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	1st Prize in China Undergraduate Mathematical Contest in Modeling (CUMCM)
2007, 2008	National Scholarship *(highest scholarship in China; top 2% of all university students)*

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 *CAN1* 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, Nature, The EMBO Journal, PLOS Biology, PLOS Genetics, PLOS Computational Biology, PLOS ONE, Molecular Biology and Evolution, Genome Biology and Evolution, Molecular Ecology Resources, Journal of Molecular Evolution, Bioinformatics, BMC Genomics, Evolutionary Bioinformatics, Scientific Reports, Frontiers in Bioscience

Teaching

Spring 2025	BIO439/539: Computing for Research (116 online students)

Fall 2024	BIO 340: General Genetics (250 students)
Apr. 2022	Instructor and facilitator for Girls Who Code (teaching coding for local high-school girls)

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

Outreach and Service

2024, 2025	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