# Qixin He

## Curriculum Vitae

Department of Biological Sciences, Purdue University

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I lab website

Github

#### Current Position

2021-present Assistant Professor, Department of Biological Sciences, Purdue University, West Lafayette.

Research: Evolutionary models to understand genetic diversity and disease transmission

## Professional Preparation

2015-2020 **Postdoctoral scholar**, *Department of Ecology and Evolution*, University of Chicago.

Advisor: Mercedes Pascual

2008–2014 **PhD, Ecology and Evolutionary Biology**, *EEB*, University of Michigan, Ann Arbor.

Advisor: L. Lacey Knowles

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

effects

2004–2008 Bachelor of Science, Biological Sciences, Fudan University, Shanghai.

#### Publications

- 2021 Qixin He\*, Shai Pilosof\*, Kathryn E. Tiedje, Karen P. Day, and Mercedes Pascual. Frequency-Dependent Competition Between Strains Imparts Persistence to Perturbations in a Model of Plasmodium falciparum Malaria Transmission. Frontiers in Ecology and Evolution, volume 9, page 319, 2021. \*Equal Contributions.
- 2021 **Qixin He** and Mercedes Pascual. An antigenic diversification threshold for falciparum malaria transmission at high endemicity. *PLOS Computational Biology*, volume 17, page e1008729, 2021.
- 2021 Rahul Subramanian, **Qixin He**, and Mercedes Pascual. Quantifying asymptomatic infection and transmission of COVID-19 in New York City using observed cases, serology, and testing capacity. *Proceedings of the National Academy of Sciences*, volume 118, page e2019716118, 2021.
- 2020 Jiaqi Tan, Xian Yang, **Qixin He**, Xia Hua, and Lin Jiang. Earlier parasite arrival reduces the repeatability of host adaptive radiation. *The ISME Journal*, volume 14, pages 2358–2360, 2020.
- 2019 Andréa T. Thomaz\* and **Qixin He**\*. When are populations not connected like a circuit? Identifying biases in gene flow from coalescent times. *Molecular Ecology Resources*, volume 19, pages 1381–1384, 2019. \*Equal Contributions.
- 2019 Jiaqi Tan\*, Qixin He\*, Jennifer T. Pentz, Cheng Peng, Xian Yang, Meng-Hsiu Tsai, Yongsheng Chen, William C. Ratcliff, and Lin Jiang. Copper oxide nanoparticles promote the evolution of multicellularity in yeast. *Nanotoxicology*, volume 13, pages 597–605, 2019. \*Equal Contributions.
- 2019 Shai Pilosof, **Qixin He**, Kathryn E. Tiedje, Shazia Ruybal-Pesántez, Karen P. Day, and Mercedes Pascual. Competition for hosts modulates vast antigenic diversity to generate persistent strain structure in Plasmodium falciparum. *PLOS Biology*, volume 17, page e3000336, 2019.
- 2018 Qixin He, Shai Pilosof, Kathryn E. Tiedje, Shazia Ruybal-Pesántez, Yael Artzy-Randrup, Edward B. Baskerville, Karen P. Day, and Mercedes Pascual. Networks of genetic similarity reveal non-neutral processes shape strain structure in Plasmodium falciparum. Nature Communications, volume 9, page 1817, 2018.

- 2017 **Qixin He**, Joyce R Prado, and Laura Lacey Knowles. 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. *Molecular Ecology*, volume 26, pages 6908–6920, 2017.
- 2017 **Qixin He** and L Lacey Knowles. Rapid adaptation with gene flow via a reservoir of chromosomal inversion variation? *bioRxiv*, page 150771, 2017.
- 2016 **Qixin He** and L Lacey Knowles. Identifying targets of selection in mosaic genomes with machine learning: applications in a nopheles gambiae for detecting sites within locally adapted chromosomal inversions. *Molecular ecology*, volume 25, pages 2226–2243, 2016.
- 2016 L Lacey Knowles, Rob Massatti, Qixin He, Link E Olson, and Hayley C Lanier. Quantifying the similarity between genes and geography across alaska's alpine small mammals. *Journal of Biogeography*, volume 43, pages 1464–1476, 2016.
- 2015 Hayley C Lanier, Rob Massatti, **Qixin He**, Link E Olson, and L Lacey Knowles. Colonization from divergent ancestors: glaciation signatures on contemporary patterns of genomic variation in collared pikas (ochotona collaris). *Molecular Ecology*, volume 24, pages 3688–3705, 2015.
- 2013 **Qixin He**, Danielle L Edwards, and L Lacey Knowles. Integrative testing of how environments from the past to the present shape genetic structure across landscapes. *Evolution*, volume 67, pages 3386–3402, 2013.
- 2012 L Lacey Knowles, Hayley C Lanier, Pavel B Klimov, and **Qixin He**. Full modeling versus summarizing gene-tree uncertainty: method choice and species-tree accuracy. *Molecular phylogenetics and evolution*, volume 65, pages 501–509, 2012.
- 2010 Huateng Huang, **Qixin He**, Laura S Kubatko, and L Lacey Knowles. Sources of error inherent in species-tree estimation: impact of mutational and coalescent effects on accuracy and implications for choosing among different methods. *Systematic biology*, volume 59, pages 573–583, 2010.
- 2009 Wei Yin, Cuizhang Fu, Li Guo, **Qixin He**, Jun Li, Binsong Jin, Qianhong Wu, and Bo Li. Species delimitation and historical biogeography in the genus helice (brachyura: Varunidae) in the northwestern pacific. *Zoological Science*, volume 26, pages 467–475, 2009.
- Jun Li, **Qixin He**, Xia Hua, Jie Zhou, Huidan Xu, Jiakuan Chen, and Cuizhang Fu. 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. *Global Ecology and Biogeography*, volume 18, pages 264–272, 2009.
- 2009 Xia Hua, W Wang, W Yin, Qixin He, B Jin, Jun Li, Jiakuan Chen, and Cuizhang Fu. Phylogeographical analysis of an estuarine fish, salanx ariakensis (osmeridae: Salanginae) in the north-western pacific. *Journal of Fish Biology*, volume 75, pages 354–367, 2009.

#### Software & Pipelines

iDDC He, Edwards & Knowles (2013) Evolution

X-Origin He, Prado & Knowles (2017) Molecular Ecology

varmodel He et al. (2018) Nature Communications

#### Presentations

#### Invited Talks

- Jan 2021 **Qixin He** and Mercedes Pascual. An antigenic diversification threshold for falciparum malaria transmission at high endemicity. In *Workshop on Limits to Diversity Assembly*, International Centre for Theoretical Physics, Italy, Jan 2021.
- Nov 28 2018 **Qixin He**, Shai Pilosof, Kathryn E. Tiedje, Shazia Ruybal-Pesántez, Yael Artzy-Randrup, Edward B. Baskerville, Karen P. Day, and Mercedes Pascual. Why is malaria a chronic disease? immune selection promotes malaria antigenic diversity at genetic and strain levels across time. In *Departmental Seminar*, University of Oklahoma, Norman, OK, Nov 28 2018.

July 11 2018 Qixin He, Shai Pilosof, Kathryn E. Tiedje, Shazia Ruybal-Pesántez, Yael Artzy-Randrup, Edward B. Baskerville, Karen P. Day, and Mercedes Pascual. Agent-based simulations and network analyses reveal the strain structure of falciparum malaria. In *Melbourne Integrative Genomics*, University of Melbourne, Australia, July 11 2018.

#### Conference Presentations

- **Qixin He** and Mercedes Pascual. An antigenic diversification threshold for infectious diseases by combining population genetic and epidemiological processes. In *Midwest Population Genetics*, University of Wisconsin, Madison, 2021.
- **Qixin He** and Mercedes Pascual. An antigenic diversification threshold for falciparum malaria and its control at high endemicity. In *EEID*, Online, 2021.
- **Qixin He** and Mercedes Pascual. An antigenic diversification threshold for falciparum malaria and its control at high endemicity. In *Evolution*, Online, 2021.
- **Qixin He** and Mercedes Pascual. An antigenic diversification threshold for falciparum malaria and its control at high endemicity. In *ESA*, Online, 2020.
- **Qixin He** and Mercedes Pascual. A novel epidemiological threshold related to parasite antigenic diversification. In *Epidemics*, Charleston, SC, USA, 2019.
- **Qixin He** and Mercedes Pascual. Evolutionary and ecological determinants of functional diversification in antigen gene families. In *Evolution*, Providence, RI, USA, 2019.
- **Qixin He** and Mercedes Pascual. Networks of genetic similarity reveal the role of non-neutral processes in shaping the strain structure of *Plasmodium falciparum*. In *ESA Symposium: Turn and Face the Strain: Changing Signatures of Niche Processes in Disease and Community Diversity*, Santa Babara, CA, 2017.
- **Qixin He** and Mercedes Pascual. Networks of genetic similarity reveal the role of non-neutral processes in shaping the strain structure of *Plasmodium falciparum*. In *ESA Symposium: Turn and Face the Strain: Changing Signatures of Niche Processes in Disease and Community Diversity*, Portland, OR, 2017.
- **Qixin He**, Shai Pilosof, and Mercedes Pascual. Does specific immunity selection structure the plasmodium falciparum population into strains from the perspective of the major blood antigen *Pf* emp1? In *Evolution*, Austin, TX, 2016.
- **Qixin He**, Shai Pilosof, and Mercedes Pascual. Does specific immunity selection structure the plasmodium falciparum population into strains from the perspective of the major blood antigen *Pf* emp1? In *ISEMPH*, Durham, NC, 2016.
- **Qixin He** and L. Lacey Knowles. Locating a selection signature inside chromosomal rearrangements fortests of adaptive divergence in *Anopheles gambiae*. In *Evolution*, Raleigh, NC, 2014.
- **Qixin He** and L. Lacey Knowles. Integrative testing of how environments from the past to the present shape genetic structure across landscapes. In *Evolution*, Snowbird, Utah, 2013.
- 2013 Qixin He and L. Lacey Knowles. Genomic tests of whether chromosomal rearrangements facilitatedlocal adaptation in anopheles gambiae based on coalescent expectations. In *Evolution*, Lisbon, Portugal, 2013.
- **Qixin He** and L. Lacey Knowles. Utility of next-generation sequencing for phylogenomic analysis. In *Evolution*, University of Oklahoma, Norman, OK, 2011.
- **Qixin He**, Diego F. A-Serrano, Huateng Huang, and L. Lacey Knowles. An approach for coupling ecological, demographic, and genetic models to test spatially-explicit phylogeographic hypotheses. In *Evolution*, Portland State University, Portland, OR, 2010.
- **Qixin He** and L. Lacey Knowles. Rapid evolution via standing variation: an adaptive seed bank in chromosomal inversions. In *Evolution*, University of Idaho, Moscow, ID, 2009.

#### **Posters**

- 2018 **Qixin He**, Shai Pilosof, Kathryn E. Tiedje, Shazia Ruybal-Pesántez, Karen P. Day, and Mercedes Pascual. Static and temporal signatures of immune selection in *Plasmodium falciparum* revealed through network analyses of var genes and their repertoires. In *First Malaria World Congress*, Melbourne Convention & Exhibition Centre, Australia, 2018.
- 2012 **Qixin He**, Shai Pilosof, Kathryn E. Tiedje, Shazia Ruybal-Pesántez, Karen P. Day, and Mercedes Pascual. Species-tree estimation using snp data from deep sequencing in non-model organisms. In *Evolution*, Ottawa Convention Centre, Canada, 2012.
- 2009 **Qixin He** and L. Lacey Knowles. Can the intrinsic limitations of dna sequences for phylogenetic estimation be overcome? In *5th Annual Early Career Scientists Symposium: Using Phylogenies in Ecology*, University of Michigan, Ann Arbor, MI, 2009.

### Awards & Research Support

- April 2014 **Tinker Scholarship**, outstanding student of the Museum of Zoology, University of Michigan.
- April 2013 Edwin H. Edwards Fellowship, University of Michigan.
- April 2013 **EEB student outstanding paper award**, *Q. He, D. Edwards, L. L. Knowles (2013)*, University of Michigan.
- April 2012 **Hinsdale Museum of Zoology Scholarship Award**, *Museum of Zoology*, University of Michigan, (\$4000).
- March 2012 NSF Doctoral Dissertation Improvement Grant, NSF, (\$15,000).
- April 2011 **Hinsdale Museum of Zoology Scholarship Award**, *Museum of Zoology*, University of Michigan, (\$5000).
- March 2011 International Research Award, International Institute, University of Michigan, (\$3000).
  - May 2010 Block Grant funds, EEB, University of Michigan.
  - May 2007 National Talent Training Fund in Basic Research (J0630643), NSF, China.

    Project: Elevational diversity pattern of Schizothorax fishes: ecological and evolutional causes

## Teaching Experience

2008–2009 Graduate Student Instructor, Bio171: introductory biology, University of Michigan.

#### Professional Societies

2008-present The Society for the Study of Evolution (SSE), Ecological Society of America (ESA)

#### Reviewer

PNAS, Heredity, Systematic Biology, Molecular Ecology, Molecular Ecology Resources, Evolution, PLoS Computational Biology, Communications Biology, Journal of Biogeography, Virus Evolution, PLoS One, FONDECYT Chilean National Science and Technology grants

#### Service and Outreach

- 2010, 2021 Undergraduate student mentor, Conference: Evolution.
  - Mentored Richard Coleman and Milinda Thompson
- 2010–2011 **EEB seminar committee**, University of Michigan.
  - 2013 **Organization committee**, *Ninth annual Early Career Scientists Symposium*, University of Michigan.
  - 2015 Co-organizer, Oral session "community and ecosystem effects of rapid evolution", ESA.
- 2019-2021 Instructor, Flu for fun, EYH-workshop for middle school girls, Chicago.