

# Thomas E. Keller

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## Education

Ph.D. Biology, University of Texas at Austin, 2012  
*The evolution of RNA and the actin protein family*

*Committee:* Jim Bull (co-advisor) , Claus Wilke (co-advisor), Thomas Juenger, Lauren Ancel Meyers, and Sara Sawyer.

B.S. Zoology, University of Florida, 2005.

*Minor:* Wildlife Ecology and Conservation.

*Honors:* *Magna Cum Laude*, University Scholar, Dean's list 2003-2005.

## Skills

*Areas:* Evolutionary Biology, Bioinformatics, Epigenomics, Genomics, Phylogenetics

*Languages:* Python, Biopython, Cython, R, Bioconductor, BASH, Mathematica, C, C++, Perl, SQL

*Tools:* L<sup>A</sup>T<sub>E</sub>X, Linux, RNA-seq, NGS, CHIP-seq

## Academic Experience

### *Georgia Institute of Technology, School of Biology*

Temporary Tech Dr. Soojin Yi, November 2015–January 2016.  
Temporary extension to finish submission and publication of several papers.

Postdoctoral Researcher Dr. Soojin Yi, August 2012–August 2015.  
Responsibilities included writing software to conduct NSF-funded research and mentoring students. Total scientific output will be three first author and two co-author papers. One study examined multivariate associates between plant epigenetics and climate, both new areas of research in the lab. A second study examined primate brain regions for epigenetics regions of similarities and differences between humans and their near relatives. In these studies and others I used NGS techniques including mapping, RNA-seq, motif-searching, CHIP-seq, among others. Efficiently processing this data required the use of a computer cluster, which meant I learned a bit about distributed systems. Data collection was done primarily with Python. Statistical analyses and figures for analyses for publication were done with R and Bioconductor.

### *University of Texas at Austin, School of Biological Sciences*

Research and Teaching Assistant  
Jim Bull, Claus Wilke, Matthew Cowperthwaite  
August 2006–May 2012.

Responsibilities included supervising undergraduates and working on NIH-funded research and preparing results for publication. In addition I was a teaching assistant for a survey course on biology for non-majors as well as an introduction to computational biology. Simulation code and data collection was primarily in Python or Cython. Statistical analyses and figures for analyses for publication were performed with R and Bioconductor. Total scientific output was three first-author and two co-author publications.

### *University of Florida, Department of Zoology*

Research Assistant, Charlie Baer, Fall 2004–Spring 2005. Assisted in mutation accumulation experiments with *C. elegans* and other nematodes that investigated how fitness declines as deleterious mutations accumulate in the absence of negative selection.

## Research

### *Publications*

1. I. Mendizabal, L. Shi, **T. E. Keller**, G. Konopka, T. M. Preuss, T. Tsieh, E. Hu, Z. Zhang, B. Su, S. V. Yi. Comparative methylome analyses reveal epigenetic loci implicated in transcription regulation of human brains. Submitted to *PLoS Genetics*.
2. **T. E. Keller**, J. E. Lasky, S. V. Yi. The multivariate association between genome-wide DNA methylation and climate across the range of *Arabidopsis thaliana*. In press, *Molecular Ecology*, doi 10.1111/mec.13573 .
3. **T. E. Keller**, P. Han\*, S. V. Yi. Evolutionary transition of promoter and gene body DNA methylation across invertebrate-vertebrate boundary. *Molecular Biology and Evolution* 33:1019-1028, 2016.
4. I. Mendizabal, **T. E. Keller**, J. Zeng, S. V. Yi. Epigenetics and evolution. *Integrative and Comparative Biology* 54 31–42 2014.
5. **T. E. Keller**, S. V. Yi. DNA methylation and evolution of duplicate genes. *Proceedings of the National Academy of Sciences* 111:5932–5937 2014.
6. **T. E. Keller**, C. O. Wilke, J. J. Bull. Interactions between evolutionary processes at high mutation rates. *Evolution* 66:2303–2314, 2012.
7. **T. E. Keller**, S. D. Mis\*, K. E. Jia\*, C. O. Wilke. Reduced mRNA secondary-structure stability near the start codon indicates functional genes in prokaryotes. *Genome Biology and Evolution* 4:80–88, 2012.
8. E. B. O’Dea, **T. E. Keller**, C. O. Wilke. Does mutational robustness inhibit extinction by lethal mutagenesis in viral populations? *PLoS Computational Biology* 6:e1000811, 2010.
9. R. Springman, **T. Keller**, I. Molineux, J. J. Bull. Evolution at a high imposed mutation rate: adaptation obscures the load in Phage T7. *Genetics* 184:221–232 , 2010.
10. M. P. Salomon, D. Ostrow, N. Phillips, D. Blanton\*, W. Bour\*, **T. E. Keller\***, L. Levy\*, T. Sylvestre\*, A. Upadhyay\*, C. F. Baer. Comparing mutational and standing genetic variability for fitness and size in *Caenorhabditis briggsae* and *C. elegans*. *Genetics* 183:685–92, 2009.
11. **T. E. Keller**, I. J. Molineux, J. J. Bull. Viral resistance evolution fully escapes a rationally designed lethal inhibitor. *Molecular Biology and Evolution* 26:2041–46, 2009.
12. D. Ostrow, N. Phillips, A. Avalos\*, D. Blanton\*, A. Boggs\*, **T. Keller\***, L. Levy\*, J. Rosenbloom\*, C. F. Baer. Mutational bias for body size in rhabditid nematodes. *Genetics* 176:1653–61, 2007.

13. C. F. Baer, N. Phillips, D. Ostrow, A. Avalos\*, D. Blanton\*, A. Boggs\*, **T. Keller\***, L. Levy\*, E. Mez-erhane\*. Cumulative effects of spontaneous mutations for fitness in *Caenorhabditis*: role of genotype, environment and stress. *Genetics* 174:1387–95, 2006.

\* Undergraduate co-author

## Conference Presentations

Evolution in actin: a protein family drama.

International Evolution Society Conference, Norman, OK, 2011.

Interactions between evolutionary processes at high mutation rates.

International Evolution Society Conference, Portland, OR, 2010.

Quasispecies adapts to overcome mutation load: a problem for lethal mutagenesis?

Gordon Conference for Microbial Population Genetics, Andover, NH, 2009.

Evolution at high mutation rates: not as bad as we think.

International Evolution Society Conference, Minneapolis, MN, 2008.

## Conference Posters

DNA methylation and the evolutionary divergence of duplicate genes.

Society for Molecular Biology and Evolution, San Juan, Puerto Rico, 2014.

Divergence of methylation maps in humans and higher primates.

International Conference on Bioinformatics, Atlanta, GA, 2013.

## Mentoring

Supervised four undergraduate students and one high school student, which led to two publications.

Supervised one Master's student August 2014- August 2015.

## Professional Activities

Member, Society for the Study of Evolution, 2008–Present.

Member Society for Molecular Biology and Evolution 2013–Present.

## Professional Service

Reviewer, BMC Evolutionary Biology

Reviewer, Evolutionary Applications

Reviewer, Genome Research

Reviewer, PLoS Computational Biology

## Honors, Awards, & Fellowships

National Science Foundation Graduate Student Fellowship (Honorable Mention), 2007.

National Science Foundation Graduate Student Fellowship (Honorable Mention), 2006.

Houston Rodeo Fellowship, University of Texas at Austin, 2006.

Last updated: March 24, 2016