Chenlu Di

Email: chenludi6@gmail.com
cdi@email.arizona.edu

Dept. of Ecology and Evolutionary Biology

Education

Department of Ecology and Evolutionary Biology, University of Arizona
Ph.D. candidate

08/2016-present

College of Agriculture & Biotechnology, Zhejiang University
Major in Applied Biological Science, B.S. in Agronomy

09/2012- 07/2016

Research grants

2015-2016	Project leader, Science & Technology Innovation Plan (Xinmiao Talents Plan) of College Students in Zhejiang Province	~$1,000
2015-2016	Project leader, Zhejiang University Student Research Training Program	~$350
2014-2015	Project leader, Zhejiang University Student Independent research platform	~$160

Prizes and scholarships

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**, Diego Salazar Tortosar, M. Elise Lauterbur and David Enard. Decreased recent adaptation at human mendelian disease genes as a possible consequence of interference between advantageous and deleterious variants. *Elife* **10**:e69026. 2021.

2. **Chenlu Di** and David Enard. Gene set enrichment analysis of genome scans for positive selection. In revision.

3. **Chenlu Di**, Andreas L. S. Meyer and John J. Wiens. A major likelihood approach gives problematic estimates of diversification dynamics and rates. In revision.

4. Peter Chesson and **Chenlu Di**. A comprehensive theoretical framework for the Janzen-Connell hypothesis. In prep.

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. Genes derived from ancient polyploidy have higher genetic diversity and are associated with domestication in Brassica rapa. New Phytol, 230: 372-386. 2021

6. Xiaobai Li, Weirui Li , **Chenlu Di**, Ming Xie, Liang Jin, Cheng Huang and Dianxing Wu. 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. 2016

Skill Sets

Coding skill: R/Python/Unix programming environments; Running jobs on remote clusters; Using containers; Text, table, and file manipulation with regular expressions; Pipeline construction; Some experience in Java and Gauss; Reading scripts in Perl and Julia.

Knowledge of public human genomic resources: Ensembl genomes database**,** 1000 Genomes Project, Uniprot, 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; Using AIC for model selection and comparison.

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

Research experience

Dissertation Project, The relationship between adaptation and human diseases. *Treatment and prevention of human disease can benefit from understanding human adaptation to diseases.*	06/2018 -present David Enard Lab (UA)

- Chapter 1: Testing and packaging a gene enrichment test pipeline that controls for confounding factors (Paper in revision)
- Chapter 2: Evidence that interference between deleterious and advantageous mutations impedes recent adaptation in human Mendelian

disease genes (Paper published in eLife)
- Chapter 3: How does past adaptation, especially past adaptation to viruses, happen at the protein level? (Paper in prep)

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
- 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 and talks

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), Oral presentation
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, Oral presentation (competitive)
The causes of strongly depleted recent adaptation in human disease genes

2020   Club EvMed — Virtual Evolutionary Medicine Conversations, Oral presentation
The causes of strongly depleted recent adaptation in human disease genes

2020   Annual Arizona Astrobiology Research Symposium, Oral presentation
The causes of strongly depleted recent adaptation in human disease genes

2019   Bay Area Population Genomics, Oral presentation
The causes of strongly depleted recent adaptation in human disease genes

Teaching experience

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

Local / Community Service and Outreach

2019-present   Executive member of Chinese Genomics Meet-up online, a US non-profit organization. Secretariat since 2022

2021   Volunteer in ResBaz Arizona: helping with an online workshop on Python

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

2015   Volunteer in children education on evolution in Zhejiang Province Museum of Natural History

2013   Weekly volunteer in Liuxia Public Medical Station for a year