

Bin Z. HE, Ph.D.

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SCHOLARLY PROFILE

As an evolutionary geneticist, I study the evolution of gene regulatory network (GRN) for stress responses between commensal and free-living yeast. I employ a combination of functional genomics, biochemistry and molecular phylogenetics to tackle this challenging question.

EDUCATION

- 2006-2012 **The University of Chicago**, Chicago, IL
Ph.D. in Ecology and Evolution, Advisor: Martin Kreitman
Thesis title: "Using *Drosophila* Natural Variation to Study the Role of Positive Selection in Cis-Regulatory Evolution and the Genetic Basis of a Complex Trait"
- 2002-2006 **Peking University**, Beijing, China
B.S. , Advisor: Qi Ouyang
Thesis title: "Using microfluidics device to investigate bacteria persistence phenomenon"

PROFESSIONAL APPOINTMENT

- 2018- **Assistant Professor**
Biology Department, University of Iowa
- 2017-2018 **Associate research scholar**
Lewis-Sigler Institute for Integrative Genomics, Department of Ecology and Evolutionary Biology, Princeton University
Affiliation: Peter Andolfatto lab, Julien Ayroles lab
Research: Evolution of gene regulatory networks controlling stress response in yeast
- 2012-2017 **Postdoctoral researcher**
FAS Center for Systems Biology, Harvard University, HHMI
Advisor: Erin O'Shea
Research: Evolution of phosphate starvation response pathway in a commensal yeast

GRANTS AND AWARDS

- 2016 The Allied Genetics Conference, GSA Trainee Travel Award (\$300)
- 2012 Sigma Xi Research-in-Aid Grant (\$950)
- 2012 Women's Board Travel Fund, BSD, University of Chicago (\$400)
- 2011 1st Asia Pacific *Drosophila* Research Conference, Travel Fellowship (\$1000)
- 2011 Honorary mention, Harper Fellow for best Ph.D. thesis at The University of Chicago
- 2009-2010 University of Chicago Hinds Fund (\$2000)

PUBLICATIONS

Peer-reviewed journal articles

- [1] **He, BZ***, Zhou, X, and O'Shea, EK* (2017). Evolution of reduced co-activator dependence led to target expansion of a starvation response pathway. *eLife* 6, e25157. (* co-corresponding authors)
- [2] Chen J-Y, Shen QS, Zhou W-Z, Peng J, **He BZ**, Li Y, Liu C-J, Luan X, Ding W, Li S, Chen C, Tan C-M, Zhang YE, He A, Li C-Y. (2015) Emergence, Retention and Selection: A Trilogy of Origination for Functional *De Novo* Proteins from Ancestral LncRNAs in Primates. *PLoS Genet* 11(7), e1005391.
- [3] Yang H*, **He BZ***, Ma H, Tsauro S-C, Ma C, Wu Y, Ting C-T, Zhang YE. (2014) Expression Profile and Gene Age Jointly Shaped the Genome-Wide Distribution of Premature Termination Codons in a *Drosophila* *Melanogaster* Population. *Mol Biol Evol*, 32 (1), 216-228 (* co-first authors)
- [4] **He BZ***, Ludwig MZ, Dickerson DA, Barse L, Arun B, Vilhjálmsón BJ, Park SY, Tamarina NA, Selleck SB, Wittkopp PJ, Bell GI, Kreitman M*. (2014) A *Drosophila* Model to Investigate Natural Variation Effect in Response to Expression of a Human Misfolded Protein. *Genetics* 196 (2), 557-567 (* co-corresponding authors)
- [5] Park SY, Ludwig MZ, Tamarina NA, **He BZ**, Carl SH, Dickerson DA, Barse L, Arun B, Williams C, Miles CM, Philipson LH, Steiner DF, Bell GI, Kreitman M. (2014) Genetic Complexity in a *Drosophila* Model of Diabetes-Associated Misfolded Human Proinsulin. *Genetics* 196 (2), 539-555
- [6] **He BZ***, Holloway AK, Maerkl JS, Kreitman M*. (2011) Does positive selection drive transcription factor binding site turnover? A test with *Drosophila* cis-regulatory modules. *PLoS Genet* 7(4): e1002053. (* co-corresponding authors)
- [7] **He B**, Kreitman M. (2010) Evolution of Cis-Regulatory Modules. In: *Darwin's Heritage Today: Proceedings of the Darwin 200 Beijing International Conference*, Long M, et al., eds, Higher Education Press, Beijing, China
- [8] Lu J, Shen Y, Wu Q, Kumar S, **He B**, Shi S, Carthew RW, Wang SM, Wu CI. (2008) The birth and death of microRNA genes in *Drosophila*. *Nature Genetics* 40 (3), 351-355.
- [9] Lou C, Yang X, Liu X, **He B**, Ouyang Q. (2007) A quantitative study of λ -Phage SWITCH and its components. *Biophysical Journal* 92 (8), 2685-2693.

PROFESSIONAL SERVICE

Reviewer for *Journal of Molecular Evolution*, *PLoS Genetics*, *PLoS Computational Biology*, *PLoS One*, *Genetics*, *Molecular Biology and Evolution*, *Genome Biology and Evolution*, *Cell Reports*, *Genome Research*

SELECTED PRESENTATIONS

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| 2017 | ASBMB Special Symposium on Evolution and Core Processes in Gene Expression, Kansas City, MO |
| 2016 | The Allied Genetics Conference, Orlando, FL |
| 2014 | Experimental Approaches to Ecology and Evolution using Yeast & Other model organisms, Heidelberg, Germany |
| 2013 | 54th <i>Drosophila</i> Research Conference, Washington, DC |
| 2011 | Society of Molecular Biology and Evolution Annual Conference, Kyoto, Japan |
| 2011 | First Asia-Pacific <i>Drosophila</i> Research Conference, Taipei |
| 2010 | Midwest Ecology and Evolution Conference, Ames, Iowa |