# 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** 

Bachelor in Applied Biological Science, B.S. in Agronomy

09/2012-07/2016

### **Employment**

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

Postdoctoral Researcher

#### **Publications**

- 1. **Chenlu Di**, Kirk E Lohmueller, 2024. Revisiting dominance in population genetics. *Genome Biology and Evolution*, 16, no. 8: evae147.
- 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. (old model)
- 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.
- 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.

#### Paper in revision

5. Chenlu Di\*, Carlos Eduardo G. Amorim\*, Meixi Lin, Clare Marsden, Christina A. Del

Carpio, Jonathan C. Mah, Jacqueline A. Robinson, Bernard Y. Kim, Jazlyn A. Mooney, Omar E. Cornejo, Kirk E. Lohmueller. 2024. Evolutionary consequences of domestication on the selective effects of new amino acid changing mutations in canids. *bioRxiv* 2024.11.13.623529. (\*contributed equally)

 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. (in revision at *Molecular Biology and Evolution*)

### Preprint

7. **Chenlu Di**, Swetha Ramesh, Jason Ernst, Kirk E. Lohmueller. 2025. The landscape of fitness effects of putatively functional noncoding mutations in humans. bioRxiv 2025.05.14.654124

#### **Prizes and Scholarships**

2025	Society of Molecular Biology and Evolution: Young Investigator Attendance Award
2021, 2022	The Galileo Circle Scholarship
2018, 2019, 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

### Conference, Talks and Posters

#### Invited talks

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 Presented by Peter Chesson
2024	Invited talk at Westlake University, China The interplay between natural selection and diseases in human genome

## Oral presentations

2024	Young Evolutionary Researchers' Symposium at Zhejiang University, China The landscape of fitness effects of putatively functional noncoding mutations in humans
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	
2024	Society for Molecular Biology and Evolution (SMBE)  The distribution of fitness effects of mutations in enhancers, promoters and conserved non-coding regions
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

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

Workshop

2021 ResBaz Arizona: assistant at a python workshop

## **Professional Service**

**Reviewer:** BCM genomics, Ecology

## **Local / Community Service and Outreach**

2024	Judges at poster fair for undergrads, Department of Ecology and Evolutionary biology, University of California, Los Angeles
2023	Mentor for undergrads for Society for Molecular Biology and Evolution (SMBE) conference at Ferrara, Italy
2019-2023	Executive member of Chinese Genomics Meet-up online (a US non-profit organization).
2022-2023	Secretary of Chinese Genomics Meet-up online (a US non-profit organization).
2021	Volunteer in ResBaz Arizona: a python workshop
2021	Judges at poster fair for undergrads, Department of Ecology and Evolutionary biology, University of Arizona