

Zikun Yang

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EDUCATION

SHANGHAI JIAO TONG UNIVERSITY

Sept 2022 - Present

School of Life Sciences and Biotechnology

Major in Biology Science (ZHIYUAN HONORS PROGRAM)

- GPA:3.84/4.3
- Functional Genomics(4.3), Bioinformatics(4.3), Application of Data Science(4.3), Mathematical Analysis II(4.0)
- Zhiyuan Scholarship

PUBLICATION

- Mao Y X, Li Y, **Yang Z**, et al. Comparative transcriptome analysis between rhesus macaques (*Macaca mulatta*) and crab-eating macaques (*M. fascicularis*)[J]. *Zoological Research*, 2024, 45(2): 299.
- Zhang, S., Xu, N., Fu, L., Yang, X., Li, Y., **Yang, Z.**, ... & Mao, Y. (2024). Comparative genomics of macaques and integrated insights into genetic variation and population history. *bioRxiv*, 2024-04.

RESEARCH EXPERIENCE

Bioinformatic Scientific Training in [MAO'S LAB](#) - SJTU

Jun 2022 - present

- **keywords:** Comparative Genomics, Phylogeny Analysis, transcriptome analysis
- Below are representative work detail:
- **CNV Identification and Analysis:** Based on previous RNA-seq data, *FAM220A*, a gene associated with the positive regulation of protein binding activity, displayed differential expression in multiple tissues between human and macaque. To explain the expression difference from genetic aspect, I analysed the copy number of *FAM220A* in human, macaque and even apes, built the phylogenetic tree of these duplicated genes and eventually identified 2 ape-specific segmental duplications in human. The findings are published on *Zoological Research*. This work partially explained the differential expression of *FAM220A* between human and macaque and offered an example of how structural variants can significantly impact gene expression.
- **Genotyping and Phylogeny Analysis:** Copy number estimation based on reads statistics provided clues to the potential copy number variants(CNV) of *CYP2C76* between rhesus macaque and crab-eating macaque. Hence I genotyped *CYP2C76* tandem repeats variants in the diploid genomes of 5 Crab-eating macaque individuals and 5 Rhesus macaque individuals, utilized *beast2* software to construct the phylogenetic tree of duplicated genes and inferred the evolutionary process of distinct haplotypes. This scientific training experience empowered me to identify population genetic features and analyse them from an evolutionary standpoint.
- **Recent work:** I am exploring the structure of subtelomeric regions of human chromosome 2 (HSA2) in primates and examining their epigenetic signatures.

ACADEMIC PROJECTS

SJTU Participation in Research Program (PRP)

Sept 2023 - Mar 2024

Project Member

- Under mentor's guidance, we genotyped gene knockout fetal mice and took brain tissues to determine whether there is development difference of the cerebral cortex between KO and control mice through immunofluorescence staining .
- Techniques used: PCR, fetal mice dissection etc.
- Excellent Defense Project

ACTIVITIES

SJTU Student Science and Technology Association

Mar 2023 - present

Secretary

- responsible for the arrangement and execution of the school entrepreneurship competition field service.

ADDITIONAL

- Personal Page:[Eric-Y-S.github.io](#)
- Technical Skills: R, C++(Basic), Python(Proficient)
- Language Skills: English (CAT4:636, CET6:625, TOEFL:98), Mandarin (Native)

REFERENCE

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Qing Lu

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