

# Tyler Duncan Hether

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## Education

Ph.D. Bioinformatics & Computational Biology, University of Idaho. 2016

*Dissertation:* “Genetic Networks, Adaptation, & the Evolution of Genomic Islands of Divergence”.

M.S. Biology, University of Central Florida. 2010

*Thesis:* “Using landscape genetics to assess population connectivity in a habitat generalist”.

B.S. Biology, University of Central Florida. 2006

## Programming & Scripting Languages (in descending order of expertise)

R, bash/linux,  $\text{\LaTeX}$ , C++, python, mathematica, & perl

## Employment

University of Oregon 2016–present.

University of Idaho 2010–2016.

University of Central Florida 2006–2010.

## Research Support

Eugene Magelby Natural Sciences Scholarship, 2015–2016

NSF DDIG “The role of genetic interactions in adaptation”, 2014–2016

Bioinformatics & Computational Biology Fellowship “Develop computational tools to analyze recombination rate variation from low-coverage sequence data”, 2014–2016

NSF BEACON Graduate Fellowship “The Genetic Architecture of Multi-dimensional Adaptation & Speciation”, 2011–2013

Sigma Xi Grants-in-Aid of Research “Evaluating the role of landscape features on gene flow”, 2008–2009

## Publications

**Hether, T.D.**, Wiench C.W., and Hohenlohe P.A. Novel molecular and analytical tools for efficient estimation of rates of meiotic crossovers and non-crossover gene conversions. *In review*

Hand, B.K, **T.D. Hether**, R.P. Kovach, C.C. Muhlfeld, S.J. Amish, M.C. Boyer, S.M. O'Rourke, M.R. Miller, W.H. Lowe, P.A. Hohenlohe, & G. Lukart. 2015. Genomics and introgression: Discover and mapping of thousands of species-diagnostic SNPs using RAD sequencing. *Current Zoology* 61 (1): 146-154

**Hether, T.D.** and P.A. Hohenlohe. 2014. Genetic regulatory network motifs constrain adaptation through curvature in the landscape of mutational (co)variance. *Evolution* (68) 4: 950-964.

Rosenblum, E.B., B.A. Sarver, J.W. Brown, S. Des Roches, K. M. Hardwick, **T.D. Hether**, J.M. Eastman, M.W. Pennell, and L.J. Harmon. 2011. Goldilocks meets Santa Rosalia: an ephemeral speciation model explains patterns of diversification across time scales. *Evolutionary Biology*. 39, number 2, 255-261.

**Hether, T.D.** and E.A. Hoffman. Machine learning identifies specific habitats associated with genetic connectivity in *Hyla squirella*. 2012. *J. Evolutionary Biology* 25, issue 6, 1039-1052

Degner, J.F., D.M. Silva, **T.D. Hether**, J.M. Daza, E.A. Hoffman. 2010. Fat frogs, mobile genes: unexpected phylogeographic patterns for the ornate chorus frog (*Pseudacris ornata*). *Molecular Ecology* 19, issue 12, 2501-2515.

Jenkins D.G, ..., **T.D. Hether**, et al. 2010. Isolation by distance: 20th century relic or reference standard for 21st century landscape genetics? *Ecography* 33, issue 2, 315-320.

**Hether, T. D.** and E. A. Hoffman. Characterization of five dinucleotide and six tetranucleotide polymorphic microsatellite loci for the squirrel treefrog (*Hyla squirella*). Appeared in D. Abdoullaye, I. Acevedo, A.A. Adebayo, et al. 2010. Permanent Genetic Resources added to Molecular Ecology Resources Database 1 August 2009-30 September 2009. *Molecular Ecology Resources* 10, 232-236.

Degner, J. F., **T. D. Hether**, and E. A. Hoffman. 2009. Eight novel tetranucleotide and five cross-species dinucleotide microsatellite loci for the ornate chorus frog (*Pseudacris ornata*). *Molecular Ecology Resources* 9, 622-624.

## Selected Talks & Presentations

Evo-Wibo. Presentation title: "Evolving genomic islands from standing genetic variation: an experimental approach with the budding yeast". Primary author, 2016.

University of Idaho's IBEST Science Update. Talk title: "Experimental Evolution of Local Adaptation in Yeast", 2014.

Evolution. Poster title: "Genetic network architecture, mutation rate, and correlational selection affect G-matrix stability". Primary author, 2014.

BEACON seminar series. Talk title: "Recombination rate and gene conversion heterogeneity: implications for 'genomic islands' of divergence". Primary author, 2013.

Evolution. *Hamilton Award Nominee*. Presentation Title: "Genetic regulatory motifs constrain adaptation through curvature in the landscape of mutational variation" Primary author, 2013.

IBEST Science Exposition, University of Idaho. Poster Title: "Spatial autocorrelation structure of genomic sequence divergence under neutrality using coalescent simulations" Contributing author, 2012.

Evolution. Poster Title: "Genetic Network Architecture and the G-matrix Under Divergent Selection" Primary author, 2012.

Seventh Annual Southeastern Ecology and Evolution Conference (SEEC), Atlanta, Georgia. Presentation Title: "Using landscape genetics to evaluate habitat permeability in an abundant frog" Primary author, 2010.

Biogeography Conference, Baja, Mexico. Poster Title: "Isolation by distance is dead: long live IBD" Contributing author, 2009.

Evolution. Presentation Title: "Testing for selection along a cline of color change in a polymorphic frog" Contributing author, 2008.

## Educational Outreach

"NIMBioS Evolutionary Quantitative Genetics Workshop", 2015 – Helped teach quantitative genetics to graduate students and postdocs

"Creatures of the night", 2011 – Helped teach chiropteran natural history elementary children

"White Sands Institute", 2011 – Helped teach lizard evolution to middle school children

"Save the Frogs Day", 2011, Helped teach amphibian decline awareness and habitat requirements to preschool children.

## Journal Referee

Biological Journal of the Linnean Society, Evolution, & Molecular Ecology

Last updated: June 17, 2016

<https://sites.google.com/site/buddingyeastbiologist/>