

Pengyao Jiang

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<https://pyjiang.github.io/>

Academic Employment

01/2024 – now	Assistant Professor in Biodesign Center for Mechanisms of Evolution and School of Life Sciences Arizona State University, Tempe, AZ
12/2022 – 11/2023	Acting Instructor in Genome Sciences University of Washington, Seattle, WA
01/2018 – 11/2022	Postdoctoral Scholar in Genome Sciences University of Washington, Seattle, WA Mentor: Kelley Harris, co-mentor: Maitreya Dunham
07/2017 – 12/2017	Postdoctoral Scholar in Ecology and Evolution The University of Chicago, Chicago, IL Mentor: John Reinitz, co-mentor: Martin Kreitman

Education

09/2010 – 06/2017	Ph.D. in Ecology and Evolution The University of Chicago, Chicago, IL Mentor: John Reinitz, co-mentor: Martin Kreitman
09/2006 – 06/2010	B.E. in Computer Science and Technology East China Normal University, Shanghai, China
02/2009 – 07/2009	Exchange student, Shanghai Jiao Tong University

Selected Honors and Awards

2020	Parker Travel Award for best poster at UW Genome Sciences retreat
2015	Systems Biology short course at UC Irvine full scholarship
2012	MBL Gene regulatory network course scholarship award
2010	Outstanding Graduates in Shanghai
2009	1 st Prize in China Undergraduate Mathematical Contest in Modeling (CUMCM)
2007, 2008	National Scholarship (<i>highest scholarship in China; top 2% of all university students</i>)

Publications and preprints

Armstrong JO*, **Jiang P***, Tsai S, Phan MM, Harris K, Dunham MJ. *URA6* mutations provide an alternative mechanism for 5-FOA resistance in *Saccharomyces cerevisiae*. *bioRxiv*. (2024):2024-06.

<https://doi.org/10.1101/2024.06.03.597250> (* Contributed equally)

Garge RK, Geck RC, Armstrong JO, Dunn B, Boutz DR, Battenhouse A, Leutert M, Dang V, **Jiang P**, Kwiatkowski D, Peiser T, McElroy H, Marcotte EM, Dunham MJ. Systematic Profiling of Ale Yeast Protein Dynamics across Fermentation and Repitching. *G3: Genes, Genomes, Genetics*. (2024) Mar;14(3):jkad293.

<https://doi.org/10.1093/g3journal/jkad293>

Jiang P, Kreitman M, Reinitz J. The effect of mutational robustness on the evolvability of multicellular organisms and eukaryotic cells. *Journal of Evolutionary Biology* 36(6), 906–924 (2023).
<https://onlinelibrary.wiley.com/doi/10.1111/jeb.14180>

Yeh CL, **Jiang P**, Dunham MJ. High-throughput approaches to functional characterization of genetic variation in yeast, *Current Opinion in Genetics & Development* 76 (2022): 101979.
<https://www.sciencedirect.com/science/article/pii/S0959437X22000880>

Jiang P, Ollodart AR, Dunham, MJ. A Modified Fluctuation Assay with a *CANI* Reporter in Yeast. *Bio-protocol* 12, no. 11 (2022): e4435-e4435. <https://bio-protocol.org/e4435>

Jiang P, Ollodart AR, Sudhesh, V, Herr AJ, Dunham MJ and Harris K. A modified fluctuation assay reveals a natural mutator phenotype that drives mutation spectrum variation within *Saccharomyces cerevisiae*. *eLife* (2021);10:e68285, <https://elifesciences.org/articles/68285>

Jiang P, Ludwig MZ, Kreitman M, Reinitz J. Natural variation of the expression pattern of the segmentation gene *even-skipped* in melanogaster. *Developmental biology* (2015), 405(1), 173-181.
<https://www.ncbi.nlm.nih.gov/pubmed/26129990>

He BZ, Ludwig MZ, Dickerson DA, Barse L, Arun B, Vilhjálmsson BJ, **Jiang P**, Park SY, Tamarina NA, Selleck SB, Wittkopp PJ, Bell GI, Kreitman M. Effect of genetic variation in a *Drosophila* model of diabetes-associated misfolded human proinsulin. *Genetics* 196, no. 2 (2014): 557-567.
<https://www.ncbi.nlm.nih.gov/pubmed/24281155>

Xu S, Jiao S, **Jiang P**, Ao P. Two-time-scale population evolution on a singular landscape. *Physical Review E*, (2014), 89(1), 012724. <https://www.ncbi.nlm.nih.gov/pubmed/24580274>

Jiao S, Xu S, **Jiang P**, Yuan B, Ao P, Wright–Fisher dynamics on adaptive landscape, *IET Systems Biology*, 7(5), 153-164. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8687433/>

Manuscripts in Preparation

Kim AR, **Jiang P**, Kang CK, Kreitman M, Ludwig MZ, Sharp DH, Reinitz J, Functional analysis of the *even-skipped* S2E enhancer in *Drosophilidae* and *Sepsidae*.

Jiang P, Sudhesh V, MM Phan, Bansal I, AJ Herr, MJ Dunham, Harris K, The natural history and effect of long-standing mild-effect mutator allele in *S. cerevisiae* populations

Reviewer

Science, The EMBO Journal, PLOS Biology, PLOS Genetics, PLOS Computational Biology, PLOS ONE, Genome Biology and Evolution, Molecular Ecology Resources, Journal of Molecular Evolution, Bioinformatics, Evolutionary Bioinformatics, Scientific Reports, Frontiers in Bioscience

Teaching

Apr. 2022	Instructor and facilitator for Girls Who Code (teaching coding for local high-school girls)
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Jan. 2012 – Teaching Assistant: Molecular Evolution I: Fundamentals and Principles
 Mar. 2012

Presentations

- 2024 Arizona State University, CME Tuesday seminar, **Oral**
 Measuring mutation spectrum from pooled mutants using Pacbio long-read sequencing in yeast
- 2024 North Carolina State University (*invited talk* for the Evolutionary Genetics Seminar), **Oral**
 Mutation rate and spectrum variation and evolution in *Saccharomyces*
- 2024 Arizona State University, MCB Colloquium, **Oral**
 Planned and unplanned: Natural variation's impact on mutation rate and spectrum and novel mutants growing in 5-FOA in *Saccharomyces cerevisiae*
- 2024 The Allied Genetics Conference (TAGC), Poster
 Mutation rate and spectrum variation and evolution in *Saccharomyces*
- 2023 SMBE Satellite Meeting on Mechanisms of Cellular Evolution, **Oral**
 The effect of mutational robustness on the evolvability of multicellular organisms and eukaryotic cells
- 2023 Pacific Northwest Yeast Club, **Oral**
 Mutation rate and spectrum variation and evolution in *Saccharomyces*
- 2022 University of Iceland (*invited talk* for Biology Seminar), **Oral**
 Uncovering natural histories of mutator alleles in budding yeast
- 2022 Yeast Genetics Meeting, **Oral**
 Uncovering natural histories of mutator alleles in budding yeast
- 2022 Population, Evolutionary, and Quantitative Genetics Conference (PEQG), Poster
 Uncovering natural histories of mutator alleles in budding yeast
- 2021 Society for Molecular Biology & Evolution (SMBE), Virtual Poster
 Mutation rate and spectrum variation in *S. cerevisiae* natural isolates
- 2021 The Biology of Genomes, Virtual Poster
 Mutation rate and spectrum variation in *S. cerevisiae* natural isolates
- 2020 The Allied Genetics Conference (TAGC), Virtual Poster
 Mutation rate and spectrum variation in *S. cerevisiae* natural isolates
- 2019 Gordon conference on Molecular Mechanisms in Evolution, Poster
 Mutation rate and spectrum variation in *S. cerevisiae* natural isolates
- 2016 SIAM Life Sciences, **Oral**
 The relationship between mutational robustness and adaptation
- 2016 The Allied Genetics Conference (TAGC), Poster
 The relationship between mutational robustness and adaptation

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| 2015 | Annual Drosophila Research Conference, Poster
Testing the role of <i>Caudal</i> in activating <i>eve</i> stripe 2 expression in sepsid fly <i>T. putris</i> |
| 2014 | Midwest Drosophila Conference, Oral
Natural variation in <i>eve</i> expression in <i>D. melanogaster</i> |
| 2014 | Annual Drosophila Research Conference, Poster
Natural variation in <i>eve</i> expression in <i>D. melanogaster</i> |

Outreach and Service

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| 2024 | ASU Undergraduate Research Symposium poster judge |
| 2022 | Symposium of Molecular Evolution: In Honor of Marty Kreitman's Scientific Career
organizing committee member |
| 2022 | PEQG Conference poster judge on Evolutionary Genetics |
| 2021 | Moderator of Undergraduate Research Symposium at University of Washington |
| 2021 | SMBE Conference online hub organizing committee member |
| 2021 | Genome Sciences Alumni Symposium planning committee member |
| 2021 | Skype a scientist, with 5th grade Medina Elementary School students |
| 2018 | Fulbright interviewer at University of Washington |
| 2018 | Science judge for Northwest Association for Biomedical Research (NWABR) "Biomedical Breakthroughs and My Life" Middle School Contest |