

# Curriculum Vitae

---

## Personal Information

**Family Name:** Lan

**Given Name:** Lan

**Nationality:** China

**E-mail:** lanlan1995.research@gmail.com; [34648864@student.murdoch.edu.au](mailto:34648864@student.murdoch.edu.au)

**Google Scholar page:** <https://scholar.google.com.hk/citations?user=fUjYGrgAAAAJ&hl=en>

**X homepage:** [https://x.com/Lan\\_Orz](https://x.com/Lan_Orz)

**Github:** <https://github.com/LanLBio>

---

## Education & Career

Dec. 2022 – Present (supposed to be Dec. 2025)      PhD Study on Bioinformatics

Murdoch University

Sep. 2021 – Aug. 2022      Research assistant

Agricultural Genomics Institute at Shenzhen (AGIS), Chinese Academy of Agricultural Sciences (CAAS)

Sep. 2020-Aug. 2021      Research assistant

Chongqing Normal University

Sep. 2017 - Jul. 2020      Master's degree in Biochemistry and Molecular Biology

Chongqing Normal University

Sep. 2013 - Jul. 2017      Bachelor's degree in Biotechnology

Yanbian University

---

## Research Summary

I am an inquisitive and versatile genome adventurer with extensive experience across multiple research institutions, where I have cultivated a broad scientific perspective spanning both animal (honeybee species) and plant systems.

I am expert in genomic data analysis, master the extensive methods of comparative genomic and population genomic analysis. My research is at the interface of genetics, evolution and genome selection. My research aims to: **First**, understand genetic changes underlying the domestication and environmental adaptation and phenotypic divergence. **Second**, explore demographic and evolutionary histories of the current species and predict their future adaptations and distributions in response to global climate change.

My work is driven by a deep passion for genomic exploration and a commitment to challenging conventional boundaries. With a strong foundation in genomics and a proven track record of

interdisciplinary collaboration, I bring an adventurous spirit and an insatiable curiosity for innovation. I actively seek intellectual intersections across disciplines to spark transformative ideas. My goal is to leverage both my technical expertise and creative problem-solving skills to advance scientific knowledge and contribute to meaningful, inspiring breakthroughs.

---

## Research Experience

### Murdoch University

State Agricultural Biotechnology Centre (SABC), College of Science, Health, Engineering and Education,  
Jul.2024 – Present      PhD candidate      Supervisor: Chengdao Li (c.li@murdoch.edu.au)

- Digging into the subtle signal from the introgression and incomplete lineage sorting (ILS) events. Combining the genome selection results with the rebuilt domestication/breeding/evolutionary history to define new breeding milestones for cereals (including barley, oats and Lupinus).
- Focusing on deciphering the breeding history of different cereals, exploring potential selected regions and genes during breeding history.
- Exploring the genes and markers that regulate important agronomic traits to support the improvement of cereal crops.

### AGIS, CAAS

Plant genomics center, Aug.2021 - Jul.2024      Research assistant & PhD candidate      Supervisor: Zhiqiang Wu ([wuzhiqiang@caas.cn](mailto:wuzhiqiang@caas.cn))

- Started my PhD study under the collaboration project between Murdoch University and AGIS, Chinese Academy of Agricultural Sciences.
- Focused on floral genomics, utilizing cutting-edge pangenome and comparative genomic approaches to reveal evolutionary patterns and trait variations in *Bougainvillea*, *Dianthus caryophyllus*, and Rose species.
- Published the first high-quality, chromosome-level *Bougainvillea* genomes and the first telomere-to-telomere (T2T), haplotype-resolved *Dianthus caryophyllus* genome. Uncovered the evolutionary history of multiple whole-genome duplication events and widespread ancestral introgression within the Caryophyllales. Investigated the relationship between genome architecture and gene expression levels, and identified that transposable element (TE) insertions can significantly suppress gene expression.
- Organized the workshops on advanced genomics, covering topics such as T2T genome assembly, pangenome construction, and their practical applications in genomic research.
- Since 2022, join the non-profit academic research group of Chinese Genomics Meet-up (CGM), help manage the academic communities and events.

## Chongqing Normal University

School of Life Sciences, Sep.2017 - Jul.2021

Master's degree

Supervisor: Jinshan Xu

(xujinshan2008@cqnu.edu.cn)

- I started my bioinformatics training in population genetics, continuously building my theoretical knowledge and research skills in genomics.
  - Focused on the *Apis cerana* comparative genomics and population genetics studies. Reveal the different evolutionary results of olfactory receptors in *Apis cerana* from different geographical environments. Identified the basic molecular mechanism for high-altitude groups which can help to adapt to low temperatures.
- 

## Research skills

- ✓ My research career began in 2017 with my Master's degree, and since then, I have continuously developed and refined my expertise in bioinformatics.
  - ✓ I focus on genomics, with expertise spanning population genomics, comparative genomics, complex genome assembly (including telomere-to-telomere and polyploid assemblies), pangenome construction, evolutionary selection analysis, and phylogenetic reconstruction.
  - ✓ Extensive knowledge and experience in various sequencing technologies, assembly methods, genome annotation pipelines, and comparative genomics analysis workflows.
  - ✓ Expertise in population genomics, including variant calling, population structure analysis, dynamic demographic history reconstruction, genome-wide association studies (GWAS), and detection of both hard and soft selective sweeps.
  - ✓ I have a strong interest in phylogenetics, with proficiency in analyzing introgression and incomplete lineage sorting (ILS) events. I strive to explore the connections among different types of selection, breeding and evolutionary history, and introgression/ILS dynamics.
  - ✓ Proficient in utilizing a wide range of genomic analysis software and pipelines (e.g., GATK, hifiasm, etc.), and continuously integrating innovative methodologies into my research workflow to ensure cutting-edge genomic analyses.
  - ✓ Experienced in Python, R, and Linux environments.
- 

## Awards

1. In 2023, The outstanding oral presentation award, Yangling, China, from Chinese Society for Horticultural Science.
2. In 2023, The third-class award of excellent presentation award, Shenzhen, China, from Shenzhen Botanical Society.
3. In 2017-2020, Scholarships for postgraduate studies, Chongqing, China, from Chongqing

Normal University.

4. In 2017, the second-class award of “Challenge Cup” Chinese College Student Entrepreneurship Plan Competition, China, in Jilin province.
  5. In 2017, the third-class award of “Challenge Cup” Chinese College Student Entrepreneurship Plan Competition, China, on a nationwide scale.
- 

## **Publications (#as first author, \*as correspondence author)**

1. **Lan L#**, Zhao H#, Xu S, Kan S, Zhang X, Liu W, Liao X, Tembrock LR, Ren Y, Reeve W, Yang J\*, Wu Z\*: A high-quality *Bougainvillea* genome provides new insights into evolutionary history and pigment biosynthetic pathways in the Caryophyllales. *Horticulture Research* 2023, 10(8):uhad124. **(As cover article). IF=8.7, JCR=Q1.**
2. **Lan L#**, Leng L#, Liu W#, Ren Y, Reeve W, Fu X, Wu Z\*, Zhang X\*: The haplotype-resolved T2T carnation (*Dianthus caryophyllus*) genome reveal the correlation between genome architecture and gene expression. *Horticulture Research* 2023, 11(1). **IF=8.7, JCR=Q1.**
3. XXX#, **Lan L#**, XXX#, XXX#, XXX, XXX, XXX, XXX, XXX, XXX, XXX, XXX, XXX, XXX \*, XXX \*, Wu Z\*, XXX \*: The pangenome of the XXX uncovers massive structure variations for allele mining to empower breeding. *Nature Genetics*, under third round review.
4. **Lan L#**, Li H#, Xu S, Xu Y, Leng Q, Zhang L, Wu L, Yin J, Wu Z\*, Niu J\*: Chromosome-level and haplotype-resolved genome assembly of *Bougainvillea glabra*. *Scientific Data* 2025, 12(107). **IF = 5.8, JCR=Q1.**
5. **Lan L#\***, Hu H, Jia Y, Zhang X, Jia M, Li C, Wu Z: Tips for improving genome annotation quality. *Genomics Communications* 2025, 2(1).
6. Shen JS#, **Lan L#\***, Kan S, Cheng H, Peng D, Wan Z, Hu Y, Huang X, Li X, Ye Y, Tembrock L, Wu Z\*, Jin S\*: A haplotype - resolved genome for *Rhododendron* × *pulchrum* and the expression analysis of heat shock genes. *Journal of Systematics and Evolution* 2024, 62(3):489-504. **IF=3.4, JCR=Q1.**
7. **Lan L#**, Shi P, Song H, Tang X, Zhou J, Yang J, Yang M, Xu J\*: De novo genome assembly of chinese plateau honeybee unravels intraspecies genetic diversity in the eastern honeybee, *Apis cerana*. *Insects* 2021, 12(10):891. **IF=3.1, JCR=Q1.**
8. Lin D#, **Lan L#**, Zheng T, Shi P, Xu J\*, Li J\*: Comparative genomics reveals recent adaptive evolution in Himalayan giant honeybee *Apis laboriosa*. *Genome Biology and Evolution* 2021, 13(10):evab227. **IF=4.0, JCR=Q2.**
9. Kan S#, Liao X#, **Lan L**, Kong J, Wang J, Nie L, Zou J, An H, Wu Z\*: Cytonuclear interactions and subgenome dominance shape the evolution of organelle-targeted genes in the *brassica* triangle of U. *Molecular Biology and Evolution* 2024, 41(3):msae043. **IF=11, JCR=Q1.**
10. Zhang X#, Wu Q#, **Lan L**, Peng D, Guan H, Luo K, Bao M, Bendahmane M\*, Fu X\*, Wu Z\*: Haplotype-resolved genome assembly of the diploid *Rosa chinensis* provides insight into the mechanisms underlying key ornamental traits. *Molecular Horticulture* 2024, 4(1):14. **IF=10, JCR=Q1.**
11. Shi P#, Zhou J, Song H, Wu Y, **Lan L**, Tang X, Ma Z, Vossbrinck CR, Vossbrinck B, Zhou Z, Xu J\*: Genomic analysis of Asian honeybee populations in China reveals evolutionary relationships and adaptation to abiotic stress. *Ecology and Evolution* 2020, 10(23):13427-13438. **IF=2.3, JCR=Q2.**