

Chenlu Di

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University of California, Los Angeles

Dept. of Ecology and Evolutionary Biology

Education

Department of Ecology and Evolutionary Biology, University of Arizona 08/2016-01/2023

Ph.D. in Ecology and Evolutionary Biology

Zhejiang University 09/2012- 07/2016
Bachelor in Applied Biological Science, B.S. in Agronomy

Employment

Kirk Lohmueller Lab, Department of Ecology and Evolutionary Biology, University of California Los Angeles 01/2023-

Postdoc researcher

Prizes and scholarships

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| 2021,2022 | The Galileo Circle Scholarship |
| 2018-2021 | William A. Calder III scholarship |
| 2016 | Distinguished student social work award |
| 2016 | Distinguished poster in the National Agriculture conference for college students, Hefei, China |

Publications

1. **Chenlu Di** and Kirk Lohmueller. 2023. Revisiting dominance in population genetics. in minor revision, *Genome Biology and Evolution*.
2. **Chenlu Di**, Jesus Murga Moreno and David Enard. 2022. Stability evolution as a major mechanism of human protein adaptation in response to viruses. bioRxiv 2022.12.01.518739; doi: <https://doi.org/10.1101/2022.12.01.518739>; in revision, *Molecular Biology and Evolution*.
3. **Chenlu Di**, Jesus Murga Moreno, Diego Salazar Tortosar, M. Elise Lauterbur and David Enard. 2021. Decreased recent adaptation at human mendelian disease genes as a possible consequence of interference between advantageous and deleterious variants.

Elife 10:e69026.

5. Xinshuai Qi, Hong An, Tara E. Hall, **Chenlu Di**, Paul D. Blischak, Michael T.W. McKibben, Yue Hao, Gavin C. Conant, J. Chris Pires and Michael S. Barker. 2021. Genes derived from ancient polyploidy have higher genetic diversity and are associated with domestication in *Brassica rapa*. *New Phytologist*, 230: 372-386.
6. Xiaobai Li, Weirui Li, **Chenlu Di**, Ming Xie, Liang Jin, Cheng Huang and Dianxing Wu. 2016. Development of Genic Simple Sequence Repeat Panels for Population Classification of Chinese Cymbidium Species, *Journal of the American Society for Horticultural Science*, 141(2):125–130.

Manuscript in prep:

1. Peter Chesson and **Chenlu Di**. A comprehensive theoretical framework for the Janzen-Connell hypothesis. In prep.
2. **Chenlu Di** and Kirk Lohmueller. The landscape of the distribution of fitness effects of non-coding mutations in the human genome. In prep.

Research experience

Effects of non-coding mutations

02/2023-

Evolutionary studies on non-coding mutations can provide clues of mechanisms and treatments of human complex diseases.

Kirk
Lohmueller
lab (UCLA)

Polymorphisms in non-coding regions have been found to be associated with many complex diseases. However, little has been known about how non-coding mutations influence fitness. I am currently inferring the fitness effects of non-coding mutations, such as mutations on enhancers, promoters, and other annotated genomic regions using human 1000 Genome data.

06/2018

Dissertation Project, The relationship between adaptation and human diseases.

-12/2022

David Enard
Lab (UA)

Treatment and prevention of human disease can benefit from understanding human adaptation to diseases.

- Chapter 1: Testing and packaging a gene enrichment test pipeline that controls for confounding factors
- Chapter 2: Evidence that interference between deleterious and advantageous mutations impedes recent adaptation in human Mendelian disease genes (Paper published in eLife)
- Chapter 3: Adaptation against past viral infections happened by changing

protein stabilities at less exposed sites in virus-interacting proteins (Paper in biorxiv.)

Side Project, Janzen-Connell hypothesis

- Comprehensive theoretical framework for how natural enemies promote diversity of species, genotypes, and plant mating systems, updating the Janzen-Connell hypothesis (Paper in prep.)
- Individual-based, geographic information integrated simulation (GAUSS)
- Constructing community ecological model

06/2018
-present
Peter
Chesson Lab
(UA)

Co-researcher, Genes derived from ancient polyploidy have high genetic diversity and are associated with domestication in *Brassica rapa*

- Found that in *Brassica rapa*, there is more genetic diversity but less variation in expression levels in paleologs compared with non-paleologs (Paper published in New Phytologist)

09/2016-
12/2016
Michael
Barker lab
(UA)

A major likelihood approach gives problematic estimates of diversification dynamics and rates

- Evaluated the accuracy of RPANDA, an R package used to infer the diversification models and rates using simulated phylogenetic trees

01/2017
-06/2019
John Wiens
lab (UA)

Co-researcher, Screening hepatitis C virus in 1970's serum samples

- Tried to recover hepatitis C virus sequences using a highly sensitive method developed by Worobey lab

Fall, 2016
Michael
Worobey lab
(UA)

Project Leader, CRISPR/Cas9 based screening of DNA repair genes and exploring the mechanism of CRISPR in cells with high DNA repairing ability

2014-2016
Ye Zhao Lab
(ZJU)

Research Assistant, Development of genic SSR panels for population classification of Chinese cymbidium species

- Built genic SSR panels through selecting markers by WHICHLOCI (Paper published in Journal of ASHS)

04/2015-
05/2015
Xiaobai Li
Lab (ZJU)

Research Assistant, Search for mutations in miscanthus that controls its non-shattering phenotype

- Phylogenetic analysis of *Miscanthus* based on qSH1 gene.
- Analysis of the geographic distribution of gathered samples of *Miscanthus*

07/2015-
08/2015
Erik Sacks
Lab (UIUC)

Conference, talks and posters

Invited talk

- 2024 2024 Plant Ecology Workshop in Taiwan, Keynote Speech Section
The Janzen-Connell Hypothesis for Diversity Maintenance in Tropical Forests: Lessons From General Ecological Theory
 Co-author, Peter Chesson gave the actual talk.

Oral presentation

- 2024 Southern California Evolutionary Genetics and Genomics Meeting
Inference of fitness effects of mutations in non-coding regions of the human genome
- 2023 University of California, Los Angeles, QCBio Research-in-Progress Seminar
Inference of fitness effects of mutations in non-coding regions of the human genome
- 2022 Women in Data Science Tucson Virtual Conference
Explore the evolution in human disease genes by public human genomic data
- 2021 Society for Molecular Biology and Evolution (SMBE)
Decreased adaptation at human disease genes as a possible result of low recombination between deleterious and advantageous variants
- 2021 Cold Spring Harbor Laboratory (CSHL) Probabilistic Modeling In Genomics, (competitive)
The causes of strongly depleted recent adaptation in human disease genes
- 2020 Club EvMed — Virtual Evolutionary Medicine Conversations
The causes of strongly depleted recent adaptation in human disease genes
- 2020 Annual Arizona Astrobiology Research Symposium
The causes of strongly depleted recent adaptation in human disease genes
- 2019 Bay Area Population Genomics
The causes of strongly depleted recent adaptation in human disease genes

Posters

- 2023 Society for Molecular Biology and Evolution (SMBE)
How human protein adapt in response to viruses? Altering protein stability as a major mechanism
- 2022 Population, Evolutionary, and Quantitative Genetics Conference
Does adaptation to past viral infections drive the changes in protein stabilities for virus-interacting proteins?

Teaching experience

Lectures

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| Fall, 2021 | Graduate teaching assistant in Intro Biology online course |
| Spring, 2019-2021 | Graduate teaching assistant in Population genetics |
| Fall, 2016-2020 | Graduate teaching assistant in Genetics |

Spring, 2017 Graduate teaching assistant in Evolution

Spring, 2018 Graduate teaching assistant in Animal Sexual Behavior

Workshops

2021 ResBaz Arizona: assistant in a python workshop

Local / Community Service and Outreach

2019-2023 Executive member of Chinese Genomics Meet-up online (a US non-profit organization). Secretariat since 2022.

2021 Volunteer in ResBaz Arizona: ran a python workshop

2021 Poster Fair judges for undergrads, Department of Ecology and Evolutionary biology, University of Arizona

Skill Sets

Coding skill: Skilled at R/Python/Unix, high-throughput computing and pipeline construction. Some experience in Julia, Java and Gauss and building containers.

Knowledge of public human genomic resources: Ensembl genomes database, 1000 Genomes Project, UCSC genome browser, Uniprot, AlphaFold, SWISS-MODEL and the UK Biobank and DisGeNet.

Modeling: Individual and population-based modeling in community ecology and some experience in simulating population dynamics with SLiM.

Statistical tools: Generalized linear models (GLM) including mixed models (GLMM); Permutation tests; approximate bayesian computation (ABC); Using AIC for model selection and comparison.

Experimental: DNA and RNA extraction; DNA recombination; culturing bacteria; viron extraction; fluorescence microscope, western blot.