



December 2019

Vol. 32, No. 3

THE Open Reading Frame

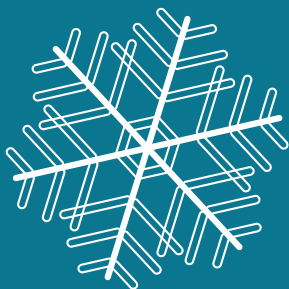
Newsletter of the Genetics Section of the American Fisheries Society

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President’s Message

Welcome to the winter 2019 edition of the Genetics Section newsletter. On behalf of the executive committee (Wendylee Stott, Marlis Douglas, and Wes Larson) we are looking forward to a new year where we continue to facilitate communication among members of the Section and to work towards goals such as helping with student travel to conferences.



Dr. Andrew Whiteley
AFSGS President

During 2019, the Genetics Section was active at the national meeting in Reno. We granted awards for graduate student achievement (through two Wright Awards), excellence in a paper contributed to AFS journals (through the Phelps Award), and excellence in early career contributions (through the Early Career Award). We are grateful to all the volunteers that helped select winners of these awards and, in thinking about next year’s round of awards, for their continued service to the section.

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President's Message cont'd

Looking ahead, the next national meeting will be held in Columbus, Ohio from August 30th – September 3rd. This meeting will be the 150th Annual AFS Meeting and the parent society is planning some extra events to celebrate the anniversary. Please start thinking about symposia that you might want to organize and reach out to an Executive Committee member if you would like to request Genetic Section sponsorship. Please also consider a number of ways you could get involved with the section. We are looking for volunteers to build a Genetics Section exhibit highlighting the past, present, and future of the use of genetics and genomics in fisheries biology. We are also looking for a new member for the committee that evaluates nominees for the Early Career Award each year. Finally, there is a big push from the parent society to make Climate Change a priority, most immediately through a position statement with partner societies. If you are interested in getting involved, let me know!

Happy Holidays,

Andrew

Genetics Section Awards Presented at Reno Business Meeting



Stevan Phelps Memorial Award - Best Genetics Paper in AFS Journal

Variance in reproductive success is driven by environmental factors, not mating system, in bonytails

Megan Osborne, Alyssa Sanchez, Thomas Dowling, and Thomas Turner

Transactions of the American Fisheries Society, Vol 147:1100-1114

Bonytail *Gila elegans* is a large, long-lived, endemic fish that was once abundant and broadly distributed throughout the Colorado River basin. Establishment of non-native species and habitat alterations caused by damming of rivers have caused this species to be functionally extirpated in the wild and it is now federally listed as endangered. Knowledge of mating systems and sources of variance in reproductive success is important



for management of endangered fish because high variance in reproductive success leads to substantial losses of genetic variation when few individuals reproduce successfully. However, studying the reproductive ecology of aggregate broadcast spawning fishes is difficult because it is not usually possible to sample all potential parents and unambiguously assign their offspring. We used molecular-based parentage analysis to understand the reproductive ecology of Bonytail, and to evaluate whether protected off-channel habitats could be used as an alternative to hatchery production. Genetic information was collected from adults and offspring stocked into two predator-free backwaters across three years. We determined that the majority of adults contributed to progeny production across years and backwaters. Both sexes had more than one mate, and there was a positive correlation between the number of mates and family size. Results also suggested that environmental factors are the primary influence to variance in reproductive success. Results provided by this study support the use of predator-free backwaters as an effective conservation tool for reintroducing Bonytail to its native habitat.



We are continuing this research on Bonytail and Razorback Sucker at the Imperial National Wildlife Refuge to further our understanding of their reproductive ecology to help inform conservation activities for these species. This research was funded by the U.S. Bureau of Reclamation- Lower Colorado River Multi-Species Conservation Program (<https://www.lcrmscp.gov/>)

James E. Wright Graduate Award

Emily Dziedzic, Master's Student, Oregon State University



As a Master's student in the Department of Fisheries and Wildlife at Oregon State University (OSU) I have been lucky to be able to forge my own path to some extent. With the help of my advisor, Taal Levi, I developed a project with the Oregon Department of Fisheries and Wildlife (ODFW) REDD group and the US Forest Service Pacific Northwest Research Station (PNWRS) to create a reference sequence database of mitochondrial genomic information for all the freshwater vertebrates of Oregon. The project is called the Oregon Biodiversity Genome Project and we are close to completing collection and mitochondrial sequencing for freshwater fishes statewide. Collection has been undertaken almost entirely by ODFW and PNWRS and I have carried out wet lab work and bioinformatics for mitogenome assembly.

The genomic data I have curated is being used to develop environmental DNA detection tools for target species like Bull Trout and Umpqua Chub and has been shared with researchers at Rocky Mountain Research Station and the Cronn lab at OSU. The ultimate goal is to create a multispecies detection tool to be used throughout the state of Oregon and my collaborators and I are exploring a variety of different methods to achieve that aim.

Being presented with the James E. Wright Graduate Award has given me a sense of accomplishment and I am grateful for this validation. It is important to feel that our endeavors are of value and having my work be recognized by my peers has provided me with a sense of personal achievement. I am very much looking forward to continuing my research and could not be happier to be engaged in fisheries genetics at such an exciting time for our field. Many thanks to the American Fisheries Society Genetics Section and to all of my collaborators and mentors—particularly Taal Levi, Richard Cronn, Brooke Penaluna, Brain Sidlauskas, Jamie Anthony, Tom Friesen, Trevan Cornwell, and Staci Stein—for their help and support.

James E. Wright Graduate Award

Aviva Fiske, PhD Student, University of California, Davis

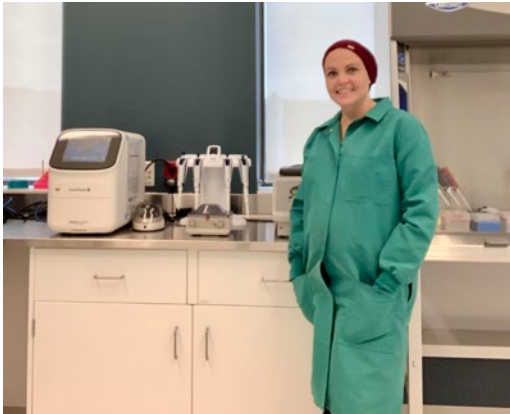
As a PhD student at the University of California, Davis, my research focuses on developing molecular genetic techniques for the conservation of white sturgeon. Previous work has indicated that minimizing the amount of time spent in the hatchery can help avoid domestication selection and potentially lead to higher survival rates for juvenile sturgeon in the river. The goal of my current work is to allow for the release of sturgeon larvae from hatcheries rather than raising the larvae to juveniles before release, with the aim of reducing the amount of time spent in the hatchery. However, because all hatchery born fish must be marked in some way before release and physical marking is not possible in larval fish, larval white sturgeon are currently not released from hatcheries. To facilitate release of larvae I am using a recently developed white sturgeon SNP panel and GT-Seq (genotyping in thousands) to assign juvenile sturgeon from the Kootenai River spawned in the hatchery to their broodstock parents using parentage analysis. This type of genetic "tagging" could allow for the identification of hatchery fish using the genetics of their broodstock parents, eliminating the need for physical marking of fish released from the hatchery.



In addition to developing parentage based tagging techniques, I have been using the genetic diversity of juvenile and larval white sturgeon collected from the Snake River to estimate the effective population size of adult white sturgeon in Hells Canyon. My previous work also involved using a blood smear technique and red blood cell size to infer the genetic ploidy of white sturgeon from three different ploidy classes. The James E. Wright Award was a huge help in allowing me to attend the national AFS meeting, which was a unique opportunity for me to learn from other fish geneticists. Previous conferences that I've attended have focused primarily on sturgeon biology and ecology rather than on genetics, and attending this meeting was a wonderful opportunity to learn from and collaborate with other fish geneticists.

Genetics Section Early Career Award

Dr. Cassidy Shaw, Fish Health Biologist, Vermont Fish and Wildlife Department



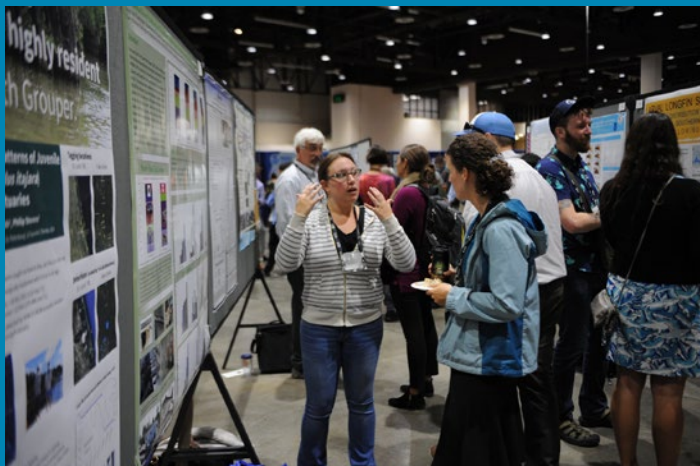
I am both honored and delighted to have been selected for the genetics section early career award. Thus far in my career I have been using next generation sequencing technology to answer a variety of questions related to the field of fish health. The ability to apply these technologies to non-model fish species has opened many doors in this field. I have been able to use RNA-seq to establish biomarkers for fishes exposed to emerging contaminants, evaluate the expression of genes in normal and disease fishes and uncover new and exciting fish pathogens. In my current position with the VT Fish and Wildlife Department the utilization of existing and emerging technologies is allowing for the advancement of established methods in fish health diagnostic testing. Furthermore, techniques in genetics allow us to improve our methods in aquaculture through the evaluation of the

genetic characteristics of broodstock, pathogen source tracking and identification of novel pathogens. None of my work would have been possible without the mentorship of outstanding scientists during my time as a student and post-doc. I am very grateful to my colleagues who have assisted me along the way and to the genetics section for supporting and promoting the impressive work performed by fisheries biologists and geneticists. I look forward to continuing to be a part of the future of this field and connecting with colleagues from the section at the next national meeting!

Sights from the AFS Meeting in Reno



Louis Bernatchez, Robin Waples, and Tom Dowling at the AFS Genetics Section Social. Photo: Marlis Douglas



In case you missed it...

Recent genetics papers from AFS journals and beyond

Editor's note: Click citations for link to papers



Genomic characterization of Coho salmon spawning populations from the Hood Canal. J. Bohlin, J. Von Bargen, and P. Bahls, TAFS, in press.

Tracking stocking success in a long-lived species through genetics and demographics: evidence of natural reproduction in lake sturgeon after twenty-two years. A.B. Welsh, D.M. Carlson, S.L. Schlueter, and J.R. Jackson, TAFS, in press.

RAD-seq refines previous estimates of genetic structure in Lake Erie walleye (*Sander vitreus*), K.Y. Chen, P.T. Euclide, S.A. Ludsins, et al., TAFS, in press.

A practical guide to sample preservation and pre-PCR processing of aquatic environmental DNA. G. Kumar, J.E. Eble, and M.R. Gaither, Molecular Ecology Resources, in press.

A clockwork fish: Age prediction using DNA methylation-based biomarkers in the European seabass. D. Anastasiadi and F. Piferrer. Molecular Ecology Resources, in press.

Contrasting genomic shifts underlie parallel phenotypic evolution in response to fishing. N.O. Therkildsen, A.P. Wilder, D.O. Conover, et al. Science 6452:487-490.

An evaluation of sequencing coverage and genotyping strategies to assess neutral and adaptive diversity. B. Benjelloun, F. Boyer, I. Streeter, et al. Molecular Ecology Resources, in press.

Adaption to extreme environments: a perspective from fish genomics. Y. Wang and B. Guo. Reviews in Fish Biology and Fisheries 29:735-747.

Genome-wide SNPs resolve spatiotemporal patterns of connectivity within striped marlin (*Kajikia audax*), a broadly distributed and highly migratory pelagic species. N.R. Mamoozadeh, J.E. Graves, and J.R. McDowell. Evolutionary Applications, in press.

Genomic data suggest environmental drivers of fish population structure in the deep sea; a case study for the orange roughy (*Hoplostethus atlanticus*). Journal of Applied Ecology, in press.

Population-level inferences from environmental DNA - Current status and future perspectives. E.E. Sigsgaard, M.R. Jensen, I.E. Winkelmann, et al. Evolutionary Applications, in press.

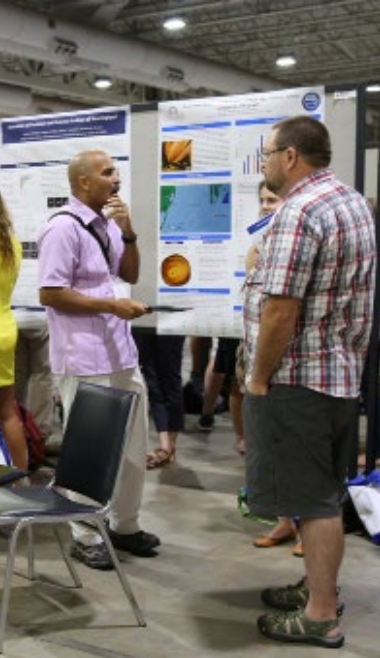
How stabilizing selection and nongenetic inheritance combine to shape the evolution of phenotypic plasticity. N.A. Levis and D.W. Pfennig. Journal of Evolutionary Biology, in press.

The genetics of phenotypic plasticity. XVII. Response to climate change. S.M. Sceiner, M. Barfield, and R.D. Holt. Evolutionary Applications, in press.

Resolving the genetic paradox of invasions: Preadapted genomes and postintroduction hybridization of bighead carps in the Mississippi River Basin. J. Wang, S. Gaughan, J.T. Lamer, et al. Evolutionary Applications, in press.



Calendar



January 2020

- 3rd-7th: American Society of Naturalists Stand-Alone Meeting, Asilomar, CA
 11th-15th: Plant and Animal Genome Conference, San Diego, CA
 14th-15th: Atlantic Salmon Ecosystems Forum, Orono, ME
 26th-29th: Midwest Fish and Wildlife Conference, Springfield, IL

February 2020

- 16th-21st: Ocean Sciences Meeting, San Diego, CA
 18th-20th: Catfish 2020 - Third International Catfish Symposium, Little Rock, AR

March 2020

- 23rd-24th: 4th International Conference on Aquaculture and Marine Biology, London, UK
 23rd-27th: 45th Eastern Fish Health Workshop, Shepherdstown, WV

May 2020

- 16th: World Fish Migration Day

June 2020

- 7th-12th: ASLO-SFS 2020 Joint Summer Meeting, Madison, WI
 11th-19th: IUCN World Conservation Congress, Marseille, France
 15th-18th: 61st Western Fish Disease Workshop, Hood River, OR

June 2020

- 19th-23rd: Evolution, Cleveland, OH
 22nd-26th: AFS Fish Health Section and Northeast Fish Health Committee Meeting, Burlington, VT
 29th-July 2nd: 14th International Congress on the Biology of Fish. Montpellier, France

August 2020

- 9th-14th: Health and Colony Management of Laboratory Fish 2020, Salsbury Cove, Bar Harbor, ME
 23th-28th: 6th International Marine Conservation Congress, Kiel, Germany
 30th-Sept 3: 150th Annual Meeting of the American Fisheries Society, Columbus, OH

September 2020

- 22nd-25th: Wild Trout Symposium XIII, West Yellowstone, MT

October 2020

- 11th-15th: 8th World Fisheries Congress, Adelaide, Australia

November 2020

- 15th-20th: 11th International Flatfish Symposium, New Castle, NH

To find dates and information for AFS chapter meetings, visit fisheries.org/about/units/chapters/



AMERICAN FISHERIES SOCIETY
150th Anniversary

Help us tell the story of the Genetics Section!

2020 marks the 150th anniversary of the American Fisheries Society. To celebrate this milestone, AFS units have been invited to create an exhibit to showcase their mission, their history, and where they're heading next.

Please consider volunteering for the committee to help create our exhibit. Section members from all career stages are encouraged to get involved.

**For more information,
 Contact Genetics Section President Andrew Whiteley**

Job Postings

Tenure track positions

University of Arizona

The Department of Ecology and Evolutionary Biology at the University of Arizona is accepting applications for an Assistant or Associate Professor position. We are particularly interested in candidates whose current or future research plans focus on adaptation to climate change and/or human health. A focus on any organism or system is welcome.

University of Maine

Assistant Professor of Ecological Bioinformatics in the School of Biology and Ecology (SBE) at the University of Maine, Orono. Anticipated start date of September 2020, with an initial appointment of 75% research and 25% teaching. We seek a bioinformatician applying computational methods to metagenomic and genomic datasets to elucidate structure and function of biodiversity or underpinnings of ecologically-relevant functional trait variation.

Texas A&M at Canyon

This full time (9 month) position at West Texas A&M University will include responsibilities in teaching (9 ACH/semester), research, and service supportive of the biology, wildlife biology, environmental science, and Biology Education programs. Candidates with expertise in the application of modern molecular methods (e.g. genomics, bioinformatics) to the study of natural populations (e.g. population genetics/genomics, evolutionary biology, or wildlife biology) are encouraged to apply.

West Virginia University

The Division of Forestry and Natural Resources within the Davis College of Agriculture, Natural Resources and Design at West Virginia University is pleased to invite applications for a nine-month tenure-track Assistant Professor in the Wildlife and Fisheries Resources (WFR) program. The position will focus on fisheries ecology with expertise in inland fisheries management and

Non-tenure track positions

Yale University

The Yale Center for Biodiversity and Global Change is seeking to fill a Staff Scientist position handling species distribution modelling and supporting geo-database management for our flagship project Map of Life.

Editor's note: Click postings for links to more information

Postdoc positions

UCLA

The UCLA La Kretz Center for California Conservation Science invites applications for its 2020 Postdoctoral Fellowship in California Conservation Science. We seek a postdoctoral scholar who conducts innovative biological research to work with the La Kretz Center and partner agencies to achieve outcomes that will direct and lead California conservation efforts.

Rutgers University

A three-year postdoctoral position is available in the Global Change Ecology & Evolution Lab at Rutgers University. The postdoc will join a NSF PIRE-funded project to study micro-evolutionary responses to a century of habitat degradation and intensive exploitation in Southeast Asia.

Czech Academy Of Sciences, Brno

The position is intended for experimental or laboratory work on brood parasitism, primarily on the cuckoo catfish and their cichlids hosts and/or bitterling fishes and their mussel hosts.

Graduate student positions

University of Maine and Partners

The Maine-eDNA EPSCoR program seeks 18 doctoral students to join a new NSF-funded \$20 million program focused on transdisciplinary eDNA research to advance freshwater and marine coastal ecosystem science and sustainability. We seek students with backgrounds and interests in aquatic ecology, marine science, bioinformatics, data science and spatial informatics, communications, and team science.

Queens University, Belfast

Understanding and predicting the success of alien freshwaterfish. Aim: To identify which species traits facilitate the introduction, establishment and spread of alien freshwater fish and predict the probability of success of potential future invaders, at global and local scale.

Pennsylvania State University

A MS student is being recruited to study invasive Flathead Catfish in Pennsylvania. The student will use molecular methods (DNA barcoding) to identify prey species consumed by Flathead Catfish. Work will include field collections, laboratory research and analysis, and writing manuscripts.

Workshops

Landscape genetics, January 15th - May 6th, 2020 - Online

This course on Landscape Genetics provides a unique opportunity for interdisciplinary training and provides an overview of the field of landscape genetics. The course caters to students in basic and applied ecology, conservation and population genetics, landscape ecology, evolutionary biology and conservation biology. A key objective of landscape genetics is to study how landscape modification and habitat fragmentation affect organism dispersal and gene flow across the landscape. Landscape genetics requires highly interdisciplinary specialized skills making intensive use of technical population genetic skills and spatial analysis tools (spatial statistics, GIS tools and remote sensing). Info: Lisette Waits, lwaits@uidaho.edu

The 4th Genomics of Disease in Wildlife Workshop - May 31st - June 6th, 2020 - Fort Collins, Colorado

Advances in genomic technology now provide an extraordinary opportunity to rapidly assess the impact of disease in wildlife biodiversity, management, and conservation. Wildlife and animal health researchers are uniquely positioned to merge ecological, biological, and evolutionary studies with genomic technologies to generate unprecedented Big Data tools in disease research. The workshop will provide a venue to accomplish this goal, will provide networking opportunities for colleagues from intersecting interests, and will advance genomic tools in wildlife and animal health disease investigations. The workshop will cover a typical workflow commonly used in NGS analyses starting with the initial raw sequence through the final stages of identifying host:pathogen variants linked with disease. Each day of the workshop will cover an essential component of the NGS workflow in succession. Info: CSU_gdw@colostate.edu.

Genome Assembly Using Oxford Nanopore Sequencing - February 10-14, 2020 - Berlin, Germany

New advances in sequencing technologies have opened the door to more contiguous genome assemblies due to the increased length of obtained fragments. Although there is a setback in accuracy, a broad range of algorithms has been developed to cope with it. This course will introduce the audience with a spectre of methods which are present in a usual assembly workflow, starting from raw data and finishing with a fully assembled genome. We will see how to obtain nucleotide sequences from raw signals, dive deeper into the most used assembly paradigm for long fragments, try out and compare several state-of-the-art assemblers, and at last, assess the quality of the obtained assembly with and without a reference genome. Structured over five days, this course consists of both theoretical and practical aspects which are intertwined through each day. The presented theoretical foundation will be applied on small bacterial datasets and visualized in order to better grasp the algorithms at hand.

Phylogenomics - May 25-29, 2020 - Berlin, Germany

Recent advances in sequencing technology, and the rapid increase in the availability of genetic data, have revolutionized the field of phylogenetics. While genomic data promise unprecedented insights into the evolution of the tree of life, they also pose new challenges that must be addressed to avoid misleading results and to fully leverage the potential of the genome-scale data sets. These challenges include the identification of orthologous sequences that are suitable as phylogenetic markers, the selection of appropriate models of sequence evolution, and the detection of gene-tree discordance due to incomplete lineage sorting and introgression. In this workshop I will present theory and exercises to infer time-calibrated phylogenies from multi-locus, RADseq, and whole-genome data sets while accounting for these confounding factors.





Section Officers

President

Andrew Whiteley
andrew.whiteley@umontana.edu

President-Elect

Marlis Douglas
mrd1@uark.edu

Past President

Wendylee Stott
wstott@contractor.usgs.gov

Secretary-Treasurer

Wes Larson
wes.larson@uwsp.edu

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Fisheries

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Listserv

Andrew Whiteley

Website

Kristen Gruenthal
kristen.gruenthal@noaa.gov

Newsletter Editor

Jared Homola
jared.homola@maine.edu