

Curriculum Vitae

Zachariah Gompert

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Degrees

Ph.D., Ecology, University of Wyoming, Spring 2012.

M.S., Population and Conservation Biology, Texas State University, 2006.

B.S., General Biology, Texas State University, 2004.

Professional Experience

Research

Graduate Research (2008–present), University of Wyoming, C. Alex Buerkle. Speciation genomics and the evolution of reproductive isolation.

Research (2007), Cambridge University, Chris Jiggins. Mate preference in *Heliconius* butterflies.

Graduate Research (2004–2006), Texas State University, Chris C. Nice. Evolutionary consequences of hybridization in the *Lycaeides* species complex.

Teaching

Lecturer (2011), University of Wyoming, instructor for Evolutionary Biology (LIFE 3500).

Teaching Assistant (2003–2006), Texas State University, TA for the following courses: Organic Chemistry, Organismal Biology, Genetics, Biostatistics.

Publications

Gompert Z, Lucas LK, Nice CC, Fordyce JA, Buerkle CA, Forister ML. Geographically variable, multifarious phenotypic divergence during the speciation process, in review.

Nosil P, **Gompert Z**, Farkas TA, Comeault A, Feder JL, Buerkle CA, Parchman TL. Genomic consequences of multiple speciation processes, in review.

Gompert Z, Lucas LK, Nice CC, Fordyce JA, Forister ML, Buerkle CA. Genomic regions with a history of divergent selection affect fitness of hybrids between two butterfly species, in review.

- Parchman T, **Gompert Z**, Benkman C, Schilkey F, Mudge J, Buerkle CA. Genome-wide association genetics of an adaptive trait in lodgepole pine, in review.
- Nice CC, **Gompert Z**, Fordyce JA, Forister ML, Lucas LK, Buerkle CA. Repeated hybrid speciation in alpine butterflies, in review.
- Gompert Z**. Population genomics as a new tool for wildlife management. *Molecular Ecology*, in press.
- Scholl CF, Nice CC, Fordyce JA, **Gompert Z**, Forister ML. Larval performance in the context of ecological diversification and speciation in *Lycaeides* butterflies. *International Journal of Ecology*, in press.
- Gompert Z**, Parchman T, Buerkle CA (2012) Genomics of isolation in hybrids. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 367:439-450.
- Fordyce JA, **Gompert Z**, Forister ML, Nice CC (2011) A hierarchical Bayesian approach to ecological count data: a flexible tool for ecologists. *PLoS ONE*, 6:e26785.
- Forister ML, **Gompert Z**, Fordyce JA, Nice CC (2011) After sixty years, an answer to the question: what is the Karner blue butterfly? *Biology Letters*, doi: 10.1098/rebl.2010.1077.
- Gompert Z**, Willmott K, Elias M (2011) Heterogeneity in predator micro-habitat use and the maintenance of Mullerian mimicry diversity. *Journal of Theoretical Biology*, 281:39-46.
- Gompert Z**, Buerkle CA (2011) Bayesian estimation of genomic clines. *Molecular Ecology*, 20:2111-2127.
- Buerkle CA, **Gompert Z**, Parchman T (2011) The $n = 1$ constraint in population genomics. *Molecular Ecology*, 20:1575-1581.
- Gompert Z**, Buerkle CA (2011) A hierarchical Bayesian model for next-generation population genomics. *Genetics*, 187:903-917.
- Merrill RM, **Gompert Z**, Dembeck LM, Kronforst MR, McMillan WO, Jiggins CD (2011) Mate preference across the speciation continuum in a clade of mimetic butterflies. *Evolution*, 65:1489-1500.
- Forister ML, **Gompert Z**, Nice CC, Forister G, Fordyce JA (2011) Ant association facilitates the evolution of diet breadth in a lycaenid butterfly. *Proceedings of the Royal Society B: Biological Sciences*, 278:1539-1547.
- Gompert Z**, Lucas LK, Fordyce JA, Forister ML, Nice CC (2010) Secondary contact between *Lycaeides idas* and *L. melissa* in the Rocky Mountains: extensive introgression and a patchy hybrid zone. *Molecular Ecology*, 19:3171-3192.

- Gompert Z**, Forister ML, Fordyce JF, Nice CC, Williamson R, Buerkle CA (2010) Bayesian analysis of molecular variance in pyrosequences quantifies population genetic structure across the genome of *Lycaeides* butterflies. *Molecular Ecology*, 19:2455-2473.
- Teeter KC, Thibodeau LM, **Gompert Z**, Buerkle CA, Nachman MW, Tucker PK (2010) The variable architecture of isolation between hybridizing species of house mouse. *Evolution*, 64:472-485.
- Gompert Z**, Buerkle CA (2010) *introgress*: a software package for mapping components of isolation in hybrids. *Molecular Ecology Resources*, 10:378-384.
- Nice CC, **Gompert Z**, Forister ML, Fordyce JA (2009) An unseen foe in arthropod conservation efforts: the case of *Wolbachia* infections in the Karner Blue butterfly. *Biological Conservation*, 142:3137-3146.
- Nolte AW, **Gompert Z**, Buerkle CA (2009) Variable patterns of introgression in two sculpin hybrid zones suggest that genomic isolation differs among populations. *Molecular Ecology*, 18:2615-2627.
- Forister ML, Nice CC, Fordyce JA, **Gompert Z** (2009) Host range evolution is not driven by the optimization of larval performance: the case of *Lycaeides melissa* (Lepidoptera: Lycaenidae) and the colonization of alfalfa. *Oecologia*, 160:551-561.
- Gompert Z**, Buerkle CA (2009) A powerful regression-based method for admixture mapping of isolation across the genome of hybrids. *Molecular Ecology*, 18:1207-1224.
- Elias M, **Gompert Z**, Willmott K, Jiggins C (2009) Phylogenetic community ecology needs to take positive interactions into account: insights from colorful butterflies. *Communicative and Integrative Biology*, 2:1-4.
- Lucas LK, **Gompert Z**, Ott JR, Nice CC (2009) Geographic and genetic isolation in spring-associated *Eurycea* salamanders endemic to the Edward's Plateau region of Texas. *Conservation Genetics*, 10:1309-1319.
- Gompert Z**, Forister ML, Fordyce JA, Nice CC (2008) Widespread mito-nuclear discordance with evidence for introgressive hybridization and selective sweeps in *Lycaeides*. *Molecular Ecology*, 17:5231-5244.
- Elias M, **Gompert Z**, Jiggins C, Willmott K (2008) Mutualistic interactions structure a neotropical butterfly community. *PLoS Biology*, 6:e300.
- Gompert Z**, Fordyce JA, Forister ML, Nice CC (2008) Recent colonization and radiation of North American *Lycaeides* inferred from mtDNA. *Molecular Phylogenetics and Evolution*, 48:481-490.

- Forister ML, Nice CC, Fordyce JA, **Gompert Z**, Shapiro AM (2008) Considering evolutionary processes in the use of single locus genetic data for conservation, with examples from the Lepidoptera. *Journal of Insect Conservation*, 12:37-51.
- Gompert Z**, Fordyce JA, Forister ML, Shapiro AM, Nice CC (2006) Homoploid hybrid speciation in an extreme habitat. *Science*, 314:1923-1925.
- Forister ML, Fordyce JA, Nice CC, **Gompert Z**, Shapiro AM (2006) Egg morphology varies among populations and habitats along a suture zone in the *Lycaeides idas-melissa* species complex (Lepidoptera: Lycaenidae). *Annals of the Entomological Society of America*, 99:933-937.
- Crutsinger GM, Collins MD, Fordyce JA, **Gompert Z**, Nice CC, Sanders NJ (2006) Plant genotypic diversity predicts community structure and governs an ecosystem process. *Science*, 313:966-968.
- Gompert Z**, Nice CC, Fordyce JA, Forister ML, Shapiro AM (2006) Identifying units for conservation using molecular systematics: the cautionary tale of the Karner blue butterfly. *Molecular Ecology*, 15:1759-1768.

Research Grants

- NSF Doctoral Dissertation Improvement Grant (\$15,000), 2010
- Xerces Society, Joan Mosenthal DeWind Award (\$3750), 2009
- EPSCoR Ecology Project Research Grant (\$5000), 2008
- Society of Systematic Biologists Graduate Student Research Award (\$1650), 2008
- Texas State Honors Thesis Research Grant (\$300), 2004

Fellowships, Academic Awards, and Honors

- UW Botany Scholarship (\$1000), 2011
- NSF EPSCoR WySTEP summer fellowship (\$3000), 2009
- St. John's College Benefactors Scholarship (\$1000), 2007
- Eben-Ellege Award (\$5000), 2006
- Summer Institute in Statistical Genetics Scholarship (\$1000), 2006
- Texas State Outstanding Graduate Student Award for the College of Science, 2006
- Texas State Student Travel Grant (\$350), 2006
- NSF Graduate Research Fellowship (\$40,000 per year for 3 years), 2005

Best Graduate Student Presentation Texas State University Student Colloquium (\$100), 2005

Texas State Student Travel Grant (\$400), 2005

Howard D. Schulze Scholarship (\$300), 2004

Invited Seminars

Bayesian population genomic models for next-generation DNA sequence data. University of Wyoming, Department of Statistics seminar series. Laramie, WY (November 2011).

Bayesian models for next-generation population genomics. Smithsonian Institution and American Museum of Natural History, Next-generation Sequencing symposium. Washington, DC (April 2011).

Hybrid speciation on mountain tops: replicated cases of hybridization in blue butterflies. European Society of Evolutionary Biology, Turin, Italy (August 2009).

Homoploid hybrid speciation in an extreme habitat. Butterfly Biology, Mechanisms of Speciation symposium. Rome, Italy (July 2007).

Presentations at Conferences

Analytical methods for next-generation population genomics. Society for the Study of Evolution. Portland, OR (June 2010).

A powerful regression-based method for admixture mapping of isolation across the genome of hybrids. Society for the Study of Evolution. Moscow, ID (June 2009).

Widespread mito-nuclear discordance caused by introgressive hybridization and selective sweeps. Society for the Study of Evolution. Minneapolis, MN (June 2008).

Hybrid speciation driven by adaptation to an extreme environment. Society for the Study of Evolution. Stony Brook, NY (June 2006).

The contribution of hybridization to diversification in North American Lycaenid butterflies. Southwestern Association of Naturalists. Colima, Mexico (April 2006).

DNA barcoding: boon or boondoggle? The cautionary tale of the Karner blue butterfly. Society for the Study of Evolution. Fairbanks, AK (June 2005).

Discordance between morphological and molecular markers in Lycaeides: hybridization or parallel evolution. Southwestern Association of Biologists. Portal, AZ (October 2004).

Service

Reviewer for the journals: American Naturalists, Biological Journal of the Linnean Society, Diversity and Distributions, European Journal of Entomology, Evolution, Evolutionary Applications, Heredity, Journal of Biogeography, Journal of Heredity, Molecular Ecology, Molecular Ecology Resources, Molecular Phylogenetics and Evolution, Oecologia, and PLoS One.

Guest editor for the International Journal of Ecology special issue on ecological speciation (to be published January 2012).

Participant in NSF Research Experience for Teachers (RET; 2010), and mentor for NSF EPSCoR funded undergraduate research (2009-2010).

Mentor for University of Wyoming's Bioinformatics and Computational Biology Undergraduate Summer Research Program (2009).

Technical Skills

Bayesian data analysis using Markov chain Monte Carlo

Population genetic and genomics data analysis

Computer simulation and modeling

Computer programming in C, R, and PERL

Bioinformatics with next-generation sequence data

Molecular genetics laboratory techniques

Field ecology techniques

Memberships

The American Association for the Advancement of Science

Society for the Study of Evolution

References

Dr. C. Alex Buerkle (current collaborator and Ph.D. advisor),
Department of Botany, 3165, University of Wyoming, Laramie,
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Dr. Chris C. Nice (current collaborator and M.S. advisor),
Biology Department, Texas State University, San Marcos, TX
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Dr. James A. Fordyce (current collaborator), 569 Dabney Hall,
University of Tennessee, Knoxville, TN 37996,
jfordyce@utk.edu, Ph: 865-974-2925, Fax: 865-974-3067