

The American Fisheries Society Genetics Section Newsletter

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President's Message

My term is about over and Wendylee Stott will take over as your Genetics Section President during our business meeting at the AFS annual meeting in Kansas City in August. I have enjoyed my two years as the Section President and I'm looking forward to supporting Wendylee and the Section in the role of past-President. This is an exciting time in our field as we witness and contribute to the



Dr. Jeffrey Olsen, AFSGS president.

remarkable innovations and growth of genetic- and genomic-based tools for research, conservation and management of fisheries and aquatic resources. The variety of applications seems endless. Here are just a few regional examples: genetic mixed-stock analysis of Pacific salmon fisheries (Alaska, western Canada, western US), parentage-based tagging to monitor and evaluate Pacific salmon and steelhead populations (western US), eDNA analysis to monitor and control invasive Asian carp (midwest) and monitor freshwater and anadromous species distributions in the Arctic (northern Canada), riverscape genetics to inform conservation of brook trout (northeastern US), genetic analysis of hybridization among native and invasive bass species (southern US), next-generation sequencing to elucidate contaminant-driven selection in the American eel (eastern Canada). These few examples just scratch the surface and I'm sure you can think of many others. The point is, given the expanding role and demand for genetic tools and data in research, conservation and management, our Genetics Section can play a vital role inside and outside the American Fisheries Society in terms of communicating with and informing biologists and managers about the uses of genetic data and applications and in mentoring and encouraging students. Collectively, we represent a tremendous resource of knowledge, experience, and innovation in applying genetics to fisheries and aquatic resource management and conservation. I'm talking about everyone from our senior members and Hall of Excellence inductees to our students and young professionals, James E. Wright, Early Career, and Stevan R. Phelps Award winners. I hope you will continue to support the Section and AFS and encourage others to do so. *Continued on page 7*

AFSGS Business

CONGRATULATIONS!

Hello fellow Genetics Section members,

Please join me in congratulating our student travel award recipients for 2016. This is an amazing group and you can see from their presentation titles the depth and breadth of genetic applications in fisheries and aquatic resource management and conservation. As a side note, the researchers advising our two James E Wright award recipients were past Wright award winners (Amy Welsh - 2004; Jamie Roberts - 2009).

James E Wright annual travel award to the 2016 AFS national meeting, Kansas City MO

Nathan Lucas, University of Connecticut
"Using Riverscape Genetics to Inform Conservation of Eastern Brook Trout Populations"
Co-advisors: Jason Vokoun, Amy Welsh

Jackman Eschenroeder, Georgia Southern University
"Hybridization and Replacement of Roanoke Bass with Invasive Rock Bass in Virginia: A Genetic Analysis of the Problem"
Advisor: Jamie Roberts

2016 Coastwide Salmonid Genetics meeting, Astoria OR

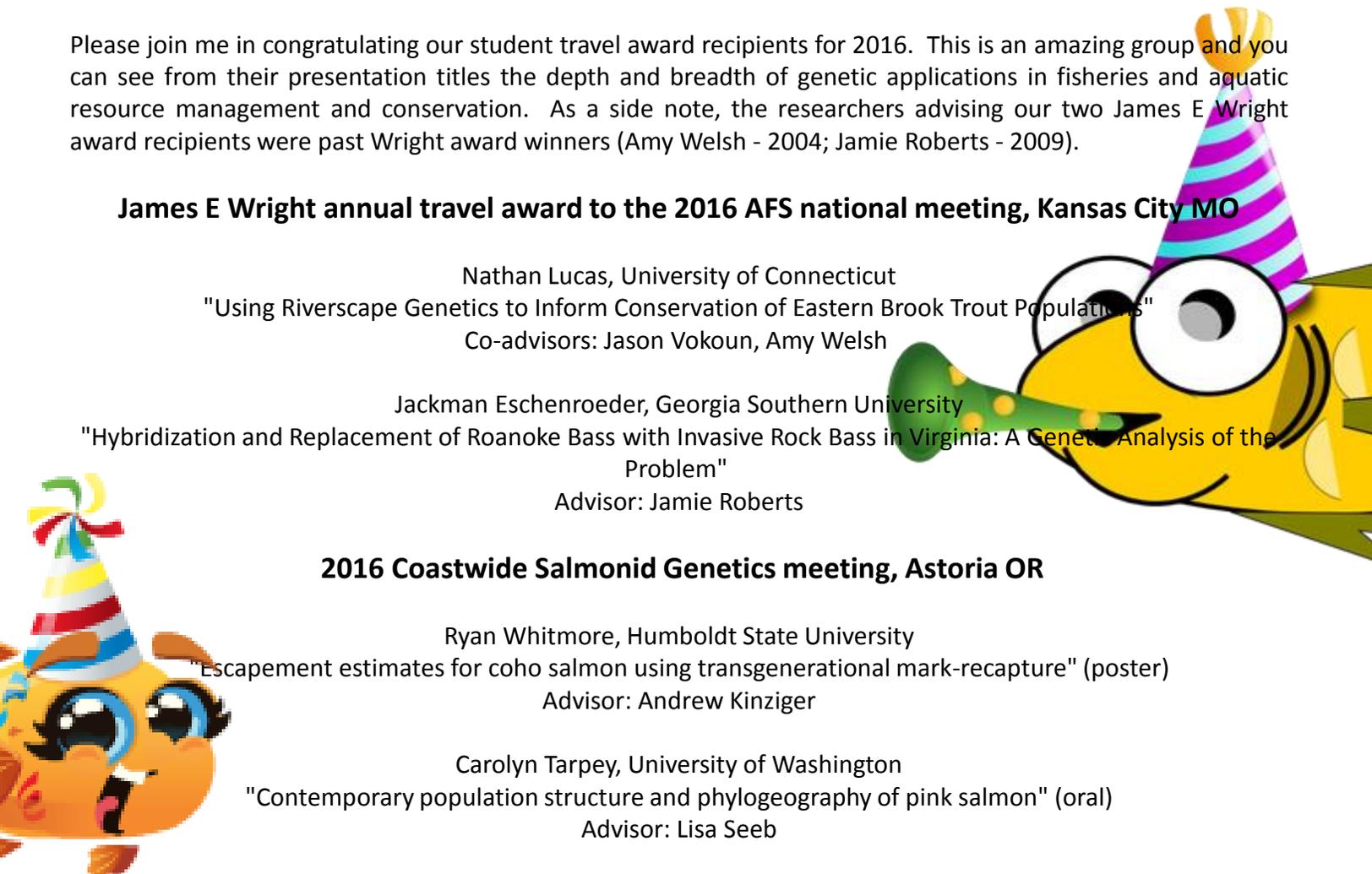
Ryan Whitmore, Humboldt State University
"Escapement estimates for coho salmon using transgenerational mark-recapture" (poster)
Advisor: Andrew Kinziger

Carolyn Tarpey, University of Washington
"Contemporary population structure and phylogeography of pink salmon" (oral)
Advisor: Lisa Seeb

2016 Fisheries Society of the British Isles annual meeting, Bangor University, UK

Taylor Wilcox, University of Montana
"Understanding environmental DNA detection probabilities: A case study using a stream-dwelling char"
Advisor: Michael Schwartz

Note: The James E Wright award is the section's only annual student travel award. The other student travel awards (to the 2016 Coastwide Salmonid Genetics and FSBI meetings) were requested by the respective program organizers. The Genetics Section welcomes and encourages requests for student travel stipends from organizers of meetings or symposia focusing on genetic applications to fisheries and aquatic resource management and conservation.



Publications

Paying attention to assumptions: Coalescing genes and reproductive skew in marine species

We have known for some time that family sizes in marine organisms are highly variable (Beckenbach 1994; Hedgecock 1994). Most marine invertebrates and fishes have type III life histories in which large numbers of eggs and larvae are spawned--sometimes in the tens of millions--but only a few survive. Most larvae succumb to predation, or are advected by currents away from nursery areas or suitable settlement areas. Hence, just a few individuals often contribute disproportionately to the next generation, a process called reproductive skew.

The effects of reproductive skew on effective population size have been documented in the fisheries literature by discrepancy between the genetic effective population of a population (N_e) and the census size (N_c). For many species, N_e can be as many as 5 or 6 orders of magnitude smaller than N_c . The much smaller value of N_e makes many commercially important marine species especially vulnerable to the loss of genetic diversity from overexploitation (Smith 1994, Kenchington 2003). For example, low genetic diversity was detected with microsatellite DNA markers in heavily fished populations of New Zealand snapper (Hauser et al. 2002).

Less well known are the effects of reproductive skew on the analysis of genetic data. Simulations are widely used to produce sample distributions to test statistical hypotheses. Analyses of mitochondrial DNA sequences employ simulations of gene genealogies created with coalescent algorithms. In the classic the forward-looking Wright-Fisher model, each individual potentially passes on two genes. Some individuals pass on only one gene or sometimes no genes. However, a more efficient way of simulating gene genealogies is to work backward from a collection of genes in a sample.

The most widely used coalescent algorithm is based on the Kingman coalescent (Figure 1, left), which, like the Wright-Fisher model of evolution, assumes a bifurcation at each node in the genealogy. Bifurcations, however, do not adequately capture the effects of reproductive skew (Tellier & Lemaire 2014) and do a poor job capturing the complexity of data for marine species, such as Atlantic cod (Eldon and Wakeley 2006, Árnason & Halldórsdóttir 2015).

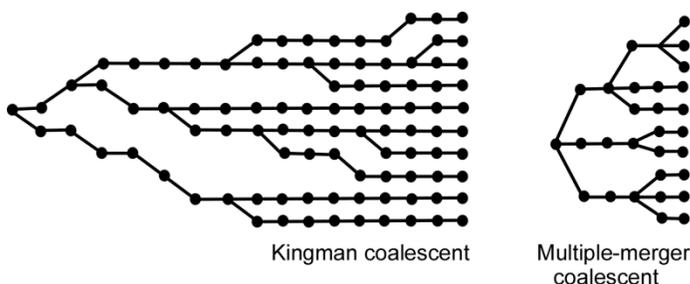


Figure 1. Hypothetical female gene genealogies under the backward-looking, Kingman model of coalescence (left) and under the multiple-merger coalescent model (right). Closed circles represent successfully reproducing individuals within a gene lineage. Extinct lineages are not shown in a coalescent genealogy.

Better coalescence simulations incorporate the effects of the profoundly large skew in the sizes of families in marine species by letting more multiple gene lineages coalesce to the same ancestor. Backward simulations under a multiple-coalescence model produce a fundamentally different gene genealogy (Figure 1, right). These figures show hypothetical gene genealogies that can be imperfectly captured by tracking mutations along the branches. The shallow, multiple-merger genealogy pictured here could produce a single star-shaped molecular

Publications

Paying attention to assumptions: Coalescing genes and reproductive skew in marine species *continued*

Continued from page 3

phylogeny, depending on the mutation rate. In general, time scales of multiple merger coalescents can be considerably shorter than for the Kingman coalescent (Schweinsberg 2003, Eldon et al. 2015, Árnason and Halldórsdóttir 2015). Fewer coalescences are required to reach the most recent common ancestor of the sample. These faster time scales have implications for the dating of population events with genetic markers.

Star-shaped mtDNA genealogies are almost universally observed in marine species, in which one or two high-frequency haplotypes are connected to numerous low-frequency haplotypes or singletons by only one mutation. This pattern appears in North Atlantic haddock (Figure 2, left; from Eiríksson 2015). Star-shaped gene genealogies produce a unimodal nucleotide mismatch distribution (Figure 2, right). These patterns are usually interpreted to indicate a recent population expansion, and warming after the Last Glacial Maximum is generally invoked to account



North Atlantic Haddock (NOAA)

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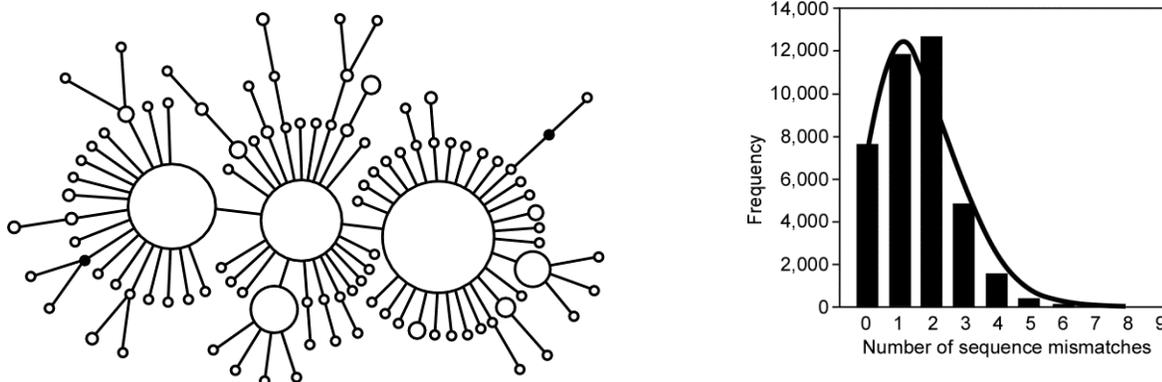


Figure 2. Mitochondrial DNA haplotype network (left) and mismatch distribution (right) in Atlantic haddock (from Eiríksson 2015). Left: A circle represents a haplotypes and size its relative frequency. Lines connecting haplotypes represent one mutation distance between haplotypes. Right: nucleotide mismatch distribution (bars) showing the expected distribution (solid line) after a population expansion. Haddock has a type III life history pattern, in which a large number of larvae, often in the millions, are produced, but offspring from only a few families survive.

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Publications

Paying attention to assumptions: Coalescing genes and reproductive skew in marine species *continued*

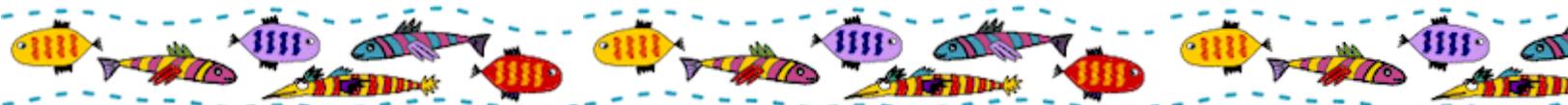
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Unfortunately, a demographic explanation for star-shaped genealogies may not be correct in all cases. Other mechanisms can produce the same pattern. Most researchers still use a coalescence model that may not be appropriate for their species. The reason for this is the pervasive use of the Kingman coalescent in software. Only now are programs being developed to accommodate species with large variances in reproductive success (<http://page.math.tu-berlin.de/~eldon/programs.html>; <http://www.eddiesalinas.com/COMET/>). Many population geneticists in AFS strive to provide information to management, and genetic markers have been invaluable for delineating stock boundaries to support stock assessments and for identifying declining genetic diversity in overexploited populations. However, the use of the Kingman coalescent for marine species casts doubt on many historical biogeographic models and estimates of population parameters.

Article by Stewart Grant, PhD

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Workshops

7th Annual Workshop on Genomics

8-21 January 2017

Czech Republic

Application Deadline: 15 September, 2016 is the preferred application deadline, after which time people will be admitted to the course following application review by the admissions committee. However, later applications will certainly be considered for admittance or for placement on a waiting list. Registration Fee: \$1800 USD. Fee includes opening reception and access to all course material, but does not include other meals or housing. Special discounted pricing has been arranged for hotels, pensions and hostels. Information regarding housing and travel will be made to applicants following acceptance. APPLY HERE: <http://evomics.org/2017-workshop-on-genomics/> Useful Links: Direct Link to the Full Workshop Schedule: <http://evomics.org/workshops/worksho...cesky-krumlov/> General Workshop information: <http://evomics.org> Frequently Asked Questions (FAQ) about the Workshop and Ěeský Krumlov can be found here: <http://evomics.org/workshops/faq/> Workshop Overview: The Workshop on Genomics consists of a series of lectures, demonstrations and computer laboratories that cover various aspects of genomics focusing primarily on the analysis of modern sequencing data. Faculty are chosen exclusively for their effectiveness in teaching theory and practice. The course is designed for established investigators, postdoctoral scholars, and advanced graduate students. Scientists with strong interests in the uses of modern sequence data, analytical methods, and the use of modern sequence data to study non-model organisms, variant detection and analysis, genome visualization tools and related areas are encouraged to apply for admission. Lectures and computer laboratories total ~90 hours of scheduled instruction. No programming experience is required. Topics to be covered include: - Sequencing technologies - Genomics study design - Manipulation of sequence data using the command-line and quality assessment and control techniques - Analyzing genomic data in

the "cloud" using Amazon Web Services (AWS) - Assembly and alignment: basic analyses used for de novo and re-sequencing studies - The use of next-generation sequence data to study non-model organisms - RAD (Restriction site Associated DNA) sequence analysis - Metagenome analysis (with WGS and amplicon) - Evolutionary genomics Co-directors: Naiara Rodríguez-Ezpeleta, Dag Ahren, Scott A. Handley, Konrad Paszkiewicz, and Karin Rengefors For more information and online application see the Workshop web site - <http://evomics.org> "Handley, Scott" <shandley@pathology.wustl.edu>

14th Annual Ecological Genomics Symposium

28-30 October, 2016

Kansas City, MO

This year marks the 14th anniversary of the Ecological Genomics Symposium. We have put together an outstanding lineup of ten speakers. Symposium details can be found at <http://ecogen.k-state.edu/symposia/2016/2016.html>. The meeting will convene at 7:00 p.m. on Friday, October 28, and conclude at Noon on Sunday, October 30.

REGISTRATION: Please register online today at: <http://ecogen.k-state.edu/symposia/2016/2016registration.html>.

You may also register to attend the optional Saturday night banquet for an additional fee of \$50. POSTER ABSTRACTS: Poster topics should be related to the field of Ecological Genomics. A LIMITED NUMBER OF SUBMITTED POSTER ABSTRACTS WILL BE SELECTED FOR ORAL PRESENTATIONS. Instructions for submitting your abstract online are at:

<http://ecogen.k-state.edu/symposia/2016/2016abstract.html>.

DEADLINE to be considered for oral presentation: September 16, 2016. VENUE: The symposium will take place at the Kansas City Marriott on the beautiful Country Club Plaza in Kansas City, Missouri. Reserve your hotel room online by visiting the Symposium website. Deadline: October 7, 2016.

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Workshops continued

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14th Annual Ecological Genomics Symposium

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FEATURED SPEAKERS: · Hans Hofmann, University of Texas at Austin · Kirsten Hofmockel, Iowa State University · Robin Hopkins, Harvard University · Christian Landry, Département de biologie, Université Laval, Québec, Canada · Blake Matthews, Eawag, Swiss Federal Institute of Aquatic Science and Technology · Suzanne McGaugh, University of Minnesota · Geoffrey P. Morris, Kansas State University · Kenneth M. Olsen, Washington University in St. Louis · Amy Toth, Iowa State University · James R. Walters, University of Kansas

DEADLINES: Friday, 9/16 Early Registration at discounted rates Friday, 9/16 Poster Abstracts for oral presentation consideration Friday, 10/7 Hotel Reservations Friday, 10/21 Poster Abstract for poster presentation ADDITIONAL INFORMATION will be posted on our website, <http://ecogen.k-state.edu/symposia/2016/2016.html>, as details are finalized. FUNDING for this symposium is provided by Kansas State University and Genome. Jennifer Rhodes <jenniferrhodes@ksu.edu>

Calendar

SEPTEMBER 2016

19th-23rd Meeting. ICES Annual Science Conference. Riga, Latvia.

29th-Oct 1st Meeting. 4th International Conference on Aquaculture & Fisheries. London, UK.

OCTOBER 2016

14th Meeting. 14th annual Ecological Genomics Symposium. Kansas City, MO.

2nd -6th Conference. International Trout Congress. Bozeman, MT.

28th – 30th Symposium. 14th Annual Ecological Genomics Symposium. Kansas City, MO.

NOVEMBER 2016

28th – 30th Meeting. 4th International Conference on Fisheries and Aquaculture. San Antonio, TX.

DECEMBER 2016

12th -16th Meeting. AGU's 2016 Fall Meeting-Damming Tropical Rivers. San Francisco, CA.

JANUARY 2017

8th -21ST Workshop. 7th annual workshop on genomics. Czech Republic.

20th Deadline. Symposium proposals due for the 147th annual AFS meeting.

Presidents message continued

Continued from page 1

For those of you traveling to Kansas City for the AFS annual meeting (August 21-25) I hope you will also attend the Genetics Section business meeting and social. This year our meeting will be on Monday, August 22 at 5:30p in the Chouteau A room of the Sheraton Kansas City. The time and venue for the social will be announced soon via the Genetics Section listserv.

Finally, I would like to thank a few members in particular for their help and time commitment during the last two years: Meredith Bartron (past president), Wendylee Stott (president-elect) Amy Welsh (secretary/treasurer, James E Wright Award committee chair) Joy Young (newsletter editor), Kristen Gruenthal (website manager), Helen Neville (membership committee chair and Early Career Award committee chair), Ken Currens (Stevan R Phelps Award committee chair), Andrea Drauch-Schreier (James E Wright Award committee chair).

Jobs

Graduate positions

M.S. or Ph.D. Graduate Research Assistantship on genetic marker-assisted management of Virginia sportfishes. Seeking a motivated and hardworking M.S. or Ph.D. candidate to work on application of population genetics to define the most appropriate units for fishery management at the regional scale. This position is funded for three years, and the student will be supported by a research assistantship. A doctoral student may expect to serve as a teaching assistant for one or two semesters during the doctoral program.

The goal of this study is to conduct population genetic studies of Striped Bass and Walleye. For Striped Bass, the objectives are to: 1. assess ancestry, genetically effective population size, and inbreeding of selected Striped Bass populations in Virginia, 2. gain understanding of how Virginia populations fit within the regional population genetic context, and 3. against that background, formulate genetically cognizant recommendations for management of Virginia Striped Bass populations. For Walleye, the objectives are to: 1. continue the existing program of genetic marker-assisted selection for New River Walleye, 2. define a more precise protocol for marker-assisted selection of New River Walleye, 3. evaluate the success of the marker-assisted selection and hatchery-based augmentation program to date, 4. Characterize the demography and genetic character of Tennessee and Big Sandy drainage Walleye stocks, and 5. assess genetic differentiation among regional Walleye populations.

Qualifications: Minimum qualifications include a B.S. or M.S. in fisheries, a related field, or genetics, as well as competitive GPA and GRE scores. Candidate should have a strong work ethic, ability to work independently and as part of a team, advanced problem-solving skills, high motivation, and deep underlying interest in applied population genetics. Experience with molecular genetic markers is highly desirable. **Stipend:** \$21,636 for M.S. student and \$22,884 for Ph.D. student, plus tuition and student health benefits. **Closing date:** As soon as suitable candidate is found. Review begins immediately.

Expected starting date: Fall semester 2016 or Spring 2017. **To apply:** Interested applicants should submit a letter of interest, contact information for three references, unofficial transcripts, and CV to: Dr. Eric Hallerman (ehallerm@vt.edu; please put "MAS of sportfishes" in the subject line). The selected applicant will need to apply to the Virginia Tech Graduate School before acceptance.

PhD Student position in Fish Evolutionary Ecology, Alternative life histories: evolutionary ecology and genetics of facultative anadromy in Brown Trout. Cork, Ireland. We seek a highly motivated graduate who wants to gain a PhD in the area of evolutionary ecology/genetics working in collaboration with scientists at University College Cork (UCC) the Marine Institute of Ireland and Queens University Belfast (QUB). This 4 year position is funded through a European Research Council (ERC) Starting Grant and will attract an annual tax-free stipend of euro 18000 plus an amount equivalent to EU fee rates (non-EU members may apply but would need to cover extra fees themselves). What it's about: Understanding how and why individuals develop strikingly different phenotypes and life histories in variable environments is a major goal in evolutionary ecology. It is also a prerequisite for conserving important biodiversity within species and predicting the impacts of environmental change and management interventions on natural populations. This PhD will form part of a larger ERC-funded research program to understand the causes and consequences of facultative anadromy in brown trout (*Salmo trutta*) the phenomenon whereby some individuals in a population migrate to the sea for part of their lives while others remain resident in freshwater and never go to sea. See <http://tinyurl.com/z7uxs5r> for a recent review. The successful candidate will be involved in a large-scale reciprocal transplant, field experiment where the goal is understand how genes and environment interactively determine alternative life histories. *Continued on page 9*

Jobs continued

Graduate positions continued

Continued from page 8 A background in or familiarity with the concepts of quantitative genetics would be particularly useful and there is also ample scope and resources for developing population/landscape genomics or gene expression approaches to probe the genetic basis of anadromy/migration and associated traits. The student will be supervised by Drs Tom Reed (UCC) and Phil McGinnity (UCC and Marine Institute) and will work in a growing team of salmonid researchers with a broad network of collaborators across academic and governmental institutions in Ireland and abroad. The student will be primarily based at the School of Biological Earth and Environmental Sciences (BEES) at University College Cork (UCC) in the south of Ireland which offers a vibrant and diverse research environment. The student will also be expected to spend periods of time at the Marine Institute's Newport Catchment Facility (<http://tinyurl.com/j5o4d8a>). Candidates should possess at minimum a 2.1 BSc (Hons) degree in a relevant discipline (e.g. Ecology Evolution, Zoology, Genetics). Applicants must be self-motivated with good numerical communication, organizational and writing skills. Experience working with fish would be advantageous but not essential; as would molecular laboratory and/or bioinformatics skills. The studentship is open to non EU students though only EU fee rates will be covered. Informal Enquiries: Please contact Dr Tom Reed (Email: treed@ucc.ie) Remuneration: This position covers an amount equivalent to EU fee rates (non-EU members may apply but would need to cover extra fees themselves) plus a tax-free stipend of 18000 p.a. To apply please send by email a CV details of 2 referees, and an accompanying letter of application outlining your relevant experience and why you want to do this studentship to Dr T. Reed School of Biological Earth & Environmental Sciences, University College Cork, Enterprise Centre Distillery Fields, North Mall, Cork, Ireland. Email: treed@ucc.ie Dates: Start date autumn/winter 2016. Webpage of PI: <http://research.ucc.ie/profiles/D026/treed> treed@ucc.ie

Post doc positions

Postdoctoral Fellow – Wildlife & Fisheries Biology (DFNR 16-0087). The West Virginia University Research Corporation (WVURC) seeks to hire a Postdoctoral Fellow – Wildlife & Fisheries Biology for the Division of Forestry and Natural Resources at West Virginia University. This position supports the Appalachian Freshwater Initiative, an NSF EPSCoR funded project within the School of Natural Resources. The incumbent will develop and test strategies to improve and streamline environmental DNA (eDNA) sampling and laboratory techniques for assessing amphibian, fish, and invertebrate assemblages in headwater Appalachian streams and wetlands. Specifically, the incumbent will advance WVU capabilities in eDNA technology including sampling, handling, and storage, protocols; increasing reliability of survey and research methodology; and increasing efficiency of eDNA extraction and processing techniques. The incumbent will perform primary data collection in the field and the lab on presence of wetland and aquatic organisms. Substantial contributions to scholarly outputs including publications, presentations, and grant applications is expected. This position will contribute to a multi-disciplinary and multi-institutional study designed to improve management of aquatic environments in West Virginia

Qualifications: A PhD in wildlife, fisheries, ecology, genetics, or a similar field, and experience in contemporary eDNA techniques and sampling techniques for organisms in aquatic or wetland environments are required. Preference will be given to candidates with previous publications on vertebrate genetics. **Salary:** Competitive salary and benefits offered. **To apply:** For a complete job description and to apply for this position, please visit <http://hr.research.wvu.edu> and click on the "View Jobs" link. AA/EOE/Minorities/Females/Vet/Disability/E-verify compliant employer

Jobs continued

Post doc positions continued

Post-Doctoral Fellow, Catfish & Carp Genetics/Genomics. This is a 12-month non tenure-track position at Auburn University, AL. The successful candidate will work on a variety of applied genetic and genomic projects on catfish and carp employing techniques such as RAD-seq, RNA-seq, electroporation and microinjection, gene editing analyses, gene cloning, maxi preps, PCR, qPCR, DNA and RNA analysis, Southern blotting, primer design, sgRNA design and targeted SNP genotyping. For a FULL description, please visit <http://aufacultypositions.peopleadmin.com/postings/1728>. **Qualifications:** We are seeking a highly motivated and creative post-doctoral researcher with a PhD in Cell Biology, Molecular Biology, Genomics, and/or a PhD in an agricultural science with a dissertation emphasis on genetics and/or genomics. Experience in molecular biology techniques is required. **Salary:** Commensurate with education and experience. **End date:** Review of applications will begin July 1, 2016 and will continue until the position is filled. **Contact:** Dr. Rex Dunham/dunhara@auburn.edu. Applicants must apply for the position electronically at <http://aufacultypositions.peopleadmin.com/postings/1728>. Auburn University is an EEO/Vet/Disability

Postdoctoral Fellow Position with Fisheries and Oceans Canada on modelling the impacts of Atlantic salmon aquaculture on wild Atlantic Salmon populations. Overview: Fisheries and Oceans Canada is seeking applicants for a full-time postdoctoral fellow position on modeling relationships between wild and farm escaped Atlantic salmon in the North Atlantic. This is a 24-month position that will be based at the Bedford Institute of Oceanography, Halifax Nova Scotia, beginning in the fall of 2016. The position may be extended contingent upon performance and funding. The PDF will be mentored by Dr. Ian Bradbury, and directly collaborate with both students and fellows in the lab as well as an international modeling team working on the topic.

The successful candidate will undertake analyses and modelling to investigate the genetic and ecological impacts of escaped farmed salmon on wild populations. This project will directly inform management and conservation efforts of Atlantic salmon in Atlantic Canada. Requirements: Candidates must have a Ph.D. in fisheries science, population genetics, genomics, oceanography or a related field. The position requires strong mathematical, and computational skills, and previous experience with individual based models, or population dynamics models would be an asset. Candidates should have experience in the R and/or MATLAB programming languages. In addition, candidates are expected to have a demonstrated ability to work independently and possess strong organizational and communication skills. The successful applicant will be expected to lead and contribute to journal articles, reports, and presentations to both stakeholders and scientific audiences. As this position will collaborate with an international team, the candidate should be willing and able to travel domestically and internationally on a regular basis. To apply: Please submit a CV, and letter of interest to Dr. Ian Bradbury - ibradbur@me.com, Review of applications will begin on July 30th, 2016, but the position will remain open until filled. Questions should be referred to ibradbur@me.com. Ian Bradbury <ibradbur@me.com>

Comic

Pipette Tip Personalities

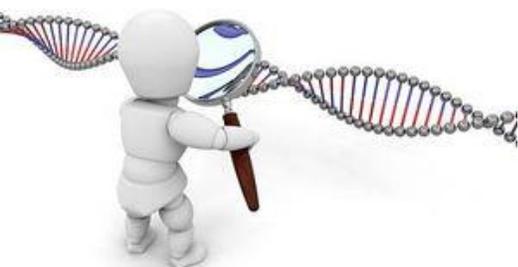


Jobs continued

Professional positions

Assistant Marine Scientist. South Carolina Department of Natural Resources, Charleston, SC. **Position summary:** The successful candidate will join our population genetics team to contribute to our population genetic and molecular tool research projects on marine and freshwater fishes in areas of stock enhancement, fisheries management, conservation, and tool development. Specific duties will include field and laboratory research, data collection and analysis, collection and data management, preparation of reports and presentations, authoring technical manuscripts, coordination and supervision of team personnel, proposal preparation, and budget management. Some projects will include work on multi-disciplinary teams. **Requirements:** Applicants will be required to have an Ph.D. degree in biology, marine science, or genetics. Individuals should have demonstrated abilities to conduct population genetics research including experimental design, data collection and analyses, and report preparation. Publication record and experience with microsatellites and automated sequencing systems required; successful grant funding record preferred. Applicants must also have knowledge of marine and/or freshwater fishes of the southeastern US and the capability to work independently. Strong communication, quantitative, organizational, computer, writing and inter-personal skills required. **Other preferred knowledge, skills and abilities:** Valid SC driver's license and a copy of driving record are required. Applicant must have dependable transportation and a satisfactory driving record. A current CV is requested to supplement the required state application. **To apply:** Submit a state application and letter of interest via the SC State Job Website (www.jobs.sc.gov). For more information, contact Tanya Darden (dardent@dnr.sc.gov; 843-725-4876).

Lecturer in Molecular Ecology and Genomics. Bangor University, School of Biological Sciences, UK. **Position summary:** We invite applications to this permanent full time appointment in the School of Biological Sciences. The successful candidate will be expected to make a significant contribution to molecular ecology and genomics research in the School and College, and to develop a research programme in their specialist area that will attract external funding and international recognition. They will also contribute to the teaching of Biology and related subjects at undergraduate and postgraduate levels. The successful candidate will be educated to PhD standard or equivalent and have previous experience across a broad range of sub-disciplines within biological science. To match our vision for the development of biology in the school we would particularly welcome candidates to carry out research in the area of molecular ecology and genomics. The applicant would be expected to contribute to teaching, e.g. in molecular ecology and genomics/bioinformatics, or in forensic biology, incorporating quantitative and statistical approaches from the cellular to community level. The post holder will be expected to make a strong contribution to our existing ethos of inter-disciplinarity and team work in research and teaching, enhancing and complementing our existing areas of expertise. The appointment will be made in the range of Lecturer 1 31,656 - 37,768 (Grade 7) or Lecturer 2 38,896 - 46,414 (Grade 8) per annum, depending on previous experience. **Salary:** Grade 7: 31,656-37,768 or Grade 8: 38,896-46,414 p.a. **To apply:** Informal enquiries can be made by contacting Prof G Carvalho (tel: +44 (0) 1248 382100, e-mail: g.r.carvalho@bangor.ac.uk, or Dr. S Creer (tel: +44 (0) 1248 382302), email: s.creer@bangor.ac.uk from the 1st September onwards. Please include the above job reference number BU01253 in your header title for email enquiries. Interviews will be scheduled for the second half of October, or early November 2016. Rhif Elusen Gofrestredig 1141565 - Registered Charity No. 1141565 John Mulley <j.mulley@bangor.ac.uk>



Farewell

I have enjoyed working with and learning from many genetics section members for the past four years, and am ready to move on to the next phase in my life. Unfortunately, due to time constraints and increasing work duties, I am not able to continue as newsletter editor.

If you are interested in picking up the torch, please contact one of the section officers listed below. I am happy and very willing to help to make the transition as smooth as possible. This includes passing on the newsletter templates, and tips, trips and resources for generating material.

It has been an amazing journey. I volunteered to edit the newsletter at my first genetics section meeting at the 142nd annual AFS meeting in Minneapolis, MN. I was in the middle of my graduate work and wanted to get more involved in the society and network with like-minded scientists. I took over the newsletter from Dr. Joel Carlin after 14 years of incredible service and commitment. The shoes seemed very large, but I enjoyed the challenge of seeking new and fresh material for each newsletter.

It has indeed been a rewarding experience. I thank you all, and look forward to seeing you at the meetings!

Joy Young, PhD

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This could be YOU!!!

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