Implementing the WSSD decision of restoring marine ecosystems by 2015 – Scientific information support in the public domain. *Marine Policy*, 30:455-461.

New understanding, fresh narratives

So, we are looking for new perspectives on 'old problems' that should be

- Cross-fertilised from a variety of fields of experience and enquiry to ensure robustness,
- Grounded locally, where operational capabilities are,
- but conscious of global connections.

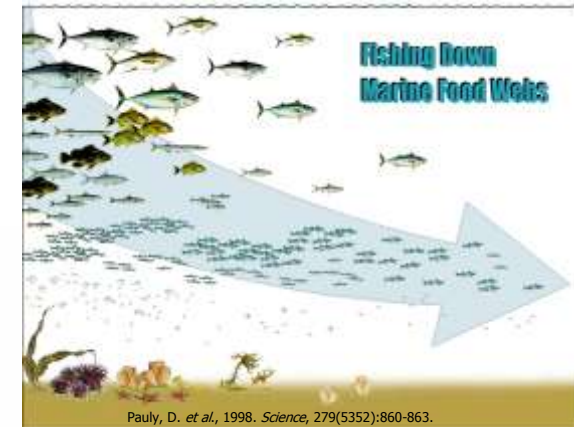
They should be understandable to and understood by the many

Thus: How to tell stories about the ocean that engage? One well-known visual example.

The Challenges are becoming bigger and more interconnected

Need to question eternal growth: reality check

- The resources on Earth are finite, even though we are very ingenious in finding new technical fixes - right now by borrowing from the future
- Our Earth is quite unique within the accessible parts of the universe, we better make it work
- We produce enough food to feed everybody, but 1 billion is obese and 1 billion is hungry
- Three major "environmental" challenges: Overfishing, climate change with acidification and pollution – how to act more



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Spaceship Earth – International Roundtable at PWIAS



Scientists, practitioners, artists from different places and cultures were invited to 5 days of intense exchange using participatory research methods.

The aim was to generate new insights through crossfertilization and unconventional ways of learning in order to initiate new projects and other actions for ocean health.



Listening to and telling stories that matter



Sharing examples of good experiences in different fields allowed to harvest a fair number of principles that contribute to "success" and can be used in future action.

Another method used to blend what we already know in different professions and cultures was "mind mapping". We clustered ideas around big concepts.



Levers and Learning Journeys



Analysing our mindmap and the big challenges to the ocean, we extracted what we considered "levers" enabling action for positive change.

Instead of "broadcasting" individual work results, with often little impact, we went on learning journeys the following day to find innovative ways for acting on the levers identified.



The "big issues" we identified

- Resource overexploitation
- Climate collapse
- Pollution
- Institutions
- Global capital
- Social inequality
- Human affect and emotions
- The connectedness of issues

"Levers for action" are, among others, passionate people, engaging narratives ...

Learning journeys spawning projects



Groups and individuals focused on different levers reporting back from their learning journeys, through recitals, film, scientific papers, exhibition planning thus opening minds for new opportunities.

The scene was set for project planning using the Pro-Action Café format in smaller groups and reporting the results back to the whole group again.



Working on project proposals arising

- How to model Spaceship Earth? - Alan Mackworth
- Can we capture our experience in an open access book? - Cornelia Nauen
- What other written output can we produce? - Rashid Sumaila
- What does it take to bring "Fish-Credits" currency on its way? - Paolo Dini
- Can we expand the conversation to include eco-theology and build on the aboriginal spirituality? - Nigel Haggan
- What do we need to do to produce a contrasted global video interview about the ocean? - Dyhia Belhabib

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Spaceship Earth, Nauen, C.

Robi Smith's art inspired by FishBase



For more ...

<http://www.spaceshipearth.pwias.ubc.ca>

<http://www.mundusmaris.org>

We encourage and welcome cooperation

to use FishBase for developing ever more engaging stories that shift perceptions about what is necessary and possible and enable positive change.



Thanks!

info@mundusmaris.org

Cornelia Nauen holds a PhD in marine ecology/fisheries science from Kiel University, Germany. She worked in FAO's Fisheries Department starting in the late 1970s in relation to the species identification programme (biodiversity) and on aquatic and coastal pollution issues (consumer safety levels in and advisories). Between 1986 and 2012, she served in the European Commission in development cooperation and in international science cooperation. Subject areas were aquatic resources management and restoration, water systems and policy and lately science and innovation policy cooperation with Latin America. Critically engaged science to support policy and action for social inclusion and living and being in sustainable ways were a major focus. Since 2010 she heads the international non-profit association Mundus Maris – Sciences and Arts for Sustainability. Mundus Maris seeks to combine scientific concepts with practice embedded in local and global cultural spaces. It supports awareness raising and education about the ocean, e.g. through promoting conversations that matter and enable action. In May 2014, she co-organised the international Roundtable “Spaceship Earth” at the Peter Wall Institute for Advanced Studies at UBC Vancouver.



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IsotopeBase, Miller, T. and Palomares, M.L.D.

ISOTOPEBASE: A NEW STABLE ISOTOPE-BASED TROPHIC
ADDITION TO FISHBASE AND SEALIFEBASE¹¹

Todd MILLER, Division of Fish and Wildlife, Commonwealth of the Northern Mariana Islands, Saipan, Marianas Protectorate; tmiller.dfw@gmail.com and Maria L.D. Palomares, *Sea Around Us*, Fisheries Centre, UBC, Vancouver, Canada.

Over the last two decades stable isotope analysis (SIA) has become one of the most common and widely used tools in aquatic trophic ecology. Stable isotopes of both carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) are used in measuring organism relative trophic position, ontogenetic shifts and source production, and can be expanded in understanding organism movement/migration, biomagnification of contaminants, and as a precursor measure of eutrophication. As a result SIA has amassed a large literature base of stable isotope values and trophic level estimates across species and ecosystems that can be integrated into biodiversity information portals such as SeaLifeBase. Here we introduce IsotopeBase, a new addition to FishBase and SeaLifeBase that contains literature-based isotope values ($\delta^{15}\text{N}$, $\delta^{13}\text{C}$ and $\delta^{34}\text{S}$) and isotope-based trophic level estimates of invertebrates, fish, birds and marine mammals. The addition of IsotopeBase allows for direct linking of isotope values and trophic levels in space and time to the range of parameters provided in SeaLifeBase. In addition, IsotopeBase provides linear equations for ontogenetic length-isotope shifts in species of invertebrates and fish. Presently IsotopeBase has values for over 1,000 taxonomic groups/species from invertebrates, fish, birds and marine mammals from marine and estuarine systems around the world. The isotope values and trophic level estimates are linked to location and time, therefore providing researchers with temporal-spatial benchmarks from which to compare isotope values (baselines) and potential changes in relative trophic position of species. Limitations and assumptions in the use of stable isotopes as trophic estimates exist however, and IsotopeBase addresses these by an evaluation protocol to limit spurious assignments of trophic level and to help guide the user.

¹¹ Cite as: Miller, T, Palomares MLD (2014) IsotopeBase: a new stable isotope-based trophic addition to FishBase and SeaLifeBase, p. 78-81. In: Palomares, MLD, Taylor, E, Pauly, D (eds.), 12th FishBase Symposium, Big Old Data and Shiny New Insights: Using FishBase for Research. September 8, 2014, Beaty Museum of Biodiversity, University of British Columbia, Vancouver, Canada. A report prepared by the *Sea Around Us* to the Paul G Allen Family Foundation and the Pew Charitable Trusts.

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IsotopeBase, Miller, T. and Palomares, M.L.D.



IsotopeBase: a new stable isotope-based trophic addition to FishBase and SeaLifeBase

Todd W. Miller & Maria L. Palomares



$\delta^{15}\text{N}$ – Eutrophication

The primary stable isotopes used are from C and N

- Baseline $\delta^{15}\text{N}$ can indicate eutrophication

Areas that exhibit denitrification express high $\delta^{15}\text{N}$ values from phytoplankton, and this is expressed as high values through the food web.

Here we see copepods with elevated levels from areas that are more eutrophic relative to more offshore waters.

($\delta^{13}\text{C}$ would show a similar pattern)

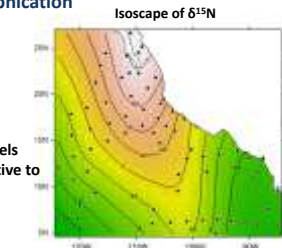


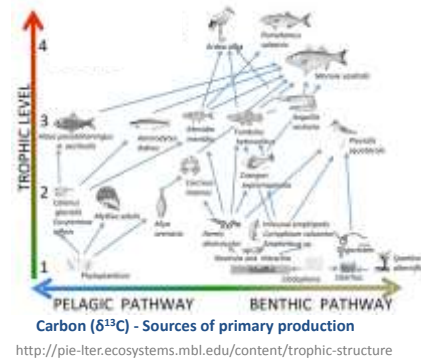
Fig. 4. Contour plot of the isoscape (within the 47th value) of atmospheric nitrogen-15 derived from the L&E model. The data sets are the sampling stations where atmospheric-copepods were sampled by togo net.

Olson et al. (2010)

Stable isotopes in ecology

The primary stable isotopes used are from Carbon and Nitrogen

Nitrogen ($\delta^{15}\text{N}$)
- Relative trophic level
- Eutrophic conditions (high $\delta^{15}\text{N}$)

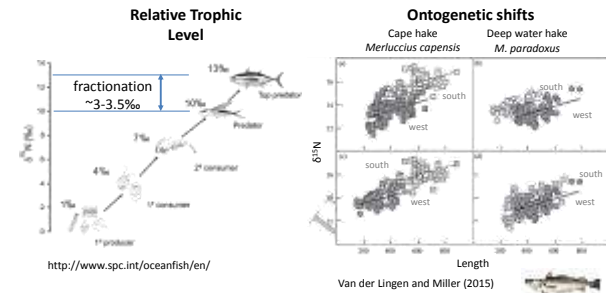


Overview of IsotopeBase Methods

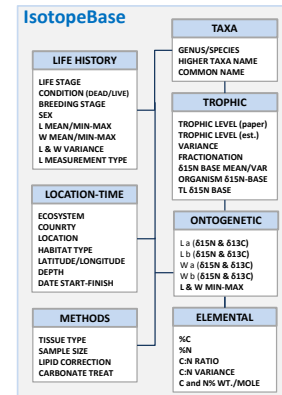
- Paper Review:** Published literature is reviewed and screened for reporting isotope values and trophic levels (when provided)
- Taxa:** IsotopeBase includes all reported organisms (algae, zooplankton, fish, birds, and marine mammals).
- Trophic levels:**
 - Record TL when given
 - When TL is not provided, in some cases IsotopeBase can calculate (if there's a baseline).
 - If TL cannot be assigned, raw isotope data is still provided.
- Other information:** life history stage, size, sample time-location, isotope methods, and how trophic level was calculated.
- Duration:** It takes ~1-2 hrs to review a paper, but this decreases with experience as the reviewer knows what to look for and how to report it.

$\delta^{15}\text{N}$ – Trophic Level Measures

Nitrogen isotopes can measure relative trophic across a wide range of taxa and size classes



IsotopeBase Structure & Integration into FishBase and SeaLifeBase



Deliverables (time-location specific)
Trophic level estimates
Ontogenetic trophic shifts (linear eq.)
Baseline isotope values for eutrophication
Baseline values for source production
Elemental %C and N, and C/N by taxa

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IsotopeBase Integration into FishBase and SeaLifeBase

IsotopeBase – current entries

3100 entries

110 papers reviewed

Total count of genera and species by group

Taxonomic group	Genus	Species
Algae	65	70
Seagrasses and plants	16	16
Gelatinous (Cnidaria)	16	16
Echinodermata (urchins, sea stars)	42	44
Gastropoda (snails)	24	24
Cephalopoda (squid, octopus)	32	32
Bivalve (clams, scallops)	53	52
Crustacea (copepods, crab, krill)	249	250
Annelida (polychaete worms)	20	20
Other inverts (corals, etc)	50	49
Fish	592	590
Sea turtles	2	2
Birds (marine)	57	57
Seals/sea lions/walrus	12	12
Dolphins/porpoise/orchas	7	7
Whales	15	15
Other mammals (otters, bears)	3	3
TOTAL	1255	1259

Deliverables (time-location specific)

Trophic level estimates
Ontogenetic trophic shifts (linear eq.)
Baseline isotope values for eutrophication
Baseline values for source production
Elemental %C and N, and C/N by taxa

IsotopeBase Integration into FishBase and SeaLifeBase

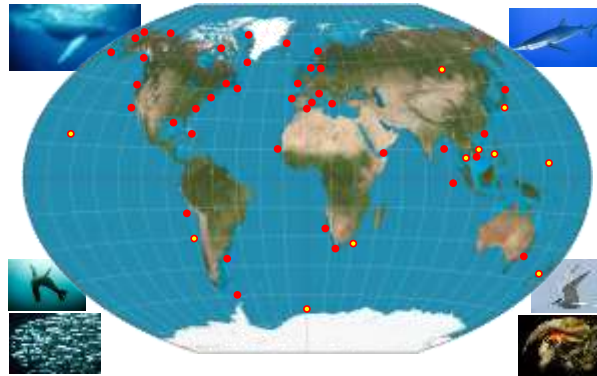


Synthesis projects for research (BSc, MSc and PhD)

- Ecosystem comparisons of food webs
- Fishing impacts on food web structure (comparative studies)
- Global nutrient dynamics – N fixation and upwelling sources
- Pollutants and regional-global variation in biomagnification
- Tracing global trends in eutrophication and hypoxia

Current Geographic Coverage of IsotopeBase

Within IsotopeBase ● Locations in-progress ○

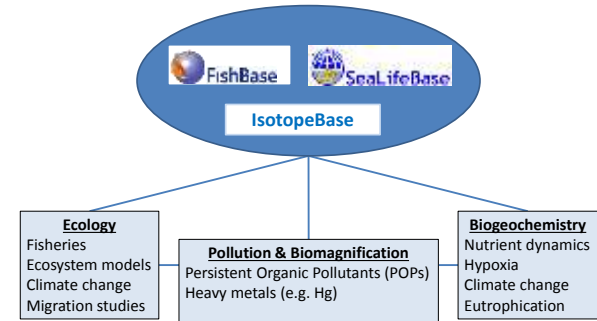


Assumptions and limitations of using stable isotopes

- 1) Fish, birds, and marine mammals move around a lot, and they may cross over different baselines.
- 2) Isotopic fractionation factor ($\delta^{15}\text{N} \sim 3.4\%$) is not well-resolved. Fractionation varies by relative trophic level and protein content of diet. IsotopeBase can always correct this as we understand more.
- 3) Tissue/isotope turnover rate – how long does it take to isotopically match diet? This can also vary.

The above will eventually be resolved as the field of isotope ecology grows. IsotopeBase can easily adjust to these changes.

IsotopeBase Integration into FishBase and SeaLifeBase



Research fields that use stable isotopes in conjunction with information from FishBase and SeaLifeBase.

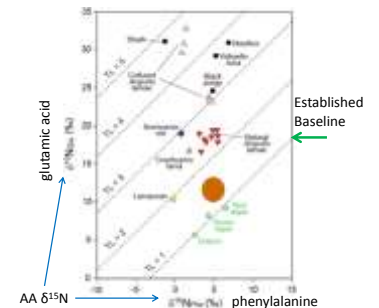
The future of IsotopeBase

From only approximately 100 papers we obtained values from over 1250 species covering the major ecosystems; there remains >1000 papers that can be added, and this number grows monthly.

New Advances:

Compound Specific Stable Isotope Analysis

- Accurate for trophic level
- Expansive
- New component of IsotopeBase



<http://www.aori.u-tokyo.ac.jp>

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IsotopeBase, Miller, T. and Palomares, M.L.D.

Conclusions

- **IsotopeBase** provides the first globally-centralized source of stable isotope data for ecologists; this information will be directly linked to the central biodiversity portals of **SeaLifeBase** and **FishBase**
- Specific deliverables from IsotopeBase are (by time and location):
 - Trophic level estimates
 - Ontogenetic trophic shifts (linear eq.)
 - Baseline isotope values for eutrophication
 - Baseline values for source production
 - Elemental %C and N, and C/N by taxa
- Limitations and assumptions for using stable isotopes – mobile/migrating animals, and unknowns in trophic fractionation (TF) and isotope turnover rates exist.
- IsotopeBase can adjust trophic level estimates as new information is obtained on TF and turnover rates.
- Advances in compound-specific stable isotope (CSSI) methods are addressing the above limitations, and IsotopeBase is planning to include CSSIs.

Todd Miller is the Head of Fisheries for the Commonwealth of the Northern Mariana Islands (CNMI), Marianas Protectorate (USA). He received his PhD from Oregon State University in Fisheries studying trophic ecology of the Northern California Current pelagic ecosystem. From there he moved to a post-doctoral and eventually Associate Professor position at Ehime University in Japan, performing food web and pollution research in Japan, Philippines, Vietnam, South Africa and Namibia. His current position in the CNMI covers life history evaluation, ecology and management of coral reef and bottom fishes. Recent projects include studying trophic plasticity of parrotfishes and surgeonfishes related to phase shifts in coral reef systems, and examining genetic connectivity of reef fishes along the Marianas Archipelago.



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Philippine capture fisheries, Hilomen, V.

PROBLEMS IN CAPTURE FISHERIES IN THE PHILIPPINES: COSTS OF INACTION¹²

Vincent HILOMEN

Biodiversity Management Bureau, Department of Environment and Natural Resources, Republic of the Philippines; vvhilomen@up.edu.ph

The various problems in capture fisheries in the Philippines were revisited and the costs of inaction were evaluated for the small trawl fishery in San Miguel Bay in the Bicol region. Length-frequency data were obtained for *Alepes djedabba*, the fourth most abundant catch in San Miguel Bay in 2001. Size at first sexual maturity for *A. djedabba* was determined at 13.4 cm. Nearly 89% of the catch of *A. djedabba* was below the size at first sexual maturity. Information on the growth rates of *A. djedabba* was obtained from FishBase to determine length of time fish reaches size at first sexual maturity from actual mean size of catch. Results show the mean size of the catch will exceed size at first sexual maturity in about 4 months. The shift in the length frequency data of fish was projected to 4 months using a natural mortality rate of 20%. The biomass of actual catch and the projected catch was evaluated and valued using current prices. Results showed that catching this fish at sizes above the size at sexual maturity increases catch biomass nearly 3 times and monetary value 4.3 times than actual practice. The gain for waiting for this fish to grow before they should recruit to the fisheries was estimated at about PhP 6,600 per day per trawl and translates to PhP 76M annually for this species alone. Important strategies to change fishing practices of locals are discussed in the paper.

¹² Cite as: Hilomen, V (2014) Problems in capture fisheries in the Philippines: costs of inaction, p. 82-85. In: Palomares, MLD, Taylor, E, Pauly, D (eds.), 12th FishBase Symposium, Big Old Data and Shiny New Insights: Using FishBase for Research. September 8, 2014, Beaty Museum of Biodiversity, University of British Columbia, Vancouver, Canada. A report prepared by the *Sea Around Us* to the Paul G Allen Family Foundation and the Pew Charitable Trusts.

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Philippine capture fisheries, Hilomen, V.

Problems in Capture Fisheries in the Philippines: Cost of inaction

Vincent V Hilomen
 Institute of Biological Sciences
 University of the Philippines Los Banos

Biodiversity Management Bureau
 Department of Environment and Natural Resources

Need to communicate problem with policy makers...

- Do not listen to usual presentation of findings and new ideas
- BUT we get their attention if shown monetary value of resources...
- There was a need to be creative...
- FishBase information...

Problems in capture fisheries in the country

- Overfishing
 - Multi-gear/multi-species fisheries
 - Gear conflicts (commercial vs artisanal)
 - Destructive fishing methods (e.g. trawl, blast fishing)
- Habitat degradation
- Burgeoning population
- Poor enforcement of relevant laws
- Research inadequacies

Focus: San Miguel Bay, Bicol Region, Philippines



Randall, JE (FishBase)

Top 10 Species:

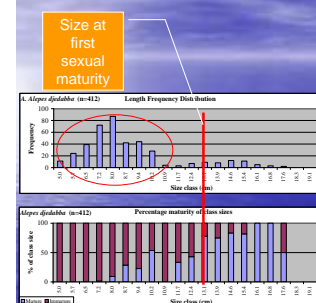
1. *Stolephorus spp.*
2. *Otolithes ruber*
3. *Dendrophyssa russelli*
4. *Alepes djedabba*
5. *Portonus pelagicus*
6. *Sardinella spp.*
7. *Acetes spp.*
8. *Trichiurus haumela*
9. *Leiognathus spp.*
10. *Penaeus spp.*

Together accounted 80% of total catch (2002 data)

Total of 9 bays included in the study

- Lingayen Gulf, Manila Bay, San Miguel Bay, Sogod Gulf, Davao Gulf, Macajalar Bay, Gingoog Gulf, Butuan Bay, Honda Bay, 2 other bays in Visayas
- Catch data history was available only for 6 of 9
- Study detected growth overfishing in all 9 bays/gulfs

Growth overfishing



- Detected in all 9 bays included in the study but intensity varies between bays
- Sizes of several species in top 10 of catch fall below size of first sexual maturity except
 - Davao Gulf
 - Honda/Puerto Princesa Bays
 - Gingoog/Butuan

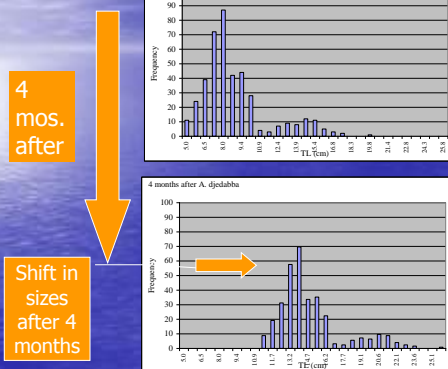
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Philippine capture fisheries, Hilomen, V.

Implications of growth overfishing

- Can lead to recruitment overfishing where the ability of stocks to naturally replenish is impaired (from bad to worse)
- Productivity is not optimal
- Substantial reduction in larger size classes
- Removing individuals with better genetic material early (those that mature at a larger size)

Shift in size structure after 4 months



What if...

- Set legal size limits to a select suite of commercially important species (initially)
 - Gear restriction (size of hooks, mesh sizes)
- Allow fish to grow a little more before harvesting
 - Collect and grow in cages
- Organize fishers into cooperatives
 - Police their ranks

Is it worth the wait?

	Current	4 mos. after	Difference	Increase
Biomass (kg)	35.9	104.1	68.2	2.9
Value (Php)	2,018.00	8,649.00	6,631.00	4.3
Bank (at 9%)	2,018.00	2033.14	15.14	1.008

Extrapolate to annual catch for San Miguel Bay

Annual Catch in San Miguel	Current	4 mos. after	Difference
Biomass (T)	411.4	1192.9	781.6
Value (Php)	23,122,857	99,112,388	75,989,531

How much do we gain for waiting? (conversely how much do we lose if we do not wait)

- Consider current data from a typical catch in one of the bays
 - Examine number and size structure of catch
- Obtain total weight of observed catch using length-weight relationship
- Allow theoretical growth period to reach sizes slightly above length at first sexual maturity (in the case of *Alepes djedabba* (salay-salay), 8 to 14 cm will be 4 months)
- Factor in 20% mortality (e.g. predation and disease)
- Re-compute total weight of theoretical catch
- Compare:
 - Previous biomass to re-computed biomass
 - Cost of previous catch to new catch
 - Extrapolate to annual catch

The gain in waiting 4 months or a mere 6 cm increase in length...

- Php 6,600 per day for mini-trawls in San Miguel Bay for example
- This translates to nearly 76M Php annually
- This figures represent potential opportunity for *Alepes djedabba* ALONE, the 4th most abundant catch in San Miguel Bay.
- So think how much is there to gain if we wait for fish to grow a little before we catch them...

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Philippine capture fisheries, Hilomen, V.

Considerations

- Waiting time for fishers ~4 mos.
- Alternative livelihood for affected fishers
- Buy out fine mesh nets and other
- Determination of size at first sexual maturity of top species
- Political will

How do we achieve compliance for legal sizes of catch

- Completely eliminate blast and all forms of poison fishing
- Buy out of fine mesh nets and provide alternative forms of livelihood
- Self policing within fisher cooperatives
- Monitor landed catch and set up penalty scheme to offenders
- Explore most profitable catch schedule
- Market denial schemes
- Information dissemination of the benefits of targeting larger fish only

THANK YOU...

Sea Around Us Project

CBD-UNEP

Vincent V. Hilomen has nearly 28 years of work experience as a marine biologist specializing in reef fish ecology, fisheries and marine protected areas. His work experience includes 26 years in the academe teaching basic and advance zoology courses, particularly, in allied fields of marine science. His academic experience include more than 23 years of studies for marine protected areas, coastal resources management, fisheries biology, and marine biodiversity projects in marginalized sectors of society in the Philippines for purposes of planning and policy formulation. He has also conducted studies for environmental impact studies, monitoring coastal environment, surveys for baseline assessment of coastal environment for a wide variety of sectors such as oil and gas, mining industry, power plants, coastal industrial areas and ecotourism. His experience covers projects in coastal baseline assessment in the ASEAN Region and the Middle East. He is presently on secondment Associate Professor in Zoology of the Institute of Biological Sciences, University of the Philippines Los Baños and is the Executive Director for Priority Programmes of the Biodiversity Management Bureau of the Department of Environment and Natural Resources.



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Trophic level of Northeastern Aegean Sea bottom trawl fishery, Keskin, Ç.

ESTIMATION OF MEAN TROPHIC LEVEL OF THE BOTTOM TRAWL FISHERY
IN THE NORTH-EASTERN AEGEAN SEA (EASTERN MEDITERRANEAN)¹³

Çetin KESKIN

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Commercial discards of bottom trawl was studied in fishing grounds around Gökçeada Island in the north-eastern Aegean Sea. All the samples were collected on board a commercial trawler under commercial fishing conditions between 70 and 410 m depth from December 2009 to February 2010. A total of 3143 kg of biomass were caught in the 28 valid hauls. Of that amount, 2101 kg (67%) were landed and 1042 kg (33%) were discarded. Eighty nine fish species comprised the 85% of the total catch. Eight fish species were always landed, 49 always discarded, and 32 appeared both in the landed and the discarded fractions. Mean weighted trophic level of the discarded fishes was significantly lower than landed. The results of this short time study show that bottom trawl fishery removes higher trophic level species from the ecosystem and support fishing down effect.

¹³ Cite as: Keskin, Ç (2014) Estimation of mean trophic level of the bottom trawl fishery in the north-eastern Aegean sea (eastern Mediterranean), p. 86-90. In: Palomares, MLD, Taylor, E, Pauly, D (eds.), 12th FishBase Symposium, Big Old Data and Shiny New Insights: Using FishBase for Research. September 8, 2014, Beaty Museum of Biodiversity, University of British Columbia, Vancouver, Canada. A report prepared by the *Sea Around Us* to the Paul G Allen Family Foundation and the Pew Charitable Trusts.

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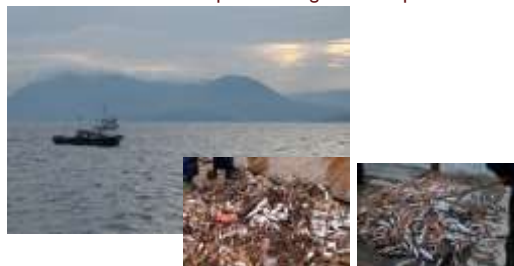
Trophic level of Northeastern Aegean Sea bottom trawl fishery, Keskin, Ç.

Estimation of mean trophic levels of the bottom trawl fishery in the North-eastern Aegean Sea (Eastern Mediterranean)

Çetin Keskin, PhD
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Objective

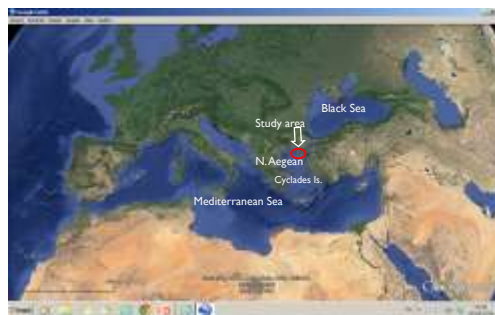
- Testing the MTL of landed species differs from that of the discarded ones
- The MTL of discarded and landed species changes with depth



Agenda

- Introduction
 - Objective of the study
- Study Area
 - Bottom trawl fishery in the NE Aegean
 - Fishing regulation in Turkey
- Sampling
- Results
- Main Points
- Suggestions

Study area



Introduction

The impact of fishing activities on the ecosystems:

- ✓ Reduced species abundances, changes in size and species composition, and modifications of species life-history traits (e.g., Gislason *et al.* 2000),
- ✓ By-catch and discards (Kelleher 2005; Davies *et al.* 2009)
- ✓ Decrease in trophic levels vs the removal of the large size, high-trophic level species (e.g., Pauly *et al.*, 2002)

General view on demersal fishery in the Aegean Sea

Demersal species landings in the Aegean Sea are about 31% of its total fisheries production (Tirasin and Ünlüoğlu, 2012).

A total of 5,725 fishing boats (32%) are located in the Aegean Sea of which:

83 are bottom trawlers,
17 are trawler-purse seiners (combined)
89 are purse seiners, and 5,056 are small scale fishing boats.

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Trophic level of Northeastern Aegean Sea bottom trawl fishery, Keskin, Ç.

The current fishing regulations in Turkey:

- i) minimum mesh size and landing sizes
- ii) closed areas and seasons
- iii) gear or fishing methods restrictions and bans
- iv) catch prohibition for some species

Sampling

- Sampling period: Winter, 2010
- Onboard a commercial vessel (24 m length and 141.5 GRT)
- Cod-end stretched diamond mesh size: 44 mm
- Depth range: 70 and 410 m
- Haul duration:
 1-2 hour <100 m
 3-4 hour in deeper waters



Target species include:

- Red mullet *Mullus barbatus*
- European hake *Merluccius merluccius*
- Pandoras (*Pagellus* spp.)
- Norway lobster *Nephrops norvegicus*
- Rose shrimp *Parapenaeus longirostris*
- Giant red shrimp *Aristeomorpha foliacea* (Risso)

Results

28 valid hauls.
 Total biomass = 3143 kg

89 fish species:
 always landed: 8
 always discarded: 49
 landed and the discarded fractions: 32

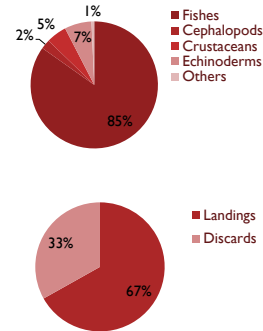


Figure 1. General summary of the results for the trawl samples analyzed.

Sampling stations



Figure 1. Map of the study area around Gökçeada Island (north-eastern Aegean Sea; eastern Mediterranean) showing the position of the trawl samples analysed (circles).

Existence groups of samples

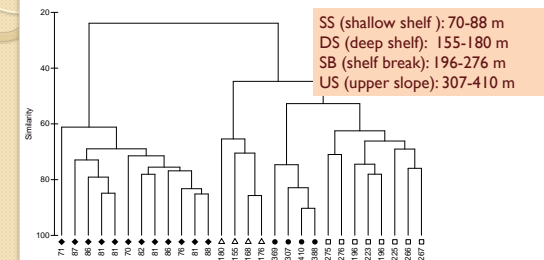


Figure 2. Cluster analysis of the species abundance (individuals/h) in the trawl samples.

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Discards and landings for each group

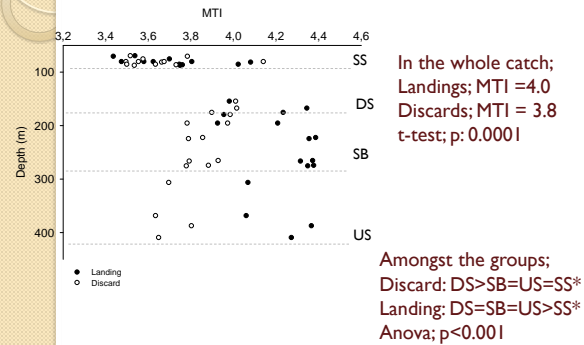
Table 3. Biomasses (kg/h) of discards (D) and landings (L) by groups in the North-eastern Aegean Sea. * p<0.01

	SS (70-88 m)	DS (155-180 m)	SB (196-276 m)	US (307-410 m)	Post-hoc
n	12	4	8	4	
D	32.89±13.13	14.03±2.8	12.72±13.56	10.77±1.84	SS>DS=SB=US*
L	45.64±19.3	31.04±3.8	25.37±9.19	35.37±20.01	SS=DS=SB=US

Finally,

The negative impact of trawl fishery cannot be handled only with the present fishing regulations in Turkey, since this can affect food web structure and ecosystem functioning.

Mean Trophic Index by each group for discards and landings



Suggestions

- For better fisheries governance,
- Strict enforcement of the fisheries rules is requested and needed
 - There are some closed areas (Saroz Bay) and around Gökçeada Island, but;
 - Management plan for the Saroz Special Protected Area is needed, but there is NO MANAGEMENT Plan right now
 - For Gökçeada, a very small protected area exists, but this area should be enlarged.

Major points

- ✓ In the North-eastern Aegean, The MTI of the discarded fish was significantly smaller than that of the landed fish.
- ✓ The MTI of the whole catch (3.9) was lower than in the past [MTI₁₉₉₈ = 4.1; It was estimated by using Gurbet and Kara (1999)]
- ✓ Mediterranean hake, *Merluccius merluccius*, the deeper self water (155-180 m) around Gökçeada was the main discarded fish with high troph (discard size changed: 10 to 23 cm; mod: 14 cm).

• NEVERTHELESS:

- Protection of the fisheries stocks in the Northern Aegean Sea, concerted action is needed between Turkey and Greece, mostly with shared stocks.
- High Sea marine protected area is one of the option for the protection of the demersal stocks .

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Trophic level of Northeastern Aegean Sea bottom trawl fishery, Keskin, Ç.

Çetin Keskin received MSc and PhD degrees in Fisheries Science from the Institute of Science, University of İstanbul in 1994 and 2002, respectively. In 1994, she became a Research Assistant at the Department of Marine Biology, Faculty of Fisheries at the University of İstanbul, and stayed on to become Assistant Professor in 2006, and Associate Professor in 2013. Her current research interests include diversity, distribution and community structure of fishes in the eastern Mediterranean. FishBase has been one of her interests after her postdoc in 2013 at the Fisheries Centre, UBC.



12th FishBase Symposium
Big Old Data and Shiny New Insights: Using FishBase for Research

Brazilian freshwater fish species by state, Freire, K. et al.

OCCURRENCE OF BRAZILIAN FRESHWATER FISH SPECIES BY STATE¹⁴

Kátia de Meirelles Felizola FREIRE, Laboratório de Ecologia Pesqueira (LEP), Departamento de Engenharia de Pesca e Aquicultura (DEPAQ), Universidade Federal de Sergipe (UFS), Rua Mal. Rondon S/N, Jardim Rosa Elze, São Cristóvão-Sergipe-Brasil, CEP: 49100-000; kfreire2006@yahoo.com.br and Isaac Trindade Santos, LEP/UFS; Thaisa Accioly de Souza, Laboratório de Oceano, Departamento de Botânica, Ecologia e Zoologia, Universidade Federal do Rio Grande do Norte (UFRN), Campus Universitário Lagoa Nova, Natal – Rio Grande do Norte – Brasil, CEP: 59078-970; Danyhelton Douglas Farias Dantas, Laboratório de Ecologia Aquática (LEA)/UFRN; Ronaldo Angelini, Departamento de Engenharia Civil/UFRN

Brazil possesses the highest diversity of freshwater fishes in the world, with 3,152 species reported. It is followed by China, Indonesia, the Democratic Republic of the Congo, and United States of America with 1,605, 1,209, 1,138, and 1,001 species, respectively. All the other countries have less than 1,000 freshwater fish species. Brazil has a large continental area and very diverse hydrographic basins. One of the initial steps when planning to carry out a study is to secure a checklist of species found in that study area (such as state, river, basin). Except for some rare cases, such as the state of Pernambuco for which an electronic atlas was prepared, there is no list easily available for freshwater fish species by state in Brazil. FishBase currently has a partial list for freshwater species that reports 1-68 species by state, which is unrealistic and reveals that no effort was done yet to compile a more comprehensive list. Thus, we propose a study to be primarily based on CLOFFSCA to remedy this situation. This database will be complemented by information provided by local sources, and the data will be made available through FishBase. This new list, together with a database for common names for freshwater fish species, previously compiled by the first author will allow for the reconstruction of catch statistics for Brazilian continental waters that should also be made online for wider and easy usage. Preliminary results indicate the occurrence of 11-444 species by state, with the highest fish diversity found in the state of Amazonas, whereas the highest diversity of marine fishes is found in the state of Rio de Janeiro.

¹⁴ Cite as: Freire, K, Trindade-Santos, I, de Souza, TA, Farias Dantas, DD, Angelini, R (2014) Occurrence of Brazilian freshwater fish species by state, p. 91-94. In: Palomares, MLD, Taylor, E, Pauly, D (eds.), 12th FishBase Symposium, Big Old Data and Shiny New Insights: Using FishBase for Research. September 8, 2014, Beaty Museum of Biodiversity, University of British Columbia, Vancouver, Canada. A report prepared by the *Sea Around Us* to the Paul G Allen Family Foundation and the Pew Charitable Trusts.

12th FishBase Symposium Big Old Data and Shiny New Insights: Using FishBase for Research

Brazilian freshwater fish species by state, Freire, K. et al.

OCCURRENCE OF BRAZILIAN FRESHWATER FISH SPECIES BY STATE

Kátia de Meirelles Felizola Freire*, Isaac Trindade Santos, Thaisa Accioly de Souza, Danyhelton Douglas Farias Dantas & Ronaldo Angelini

*Universidade Federal de Sergipe, Brazil/CAPEs

FishBase Symposium, Vancouver – September 8, 2014

INTRODUCTION

- Brazil has the highest diversity of freshwater fish species in the world: 3163 spp. (Froese & Pauly, 2014)
- It is followed by China (1605), Indonesia (1209), the Democratic Republic of the Congo (1138), and United States of America (1001)
- Brazil has a large continental area and very diverse hydrographic basins.
- Except for some rare cases, such as the state of Pernambuco for which an electronic atlas was prepared, there is no list easily available for freshwater fish species by state in Brazil.



OBJECTIVE

- To compile data of occurrence of Brazilian freshwater fish by state for all 26 states
- To report occurrence by main water bodies and establish the link between these water bodies and the basins defined by ANA (Brazilian Water National Agency)
- To set the stage to the reconstruction of commercial catches in Brazilian inland waters



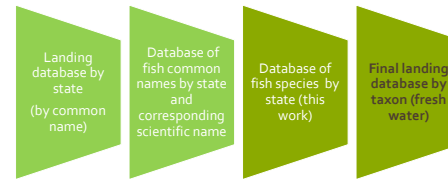
METHODS

- Compilation started with a national publication
- ✓ Backup, P.A., N.A. Menezes & M.S. Ghaziz, 2007. Catálogo das espécies de peixes de água doce do Brasil. Museu Nacional, Rio de Janeiro. 195 p.
- ✓ Reis, R.E., S.O. Kullander & C.J. Ferraris Jr, 2003. Check list of the freshwater fishes of South and Central America (CLOFFSCA). EDIPUCRS, Porto Alegre. 734 p.

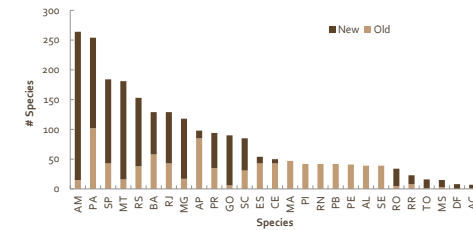


METHODS

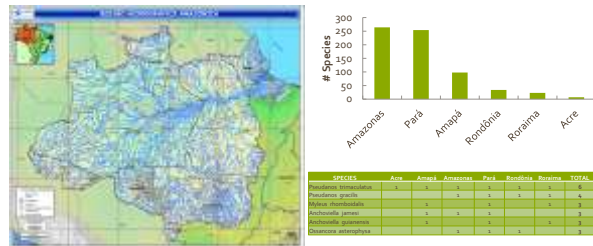
- Remote Data Entry into the Philippine server (www.fishbase.ph) – Isaac Trindade
- Database in MS Access with occurrence by river/basin/stream



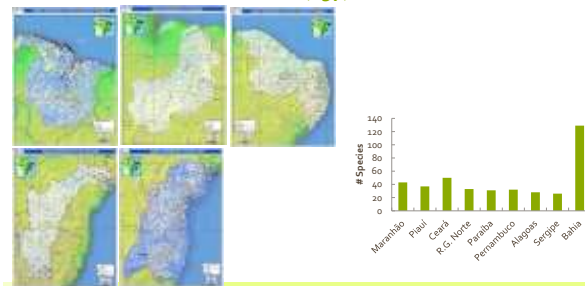
RESULTS



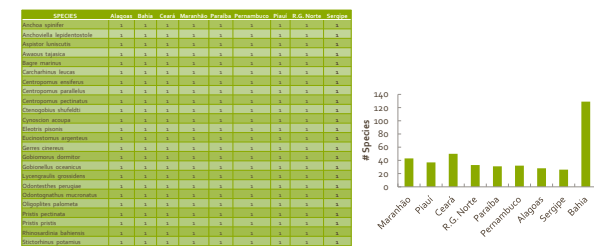
RESULTS – Northern Brazil (592)



RESULTS- Northeastern Brazil (197)



RESULTS- Northeastern Brazil (197)



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Brazilian freshwater fish species by state, Freire, K. et al.

ACKNOWLEDGEMENTS

- ❖ FishBase Consortium for allowing me to present recent advances in data entry for Brazil
- ❖ CAPES (Coordenação de Aperfeiçoamento de Pessoal de Nível Superior) for covering my trip expenses
- ❖ To Emily and Josephine (FishBase) for kindly and readily attend all my numerous data requests



<http://www.cpt.com.br/artigos/peixes-de-agua-doce-do-brasil-aracata-osteoglossum-br/rihossun>

Kátia Freire was born in Sergipe, Brazil and moved to Rio Grande do Sul to do her undergraduate study in Oceanology. She got her MSc in Biological Oceanography also in Rio Grande do Sul, while studying feeding habits of *Engraulis anchoita* in southern Brazil. She moved to Rio Grande do Norte where she did a specialization in Statistics. She worked in Paraíba and Pernambuco as a professor and researcher, respectively. In 2000, she moved to Vancouver, Canada to pursue her PhD with Dr. Daniel Pauly studying the impact of fisheries on the ecosystem of north-eastern Brazil. Back in Brazil she got teaching/researcher positions in the states of Bahia, Rio Grande do Norte and more recently Sergipe. Katia's other interests include children's books, common names of fishes, and instrumental English. She has been contributing to FishBase since 2001 and to SeaLifeBase since 2010. Katia joins the FishBase Symposium with funding via the CAPES/Brazil.



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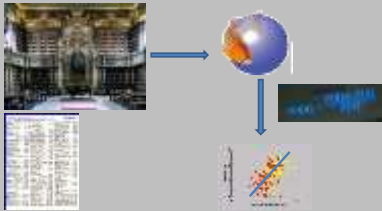
CLOSING REMARKS

CLOSING OF THE 12TH FISHBASE SYMPOSIUM: BIG OLD DATA AND SHINY NEW INSIGHTS: USING FISHBASE FOR RESEARCH¹⁵

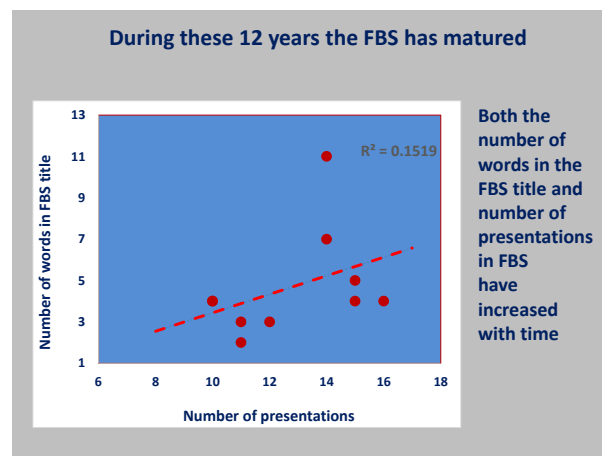
Konstantinos I. Stergiou

Aristotle University of Thessaloniki and
Institute of Marine Biological Resources and Inland Waters; kstergio@hcmr.gr

Closing of the 12th FishBase Symposium
Big Old Data and Shiny New Insights: Using FB for Research



Kostas Stergiou
Institute of Marine Biological Resources and Inland Waters, Hellenic Centre for Marine Research, Athens, Greece
School of Biology, Aristotle University of Thessaloniki, Thessaloniki, Greece



There was a variety of presentations, revolving around the importance of FishBase in “big” data research meta-analyses:

- taxonomy/nomenclature
- FishBase going FishBayes
- Management, socio-economics, effects of fishing
- global change
- country-specific fisheries-related case studies
- links with other fish-related projects/databases (osteological, barcoding, isotope base)

¹⁵ Cite as: Stergiou, K (2014) Closing of the 12th FishBase Symposium: Big Old Data and Shiny New Insights: Using FishBase for Research, p. 95-97. In: Palomares, MLD, Taylor, E, Pauly, D (eds.), 12th FishBase Symposium, Big Old Data and Shiny New Insights: Using FishBase for Research. September 8, 2014, Beaty Museum of Biodiversity, University of British Columbia, Vancouver, Canada. A report prepared by the *Sea Around Us* to the Paul G Allen Family Foundation and the Pew Charitable Trusts.

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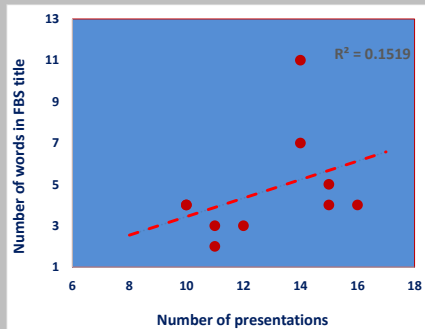
CLOSING REMARKS

The FishBase Symposium (FBS)...

5 September 2002 1st FBS in
Royal Museum for Central Africa,
Tervuren, Belgium
8 oral presentations

Since then, FBS has been an integral part of the
FBC annual meetings

During these 12 years the FBS has matured



Both the number of words in the FBS title and number of presentations in FBS have increased with time

History of the FishBase Symposium (FBS)

FBS	Title	Year	Location	Date	Place	Talks
1 st		2002	Tervuren, Belgium	5 Sep	RMCA	8
2 nd	FishBase uses	2004	Paris, France	2 Sep	MNHM, Grande Galerie de l'Évolution	11
3 rd	Fish and more	2005	Thessaloniki, Greece	31 Aug	AUTH, Central Library	12
4 th	Fish in ecosystems	2006	Vancouver, Canada	6 Sep	FC-UBC, Aquatic Ecosystems Research Laboratory	11
4	Fish Diversity and Aquatic Databases	2007	Tervuren, Belgium	5 Sep	RMCA, Okapi Room	15
6 th		2008	Qingdao, China	1 Sep	CAFS, Yellow Sea Fisheries Research Institute, R.1601	17
7 th	Darwin, names and databases	2009	Rome, Italy	9 Sep	FAO, Iran Room	10
8 th	20 years of FishBase	2010	Kiel, Germany	6 Sep	IFM-GEOMAR	16
9 th	Biogeographical modelling in FishBase	2011	Stockholm, Sweden	5 Sep	NHM	10
10 th	Fish diversity: a look from different angles	2012	Tervuren, Belgium	11 Sep	RMCA, Conference room (CAPA Building)	14
11 th	More fish and more	2013	Thessaloniki, Greece	2 Sep	AUTH, Center for Dissemination of Scientific Results	15

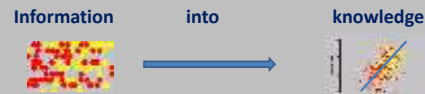
Impact of FishBase

FishBase has been evolved into a highly

- dynamic
- versatile
- ecological tool for

fish and fisheries research.

This is because it has transformed



Overall, during 2002-2014:

- 12 symposia organized
- 8 cities in 8 countries
- number of talks delivered increased to about 14-16
- 153 talks

These talks were on various aspects related to:

- Informatics
- Fish and non-fish
- Charles Darwin
- Biodiversity
- Modeling
- Ecosystems, conservation, management.

FishBase as a reference has penetrated into the




- primary aquatic
- general literature
- review literature
- aquatic and general books and textbooks

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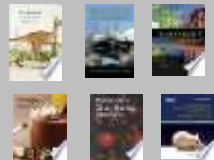
CLOSING REMARKS

Penetration into books and textbooks

FishBase is cited in many aquatic textbooks



FishBase is cited in many general, mainly life science, textbooks



FishBase ranks among the top most influential documents ever published in the fish, fish biology and fisheries literature

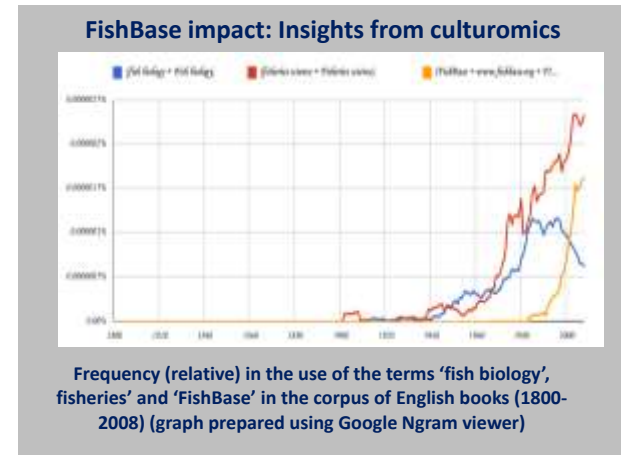
With > 4500 citations (i.e. >300 citations/year)
(or 4 citations for each 1 page of archive)

FishBase belongs to the:

- 0.03% most highly cited items ever published



during the last 100 years, irrespective of discipline
(based on Garfield 2005).



In 1985-1994, Kostas was a research associate at the National Centre for Marine Research (NCMR, now HCMR, Greece). In 1995-2001, he served as an Assistant Professor, and since 2006 as a Professor at the School of Biology, Aristotle University of Thessaloniki. He teaches both under-graduate and graduate courses on Ichthyology, Fisheries Biology, Fisheries Resources and Management and Time-Series Analysis. He was the Director of the Laboratory of Ichthyology, School of Biology in 2007-2013. His research interests are on fish life-history and population dynamics, fisheries ecology, modeling and forecasting, and ecosystem management, and bibliometrics. He was a member of the EU STCFM committee (1997-2002) and the Coordinator of the Fishery Science Task of CIESM (International Commission for the Scientific Exploration of the Mediterranean Sea). In 2001-2004, he became the Head of the CIESM Subcommittee on Living Resources and co-Chair of the CIESM Committee on Living Resources and Marine Ecosystems in 2004-2007. He acted as the National Coordinator of FishBase for Greece (since 1998) and since 2004 is the representative of the Aristotle University (School of Biology, Department of Zoology) to the FishBase Consortium. He serves on the Editorial Board of the journals Fisheries Research, Ethics in Science and Environmental Politics and Journal of Biological Research. He is also a contributing editor of the journal Marine Ecology Progress Series, Associate Editor for the FishBase Section (responsible for 'Short Communications in Ichthyology') in the journal Acta Ichthyologica et Piscatoria, Associate Editor for the journal Mediterranean Marine Science and Academic Editor of the journal Plos-One. He has contributed about 135 papers in peer-reviewed journals, 20 book chapters, one book, as well as more than 220 other publications (i.e. conference proceedings, special publications, newspaper and magazine articles) and co-authored 25 technical reports.



ACKNOWLEDGEMENTS

We wish to thank the sponsors who made the participation of most of our speakers possible, the key people being:

- Mr Mathieu Leporini, Scientific Attaché, Consulate General of France in Vancouver;
- Dr Yoshitaka Ota, Program Co-Director of the Nereus Program; and
- Dr Mary Ann Bimbao, Executive Director, FishBase Information and Research Group.

We equally wish to thank those who helped in the organization of this Symposium:

- Ms Alice Dubot, Press and Communications Advisor, Consulate General of France in Vancouver;
- Ms Nicole Gibillini, Sea Around Us Communications Officer, UBC Graduate School of Journalism;
- Ms Mairin Kerr, Marketing, Communications and Events Coordinator and Ms Jacqueline Chambers, Education and Outreach Manager, Beaty Biodiversity Museum;
- Mr Michael Yap, Ms Joann Glorioso, Ms Rachel Atanacio and Mr Daryl Nikasius Santos, FishBase Information and Research Group;
- Ms Dayna Szule, Sea Around Us Administrative Assistant, whose help was instrumental in ironing the small but many details of this Symposium's organization and Ms Pamela Rosenbaum, Fisheries Centre Manager, who guided us through the many other details we overlooked.

Finally, we are grateful to the Paul G Allen Family Foundation for the generous grant to the Sea Around Us, which includes a sub grant to the FishBase Information and Research Group.

This report is the product of a scientific collaboration between the Pew Charitable Trusts and the Sea Around Us.

www.seaaroundus.org

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