

Quanyu Chen

Center for Evolutionary & Organismal Biology | Zhejiang University | Hangzhou, China

Email: chenquanyu@zju.edu.cn

[Google Scholar](#) | [GitHub](#) | [ORCID](#) | [Twitter](#) | [Bluesky](#)

EDUCATION

Zhejiang University

Hangzhou, China

Ph.D. Candidate In Biomedical Sciences

Sep. 2025 - Present

- Center for Evolutionary & Organismal Biology
- Advisor: Prof. Guojie Zhang
- ZhongKeMeiLing Excellence Scholarship

Zhejiang University

Hangzhou, China

B.S. in Life Sciences (Overall GPA: 3.89/4.00)

Sep. 2021 - Jun. 2025

- ShangDe Student Scholarship (awarded to top 30 students university-wide)
- Zhejiang University Second- and Third-Class Scholarships
- Yamato Thermomagnetic Scholarship
- National Encouragement Scholarship

RESEARCH INTERESTS

My research combines pangenomics with multi-omics to link the evolutionary history of complex genomic variation to its phenotypic consequences, with the goal of informing precision medicine across populations.

Pangenomics and Complex Genomic Variation

- I use high-quality haplotype-resolved assemblies within a pangenome framework to resolve complex variation that remains difficult to characterize with short-read (NGS) sequencing and conventional reference-based approaches. Functional evidence from multiple omics layers helps explain the molecular consequences of this sequence-resolved variation.[1, 5]

Evolutionary Genomics and Medicine

- Tracing the origins of complex structural variation through comparisons among primate genomes, particularly those of great apes, and examining the contribution of archaic introgression in modern humans. Ancient DNA analyses reconstruct the spread and selection history of these variants, exemplified by the gene-culture coevolution (e.g., dietary adaptation). These evolutionary histories help explain why disease-associated variants arose and persisted, and how past adaptation relates to present-day disease susceptibility.[5, 6]

Genomics for Precision Medicine

- Pangenome references derived from high-quality haplotype-resolved assemblies support studies of how complex genomic variation contributes to disease susceptibility. Cohort-scale genotyping enables GWAS/PheWAS to identify disease-associated structural haplotypes. I integrate their shared and population-specific association effects with molecular evidence to identify disease-relevant pathways and explain population differences in susceptibility.[1, 5]

Publications

Published and Accepted

- [1] Wu, D., Yang, C., Chen, Q., et al. (2026). Hidden genetic diversity in 320 nearly-complete East Asian genome assemblies. *Nature*. Accepted. (Co-first author, listed third.) Preprint doi:10.64898/2026.07.27.740875.
- [2] Chen, B. H., Wu, D. Y., Yu, D., Dai, W., **Chen, Q.**, et al. (2026). A near telomere-to-telomere genome assembly of the Amur stickleback (*Pungitius sinensis*) reveals structural variation and parallel evolution of sticklebacks. *Zoological Research*, 47(3), 880-894. doi:10.24272/j.issn.2095-8137.2025.395.
- [3] Xie, L., Huang, Y., Huang, W., Shang, L., Sun, Y., **Chen, Q.**, et al. (2025). Genetic diversity and evolution of rice centromeres. *Nature Genetics*, 57(11), 2808-2818. doi:10.1038/s41588-025-02365-1.
- [4] **Chen, Q.**, Yang, C., Zhang, G., & Wu, D. (2024). GCI: a continuity inspector for complete genome assembly. *Bioinformatics*, 40(11), btae633. doi:10.1093/bioinformatics/btae633. (First author.)

Preprints

- [5] Chen, Q., Wang, F., Liu, A., et al. (2026). Contrasting selective pressures shape human pepsinogen A gene copy-number variation across Eurasia. doi:10.64898/2026.08.17.745382. (First author.)
- [6] Suo, M., Bi, A., Chen, Q., et al. (2026). Deciphering complete archaic introgression sequences in modern human genomes. doi:10.64898/2026.07.23.740208. (Co-first author, listed third.)
- [7] Sun, Y., Wan, S., Nie, L., et al. (2026). Multidimensional variation and population stratification across 8000 complete human centromeres. doi:10.64898/2026.07.22.740206.
- [8] Liu, J., Ni, Q., Zhang, Y., et al. (2026). Origin and structural evolution of the complex genomic regions of human Y chromosome. doi:10.64898/2026.07.27.26359059.
- [9] Yang, T., Shi, J., Chen, Q., et al. (2026). PanSVmerger: a flexible pipeline for merging multiallelic structural variants in pangenome graphs. doi:10.64898/2026.08.13.744739.

Skills

Computational and Analytical Skills

- **Genome Analysis:** Genome assembly and quality assessment, gene and repeat annotation, read alignment, and structural and copy-number variant analysis; GCI, SAMtools, BCFtools and minimap2.
- **Pangenome Analysis:** Pangenome graph construction; characterization of complex loci and structural haplotypes; Minigraph-Cactus, vg and ODGI.
- **Multi-Omics Integration:** Integration of genomic variation with proteomic and metabolomic phenotypes; functional annotation and enrichment analysis.
- **Evolutionary Genomics:** Comparative genomics across primates and phylogenetic inference; analysis of archaic-derived structural variation; population structure, linkage disequilibrium and selection analyses using modern and ancient genomes; PLINK 1.9, IQ-TREE and iTOL.
- **Cohort Analysis:** Population-scale genotyping of structural variants and complex-locus haplotype inference (PanGenie, Locityper); GWAS/PheWAS of disease-related traits and molecular phenotypes, including protein and metabolite levels.

Languages

- Chinese (Native)
- English (Professional Proficiency)