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# Open Reading Frame

Newsletter of the Genetics Section of the American Fisheries Society

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## President's Message

Welcome to the summer 2023 edition of the Genetics Section newsletter. As summer begins many of us are starting something new, be it fieldwork, being newly graduated, or a new job. These new opportunities come with challenges, but they're also a chance to learn new skills gain new knowledge, and move further along our

path. I was reading through some papers recently and it really struck me how quickly ne relatively short time that I've been

the field of fisheries genetics is changing. In the relatively short time that I've been involved in fisheries genetics I've seen the leading edge of fisheries research transition from microsatellites to SNPs, to RADseq, and whole-genome sequencing. It's truly an exciting time to be involved in fisheries genetics.

The next annual meeting will be held August 20-24 in Grand Rapids, Michigan. This year's theme is Adaptive approaches to understand and manage changes in fisheries". The conference program is available online at https://afsannualmeeting.fisheries.org/. Early-bird registration rates end July 7th.

On a sadder note, Fred Utter passed away on March 5th. Fred was one of the founders of fisheries genetics and was a true pioneer in the use of genetics for fisheries management. The impact of Fred's work and his lab was immense, including the development of genetic stock identification (GSI) which is commonly used for fisheries

management worldwide. While there isn't room here to detail his accomplishments, his contributions to fisheries genetics were recently memorialized by Allendorf et al. (2023). Perhaps most important were Fred's contributions as a mentor. By all accounts, Fred was a passionate mentor and many of his students went on to have their own impactful careers contributing to fisheries genetics and mentoring the next generation. We are fortunate to have two articles about Fred in this newsletter written by former students. These former students have themselves been inducted into the AFS Genetics Section Hall of Fame, which is a small indicator of the impact Fred has had. Through his scientific contributions and his devotion to mentoring, Fred's legacy will continue to impact fisheries genetics for years to come.

The AFS Genetics section is working on establishing the Fred Utter Memorial Award to honor Fred Utters's legacy. The award and potential future funds will recognize outstanding contributions of graduate students to the field of fisheries genetics and be managed by the Genetics Section. Contributions of any amount can be made at: fisheries.org

Garrett J. McKinney President, AFS Genetics Section



Dr. Garrett McKinney AFSGS President

### In Memoriam Fred Utter: A Mentor Like No Other

#### By Bernie May (from 50 year old memories)

My professional career began sometime during the last quarter of my undergraduate degree in a Fish Genetics course given by Bill Hershberger in the College of Fisheries at the University of Washington in 1973. An MS student named Fred Allendorf gave a guest lecture on the application of allozyme electrophoresis to fisheries management. It really felt like a "light bulb going on in the brain" moment. I finally knew what I wanted to do for my career. Allendorf invited anyone interested to cross the ship canal and meet his mentor – Fred Utter.

A short time later I did cross the canal to the National Marine Fisheries Service and saw Allendorf in the office he mentioned. When I spoke to him about his invitation, this man came out from behind a bookshelf sticking out his hand introducing himself as Fred Utter. He quickly invited me to join the lab that at that time included him, Allendorf, and another student finishing his PhD named Allyn Johnson.

I applied for an MS degree in Fisheries that first summer and was turned down because of my 2.47 GPA (another story for another time). Fred's boss wanted him to boot me out of the lab. Fred, true to his loyalty philosophy, kept me on and I reapplied for Winter quarter and got in after taking some of the fisheries grad courses in the Fall. Fred signed my MS thesis as chair in 1975.

Fred was a true bucket chemist. Buffers were mixed in five gallon buckets with a big metal spoon. Chemicals for staining reactions were measured by eye with a small spatula. Allozyme gel rigs included glass plates on cheap plastic boxes, short pieces of platinum wires in plastic butter dish covers, handiwipes, etc., instead of fanciful plexiglass rigs with long strips of platinum wire. His goal was to get large quantities of quality genetic data with setups anyone could afford and to focus on the science that could be done with that data.

Those two years with Fred seemed like the most intense of my life. There were students, postdocs, faculty, and other professionals visiting the lab; Allendorf and I were always included. During that first summer Fred took us in his well-used green van to UC Davis and UC Berkeley for a conference and Fred introduced us to everyone with whom he interacted. Fred sent me to represent the lab at a fish genetics conference in Beulah, Wyoming.

This conference was a Who's Who of fish geneticists including the famous Russian fish geneticist Yurii Petrovich Altukhov (whose suitcase only seemed to contain bottles of vodka and no clothes). Utter and I taught several short courses on how to do allozyme electrophoresis. A few of the students whose names I remember included Jim Seeb, Stew Grant, Klaus Richter, Joy Belsky, Jack Hitron, and Ray Guries (many of the students worked on non-fish organisms).

While Fred Utter's professional impact on fisheries genetics has been well documented (https://doi. org/10.1093/jhered/esad028), his personal impact on the lives of those he met deserves equal billing. Many others have their own stories of Fred, but they all include references to the great human being who treated all he met as full professionals, whom he instantly respected. He continued that initial respect going forward. You could lose that respect by being a bull-shitter or treating others poorly. He was never "Dr. Utter", but always "Fred". Those of us who met Fred have hopefully been good emissaries of his life messages, like: keep it simple, do good science, and be kind to and supportive of others.

I miss you, Fred.



## In Memoriam Fred Utter, 1931-2023

#### By Jim and Lisa Seeb

Fish genetics lost one of the founders of the field and one of the original Genetics Section members on March 5, 2023, when Fred Utter passed peacefully in his sleep at age 91. Fred was one of the first inductees into the Genetics Section Hall of Excellence and a former president of the Section. He was widely recognized as a key founder of the field of fish genetics for his insightful research that began in the 1960s. In 1974, Fred Utter and colleagues wrote "Biochemical Genetic Studies of Fishes: Potentialities and Limitations." (Utter, Hodgins, & Allendorf, 1974). At that time, the field of fisheries genetics was in its infancy with only a few laboratories across the globe, and those mostly studied the quantitative genetics of animal breeding. The authors of the 1974 manuscript had a bold vision for the application of molecular genetic data in fisheries research and management.

Fred received a BS degree from the University of Puget Sound in 1954, only one year after Crick and Watson described the structure of DNA. Fred started working at the US Bureau of Commercial Fisheries (precursor to the NMFS) at the Montlake Laboratory on immunological research on fishes in 1959. Fred took a sabbatical to obtain a PhD (1969) from the University of



Fred Utter in the mid-2010s.

California Davis and emerged from Davis with The Vision—applying genetic data to fisheries management. He joined the then College of Fisheries at the University of Washington as a member of the affiliate faculty, got the attention of state and federal agencies with interests in Alaska, Washington, and Oregon, and began to offer graduate student stipends for applied studies using molecular genetics. Fred and his students authored landmark papers, pioneering the use of genetic data to study population structure, hybridization, genetic marking, and other applications for these agencies (see a review of Fred's contribution to fish genetics in Allendorf, Ryman, & Waples, 2023). Notably, Fred was the first person to author a paper on the use of genetics as a criterion for defining "species" of anadromous fish for the US Endangered Species Act in 1981 (Utter, 1981).

Fred gained a well-deserved reputation for nurturing and team building (students referred to him as Mother Utter). Many students will remember his bellows of delight at seeing an exciting result in the lab. Students in the Utter Lab would band together to work on each other's projects to study unusual inheritance patterns or linkage and recombination. These studies often required travel to distant hatcheries to secure gametes and tissues, genotyping parents through the night, and then producing family matings in the morning. Fred organized carpool trips for students so they could attend and give papers at distant meetings. He scaled travel up by renting motor homes to take larger groups of students to meetings or simply visit other laboratories at universities in California, Oregon, and Montana.

By the time of his Genetic Section-sponsored retirement party at the annual meeting of the American Fisheries Society in 1997, Fred's impact through his students could already be seen by a hand-drawn family tree that spanned an entire wall of the conference room. In "retirement" Fred remained active in the field of fisheries genetics as an adjunct professor at the University of Washington, an editor of the Transactions of the American Fisheries Fisheries Society for 18 years, past president of the Genetics Section, and many other related activities.

Fred's landmark 1974 paper concluded that population genetic structure of fish would vary across geographic ranges and species and be applicable to a wide range of fisheries research, including mixed stock analyses, hatchery/wild issues, hybridization issues, studying gene duplications and genetic linkages, and forensic applications. Look at studies being published today. In place of 20 allozyme loci, you'll see whole genome sequencing of millions of SNPs, but the fisheries applications envisioned by Fred and colleagues are still the foundation for much of today's ongoing research.

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### Fred Utter, 1931-2023 cont'd

Fred was a continual presence in our careers for over four decades. We were students in the Utter lab in the 1970s and then continued as colleagues and collaborators. In later years, Fred became the elder statesman with the fish genetics community at UW, mentoring members of the Naish, Hauser, and Seeb labs.

Fred reveled in writing limericks and poetry, often musing on students and techniques. Here's one for Fred:

His time began with Watson and Crick Developing many an allozyme trick from bloodtypes to genomes Fred wrote many tomes To the fish his legacy will forever stick



Fred Utter goofing off with students in his allozyme lab in the mid-1970s.

Allendorf, F. W., Ryman, N., & Waples, R. S. (2023). In Memoriam: Fred M. Utter, a founder of fisheries genetics. Journal of Heredity. doi:10.1093/jhered/esad028

Utter, F. M. (1981). Biological criteria for definition of species and distinct intraspecific populations of salmonids under the U. S. Endangered Species Act of 1973. Can. J. Fish. Aquat. Sci., 38, 1626-1635.

Utter, F. M., Hodgins, H. O., & Allendorf, F. W. (1974). Biochemical genetic studies of fishes: Potentialities and limitations. In D. C. Malins & J. R. Sargent (Eds.), Biochemical and Biophysical Perspecitive in Marine Biology, Vol. 1 (pp. 213-237): Academic Press.

## **Hello SNPs**

By Fred Utter

With allozymes dying, fish workers were trying to replace now-defunct data bases that for decades had grown and become widely known as the key to identify places

where fish populations from various nations and regions were all intermixing. Allozymes got expensive as they got less extensive

and support for them rapidly nixing.

Allozymes hit the basement.<sup>1</sup> To find a replacement, new DNA tools claimed the day. Each crowing their merits, they were dangled like carrots,

asking management bodies to pay

to develop, then sample – until data were ample to reach a new peak very fast for mixture solution with more resolution than allozymes did in the past.

Mitochondrial genomes were first seen as phenoms to reclaim salmon management's crown, but these female lines even failed to define what was known - this made managers frown.

Microsatellites came with immediate fame and abounding in loci, alleles.

Very soon major groups had the management troops strongly sniffing at microsat's heels.

Different groups had their foci on different loci. Different setups weren't very repeatable. Analytical squeals from six dozen alleles suggested this tool was defeatable.

Among other blips, crept a tool known as SNPs with apparent explicit simplicity,

proclaiming its wares based on nucleotide pairs, from proponents of zeal and felicity.

This tool at this place is the primary basis of research intended to be

a model – of course – for revealing the source of – sometime – every fish in the sea!!

Though it seems a bit chilling – living up to this billing is our intention right from the get go.So come one and all. We are having a ball.Your problems we pledge never to let go.

<sup>1</sup>see J. Irreproducible Results 49:50, 2005

## In case you missed it...

Recent genetics papers from AFS journals and beyond

Click citations for link to papers

Lusk, S.C., et al. 2023. Evaluation of population characteristic differences between the Largemouth Bass and its backcross following a long-term Florida Largemouth Bass stocking effort. North American Journal of Fisheries Management.

George, S. D., et al. Use of environmental DNA to assess American Eel distribution, abundance, and barriers in a river–canal system. Transactions of the American Fisheries Society.

Sammons, S.M., et al. Alabama bass alter reservoir black bass species assemblages when introduced outside their native range. North American Journal of Fisheries Management.

Salisbury, S. J., et al. Geography, environment, and colonization history interact with morph type to shape genomic variation in an Arctic fish. Molecular Ecology.

Bernos, T. A., et al. Simulating the effects of long-distance dispersal and landscape heterogeneity on the ecoevolutionary outcomes of range expansion in an invasive riverine fish, Tench (*Tinca tinca*). Molecular Ecology.

Fuentes-Pardo, A.P., et al. The genomic basis and environmental correlates of local adaptation in the Atlantic horse mackerel (*Trachurus trachurus*), Evolutionary Applications.

Ryman, N., et al. Variance effective population size is affected by census size in sub-structured populations. Molecular Ecology Resources.

Baltazar-Soares, M. et al. Seascape genomics reveals limited dispersal and suggests spatially varying selection among European populations of sea lamprey (*Petromyzon marinus*). Evolutionary Applications.

Venney, C. J., et al. Captive rearing effects on the methylome of Atlantic salmon after oceanic migration: Sexspecificity and intergenerational stability. Molecular Ecology Resources.

Barria, A., et al. Genetic differentiation following recent domestication events: A study of farmed Nile tilapia (*Oreochromis niloticus*) populations. Evolutionary Applications.

Fraimout, A., et al. Inbreeding depression in an outbred stickleback population. Molecular Ecology.

Ford, M.J., et al. Genomic divergence of hatchery- and natural-origin Chinook salmon (Oncorhynchus tshawytscha) in two supplemented populations. Conservation Genetics.

Heuertz, M. et al. The application gap: Genomics for biodiversity and ecosystem service management. Biological Conservation.



## Calendar

#### <u>June 2023</u>

- June 27-29: Coastwide Salmon Genetics Conference, Boise, ID, USA
- June 27-30: Society of Wetland Scientists Annual Meeting, Spokane, WA, USA

#### <u>July 2023</u>

- July 4-6: Fish Impingement and Entrainment Conference, Liverpool, UK
- July 4-25: Benthic Cnidaria (octocorals, corals, anemones and hydroids): an immersion in their diversity, Bocas del Toro, Panama
- July 11-14: ICAST Sportfishing Trade Show, Orlanda, FL, USA
- July 24-28: Joint Meeting of the Northeast Fish Health Committee and the AFS Fish Health Section, Burlington, VT, USA

#### <u>August 2023</u>

August 20-24: 153rd Annual Meeting of the American Fisheries Society, Grand Rapids, MI, USA

#### September 2023

- Oct 9-13: 7th International Otolith Symposium, Vina del Mar, Chile
- Oct 12-16: CERF 2023 Coastal and Estuarine Research Federation's 27th Biennial Conference, Portland, OR, USA
- Oct 22-26: North American Lake Management Society 43rd International Symposium, Erie, PA, USA
- Oct 23-27: ICES PICES Joint Science Conference, Seattle, WA, USA

#### October 2023

- Nov 20-24: 11th Indo-Pacific Fish Conference and Annual Conference of the Australian Society for Fish Biology, Auckland, New Zealand
- Nov 26-Dec 2: Black in Marine Science Week, Norfolk, VA, USA

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

## Workshops

#### SLiM Workshop - Harvard University, Cambridge MA August 28-September 1, 2023

All the major topics in the SLiM manual will be covered, starting with lots of introductory material to get beginners up to speed with SLiM and its associated scripting language Eidos, and ending up at advanced topics like non-Wright-Fisher models, tree-sequence recording, continuous-space models, nucleotide-based models, and multispecies models. To apply, please send an email to dcard@fas.harvard.edu, fmaravalllopez@fas.harvard.edu, and bhaller@mac.com with: (1) your name, (2) your university or institutional affiliation including the name of the lab you are in, (3) a link to a research website or similar academic page, if you have one, (4) a 1-2 sentence description of your level of experience with SLiM and any other forward genetic simulation software, if any, (5) a 1-2 sentence summary of why you want to attend the workshop (i.e., the connection to your research), (6) 1-2 sentences about any specific topics within SLiM that you hope to learn about in the workshop, and (7) A sentence stating that you are up-to-date on your COVID vaccinations, including all booster shots recommended by the U.S. CDC.

#### Exploring Evolutionary Relationships Using BLAST August 3rd, 2023 1-3pm Eastern Time

https://ncbiinsights.ncbi.nlm.nih.gov/event/blastevolution-08-2023/

Identification of evolutionarily related DNA or protein sequences (homologs) is a crucial step in many biology workflows. NCBI's BLAST program is a standard tool for identifying homologs, and this virtual workshop will teach you best practices for using it for your analysis goals. More info through emailing workshops@ncbi.nlm.nih.gov.

#### Population genomic inference from low-coverage wholegenome sequencing data, Online 2-5 October 2023

https://www.physalia-courses.org/courses-workshops/ course64/

In this course, we will explore workflows and the underlying rationale behind producing, processing and analyzing low-coverage sequencing data for population genomic inference. Given that most species have insufficient reference data to allow reliable genotype imputation, we will focus on a genotype likelihood-based methodology that can be applied to any system. We will primarily cover methods and algorithms implemented in the ANGSD software package and associated programs, providing best-practice guidelines and a discussion of how participants can make maximal use of low-coverage whole genome re-sequencing data for their studies.

The course is aimed at researchers who might have previous experience with next-generation sequencing (NGS) data (e.g. exome/RAD/pooled sequencing) and wish to explore the potential for using low-coverage whole-genome sequencing for their studies.

All hands-on exercises will be run in a Linux environment on remote servers. Statistical analyses and data visualization will be run in R. Should you have any questions, please feel free to contact us: info@physalia-courses.org

#### **153rd AFS Annual Meeting Genetics Symposium**

#### Highlighting the Cutting Edge: Graduate and Early Career Research in Genetics-Genomics

Conservation genetics-genomics is a burgeoning field due to its rapid evolution and recent advancements of

'omics' technologies." The use of next generation sequencing methods is changing not only what we can ask but how we ask it. This symposium highlights the cutting edge of genetics-genomics research in fisheries and aquatic sciences by profiling the current research of graduate students and postdoctoral fellows. These researchers, who represent the next generation of evolutionary and conservation scientists, are using next-generation sequencing not only to answer questions, but also lead the field in new directions.

#### Supported by:

American Fisheries Society Genetics Section Student and Early Career Professionals Subsection

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