



The American Fisheries Society Genetics Section Newsletter

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President's message

The 2013 American Fisheries Society Annual Meeting is just around the corner! The theme for this year's meeting in Little Rock, Arkansas is "Preparing for the Challenges Ahead". Among the many symposium and contributed paper sessions, there will be two symposium



Meredith Bartron, AFSGS President

sponsored by the Genetics Section that highlight how genetic tools and techniques can be used to prepare for the future. Also in Little Rock will be the annual Genetics Section Business Meeting, to be held Monday, September 9, from 5:30-6:30 pm, in the Grampas Room of the Marriott Little Rock. Please join us to meet other section members, discuss section business, and to congratulate the James Wright and Stevan Phelps Award winners!

Continuing with the recent establishment of a section social, please join us Tuesday, September 10, at Boscos Restaurant and Brewing Company (500 President Clinton Ave., Little Rock, AR) starting at 7 pm for a section social! This year's social will be a little different than past years, in that it will be an informal gathering (no host, no tickets) to provide an opportunity for section members and friends to gather at the meeting to relax, catch-up, and make new connections. All are welcome! Given the uncertainty with travel for many and expected decreased attendance, the executive committee decided to limit costs to the section by making it no-host while still providing the opportunity for the get-together, as we've received much positive feedback about having the social. We hope to resume fund-raising at next year's meeting.

I hope to see you in Little Rock, and for those that are unable to join us this year, we'll provide updates and information in the next newsletter and on the website.

-Meredith Bartron

Announcements

Events at the annual American Fisheries Society

September 8th-12th Little Rock, Arkansas



LITTLE ROCK • 2013

Have you planned what talks and meetings you want to attend at the annual AFS meeting? Make sure you don't miss the following AFSGS events!

Genetics Section Business Meeting

Please join us for the Genetics Section Business Meeting on, Monday, September 9, at 5:30 pm, in the Grampas Room of the Marriott Little Rock (although please confirm the location at the meeting)

Genetics Section Social in Little Rock

Please join us for an informal gathering, starting at 7pm, Tuesday, September 10 at Bosco's Restaurant and Brewing Company (500 President Clinton Ave Little Rock, AR). Bosco's is just down the street from the Statehouse Convention Center, in the River Market District. This year's social will be no-host, so please join us at your leisure to catch-up with old friends and make new connections. All are welcome!

Monday September 9th

1:00-5:00pm Symposium Applying genetic principles and technologies to the management and conservation of fishery and aquatic resources- part 1 (Pope)

1:00-5:00pm Symposium Hatcheries and Management of Aquatic Resources (HaMAR)- part 1 (Ballroom A)

11:30am-6:00pm Posters Applying genetic principles and technologies to the management and conservation of fishery and aquatic resources (Trade show)

5:30-6:30pm Meeting Genetics Section Business Meeting (Chicot)

Tuesday September 10th

8:00am-3:00pm Symposium Applying genetic principles and technologies to the management and conservation of fishery and aquatic resources- part 2 (Pope)

8:00am-3:00pm Symposium Hatcheries and Management of Aquatic Resources (HaMAR)- part 2 (Ballroom A)

7:00pm-? Social Genetics section Social (Bosco's restaurant)

Thursday September 12th

8:00am-5:00pm Symposium Environmental DNA (eDNA) Analysis- a new genetic tool for monitoring, managing, and conserving resources and aquatic habitat (Fulton)

Feature article by Stewart Grant

Mixed stock analysis and fishery management

Mixed-stock analysis is now used routinely by many fishery management agencies. A recent article by Tyler Dann (Alaska Department of Fish and Game) and co-workers reports real-time estimates of mixed-stock components in the annual test fishery across Bristol Bay at Port Moller. Tissue samples of Sockeye Salmon are flown to the Gene Conservation Laboratory in Anchorage, analyzed for single nucleotide polymorphisms (SNPs), and used to identify fish from particular populations. This information is used by both fishery managers to open and close fisheries and by commercial fishermen to choose fishing locations.

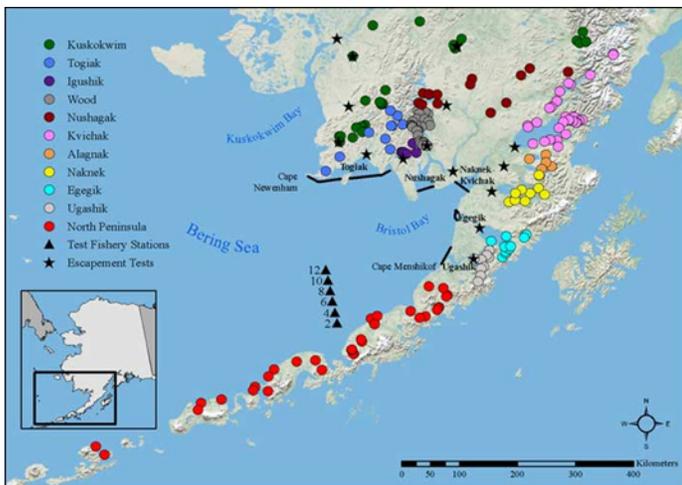


Figure 1. Map showing locations of baseline population of Sockeye Salmon in western Alaska. Various colors represent genetically distinct groups of populations (or reporting groups) used for making management decisions. However, some populations within these groups are genetically distinct. http://www.adfg.alaska.gov/index.cfm?adfg=fishinggeneconservationlab.bbaysockeye_baseline

The start of fishery genetics has roots, first in the development population genetic theory in the 1920s and 1930s, then in the development of laboratory techniques to measure genotypic diversity. In the late 1960s, Fred Utter, then at the Bureau of Commercial Fisheries (now NOAA Fisheries), was one of the first to use protein electrophoresis to study natural populations of fishes, a technique being applied to the study of genetic diversity in fruit flies. Fred quickly

grasped the usefulness of electrophoretic surveys to management of commercially harvested species such as Hake, Pollock, and Herring. The technique turned out to be especially useful for salmon.

Early surveys of 'allozyme' variability among populations of Pacific salmon spawning in the rivers and streams in the Pacific Northwest showed strong differences between populations, often between populations in the same river drainage. These results confirmed the ideas of many salmon biologists that salmon homed to their natal spawning areas to spawn, after long ocean migrations. Since most populations of salmon were genetically distinct, Fred reasoned that it might be possible to identify the population components as salmon traversed marine harvest areas on their way to spawning grounds. The identification of run components could be used by fishery managers to protect small populations from the detrimental effect of harvest.

George Milner, one of Fred's graduate students in the mid-1970s, set about using maximum likelihood to estimate the population components of a mixed-stock fishery. Several of Fred's students set about using George's FORTRAN program to understand local fisheries. The first published account of genetic mixed-stock methods dealt with Sockeye Salmon populations in Cook Inlet, Alaska. The population baseline for this study was not large, so it was uncertain how accurate the mixed-stock analysis would be. The 'ancestral' mixed-stock computer program was written on computer cards that could only be read by a large main-frame computer and used a tremendous amount of computer processing time. But subsequent studies of Cook Inlet Sockeye Salmon populations using a greater number of allozyme markers and more sophisticated versions of mixed-stock analysis confirmed the results of the earlier study.

Continued on page 5

Announcements

Recent column in "Fisheries" highlights eDNA

The AFS magazine "Fisheries" provides a great forum for the Genetics Section to periodically inform our fellow fisheries professionals of the uses of genetic methods in aquatic resource management and conservation. In this context, Marissa Jones, a graduate student at the University of Washington, School of Aquatic and Fisheries Sciences, authored a great overview of environmental DNA in the July issue of Fisheries, 38(7): 332-333. I encourage you to read Marissa's article on eDNA. It is written with non-geneticists in mind and summarizes the technique and various applications in a brief page and a half. Next up? Look for a report on parentage based tagging by Wes Larson, also from UW SAFS.

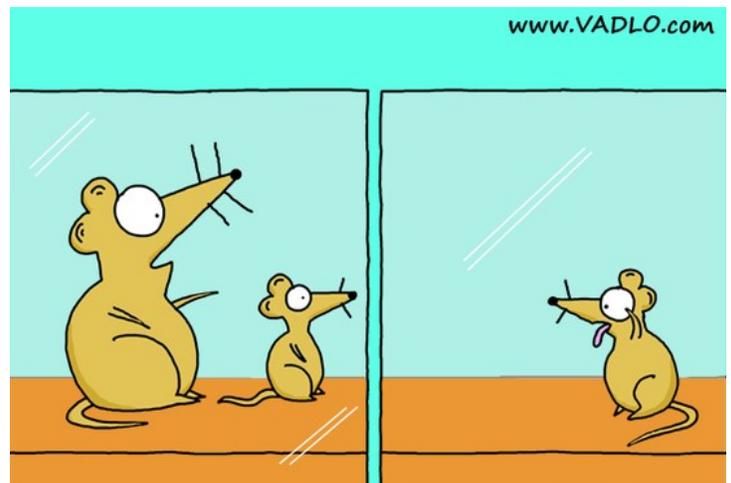
Genome 10K Workshop and Conference: The Great Challenge of Fish Genomes

I presented our current research of sequencing the American Eel (*Anguilla rostrata*) genome at the Genome 10k Workshop and Conference in Fort Lauderdale, FL that occurred April 24 - 28, 2013. Genome 10k (<https://genome10k.soe.ucsc.edu/>) is an international initiative to coordinate and facilitate the sequencing, assembly and annotation of the genomes of 10,000 species of vertebrates. This is a mammoth goal, but also realistic given the trajectory of sequencing technology. Currently the bottleneck of progress is not in the sequencing volume; you can get the raw data for 10 salmon sized genomes on a single sequencing lane; but instead it is the assembly of these short reads of 100-200 base pairs into a genome which is typically billions of base pairs. For many fish genomes, this is not unlike a 30 million piece jigsaw puzzle without the benefit a reference image of the completed picture. It was the consensus at the conference the fish genomes are particularly

difficult to assemble compared with birds and mammals. However, since fishes are the most diverse, as well as the mother of all vertebrates (phylogenetically all vertebrates are technically in the same clade as fishes), they represent the largest thrust of the genome 10k effort.

Scott A. Pavey, Postdoctoral Fellow at the Bernatchez Lab, Université Laval, 418-265-3456, scott.pavey.1ulaval.ca

Cartoon

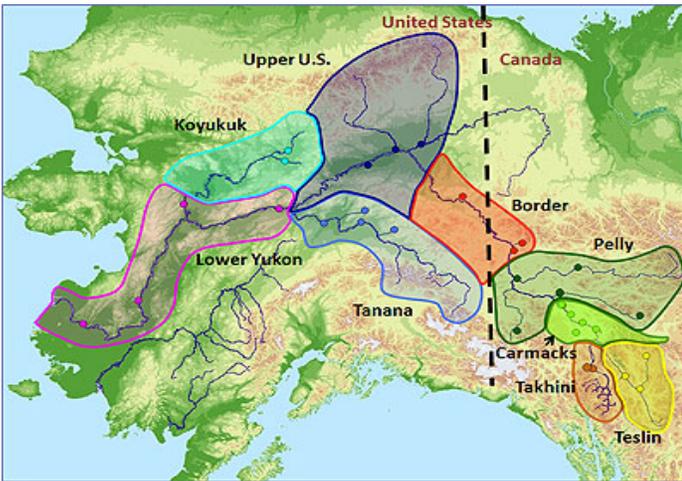


"Don't play with him, he is Wild Type."



Feature article by Stewart Grant continued

Fred Utter's original vision for the use of genetic markers in fishery management has grown far beyond its original application to regional fishery problems. Joint data bases for species that straddle international boundaries have been developed to help manage the interceptions of salmon in one country migrating to another to spawn. For example, mixed stock analysis is routinely used in the Yukon River and in transboundary rivers in southeastern Alaska. Genetic markers are also used by European countries for tracing food products, for enforcement, and for fishery management. [<http://fishpoptrace.jrc.ec.europa.eu/>]. However, the development of new molecular markers is not over. High throughput sequencing will give us better insights into the basis for adaptation that are not possible with 'neutral' markers.



Map showing regional groups of Chinook Salmon in the Yukon River system with headwaters and spawning populations in Canada. [http://www.adfg.alaska.gov/index.cfm?adfg=fishinggeneconservationlab.yukonchinook_baseline]

Further reading:

Bowen, B.W., W.S. Grant, D.J. Hillis-Starr, A. Bjorndal, A.B. Bolten and A.L. Bass. 2007. Mixed-stock analysis reveals the migrations of juvenile hawksbill turtles (*Eretmochelys imbricata*) in the Caribbean Sea. *Molecular Ecology* 16:49–60.

Dann, T.H., C. Habicht, T.T. Baker, and J.E. Seeb. 2013. Exploiting genetic diversity to balance conservation and harvest of migratory salmon. *Canadian Journal of Fisheries and Aquatic Sciences* 70:785–793.

Debevec, E. M., R. B. Gates, M. Masuda, J. Pella, J. Reynolds, and L. W. Seeb. 2000. SPAM (Version 3.2): Statistics program for analyzing mixtures. *Journal of Heredity* 91:509–511.

DeCovich, N.A., and K.G. Howard. 2011. Genetic stock identification of Chinook Salmon harvest on the Yukon River 2010. ADF&G, Fishery Data Series No. 11-65, Anchorage.

Grant, W.S., G.B. Milner, P. Krasnowski and F.M. Utter. 1980. Use of biochemical genetic markers for identification of sockeye salmon (*Oncorhynchus nerka*) stocks in Cook Inlet, Alaska. *Canadian Journal of Fisheries and Aquatic Science* 37:1236–1247.

Milner, G.B., D.J. Teel, F.M. Utter, and G.A. Winans. 1985. A genetic method of stock identification in mixed populations of Pacific salmon, *Oncorhynchus* spp. *Marine Fisheries Review* 47:1–8.

Seeb, L.W., A. Antonovich, M.A. Banks, T.D. Beacham, M.R. Bellinger, S.M. Blankenship, M.R. Campbell, N.A. Decovich, J.C. Garza, C.M. Guthrie III, T.A. Lundrigan, P. Moran, S.R. Narum, J.J. Stephenson, K.J. Supernault, D.J. Teel, W.D. Templin, J.K. Wenburg, S.F. Young, and C.T. Smith (2007): Development of a standardized DNA database for Chinook Salmon. *Fisheries* 32:540–552.

Seeb, L.W., C. Habicht, W.D. Templin, K.E. Tarbox, R.Z. Davis, L.K. Brannian, and J.E. Seeb. 2000. [Genetic diversity of sockeye salmon](#)

(*Oncorhynchus nerka*) of Cook Inlet, Alaska, and its application to restoration of populations affected by the Exxon Valdez oil spill. *Transactions of the American Fisheries Society* 129:1223–1249.

Utter, F., and N. Ryman 1993. Genetic markers and mixed stock fisheries. *Fisheries* 8:11–21.

Stewart Grant, Commercial Fisheries Division, Alaska Department of Fish & Game, Anchorage, AK. Email: william.grant@alaska.gov

Award Announcement



James E. Wright Award

We are pleased to announce the two winners of this year's James E. Wright award, which facilitates graduate student travel to the annual AFS meeting. Cassidy Hahn is a Ph.D. student at West Virginia University. She will be giving an oral presentation at the meeting in Little Rock on the effects of contaminants on gene expression endpoints in Great Lakes fishes. Darren Wood is a M.S. student at West Virginia University. His oral presentation at the meeting will be on the effects of culverts on the genetic diversity of brook trout. Be sure to congratulate our winners at the upcoming meeting!

Amy B. Welsh, email: amy.welsh@mail.wvu.edu

Stevan Phelps Award for Best Genetics Paper

I am pleased to announce that our committee has chosen

"Genetically Derived Estimates of Contemporary Natural Straying Rates and Historical Gene Flow among Lake Michigan Sturgeon Populations" by Jared Homola, Kim Scribner, Robert Elliott, Michael Donofrio, Jeannette Kanefsky, Kregg Smith, and James McNair (TAFS 141:1374-1388)

as the winner of this year's Stevan Phelps Award for Best Genetics Paper.

The Stevan Phelps Award has been given since 2000 in memory of Stevan Phelps, an early student of Fred Allendorf's at University of Montana. In the mid-1970s Stevan pioneered the establishment of population genetics laboratories in state fish and wild agencies (such as the Washington Department of Fish and Wildlife where he worked until 1999). He was instrumental in establishing the first consortium of state, federal, and university genetics laboratories along the West Coast that helped standardize rapidly developing techniques and allele and locus designations so that agencies could share data and analyses. Under his leadership genetic analyses became an accepted part of salmon management.

I am especially pleased with the choice of this paper this year because it brings together in an innovative way landscape genetics and study of patterns of historical gene flow with analyses of contemporary natural stray rates - two issues that are often studied separately but that Stevan would have seen as essential to combine to make good management decisions.

I especially want to thank my team of Amy Welsh, Adrian Spidle, and Patrick DeHaan who read through nearly 40 genetics papers published in 2012 in AFS publications.

Ken Currens, Phelps Committee Chair

Calendar

SEPTEMBER 2013

4th-6th Meeting. Genomics in Aquaculture Symposium in Bodø, Norway.

8th-12th Meeting. Annual AFS meeting in Little Rock, AR

15th Abstract deadline. Mobile Genetic Elements.

23rd-26th Meeting. Oceans 2013 MTS/IEEE in San Diego, CA.

23rd-25th Meeting. 2nd Annual World Conference of Mariculture and Fisheries. Hangzhou, China.

OCTOBER 2013

1st Abstract deadline. Oral and posters submissions for the Southern Division of the American Fisheries Society.

1st-4th Meeting. Wild Trout XI in Yellowstone National Park.

6th-10th Meeting. 10th International Symposium on Tilapia in Aquaculture.

January 2014

15th Grant deadline. Sigma Xi Grants In Aid of Research.

22nd-26th Meeting. Southern Division AFS in Charleston, SC.

24th-26th Meeting. Mobile Genetic Elements. Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.

NOVEMBER 2013

8th Grant deadline. National Science Foundation Graduate Research Fellowship Program in Life Sciences.

8th Abstract deadline. Society for Integrative and Comparative Biology annual meeting.

9th Meeting. Sigma Xi annual meeting. Communicating Science in the 21st Century. Virtual.

JANUARY 2014

3rd-7th Meeting. Society for Integrative and Comparative Biology (SICB). Austin, TX.

13th-15th Meeting. American Society of Naturalists (ASN). Pacific Grove, CA.

22nd-26th Meeting. Southern Division of the American Fisheries Society annual meeting. Charleston, SC.

26th-29th Meeting. North Central Division of the American Fisheries Society annual meeting. Kansas City, MO.

APRIL 2014

7th-11th Meeting. Western Division of the American Fisheries Society annual meeting. Mazatlan, Mexico.

JUNE 2014

8th-12th Meeting. Society for Molecular Biology and Evolution (SMBE). Puerto Rico.

Symposia

Population Genomic Data Analysis Course
2-7 Sept 2013. Flathead Lake Biological Station, Montana.

Recent approaches for estimation of population structure, gene-flow, landscape genomics, selection detection, and the analysis of next-gen sequence data. For more information visit <http://popgen.net/congen2013/>

Please send information on
symposia, jobs, articles,
and calendar events to
Joy.Young@myfwc.com to
see it published in the next
newsletter!

Jobs

Graduate positions

Ph.D. Graduate Research Assistantship in Fisheries Population Genetics/Molecular Ecology. Agency: University of Toledo, Great Lakes Genetics/Genomics Laboratory, Dept. Environmental Sciences. Location: Toledo, OH. Description: PhD research assistantship for new project on Yellow Perch and Eurasian Ruffe comparative population genetics, eDNA detection, kin selection, and chemical cues that may regulate homing.

For more information visit:
http://www.utoledo.edu/nsm/envsciences/grad/degreereq/phd_bio.html

Salary: \$23,000/yr stipend + tuition + general fees + student medical insurance all paid. Start Date: 01/05/2014. Last Date to Apply: 10/01/2013. Contact Person: Dr. Carol Stepien. Contact email: carol.stepien@utoledo.edu

Graduate Positions in Marine Population Genetics/Genomics (two positions).

Agency: University of Queensland, Australia. Location: St. Lucia, Australia. Description: The two projects are: 1) Comparative genomics and physiology of native and invasive mussel species in Australia, and 2) Range wide population connectivity and demography of a tidepool fish. For more information visit: <http://www.biology.uq.edu.au/>. Last date to apply: 9/8/2013. Contact person: Cynthia Riginos Contact email: c.riginos@uq.edu.au

Ph.D. Graduate Research Assistantship.

Agency: university of Vermont, Rubenstein Ecosystem Science Lab. Location: Burlington, VT. Description: Student will develop an interdisciplinary dissertation that combines fish acoustic telemetry with genetic analysis to examine the impacts of human-built barriers on fish movement and population structure in Lake Champlain. Last date to apply: 9/1/13 or until filled. Salary: \$26,500/yr. Contact email: ellen.marsden@uvm.edu

Graduate Assistantship (MS or PhD).

Agency: University of Maine. Location: Orono, Maine. Description: Develop and apply eDNA detection tools for invasive or imperiled aquatic species in Maine and the North East region. Graduate research may further integrate related themes such as fish conservation, population genetics and biogeography.. Last date to apply: 1/1/2014. Contact email: michael.kinnison@umit.maine.edu

Postdocs

Postdoctoral Research Scientist-Molecular Population Genetics/Ecology.

Agency: Harte Research Institute at Texas A&M University. Location: Corpus Christi, TX. Description: Position responsibilities involve development and assay of nuclear-encoded single nucleotide polymorphisms (SNPs), microsatellites, and mitochondrial DNA sequences for projects involving population genetics and molecular ecology, primarily of marine fishes. Central responsibilities include data acquisition and analysis, and preparation of reports and publications. Salary: \$35-\$40,000/yr. Last date to apply: position will remain open until filled. Contact person: John Gold. Contact email: goldfish@tamu.edu

Postdoctoral Researcher. Agency: Institute of Oceanography, National Taiwan University. Location: Taipei, Taiwan. Description: Our research group focuses

on three research axes (1) Phylogeny of ray-finned fishes at both large and small evolutionary time scales; (2) Evolutionary genomics, particularly the species diversification in relation to gene duplication; (3) Biogeography (historical biogeography and comparative phylogeography) of the Indo-West Pacific fishes. Contact person: Wei-Jen Chen. Contact email: wjchen.actinops@gmail.com

Jobs continued

Postdocs continued

Postdoctoral Position. Agency: Albert Einstein College of Medicine. Location: New York New York. Description: Research goals of the lab are to use statistical methods in conjunction with high-throughput DNA sequencing to understand patterns of genetic diversity, and to quantify how these patterns vary across individuals. We are interested in a variety of problems, including investigation of the influence of mutation, recombination, and natural selection. Contact person: Adam Auton. Contact email: adam.auton@einstein.yu.edu.

Assistant Professorship in Genetics. Agency: The Biology Department at Western Washington University. Location: Bellingham, WA. Description: Tenure-track position. Successful applicants for this position will demonstrate a strong quantitative approach in a genetics research program. They will also clearly articulate how they can translate their enthusiasm for quantitative work into a rigorous statistics course and how they can contribute to a genetics course reflecting contemporary problems in genetics. Last date to apply: 10/21/2013. For more information visit: <http://www.wwu.edu/jobs>.

Professional

Assistant/Associate Professor of Quantitative Genetics. Agency: Department of Animal Sciences, Institute of Food and Agricultural Sciences, at the University of Florida. Description: This is a 12-month tenure-track position with a 70% research and 30% teaching assignment. Major duties are to develop and implement a strong research and teaching program in quantitative genetic analysis and bioinformatics and related subject areas that will benefit Florida animal agriculture and human health industries. Applicant screening begins: 9/15/2013. Start: 10/1/2013. Contact person: PJ Hansen. Contact email: pjhansen@ufl.edu

Group Leader in Ecological and Evolutionary Genomics of Fish (Tenure track). Agency: The Swiss Federal Institute of Aquatic Science and Technology. Description: Applications are sought from individuals with an excellent research record in ecological or evolutionary genomics, an earned doctorate in a relevant field (e.g., genetics or evolution), and an interest in applying genomic research to understanding the genetic basis of variation in the behavior, ecology and adaptations of fish. Last date to apply: 9/30/2013. Contact person: Ole Seehausen. Contact email: ole.seehausen@eawag.ch

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Committees

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