

Curriculum Vitae

Qixin He, Ph. D.

Department of Ecology and Evolution, University of Chicago

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Current position

2015-current Postdoctoral scholar, Department of Ecology and Evolution, University of Chicago. Advisor: Mercedes Pascual

Professional preparation

2008-2014, Ph.D., Ecology and Evolutionary Biology, University of Michigan.

Advisor: L. Lacey Knowles. Achieved candidacy in 2010.

Thesis: Inferring histories of adaptive divergence with gene flow: genetic, demographic and geographic effects

2008, Bachelor of Science, Biological Sciences, Fudan University, Shanghai, China

Awards & Research Support

April 2014 Tinker Scholarship to outstanding student of the Museum of Zoology

April 2013 Edwin H. Edwards Fellowship

April 2013 EEB student outstanding paper award (\$500) for Q. He, D. Edwards, L. L. Knowles (2013)

April 2012 Hinsdale Museum of Zoology Scholarship Award from Museum of Zoology, University of Michigan (\$4000)

March 2012 NSF Doctoral Dissertation Improvement Grant (\$15,000)

April 2011 Hinsdale Museum of Zoology Scholarship Award from Museum of Zoology, University of Michigan (\$5000)

March 2011 International Research Award from International Institute, University of Michigan (\$3000)

May 2010 Block Grant funds from University of Michigan, Ann Arbor, USA (\$1500)

May 2007 National Talent Training Fund in Basic Research (J0630643), China: Elevational diversity pattern of Schizothorax fishes: ecological and evolutionary causes (\$700)

Teaching Experience

2009 Fall, U-M, GSI, Bio171: introductory biology

EEB 2008 Winter, U-M, GSI, Bio171: introductory biology, EEB

Publications

Q. He, L. L. Knowles. 2017. Rapid adaptation with gene flow via a reservoir of chromosomal inversion variation? *bioRxiv*. doi: <https://doi.org/10.1101/150771>

Q. He, J. Padro, L. L. Knowles. 2017. Inferring the geographic origin of a range expansion:

- latitudinal and longitudinal coordinates inferred from genomic data in an ABC framework with the program X-ORIGIN. *Mol. Ecol.* (accepted)
- Q. He**, L. L. Knowles. 2016. Identifying targets of selection in mosaic genomes with machine learning: applications in *Anopheles gambiae* for detecting sites within locally adapted chromosomal inversions. *Mol. Ecol.* DOI: 10.1111/mec.13619
- L. L. Knowles, R. Massatti, **Q. He**, H. C. Lanier, L. E. Olson. 2016. Quantifying the similarity between genes and geography across Alaska's alpine small mammals. *J. Biogeogr.* DOI: 10.1111/jbi.12728
- H. C. Lanier, R. Massatti, **Q. He**, L. E. Olson, and L. L. Knowles. 2015. Colonization from divergent ancestors: glaciation signatures on contemporary patterns of genomic variation in Collared Pikas (*Ochotona collaris*). *Mol. Ecol.* 24:3688-3705
- Q. He**, D. Edwards, L. L. Knowles. 2013. Integrative testing of how environments from the past to the present shape genetic structure across landscapes. *Evolution.* 67:3386-3402
- L. L. Knowles, H. C. Lanier, P. B. Klimov, and **Q. He**. 2012. Full modeling versus summarizing gene-tree uncertainty: Method choice and species-tree accuracy. *Mol. Phylogenet. Evol.* 65:501-509
- Huang, H., **Q. He**, L.S. Kubatko, and L.L. Knowles. 2010. Sources of Error Inherent in Species- Tree Estimation: Impact of Mutational and Coalescent Effects on Accuracy and Implications for Choosing among Different Methods. *Sys. Bio.* 59:573-83
- Li, J., **Q. X. He**, X. Hua, J. Zhou, H. D. Xu, J. K. Chen, and C. Z. Fu. 2009. Climate and history explain the species richness peak at mid-elevation for Schizothorax fishes (Cypriniformes: Cyprinidae) distributed in the Tibetan Plateau and its adjacent regions. *Glob. Ecol. Biogeogr.* 18:264-272.
- Yin, W., Fu, C., Guo, L., **He, Q.**, Li, J., Jin, B., Wu, Q. and Li, B. 2009. Species delimitation and historical biogeography of the genus *Helice* (Brachyura: Varunidae) in the northwestern Pacific. *Zool. Sci.* 26:467-475.
- Hua, X., W. Wang, W. Yin, **Q. He**, B. Jin, J. Li, J. Chen and C. Fu. 2009. Phylogeographical analysis of an estuarine fish, *Salanx ariakensis* (Osmeridae: Salanginae) in the north-western Pacific. *J. Fish Biol.* 75:354– 367

In review

- Q. He**, S. Pilosof, K. E. Tiedje, S. Ruybal-Pesántez, Y. Artzy-Randrup, E. B. Baskerville, K. P. Day & M. Pascual. Networks of genetic similarity reveal the role of non-neutral processes in shaping the strain structure of *Plasmodium falciparum*. *Nature Communications*

Presentations

- Q. He**, S. Pilosof, M. Pascual, K. Day. 2017 Networks of genetic similarity reveal the role of non-neutral processes in shaping the strain structure of *Plasmodium falciparum*. ESA 2017, Portland, OR. Invited talk for Symposium: "Turn and Face the Strain: Changing Signatures of Niche Processes in Disease and Community Diversity"
- Q. He**, S. Pilosof, M. Pascual, K. Day. 2017 Networks of genetic similarity reveal the role of non-neutral processes in shaping the strain structure of *Plasmodium falciparum*. EEID lightning talk, Santa Barbara, CA.
- Q. He**, S. Pilosof, M. Pascual, K. Day. 2017 Networks of genetic similarity reveal the role of non-neutral processes in shaping the strain structure of *Plasmodium falciparum*. ESA 2017, Portland, OR.

- Q. He, S. Pilosof, M. Pascual.** 2016 Does specific immunity selection structure the *Plasmodium falciparum* population into strains from the perspective of the major blood antigen PfEMP1? ISEMPH 2016, Durham, NC.
- Q. He, S. Pilosof, M. Pascual.** 2016 Does specific immunity selection structure the *Plasmodium falciparum* population into strains from the perspective of the major blood antigen PfEMP1? Evolution 2016, Austin, TX.
- Q. He, L.L. Knowles.** 2014. Locating a selection signature inside chromosomal rearrangements fortsets of adaptive divergence in *Anopheles gambiae*. Evolution 2014, Raleigh, NC.
- Q. He, L.L. Knowles.** 2013. Genomic tests of whether chromosomal rearrangements facilitated local adaptation in *Anopheles gambiae* based on coalescent expectations. ESEB 2013, Lisbon, Portugal.
- Q. He, L.L. Knowles.** 2013. Integrative testing of how environments from the past to the present shape genetic structure across landscapes. Evolution 2013, Snowbird, Utah.
- Q. He, L.L. Knowles.** 2011. Utility of next-generation sequencing for phylogenomic analysis. Evolution 2011. University of Oklahoma, Norman, OK.
- Q. He, L.L. Knowles.** 2011. Adaptive divergence in *Anopheles gambiae*: facilitation via standing inversion variation. EEB Lunch 2011-3-15.
- Q. He, D. F. A-Serrano, H. Huang, L.L. Knowles.** 2010. An approach for coupling ecological, demographic, and genetic models to test spatially-explicit phylogeographic hypotheses. Evolution 2010, Portland State University, Portland, OR.
- Q. He, L.L. Knowles.** 2009. Rapid evolution via standing variation: an adaptive seed bank in chromosomal inversions. Evolution 2009, University of Idaho, Moscow, ID.
- Q. He, L.L. Knowles.** 2009. Rapid evolution via standing variation: an adaptive seed bank in chromosomal inversions. EEB Lunch 2009-9-30.

Posters

- He, Q., L.L. Knowles.** 2012. Species-tree estimation using SNP data from deep sequencing in non-model organisms. Evolution 2012, Ottawa Convention Centre, Canada.
- Huang, H., Q. He, L.L. Knowles.** 2009. Can the Intrinsic Limitations of DNA Sequences for Phylogenetic Estimation be Overcome? 5th Annual University of Michigan Early Career Scientists Symposium: Using Phylogenies in Ecology

Professional Societies

The Society for the Study of Evolution (SSE), Ecological Society of America (ESA)

Reviewer

Systematic Biology, Molecular Ecology, PLoS One, PLoS Computational Biology, FONDECYT Chilean National Science and Technology grants, Journal of Biogeography

Service and Outreach

Undergraduate student mentor in Evolution 2010, advised Mentored Richard Coleman and Milinda Thompson;

EEB seminar committee, 2010-2011 academic year

Ninth annual Early Career Scientists Symposium organization committee, 2013

Co-organizer of ESA 2015 oral session “community and ecosystem effects of rapid evolution”