

Pengyao Jiang

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Department of Genome Sciences

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Training and Education

2018 – 2022 <i>Current</i>	Postdoctoral Scholar in Genome Sciences University of Washington, Seattle, WA
2010 – 2017	Ph.D. in Ecology and Evolution The University of Chicago, Chicago, IL
2006 – 2010	B.E. in Computer Science and Technology East China Normal University, Shanghai, China

Research experience

2018 – 2022	University of Washington – <i>Postdoctoral Scholar</i> Mentor: Kelley Harris , co-mentor: Maitreya Dunham Theme: Experimental and computational analysis of mutation rate and spectrum variation in yeast - Project 1: Uncovering natural mutator alleles in haploid <i>Saccharomyces cerevisiae</i> - Project 2: Meta-analysis of mutation spectrum variation in different <i>Saccharomyces</i> yeast species - Project 3: Testing the consequences of possible mutator allele gene flow between two <i>Saccharomyces cerevisiae</i> populations - Project 4: Mutation rate and spectrum variation with aging in <i>Saccharomyces cerevisiae</i>
2010 – 2017	The University of Chicago – <i>Ph.D. Student</i> Mentor: John Reinitz , co-mentor: Martin Kreitman Thesis: Experimental and computational analysis of canalization and its relation to evolution and development - Project 1: <i>eve</i> expression variation among inbred lines derived from natural isolates of <i>Drosophila melanogaster</i> - Project 2: Experimentally testing the role of <i>Caudal</i> in activating <i>eve</i> stripe 2 expression in sepsid fly <i>Themira putris</i> - Project 3: Theoretical modeling and simulation to explore the relationship of mutational robustness to adaptation in multi-cellular organisms
2009 – 2010	Shanghai Jiaotong University – <i>Exchange Student</i> Mentor: Ping Ao Thesis: Modeling the Wright Fisher model using adaptive landscape framework

Publications

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/>

Preprints

Jiang P, Kreitman M, Reinitz J. The effect of mutational robustness on the evolvability of multicellular organisms. *bioRxiv* (2021), under review at the *Journal of Evolutionary Biology*,
<https://www.biorxiv.org/content/10.1101/268862v2>

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, Bansal I, Harris K, Mutation spectra variation in the *Saccharomyces* genus.

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>)

Teaching and Mentoring

July 2022 – now	Mentoring Megan Phan: an undergraduate research student on experimentally collecting and measuring mutation spectra from natural populations and aging <i>Saccharomyces cerevisiae</i>
Apr. 2022	Instructor and facilitator for Girls Who Code (teaching coding for local high-school girls)
Aug. 2019–May 2022	Mentoring Vidha Sudhesh: an undergraduate research student on experimentally measuring mutation rates and spectra in <i>Saccharomyces cerevisiae</i>
Jan. 2019 – June 2022	Mentoring Ishan Bansal: a high school intern on computational analysis of mutation spectrum using natural polymorphisms in different <i>Saccharomyces</i> yeasts
Jan. 2012 – Mar. 2012	Teaching Assistant: Molecular Evolution I: Fundamentals and Principles

Reviewer

PLOS ONE, Scientific Reports, Genome Biology and Evolution, Bioinformatics, Evolutionary Bioinformatics, Frontiers in Bioscience

Short Courses and Workshops

2021	Teaching workshop at Genome Sciences
2021	Summer Institute in Statistical Genetics on Quantitative Genetics at UW
2020	Future Faculty Fellows workshop
2015	Systems Biology short course at UC Irvine
2012	MBL Gene Regulatory Network Course
2011	10-week Teaching Assistant Training Class at the University of Chicago

Presentations

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 <i>S. cerevisiae</i> natural isolates
2021	The Biology of Genomes, Virtual Poster Mutation rate and spectrum variation in <i>S. cerevisiae</i> natural isolates
2020	The Allied Genetics Conference (TAGC), Virtual Poster Mutation rate and spectrum variation in <i>S. cerevisiae</i> natural isolates

2019	Gordon conference on Molecular Mechanisms in Evolution, Poster Mutation rate and spectrum variation in <i>S. cerevisiae</i> 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 <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

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

Reference

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