<div align="center">**CURRICULUM   VITAE**</div>

Name: Lingbin Ni

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EDUCATION

Ph.D. in Bioinformatics, June 2023, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, China.

Minor in Computer Science and Technology, June 2017, University of Chinese Academy of Sciences, Beijing, China.

B.S. in Seed Science and Engineering, June 2016, Shandong Agricultural University, Tai'an, China.

RESEARCH EXPERIENCES

2016-2023 Institute of Genetics and Developmental Biology, Chinese Academy of Sciences

Supervisor: Prof. Zhixi Tian

1. Pan-3D genome analysis, SV identification, and expression analysis of soybean accessions

2. Genome assembly and annotation of a high-quality Chinese soybean genome

3. Development of an integrated database on soybean multi-omics

2014-2016 College of Agronomy, Shandong Agricultural University

Supervisor: Prof. Pinghua Li

1. Transcriptome analysis of multiple development stages of maize leaves

2. Field trial of maize hybrids

HONORS AND AWARDS

Excellent Poster Award, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, 2023

Postgraduate Scholarship, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences,2021

Merit Student, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, 2021

Outstanding Graduate, Shandong Agricultural University, 2016

DuPont Pioneer Scholarship, Shandong Agricultural University, 2016

Merit Student, Shandong Agricultural University, 2014

Excellent Student Scholarship, Shandong Agricultural University, 2012-2016

CONFERENCE PRESENTATIONS

Oral presentation:

State Key Laboratory of Plant Cell and Chromosome Engineering Summer Meeting, July 2022, Beijing

Poster presentation:

State Key Laboratory of Plant Cell and Chromosome Engineering Winter Meeting, February 2023, Beijing

SCIENTIFIC PUBLICATIONS

Ni L, Liu Y, Ma X, Liu T, Yang X, Wang Z, Liang Q, Liu S, Zhang M, Wang Z, et al. (2023). Pan-3D genome analysis reveals structural and functional differentiation of soybean genomes. Genome Biol 24, 12.

Ni L, Tian Z. (2023). Toward cis-regulation in soybean: a 3D genome scope. Mol Breeding (Accepted).

Liu Y, Zhang Y, Liu X, Shen Y, Tian D, Yang X, Liu S, **Ni L**, Zhang Z, Song S, Tian Z. (2023). SoyOmics: A deeply integrated database on soybean multi-omics. Mol Plant (Under review).

Gu D, Chen D, Liang Q, Zhang M, Chen L, **Ni L**, Qin H, Wu Z, Wang L, Jin L, et al. (2023). Natural variation in legume shoot branching 1 regulates shoot branching and enhances yield in soybean. Nat Plants (Under review).

Liu Y, Liu S, Zhang Z, **Ni L**, Chen X, Ge Y, Zhou G, Tian Z. (2022). GenoBaits Soy40K: a highly flexible and low-cost SNP array for soybean studies. Sci China Life Sci 65, 1898-1901.

Shen Y, Du H, Liu Y, **Ni L**, Wang Z, Liang C, Tian Z. (2019). Update soybean Zhonghuang 13 genome to a golden reference. Sci China Life Sci 62, 1257-1260.

RESEARCH INTERESTS

In the past few years, I was interested in the 3D genome organization and *cis*-regulatory elements in plants. Taking the pan-omics approach, I developed a pipeline to identify the conservation and variation across crop accessions of A/B compartments and TADs – the most important components in 3D genome. This work constructed the first pan-3D genome relative to crop domestication, and represented a detailed investigation on 3D genomic diversity beyond genomic diversity across crop accessions. Meta-analysis demonstrated that non-LTR retrotransposons played important roles in maintaining TAD boundaries, while Gypsy elements and satellite repeats are associated with establishment of private TAD boundaries. Benefiting from the high-quality genome assemblies of diverse accessions, I analysed the relationship between 3D genomic variation and genomic SVs. These results highlighted the dominant role of PAV in reshaping 3D genome, revealing the evolutionary route of diverse TE families to reshape 3D genome by driving SVs. Furthermore, I also found that 3D genome may undergo selection during domestication and improvement, which altered 3D genome atlas, and changed gene expressions by avoiding CDS variation. Additionally, as a participant, I also took part in researches of genome assembly, database development, ATAC-seq, and scRNA-seq in Tian Lab.

I enjoy using computational approaches to understand the fundamental principles underlying genomic structure and function, and applying those principles to address challenges in biology and health. Current interests include, among others, decoding the transcriptional regulation of genomes and epigenomes; developing and applying new technologies including single-cell sequencing, spatial omics, and machine learning to address foundational questions; and developing tools and resources for high-throughput sequencing analysis, which help to inform the in-depth mechanistic studies.

RESEARCH SKILLS

Biology: 3D genome, Structural variation, Gene regulation, Genome assembly, ATAC-seq, scRNA-seq

Computer science: R language, Perl language, Python language, Shell script, Database

Statistics: Biostatistics, Machine learning

MENTORING EXPERIENCES

Songfeng Liu, Zhao Wang (Institute of Genetics and Developmental Biology, Chinese Academy of Sciences)

REFERENCES

Professor Zhixi Tian (Ph.D. advisor)

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