

Fishbase Symposium 2014

FISHES AND GENES / FISKARNAS GENER

Swedish Museum of Natural History

20 October 2014



Summary



FishBase



Naturhistoriska
riksmuseet

FishBase Sweden
Naturhistoriska riksmuseet
Box 50007
104 05 Stockholm
fishbase@nrm.se
08-5195 40 00

12 november 2014

Text: Respective speaker and Michael Norén, FishBase Sweden
Cover photo: GloFish® tetras (transgene albino *Gymnocorymbus ternetzi*). www.glofish.com. CC-BY-SA.
Other photos: Linnea Rundgren. CC-BY-SA.
Published by FishBase Sweden, Stockholm

FishBase Symposium 2014 – Fishes and Genes

Introduction.....	1
Francesc Piferrer	2
<i>Genetic and environmental components of fish sex determination and differentiation</i>	2
Krista B. Oke	3
<i>Hybridization between genetically modified Atlantic salmon and wild brown trout.....</i>	3
Thomas J. Near	4
<i>Fish phylogenies swim into the 21st Century</i>	4
Mathias Geiger	5
<i>The FREDIE project – different lessons from a large scale DNA barcoding campaign</i>	5
Philip Francis Thomsen.....	6
<i>Monitoring aquatic biodiversity using environmental DNA</i>	6
Hannu Mäkinen	8
<i>The importance of adaptive genetic markers in conservation genetics – lessons from Baltic sticklebacks.....</i>	8
Mats Grahn.....	9
<i>Fishing for population structure with genomic markers</i>	9
Participant list FishBase Symposium 2014	14
Programme (in English)	18
Program (på Svenska)	19



The symposium was held in Stockholm, Monday 20 October, in the Main Auditorium of the Swedish Museum of Natural History. The 151 registered participants listened to seven experts lecturing on different aspects of fish genetics.

Introduction

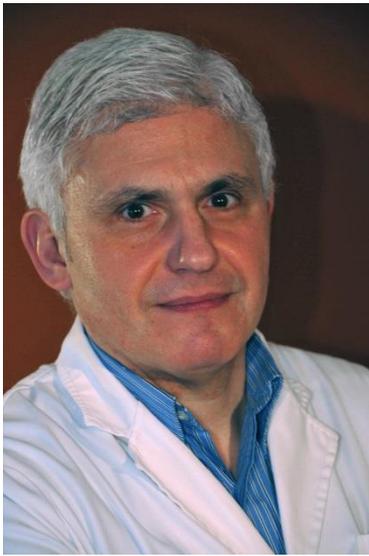
The theme for FishBase Symposium 2014 was *Fishes and Genes*. Molecular biology is increasingly a vital part of the study and management of fish, and we invited seven experts to talk about different facets of *Fishes and Genes*. The 151 registered participants were treated to lectures on a diverse range of topics: Francesc Piferrer talked about new findings on how genes and environmental factors interact to determine the sex of fishes – a subject still not fully understood. Krista B. Oke talked about her investigation of whether transgene salmon which escape from fish farms could pass on their modified genes by interbreeding with wild brown trout. Thomas Near explained how new technologies like next-generation sequencing are transforming the field of fish phylogenetics and taxonomy. Matthias Geiger talked about the lessons learned about the accuracy and reliability of standardized DNA-based species-level identification (“barcoding”) in the large-scale German barcoding initiative. Philip Francis Thomsen, a pioneer in the emerging field of environmental DNA study, talked about the possibilities and limits of eDNA. Hannu Mäkinen and Mats Grahn gave lectures on how adaptive genomic markers can be used to detect populations adapted to local conditions, even in Baltic stickleback where previous studies have failed to detect any population structure.



We were very fortunate to have Professor Dan Larhammar of Uppsala University moderating the symposium. Professor Larhammar is a distinguished molecular cell biologist, a leading proponent of science and rationality, and a member of the Royal Swedish Academy of Sciences.

Francesc Piferrer

Institute of Marine Sciences, Spanish Council for Scientific Research, Barcelona, Spain



Francesc Piferrer is a Research Professor within the department of renewable marine resources and leads the Group of Biology of Reproduction. He has contributed significantly to demonstrate the importance of estrogens in the process of sexual differentiation of fish, the development of protocols for the endocrine control of sex ratios in aquaculture and the prevention of sexual maturation. His current research focuses on the genetic and environmental regulation of sex determination and differentiation in fish, with special attention to the effects of temperature. His group is interested in epigenetic mechanisms during early development that regulate genes important for aquaculture production. He has authored more than 120 scientific publications, which have been cited about 3,000 times. Since 2011, he is in charge of the management of research projects in aquaculture within the Spanish

Ministry of Economy and Competitiveness. Among other recognitions for his work, he obtained the 2013 Jacumar Prize for Best Research in Aquaculture, awarded by the Spanish Ministry of Agriculture, Food and Environment.

Genetic and environmental components of fish sex determination and differentiation

Fish constitute the largest and most diverse group of vertebrates with over 30,000 recognized species. This great biological diversity is not only evident in morphological aspects, habitats, feeding types, etc., that fish exhibit, but also in relation to their reproduction. Thus, fish have all reproduction types known in vertebrates, including gonochorism or separate sexes, hermaphroditism, and unisexuality. However, regardless of a particular type of reproduction, the sex ratio, i.e., the number of males and females, is a central demographic parameter that influences the structure of populations and determines their reproductive potential. In this lecture, I will discuss the genetic and environmental components of fish sex determination and differentiation, the major mechanisms responsible for the sex ratio. Sex determination is the genetic or environmental process by which the sex (gender, male or female) of an individual is established in a simple binary fate decision. The inheritance of sex is based on three main effects: major sex factors, minor sex factors, and environmental differences. On the other hand, sex differentiation includes the various molecular, genetic, and physiological mechanisms that produce a male or female from a zygote of a given genotype and parents in a given environment. In the last years, major advances have been made in our understanding of these processes by combining different approaches, including molecular genetics, quantitative genetics and epigenetics. Understanding the genetic and environmental influences on the establishment of fish sex ratios has implications to understand the evolution of sex determining mechanism, for sex allocation theory and for speciation. It also has practical interest for assessing the reproductive capacity of wild populations, to monitor them in a scenario of global change, and for sex control in aquaculture production and in the eradication of invasive species.

Krista B. Oke

Department of Biology and Redpath Museum, McGill University, Montreal, Canada



Krista became interested in work on genetically modified Atlantic salmon during her undergraduate Honours degree at Memorial University of Newfoundland in St. John's, Canada. Her main interests are in the potential ecological and environmental risks that could result if genetically modified fish were to ever escape culture and enter wild ecosystems, especially in terms of the potential for hybridization. Interspecific hybridization of genetically modified fish with closely related species is an overlooked risk rarely considered in risk assessments on transgenic technologies. Specifically, Krista's work focuses on potential hybridization between genetically modified Atlantic salmon and the closely related brown trout. Krista is currently a Ph.D. candidate under the supervision of Dr. Andrew Hendry at McGill University in

Montreal, Canada. Her thesis and current interests focus mainly on evolutionary ecology and parallel evolution in North American post-glacial fishes.

Hybridization between genetically modified Atlantic salmon and wild brown trout

The development of genetically modified (GM, or transgenic) plants and animals for production has led to considerable debate over the potential environmental and ecological consequences should GM individuals escape culture. However, the potential for GM animals to hybridize with closely related wild species is an often overlooked potential risk, despite being a potential route for transgenes to invade wild populations. GM Atlantic salmon are, pending approval from the United States Food and Drug Administration, poised to become the first genetically modified animal approved for production for human consumption. In the wild, Atlantic salmon hybridize with the closely related brown trout, usually at low rates. We show through experimental crosses of wild brown trout with transgenic Atlantic salmon that transmission of the transgene into hybrid offspring is successful. Transgenic hybrids were viable and, in hatchery-like conditions, and grew faster than transgenic Atlantic salmon. In conditions that more closely emulate natural conditions, hybrids suppressed the growth of both non-transgenic and transgenic salmon. To the best of our knowledge, these results provide the first demonstration of environmental impacts of hybridization between a transgenic animals and a closely related species. Moreover, they show the successful first steps towards possible, although ultimately unlikely, introgression of a transgene into a new species. We suggest that interspecific hybridization be explicitly considered in risk assessments of transgenic technologies in animals.

Thomas J. Near

Near Lab, Ecology and Evolutionary Biology, Yale University, New Haven, U.S.A.



Tom Near is an associate professor of Ecology & Evolutionary Biology and an associate curator of the Yale University Peabody Museum of Natural History. His research is focused on developing and using molecular phylogenetic hypotheses to understand the evolutionary processes that have generated the incredible diversity of living ray-finned fishes (Actinopterygii). He has published detailed phylogenetic analyses of Antarctic notothenioids and North American endemic darters, using time-calibrated phylogenies to studying adaptive radiation and the geography of speciation. More recent studies have been directed towards the phylogeny and patterns of lineage diversification among all major lineages of ray-finned fishes.

Fish phylogenies swim into the 21st Century

The use of molecular data to infer the relationships among the major lineages of ray-finned fishes (Actinopterygii) lagged behind efforts focused on other groups of vertebrates such as birds, mammals, and squamates. A renaissance of actinopterygian phylogeny has emerged over the past several years, fueled by new datasets of DNA sequences of several nuclear genes sampled from hundreds of species. The phylogenies inferred from these comprehensive molecular datasets provide insight as to the sister lineage of all other teleost fishes, settle decades of confusion regarding the relationships of early diverging euteleosts, and offers unprecedented phylogenetic resolution of the hyper-diverse Percomorpha or the “bush at the top” of the teleost tree. Combining these new molecular datasets with morphological characters allows an integration of the fossil record to time calibrate molecular phylogenies and provide important insights into patterns of lineage diversification. The emerging phylogenetic perspective is discussed in the context of understanding mechanisms responsible for so called “living fossils,” examination of continental fragmentation events driving diversification in freshwater percomorph lineages, and patterns of evolutionary radiation in densely sampled lineages of teleosts. The future of actinopterygian phylogenetics is discussed in the context of DNA datasets built using next generation sequencing methods and the computational challenges associated with phylogenetic analysis of this type of data.

Mathias Geiger

Zoological Research Museum Alexander Koenig, Bonn, Germany



Born in Southern Germany close to Lake Würm in Bavaria State I was able to pursue my personal goal to work as biologist with freshwater fishes. After studying European ruffe (*Gymnocephalus* spp.) in my diploma thesis, I switched to Neotropical Crater Lake cichlids (*Amphilophus* spp.) from Nicaragua, on which I also wrote my dissertation about speciation and evolution. I then moved from Munich and the Bavarian State Collection to Bonn in Western Germany, where I first managed the FREDIE project at the Zoological Research Museum

Koenig and have now the coordination for the German Barcode of Life (GBOL) campaign. My research interests encompass DNA barcoding and biodiversity assessments, conservation, European freshwater fishes, cichlids and plecos, speciation, hybridization, systematics and taxonomy, biogeography, population genetics, and geometric morphometrics – at best all combined and based on a collection in a natural history museum.

The FREDIE project – different lessons from a large scale DNA barcoding campaign

In my talk I will first give an overview about the aims and structure of the FREDIE project, and will then focus on findings and highlights from the freshwater fish diversity of the Western Palearctic. Special emphasize will be put on the Mediterranean Biodiversity Hotspot, as one of the most important temperate biodiversity areas, with a remarkable diversity of freshwater fishes. Actually, 397 out of 526 species are recognized as endemic. In order to assess their diversity, and to construct a molecular identification system supporting conservation, we constructed a DNA barcode library for 498 Mediterranean freshwater fish species (98% extant species coverage) based on 3171 individuals. The congruence of clusters with morphological species ranged from 45 – 85% of species and was highly dependent on the method used to delineate clusters. Genetic discontinuities suggest the existence of up to 64 candidate species, potentially increasing fish diversity by <12%. Shared haplotypes among species highlight the limits of a barcoding approach, although mismatches tended to occur in recent (Pleistocene- or Holocene-evolved) lineages. We found reduced reliability of DNA barcoding to identify species unambiguously in a highly biogeographically structured area, but much greater accuracy when applied at the catchment scale. This scale effect has important implications for barcoding assessments, and our results suggest that fairly simple identification pipelines can be applied in local freshwater fish monitoring. Inventorying and management of large-scale diversity requires higher analytical and conceptual efforts. The barcoding of 98% of freshwater fish species of the Mediterranean Biodiversity Hotspot represents a success story for biodiversity research in the geopolitically complex region. The database will enable the recognition of conservation units within the Hotspot and will strongly support the ongoing exploration of the global freshwater fish diversity.

Philip Francis Thomsen

Center for GeoGenetics, Natural History Museum of Denmark, University of Copenhagen, Denmark



Philip's research interests are mainly focused on the applications of DNA from environmental samples to study contemporary biodiversity, both in freshwater and marine environments as well as several other sources like terrestrial sediments, museum insect specimens, human coprolites and leech gut contents. He has pioneered the work on metabarcoding of vertebrate DNA from water samples – freshwater as well as marine. He also works

with topics such as animal evolution, ecology and conservation, where he is especially focused on insects. He holds a Phd. and MSc from The University of Copenhagen, where he is currently a postdoc at the Centre for GeoGenetics. His publication record includes several high-impact journals such as *Science*, *Current Biology*, *Molecular Ecology* and *Nature Genetics*. He has disseminated his results in several international meetings and conferences as invited speaker and through popular media to the general public.

Monitoring aquatic biodiversity using environmental DNA

Aquatic ecosystems across the globe are under significant threat, suffering from various forms of anthropogenic disturbances, which is greatly impacting global biodiversity, economy and human health. Reliable monitoring of species is crucial for data-driven conservation actions in this context but remains a challenge owing to non-standardized and selective methods that depend on practical and taxonomic expertise, which is steadily declining.

Here we show that a diversity of rare and threatened European freshwater animals - representing amphibians, fish, mammals, insects and crustaceans - can be detected and quantified based on environmental DNA (eDNA) obtained directly from small water samples of lakes, ponds and streams. We successfully validate our findings in a controlled mesocosm experiment and show that eDNA becomes undetectable within 2 weeks after removal of animals, indicating that eDNA traces are near contemporary with species presence. We also demonstrate the potential of the method to detect entire assemblages of amphibians and fish by high-throughput sequencing of eDNA from a few small water samples in individual ponds. Our findings underpin the ubiquitous nature of eDNA traces in the environment and support the use of eDNA as a tool for monitoring rare and threatened species across a wide range of taxonomic groups.

Subsequently, for the first time, we investigated the potential of using metabarcoding of eDNA obtained directly from seawater samples to account for marine fish and mammal biodiversity. We show that such marine eDNA can account for fish biodiversity using high-throughput sequencing. Promisingly, eDNA covered the fish diversity better than any of 9 methods, conventionally used in

marine fish surveys. Additionally, we show that even short fish eDNA sequences in seawater degrades beyond detectable levels within days, in accordance with results obtained from freshwater eDNA. The method is also used for detection of marine mammals focusing on the cetacean species harbor porpoise. The eDNA approach consistently detected the porpoise under controlled conditions, but in natural environments the method was less successful than acoustic detections. However, at one site, long-finned pilot whale – a species rarely sighted in the target area – was detected. Although further studies are needed to validate the eDNA approach under varying environmental conditions, our findings provide a strong proof-of-concept with great perspectives for future monitoring of aquatic biodiversity and resources.

This abstract includes the work presented in the following 3 publications, and all authors should be credited for the above:

Thomsen PF, Kielgast J, Iversen LL, Wiuf C, Rasmussen M, Gilbert MTP, Orlando L, Willerslev E (2012). Monitoring Endangered Freshwater Biodiversity using Environmental DNA. *Molecular Ecology* 21, 2565-2573.

Thomsen PF, Kielgast J, Iversen LL, Møller PR, Rasmussen M, Willerslev E (2012). Detection of a Diverse Marine Fish Fauna using Environmental DNA from Seawater Samples. *PLOS ONE* 7(8), e41732.

Foote AD, Thomsen PF, Sveegaard S, Wahlberg M, Kielgast J, Kyhn LA, Salling AB, Galatius A, Orlando L, Gilbert MTP (2012). Investigating the Potential Use of Environmental DNA (eDNA) for Genetic Monitoring of Marine Mammals. *PLOS ONE* 7(8), e41781.



Hannu Mäkinen

University of Turku, Finland



I am interested in understanding how evolutionary forces such as genetic drift and selection affect allele frequency differentiation among populations. In my PhD I investigated phylogeography and adaptive divergence of sticklebacks inhabiting marine and freshwater environments in Europe. I used molecular marker based approaches to trace back evolutionary history of sticklebacks but I also aimed to locate genomic regions associated with adaptive divergence. Later I have concentrated on understanding the genetic basis of speciation in flycatchers. Currently my work at the University of Turku involves population genomics of domesticated Atlantic salmon strains and their wild conspecifics. In future, I will aim to investigate gene expression differentiation in European grayling populations inhabiting different thermal environments.

The importance of adaptive genetic markers in conservation genetics – lessons from Baltic sticklebacks

One of the aims in conservation biology is to identify intraspecific evolutionary significant units. Traditionally such units have been identified using a handful of presumably neutral genetic markers such as mitochondrial DNA or nuclear markers. This approach has provided crucial information on conservation planning in many taxa. However, studies using adaptive genetic markers i.e. those reflecting local adaptation have shown that neutral markers do not always capture relevant population structure. For example, in three-spined sticklebacks (*Gasterosteus aculeatus*) living in the Baltic Sea, the neutral markers revealed almost no genetic differentiation between populations sampled throughout the Baltic basin. Markers linked to osmoregulation genes detected four different population groups probably indicating possibly salinity related local adaptation in the Baltic basin. Lesson from the sticklebacks may change the view how conservation units should be identified especially in the marine fish populations.

Mats Grahn

Södertörn University, Stockholm, Sweden



I work as a professor of evolutionary biology at Södertörn University, Huddinge, Sweden. My research is aimed at understanding how genetic variation is preserved in wild populations despite strong natural and sexual selection, and factors such as bottlenecks and random genetic drift. To answer this I have focused on the variation in highly variable protein coding genes important for disease resistance and the maintenance of genetic variation in protein coding genes compared to non-coding neutral genes, such as microsatellites in fish and birds. The major histocompatibility complex (MHC) has a central function in the vertebrate immune system. Some MHC loci show an exceptionally high genetic variation. This extreme polymorphism is maintained by a combination of selection pressures caused by infectious pathogens and inbreeding avoidance whereby MHC affects odor preferences

and mate choice. The variation in the genes involved in the adaptation to pollutants almost rival the immune system genes and through the processes of anti-oxidative activity they may also be linked to life history traits and involved in condition dependent mate choice. However, the key factors linking genetic variation in this system to effects on the level of populations is much less understood than is the case for the MHC and I had to utilize a broader approach, relying on affordable genomic methods, mainly amplified fragment length polymorphism (AFLP). Our research deploys PCR based methods from molecular genetics and combines these with methods from quantitative genetics and behavioral ecology to test these ideas in natural or semi natural populations of corals, blue-mussels, fish and birds. I have also studied how variation in MHC affects disease resistance in farmed salmon.

Fishing for population structure with genomic markers

The architecture of gene organization into genomes imply that selection pressures from environmental factors and neutral genetic processes as genetic drift, mutation, recombination and gene flow will affect regions of the genome differently. These processes are explored in population genomics scans, mostly as a way to detect genetic regions under divergent selection in relation to environmental factors. I will present the result from some studies where we have used the same kind of methods and data to make inferences about population structure and about the nature and impact of environmental factors by estimating the potential for local adaptation. The projects have mostly used Amplified Fragment Length Polymorphism, AFLP to study the population structure in several species of fish, stickleback, salmon, mullets and siganids. Evolutionary adaptation requires intra-specific genetic diversity and genetic diversity and population genetic structure may affect the persistence of species and ecosystems by increased resistance to disturbances. Findings by us and others show that rapid change at the genomic level can occur in local populations and allow for local adaptation probably also in high gene flow situations.

I will also argue that genomic analyses of wild populations can potentially be more effective than screening for the occurrence of tolerant individuals in populations affected by environmental change. Several recent examples suggest that adaptation can involve multiple and distinct regions of the genome and highlights the danger of extrapolating from studies involving a limited number of genetic markers, and reinforces the notion that local demographic history and population-level variability are important factors influencing the ability to adapt to changing environments.

This abstract draws on the work presented in the following three PhD thesis, and all authors should be credited for the above:

Oskar Henriksson, 2013. Genetic connectivity of fish in the Western Indian Ocean. Stockholm University

Emma Lind, 2013, Genetic response to pollution in sticklebacks; natural selection in the wild, Stockholm University

Jakob Lohm, 2002, MHC and genomic diversity in Atlantic salmon (*Salmo salar* L.). Lund University.



Moderator Dan Larhammar congratulates Krista Oke to an excellent research report



Francesc Piferrer (left), Samuel Avraham and Andrea Hennyey study a three-dimensional poster.



Matthias Geiger (left) and Thomas Near in discussion during the coffee break.



Norbert Zanga, Henri Lukusa and Adèle Mputu, visiting from the Democratic Republic of the Congo.



Coffee break mingle.



Coffee break mingle.

Participant list FishBase Symposium 2014

Speakers:

Matthias Geiger	Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany
Mats Grahn	Södertörns högskola
Hannu Mäkinen	University of Turku, Åbo, Finland
Thomas Near	Yale University, New Haven, USA
Krista B. Oke	McGill University, Montreal, Canada
Francesc Piferrer	Institute of Marine Sciences, Barcelona, Spain
Philip Francis Thomsen	Københavns Universitet, Danmark

Moderator:

Dan Larhammar	Uppsala universitet
---------------	---------------------

Participants:

Hans Ackefors	Stockholms universitet
Gustaf Almqvist	Fiskesekretariatet
Per Alström	Artdatabanken
Anastasia Andersson	Stockholms universitet
Henrik C Andersson	Länsstyrelsen Stockholm
Gunnar Anéer	
Samuel Avraham	Stockholms universitet
Yordan Belivanov	
Veneta Belivanova	Naturhistoriska riksmuseet
Bengt-Erik Bengtsson	Proetus
Kristian Benkö	Aquaria Vattenmuseum
Gunnar Berglund	Stockholms kommun
David Bernvi	Stockholms universitet
Bo Björnsäter	Naturskyddsföreningen
Bertil Borg	Stockholms universitet
Ulf Borgen	
Daniel Brelin	Länsstyrelsen Uppsala
Henrik Brändén	Bioskriv
Pär Byström	Umeå universitet
Jenny Carlsson	Gentekniknämnden
Nasim Caspillo	Södertörns högskola
Johan Charlier	Länsstyrelsen Västernorrland
Nichlas Dahlén	Länsstyrelsen Gävleborg
Bo Dellling	Naturhistoriska riksmuseet

Tomas Didrikas	AquaBiota
Bernd Dinse	Haninge Akvarieförening
Emily Dock Åkerman	Naturhistoriska riksmuseet
Björn Edman	Rheoconsult
Gunilla Ejdung	Havs- och vattenmyndigheten
Nicklas Ekebom	Mälardalens Högskola
Ricky Eriksson	pensionär
Martin Franzén	Akvarievärlden AB
Gun Frostling	författare
Harald Frostling	
Matteo Fusili	Stockholms universitet
Thomas Giegold	Stockholms universitet
Lars Granat	
Niclas Gyllenstrand	Uppsala universitet
Anna Hagelin	Karlstads Universitet
Tatjana Haitina	Uppsala universitet
Stellan Hamrin	Stockholms stad
Nils Hedberg	Stockholms universitet
Per Hedberg	
Eva Hellberg	
Andrea Hennyey	Stockholms universitet
Gunilla Hjorth	Stockholms kommun
Thorbjörn Hongslo	SVA
Philip Jacobson	Stockholms universitet
Sven Jakobsson	Stockholms universitet
Eeva Jansson	Stockholms universitet
Leif Jonsson	Göteborgs Naturhistoriska Museum
Bodil Kajrup	Naturhistoriska riksmuseet
Erik Karlsson	Stockholms universitet
Ingemar Karlsson	
Christina Karlsson-Stark	
Oliver Karlöf	Stockholms stad
Berrit Kiehl	Uppsala universitet
Per Koch-Schmidt	Linnéuniversitetet
Alexander Kotrschal	Stockholms universitet
Sven O Kullander	Naturhistoriska riksmuseet
Björn Källström	Sjöfartsmuseet Akvariet
David Lagman	Uppsala universitet
Josefine Larsson	Södertörns högskola
Cecilia Lenbäck	Marine Stewardship Council
Sverker Lovén	Stockholms kommun
Henri Lukusa	SLU Uppsala
Stefan Lundberg	Naturhistoriska riksmuseet
Tyrone Lundström	Stjerberg trading
David Lundvall	Länsstyrelsen Dalarna

Thomas Lyrholm	Naturhistoriska riksmuseet
Emil Maier	Haninge Akvarieförening
Emma Maltin	Bohusläns Museum
Daniel Molin	
Aman Mottaqui-Tabar	Skogsstyrelsen
Adèle Mputu	SLU Uppsala
David Mårding	Aquaria Vattenmuseum
Margareta Mårtensson	
Ralph Mårtensson	
Thomas Mörs	Naturhistoriska riksmuseet
Sture Nellbring	Länsstyrelsen Stockholm
Jens Nielsen	Stockholms universitet
Fredrik Nilsson	Länsstyrelsen Västra Götaland
Oscar Nordahl	Linnéuniversitetet
Mats Nordenskjöld	Stockholms universitet
Lars Norelius	Uppsala kommun
Michael Norén	Naturhistoriska riksmuseet
Lennart Nyman	Man&Water
Daniel Nyqvist	Karlstads Universitet
Daniel Ocampo Daza	Uppsala universitet
Christer Olburs	
Bengt Olsson	Sportfiskarna
Lars-Olof Omfors	Stockholms akvarieförening
Nima Rafati	Uppsala universitet
Tomas Remén Loreth	Upplandsstiftelsen
Magnus Ringby	
Chrysoula Roufidou	Stockholms universitet
Piotr Rowinski	Uppsala universitet
Linnea Rundgren	Fotograf
Lisa Rydberg	Landsbyggsdepartementet
Jannikke Räikkönen	Naturhistoriska riksmuseet
Owe Salomonsson	Haninge Akvarieförening
Johnny Sandberg	
Lea Schneider	Karlstad universitet
Eva E. Sigsgaard	Københavns Universitet
Mikkel Skovrind	Københavns Universitet
Anders Stark	
Barbro Stark	Arlanda gränskontrollstation
Thomas Strid	Huddinge kommun
Fredrik Sundström	Uppsala universitet
Görel Sundström	Uppsala universitet
Linda Svensson	Sportfiskarna
Markus Sällman Almén	Uppsala universitet
Victor Söderberg	Sportfiskarna
Ryan Thoni	Saint Louis University

Robban Tranefalk
Susan Warner
Johan Watz
Lovisa Wennerström
Ulf Wiel-Berggren
Elina Viinamäki
Charlie Wijnbladh
Tomas Viktor
Anders Wilander
Steen Wilhelm Knudsen
Eva Willén
Norbert Zanga
Kaj Ådjers
Erik Åhlander

Aquaria Vattenmuseum
Karolinska Institutet
Karlstads Universitet
Stockholms universitet

Stockholms universitet
Naturskyddsföreningen
IVL
SLU Uppsala
Københavns Universitet
SLU Uppsala
SLU Uppsala
Ålands landskapsregering
Naturhistoriska riksmuseet





FishBase



Naturhistoriska
riksmuseet

FishBase Symposium 2014 — Fishes and Genes

Programme

- 09:00 - 09:30 Registration, coffee and sandwiches
Moderator: **Dan Larhammar**, Uppsala University.
- 09:30 - 09:35 Opening, **Michael Norén**, FishBase Sweden.
- 09:35 - 10:20 **Francesc Piferrer**, Institute of Marine Sciences: *Genetic and environmental components of fish sex determination and differentiation.*
- 10:20 – 10:50 Fruit break
- 10:50 – 11:35 **Krista B. Oke**, McGill University: *Hybridization between genetically modified Atlantic salmon and wild brown trout.*
- 11:35 – 12:20 **Thomas Near**, Yale University: *Fish phylogenies swim into the 21st Century.*
- 12:20 – 13:20 Lunch break
- 13:20 – 14:05 **Matthias Geiger**, Zoological Research Museum Alexander Koenig: *The FREDIE project – different lessons from a large scale DNA barcoding campaign.*
- 14:05 – 14:50 **Philip Francis Thomsen**, Copenhagen University: *Monitoring aquatic biodiversity using environmental DNA.*
- 14:50 – 15:20 Coffee break
- 15:20 – 16:05 **Hannu Mäkinen**, University of Åbo: *The importance of adaptive genetic markers in conservation genetics – lessons from Baltic sticklebacks.*
- 16:05 – 16:50 **Mats Grahn**, Södertörn University: *Fishing for population structure with genomic markers.*
- 16:50 – 17:00 Symposium Close

Time: Monday, 20th October 2014, 09:00 – 17:00.

Place: Main Auditorium (Stora Hörsalen), Swedish Museum of Natural History, Frescativägen 40, Stockholm.



FishBase



Naturhistoriska
riksmuseet

FishBase Symposium 2014 — Fiskarnas gener

Program

- 09:00 - 09:30 Registrering, kaffe och smörgåsar
Moderator: **Dan Larhammar**, Uppsala universitet.
- 09:30 - 09:35 Inledning, **Michael Norén**, FishBase Sweden.
- 09:35 - 10:20 **Francesc Piferrer**, Institute of Marine Sciences: *Genetic and environmental components of fish sex determination and differentiation.*
- 10:20 – 10:50 Fruktpaus
- 10:50 – 11:35 **Krista B. Oke**, McGill University: *Hybridization between genetically modified Atlantic salmon and wild brown trout.*
- 11:35 – 12:20 **Thomas Near**, Yale University: *Fish phylogenies swim into the 21st Century.*
- 12:20 – 13:20 Lunch
- 13:20 – 14:05 **Matthias Geiger**, Zoological Research Museum Alexander Koenig: *The FREDIE project – different lessons from a large scale DNA barcoding campaign.*
- 14:05 – 14:50 **Philip Francis Thomsen**, Copenhagen University: *Monitoring aquatic biodiversity using environmental DNA.*
- 14:50 – 15:20 Kaffepaus
- 15:20 – 16:05 **Hannu Mäkinen**, University of Åbo: *The importance of adaptive genetic markers in conservation genetics – lessons from Baltic sticklebacks.*
- 16:05 – 16:50 **Mats Grahn**, Södertörns Högskola: *Fishing for population structure with genomic markers.*
- 16:50 – 17:00 Avslutning

Tid: Måndag 20:e oktober 2014, 09:00 – 17:00.

Plats: Stora Hörsalen, Naturhistoriska riksmuseet, Frescativägen 40, Stockholm.