



The American Fisheries Society Genetics Section Newsletter

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President's message

Depending on where you reside, spring or summer has finally arrived. For many, the change of seasons corresponds with the end of another semester, the start of field season, or time to devote to lab work. It also means getting research wrapped up and analysis



Meredith Bartron, AFSGS President

completed for presentations at the annual AFS meeting in early September in Little Rock, Arkansas. It's a busy time within the section as well. We're still searching for membership for the Hall of Excellence committee, as well as soliciting nominations for our first set of inductees. Committees such as the Stevan Phelps Award committee are reviewing papers for excellence in genetic research, and the Wright Award committee will soon be reviewing student applications for student travel awards to Little Rock. In addition to your own busy schedule for the next few months, please consider participating in these or other Genetics Section activities. And don't forget to use the Genetics Section list serve to announce jobs, research news, or issues of interest. Have a great summer and see you in Little Rock!

-Meredith Bartron

Feature article by John Hargrove

Staying connected in the jungle: gene flow and patterns of connectivity in a migratory Amazon fish

Few places in the world exhibit the levels of biodiversity and endemism as is found in the Amazon basin. With over 3000 fish species distributed throughout a complex network of rivers, lakes, and seasonal flood plains, it is not surprising to find many fish species have

evolved specific life history strategies to utilize varying habitat types. Examples of adaptations include ontogenetic shifts in habitat use, long distance migration to spawning grounds (up to 5,500 km!), and the modification of feeding apparatus to exploit terrestrially deposited food resources. Given the intricate relationships that have co-evolved through time between fish fauna *continued*
page 2

Feature article by John Hargrove continued

Continued from page 1 and their environment, minimizing fragmentation and alteration of aquatic habitats is a critical (though often underemphasized) element in ensuring healthy ecosystem function.

Colossoma macropomum, Cuvier 1818, known as gamitana in Perú and tambaqui in Brazil, are of both economic and ecological significance in the Amazon basin. Because of their large size (>1 m total length, >30 kg in weight) and widespread distribution throughout the Amazon and Orinoco basins, populations of gamitana have been commercially exploited since the late 1800's and are currently considered one of the most economically important species in the Amazon (Araújo-Lima and Goulding 1997). From an ecological perspective, gamitana serve an important role as consumers and dispersers of tropical tree seeds. Adults and large juveniles take up residence in flooded forest (várzea) habitats during the wet season where they utilize modified pharyngeal teeth to forage exclusively on seeds and nuts that fall into the water. Gut contents recovered from 144 individuals contained almost 700,000 intact seeds from 21 different plant species, and fine-scale movement patterns of wild gamitana revealed these fish disperse seeds long distances to habitats favorable for seed germination (Anderson et al. 2009).

Given the significance of gamitana to both humans and local plant-recruitment dynamics, we were interested in studying population genetic structure of gamitana for multiple reasons. First, information on stock structure for gamitana is limited, and second, documenting baseline data will be of increased importance as human populations expand and the likelihood of habitat fragmentation increases. In order to address this question, we collected samples from undisturbed habitats located in the Pacaya Samiria National Reserve (PSNR), located in eastern Perú (Figure 1). In total, 131 individual fish were collected from seven floodplain lakes located along a >100 km stretch of two river drainages, the Pacaya and Samiria Rivers, located within preserve boundaries. All samples were genotyped at 13

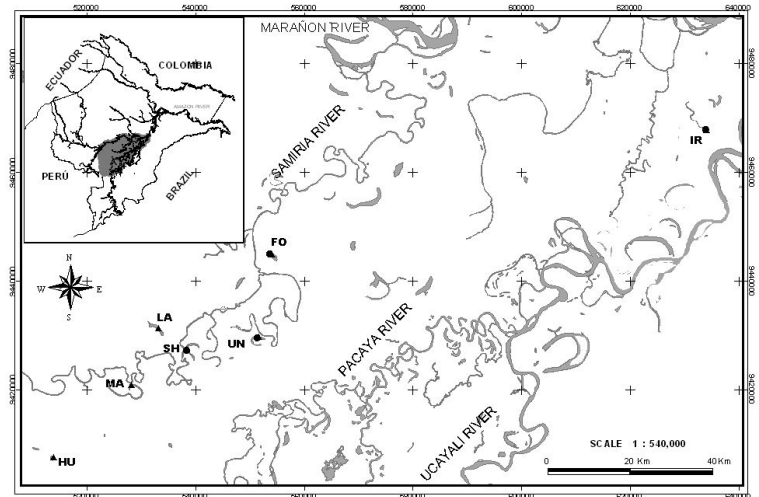


Figure 1. Pacaya Samiria National Reserve.

microsatellite loci to determine fine-scale structuring at the landscape scale and to test various migration models to determine the best fit model to explain the allelic patterns observed across populations.

We generated a variety of statistics to examine the level of differentiation between lakes, and differentiation was low overall regardless of estimator ($G_{ST} = 0.013$, $G'_{ST} = 0.087$, $D = 0.074$). All permuted statistics were smaller than those observed ($P = 0.0001$), indicating that despite low levels of differentiation, observed differences were still greater than expected under random mating. Using the Bayesian clustering analysis implemented in STRUCTURE v 2.3, we estimated the number of genetically differentiated clusters (with and without location priors) and determined that a single genetic cluster best explained the observed data ($K > 1$ displayed declining LnP vales and increased variance as the number of clusters increased). The most appropriate model of gene flow between gamitana sampling locations was tested using a Bayesian approach in MIGRATE. Five migration models were tested (model descriptions and results presented in Table 1) and model selection using log marginal likelihood (lmL) criteria indicated a stepping stone migration pattern among the Samiria River with no migration to the Pacaya

continued page 5.

Feature article by W. Stewart Grant

The 'Out of Asia' model of Red King Crab Evolution

We are all familiar with the Asian Indian story in its many guises of three blind men describing an elephant by touch. One man touches a leg and insists the elephant is a pillar. Another runs his hand along a tusk and insists it is a plowshare, and yet another mistakes the trunk for a snake. Each insists he is right. The wise person, however, knows they are examining different parts of the same animal.

We find a similar parallel in the use of various kinds of molecular markers to study population genetics of red king crab in the North Pacific (Figure 1). At one time, red king crab populations in the Bering Sea and North Pacific supported large harvests, which declined in the 1970s (Bechtol and Kruse 2009). The collapse of the fishery around Kodiak Island was particularly severe. This fishery was closed in the early 1980s and remains closed today. After the closure, management agencies supported genetics research to provide information on population structure. Genetic markers, together with population genetics theory, might be able to answer several questions. Did these population collapses affect genetic diversity? How connected are crab populations through larval drift? Would depressed populations be seeded from neighboring populations?



Figure 1. Red king crabs range across the North Pacific from the Northern Sea of Japan to Northern British Columbia. These king crabs commonly extend three feet across from one leg tip to the other.

The first genetic study of red king crab, made with allozymes, showed low levels of genetic

diversity within all the populations. Gene diversities were only about 1.5%, a value considerably lower than diversities in other marine invertebrate (Seeb et al. 1990). Russian geneticists subsequently surveyed allozyme variability in a population in the northern part of the Sea of Japan and found higher levels of genetic diversity than those found in Alaskan populations (Balakirev and Fedoseev 2000). However, it was uncertain whether NW Pacific populations were more diverse, or whether the larger estimate of gene diversity was due to the inclusion of a polymorphic allozyme locus that was difficult to score. Data for this locus had been excluded from the Alaskan dataset (Grant et al. 2011). Were there, in fact, regional differences in genetic diversity?

Allozyme data hinted at large-scale population structure, but this was largely based on a single, highly polymorphic locus (of 38 loci). Aleutian Island crabs showed a significant difference from those in Norton Sound in the northern Bering Sea, and from crabs in the Gulf of Alaska (GoA). A large sample from Bristol Bay was not available, but it was assumed that the sample from Norton Sound, which came from the same coast, was representative of crabs in Bristol Bay. Cluster analysis of the allozyme frequencies also showed that crabs in Southeast (SE) Alaska were different from other Gulf of Alaska crabs, but not all SE Alaska samples clustered into a single group. At best, allozyme markers gave us a blurred picture of genetic variability in red king crab and posed new questions. How deeply were red king crab population divided? Was it possible to infer ancestral relationships among populations?

In the 1990s, the Alaska Fish & Game lab used microsatellite DNA markers to estimate within- and between- population diversity. However, two problems diminished the usefulness of these markers. Like allozymes, only a few polymorphic loci could be developed for routine analysis. A second problem was that 'null' alleles from PCR primer failure plagued the analysis. *Continued page 6*

AFS Symposia Announcement

The Genetics Section has always been active in organizing symposia for the national AFS meeting. These symposia provide an opportunity for sharing our work with fellow geneticists but also provide us a chance to communicate with the broader AFS membership the increasingly important role that genetic principles and techniques play in research, management and conservation of fishery and aquatic resources. This year we have organized two symposia for the national meeting in Little Rock, Arkansas, September 8-12. Together, they highlight recent and future applications of genetic data in variety of fishery management and conservation contexts.



Jeff Olsen, AFSGS President elect

Applying genetic principles and technologies to the management and conservation of fishery and aquatic resources.

Chairs: Andrew Whiteley, Stew Grant, Marlis Douglas, Carol Stepien, Jeffrey Olsen.

Environmental DNA (eDNA) analysis – a new genetic tool for monitoring, managing, and conserving fishery resources and aquatic habitat.

Chairs: Jeffrey Olsen, Denise Hawkins, Meredith Bartron, Jon Amberg

I encourage you to attend the nation meeting in Little Rock and to attend both of the Sections' symposia. Information about the meeting, including all symposia and presentations, can be found at <http://afs2013.com/>.

Reminder National AFS!

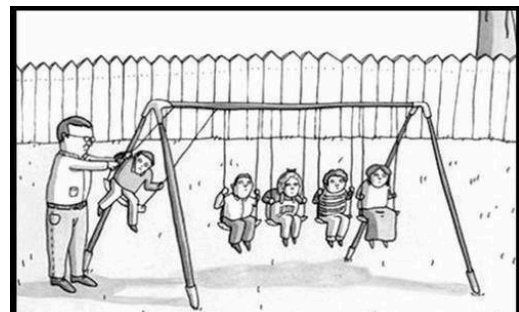


LITTLE ROCK • 2013

The Arkansas Chapter of the American Fisheries Society and 2013 AFS President John Boreman cordially invite you to attend next year's Annual Meeting, September 8-12, 2013, in the Natural State. The meeting theme is Preparing for the Challenges Ahead.

- Registration is now open!
- Visit www.afs2013.com for details

Comic



Why science teachers should not be given playground duty.

Anonymous cartoon reprinted from: Pinterest May 2013.

Feature article by John Hargrove continued

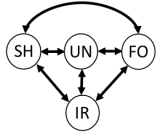

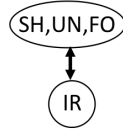
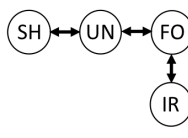
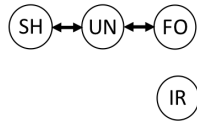
	M ₁	M ₂	M ₃	M ₄	M ₅
					
lnL	-17,491.45	-15,029.18	-26,288.23	-7373.30	-15771.99
Model rank	4	2	5	1	3
Difference from best model	-10,118.15	-7,655.88	-18,914.93	0	-8398.69
Model probability	<0.00	<0.00	<0.00	1.0	<0.00

Table 1. Log marginal likelihoods (lnL) using thermodynamic integration of two different gene flow models (M_i): M₁, full migration; M₂, panmixia; M₃, panmixia among three Samiria River samples (SH, UN, FO), with migration to Pacaya River sample (IR); M₄, stepping stone migration pattern among Samiria River samples, with no migration to IR; M₅, stepping stones migration among all four samples.

Continued from page 2 River best explained the observed data.

The findings of this research were surprising for several reasons. One, we predicted gene flow would most likely follow a model of panmixia as the only other published study to examine genetic diversity in gamitana described this species as panmictic at the Amazon Basin scale. Differences in marker selection (microsatellites vs. mtDNA sequences), scale of study (landscape vs. Amazon Basin scale), and metrics used to infer gene flow (model test vs. interpretation of fixation indices) likely explains some of the observed discrepancies. Second, specific life history characteristics of gamitana would seem likely to produce population level diversity resembling panmixia. Examples include the deposition of eggs into main river channels and subsequent passive transport of larvae to downstream habitats, long distance migrations, and historically large effective population size. These results suggest that maintaining habitat connectivity is important for maintaining gene flow in gamitana populations. Habitat fragmentation in the form of hydroelectric dams may obstruct adult migrations, destroy valuable feeding habitats, and place drifting eggs and larvae into subpar habitats. Our project provides an example of what genetic patterns exist in undisturbed habitats, and future studies should be conducted across landscapes differing in degrees of habitat conversion. Regional

protected areas like the PSNR may serve as regional sources for replenishing depleted areas for multiple fish species. Though a modest dataset, our study represent an important source of baseline information for resource managers faced with the challenging task of maintaining healthy populations of fish in an ever-changing landscape.

Specific details of this study are available in the February issue of Conservation Genetics (DOI 10.1007/s10592-012-0442-y).

John S. Hargrove, María I. Aldea-Guevara, James D. Austin

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Feature article by W. Stewart Grant continued

Continued from page 3 New primers were subsequently developed and used to study temporal and geographic variability (Vulstek 2011). Microsatellites defined two large groups of populations: those in western GoA and the eastern Bering Sea and those in SE Alaska. Interestingly, crab populations in SE Alaska showed lower levels of genetic diversity than populations in other areas (Figure 2). SE Alaska populations also

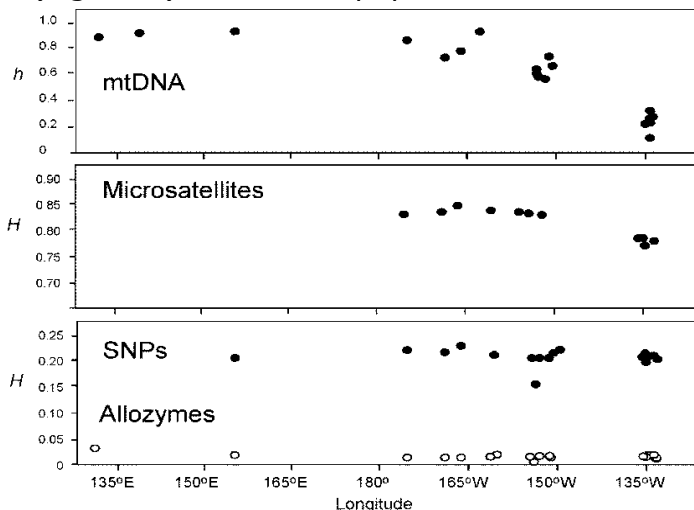


Figure 2. The distributions of genetic diversity among populations of red king crab across the North Pacific. For diploid loci, such as allozymes, microsatellites, and SNPs, heterozygosity (H) is the proportion of individuals in a population that are heterozygous, on average for the sample of genes. In mitochondrial DNA gene diversity (h) is an analogue of heterozygosity for haploid genes.

showed significant differences from one another, indicating reproductive isolation among the fjord populations. Some of these populations also showed temporal shifts, presumably due to random drift in small populations. On balance, microsatellites provided a sharper focus on some aspects of population structure, but other questions remained.

Anonymous single nucleotide polymorphisms (SNPs) were next used. SNPs are often detected with genomic scans using high throughput DNA sequencing. A survey of variability in 15 SNPs showed a similar genetic pattern as microsatellites, except a third geographic group appeared, consisting of crabs in Russia, the Aleutian Islands and Norton Sound (Grant & Cheng 2012). Surprisingly, no diversity gradient appeared

across the North Pacific (Figure 2). The absence of a gradient is likely due to an ascertainment bias in the selection of SNPs with high-frequency minor alleles, a problem that has been noted in other studies.

Next, 'barcode' mitochondrial (mt) DNA sequences showed a much steeper gene diversity gradient across the North Pacific than did the other molecular markers, with the highest diversities in the NW Pacific (Grant & Cheng 2012) (Figure 2). These results, together with the results for the other markers, supported an 'out of Asia' model of early dispersal, in which the 'mitochondrial eve' of red king crabs lived in the NW Pacific (Figure 3). MtDNA gives an alternative view of genetic structure because mitochondria are inherited maternally without recombination. Hence, mutational relationships among haplotypes and geography give insights into the dispersal histories of crab populations and the effects of Pleistocene glaciations. The groups of red king crabs appear to have originated as a result of isolation in glacial refugia.

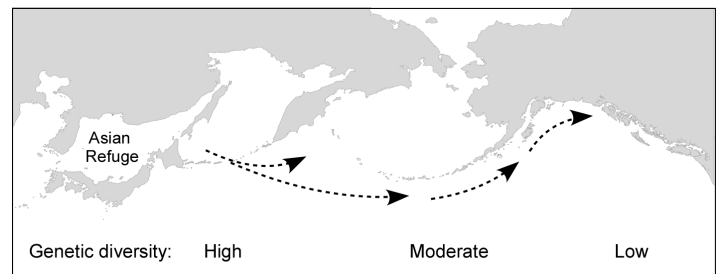


Figure 3. The 'out of Asia' hypothesis for red king crab. Populations in Southeast Alaska are at the end of the dispersal pathway. Additionally, strong allele-frequency differences and temporal shifts indicated that Southeast Alaska populations are isolated from one another in fjords and are susceptible to local extinction. This contrasts with populations in the western Gulf of Alaska and Bristol Bay, which showed virtually no genetic differences from one another.

As new molecular markers are developed, we often read the assertion that 'this is the marker of choice'. However, each new marker merely gives a complementary view of population structure and evolutionary history, because of differences in mutations rates and modes of inheritance among the markers. Population studies of red king crabs have kept pace with the development of new markers, *continued page 7*

Feature article by W. Stewart Grant continued

Continued from page 6 which together reveal the depths of evolutionary history and present-day structure. The results for each marker are blinkered by inherent limitations, so that only the analysis of all of them gives a complete picture of the 'elephant'.

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Thanks to Marianne Grant and Bert Lewis for comments.

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SDAFS Call for Workshops and Symposia



The South Carolina chapter of AFS and the Planning Committee for the 2014 Southern Division AFS Meeting invites you to historic Charleston, South

Carolina on January 23-26 for the 2014 Southern Division Spring Meeting. The Planning Committee is in the process of putting together an exciting program of Workshops, Symposia, and Technical Sessions as well as some great social events. The meeting will be held at the historic Francis Marion Hotel in the heart of downtown Charleston. Social events are going to include the student/professional mixer, trade show, student/mentor lunch, and a banquet at the South Carolina Aquarium. There is so much to do in Charleston you may even want to come early or stay late.

This is the first call for Workshops and Symposia. There have already been numerous

inquiries for Workshops and Symposia, so if you have a great idea for either, get them in soon as space is already becoming limited. Proposals for Workshops must include subject title, description (300 words or less), sponsoring organization (if relevant), chairperson or instructor, and proposed length (half day or full day). Some of the Workshops already proposed include: fish passage, dam removal, stock assessments, catfish aging, and telemetry. Proposals for Symposia must include title, subject and description (300 words or less), chairperson(s), and proposed length (half day, full day, etc.). Some of the Symposia already proposed include: Biology of Sturgeon, Reef Fish, Offshore Wind Impacts, State Wildlife Plans, and Black Bass.

Submittals for Workshops can be made at: <https://afs.confex.com/afs/sb14/work/sessions/index.cgi>

Submittals for Symposia can be made at: <https://afs.confex.com/afs/sb14/symp/sessions/index.cgi>

Award Announcement

Apply for the AFS Genetics Section Graduate Award in Memory of



James E. Wright



The Genetics Section of the American Fisheries Society is pleased to announce the James E. Wright Graduate Award. This award is presented annually by the Genetics Section at the AFS Annual Meeting and is intended to recognize excellence in graduate-level work in fisheries genetics and to assist graduate students with travel to the national meeting. The section anticipates awarding an award for \$500 to attend the 2013 AFS annual meeting in Little Rock, Arkansas. All graduate students are encouraged to apply.

Selection will be based on the following criteria:

1. Potential for success in research in fisheries genetics (60%)
2. Anticipated contribution to upcoming annual meeting, e.g. paper, poster, or other contribution (20%)
3. Service to the Society, its Sections, or Chapters (10%)
4. Demonstrated need for travel assistance (10%)

Application Procedure:

1. Applicant must be a full or affiliate member of the Genetics Section at the time of application.
2. Application package should include:
 - a. A brief curriculum vitae including anticipated degree, date of completion, and career goals.
 - b. A statement of the thesis or dissertation and abstract of progress to date.
 - c. The names and contact information for two references familiar with the applicant's background and abilities.
 - d. A statement of previous service to the Society, its Sections, or Chapters, and need for travel assistance.
 - e. A statement addressing anticipated contribution to the upcoming annual meeting.

Deadline for application is: **June 17, 2013**
All application materials should be sent via email to:
Amy B. Welsh, email: amy.welsh@mail.wvu.edu

Editor's blurb

Thank you to everyone that helped contribute to this edition of the newsletter! Your contributions makes my job a million times easier (yes, that much easier). Please continue to send me announcements, articles, photographs, comments, suggestions, critiques- basically anything you would like to see published or modified in the newsletters. As the National AFS meeting approaches, it might be a good idea to coordinate any efforts for social media broadcasting. I am calling for all tweeters, Instagram users, Facebook followers and all other media outlets currently in use! If you are planning on using social media during the meeting, let me know and I will send out the word through the newsletter so people can follow you. I would also like to propose a common hashtag to link all the information together: #AFSGS2013

Calendar

JUNE 2013

15th-20th Meeting. The World Conference on Stock Assessment Methods for Sustainable Fisheries in Boston, MA.

17th Application due. AFS Genetics Section Graduate award in memory of James E. Wright

JULY 2013

7th-11th Meeting. Society for Molecular Biology and Evolution (SMBE) in Chicago, IL

10th-15th Meeting. ASIH meeting in Albuquerque, NM

14th-19th Meeting. GRC on Ecological and Evolutionary Genomics. University of New England, Biddeford, Maine.

21st-25th Meeting. 7th International Symposium on Sturgeon in Nanaimo, BC, Canada.

AUGUST 2013

1st Abstract due. Wild Trout XI

9th Application due. AFS Best Student Poster Award from the Fisheries Information and Technology Section (FITS)

SEPTEMBER 2013

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

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

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

OCTOBER 2013

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

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

January 2014

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

Symposia

Graduate and Professional Course Non-Invasive Genetic Techniques in Wildlife Conservation

1-7 June 2013. Smithsonian-Mason School of Conservation At the Smithsonian Conservation Biology Institute, Front Royal, VA.

This workshop will review the basics of theory in the field of evolutionary quantitative genetics and its connections to evolution that is observed at various time scales. Visit <http://academy.nescent.org> or contact academy@nescent.org for more information

Evolutionary Quantitative Genetics

5-10 August 2013. National Evolutionary Synthesis Center, Durham, NC.

This course is an introduction for graduate students and professionals to the applications, benefits, and drawbacks of non-invasive genetic techniques to wildlife conservation. Visit <http://SMconservation.gmu.edu> or contact SCBITraining@si.edu for more information.

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/>

Applying Genetic principles and Technologies to the Management and Conservation of Fishery and Aquatic Resources

(Annual AFS Meeting)

Environmental DNA (eDNA) Analysis – a New Genetic Tool for Monitoring, Managing, and Conserving Fishery Resources and Aquatic Habitat

(Annual AFS Meeting)

8-12 September. Statehouse Convention Center, Little Rock, AR.

Jobs

Graduate positions and postdocs

GRADUATE RESEARCH ASST-PH.D. Hines Lab at Pennsylvania State University. Candidate will study the evolutionary genetics and developmental mechanisms underlying mimetic color variation in bumble bees. For more information on this project and other research directions in the lab visit

<http://www.personal.psu.edu/hmh19/>. Interested students should email Dr. Heather Hines (hmh19@psu.edu) with a statement of interest and curriculum vitae.

GRADUATE POSITION PH.D. Department of Evolutionary Biology, Uppsala University. Starting date 15th of August. The candidate will focus on the causes and consequences of paternal non-genetic effects transferred from the father to the offspring. You will use the zebrafish as a model system to investigate such sperm-mediated epigenetic effects by combining experimental work with next generation sequencing methods to elucidate the possible mechanisms. For more information visit <http://www.ebc.uu.se/Research/IEG/evbiol/research/Immler/>.

GRADUATE POSITION M.SC. OR PH.D. The Conservation Genetics Lab at the Great Lakes Institute for Environmental Research. Two positions. The candidate will explore the population genetics of aquatic invasive species. Position begins September 2013. For more information please contact Dr. Daniel Heath (heath@uwindsor.ca).

POSTDOC. Marine station of Banyuls/mer, France. Candidate will investigate how photoperiod and temperature interact in the synchronization of Salmonids physiological function. For more information please visit http://evol.mcmaster.ca/~brian/evoldir/PostDocs/CNRS_France.FishAdaptation.

Would you like to see a position advertised here? Let me know!
Joy.Young@myfwc.com

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What are those question marks? Your opportunity to volunteer!!!