Yafei Mao, Ph.D.

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EDUCATION

2019 Ph.D. Okinawa Institute of Science and Technology Graduate University
Evolutionary Genomics (Advisors: Dr. Noriyuki Satoh and Dr. Evan Economo)

2014 B.Sc. Nanjing University (with honor)
Life Sciences

Other Training:

May 2018 - Oct 2018	Princeton University Visiting Student (Advisor: Dr. Ricardo Mallarino)
Oct 2013 - Mar 2014	Hong Kong University of Science and Technology Visiting Student (Advisor: Dr. Mingjie Zhang)

APPOINTMENTS

Shanghai Jiao Tong University

May 2022 - present Associate Professor

University of Washington

Jun 2019 - May 2022 Postdoctoral Fellow (Advisor: Dr. Evan Eichler)

Okinawa Institute of Science and Technology Graduate University

Apr 2019 - Jun 2019 Junior Researcher
(Advisors: Dr. Noriyuki Satoh and Dr. Evan Economo)

PUBLICATIONS

Journal Articles

29. Jiang, X., Zhang, L., Yang, Z., Yang, X., Ma, K., Yoo, D., ... Sun, Q.*, Eichler, E. E.* & **Mao, Y.*** (2024). Incomplete lineage sorting of segmental duplications defines the human chromosome 2 fusion site early during African great ape speciation. ***bioRxiv***, 2024.12.12.628057. (***Cell Genomics***, in revision)
28. Yoo, D., Rhie, A., Hebbar, P., Antonacci, F., Logsdon, G. A., Solar, S. J., … **Mao, Y.** ... Makova, K. D.*, Phillippy, A. M.* & Eichler, E. E.* (2024). Complete sequencing of ape genomes. ***bioRxiv***, 2024.07.31.605654v2. (***Nature***, Accepted)
27. Zhang, S., Xu, N., Fu, L., Yang, X., Li, Y., Yang, Z., ... Sun, Q.* & **Mao, Y.*** (2025). Integrated analysis of the complete sequence of a macaque genome. ***Nature***, 1-8
26. Liang, S. A., Ren, T., Zhang, J., He, J., Wang, X., Jiang, X., ... **Mao, Y.*** & Chen, L.* (2025). A refined analysis of Neanderthal-introgressed sequences in modern humans with a complete reference genome. ***Genome Biology***, 26(1), 1-20.
25. Ma, K., Yang, X., **Mao, Y.*** (2024). Advancing evolutionary medicine with complete primate genomes and advanced biotechnologies. ***Trends in Genetics***, 41(3),201-217.
24. **Mao, Y.***, Harvey, W. T., Porubsky, D., Munson, K. M., Hoekzema, K., Lewis, A. P., ... & Eichler, E. E.* (2024). Structurally divergent and recurrently mutated regions of primate genomes. ***Cell***, 187(6):1547-1562.e13.
23. Mao, Y., Li, Y., Yang, Z., Xu, N., Zhang, S., Wang, X., ... Sun, Q.* & **Mao, Y.*** (2024). Comparative transcriptome analysis between rhesus macaques (*Macaca mulatta*) and crab-eating macaques (*M. fascicularis*). ***Zoological Research***, 45(2): 299-310.
22. Logsdon, G.A., Rozanski, A.N., Ryabov, F., … **Mao, Y.** ... & Eichler, E. E.* (2024). The variation and evolution of complete human centromeres. ***Nature***, 1-10.
21. Yang X., Wang X., Zou Y., … & **Mao, Y.*** (2023). Characterization of large-scale genomic differences in the first complete human genome. ***Genome Biology***, 24, 157.
20. He, Y.*, & **Mao, Y.*** (2023). Exploring the primate genome: Unraveling the mysteries of evolution and human disease. ***The Innovation***, 4(4).
19. Okhovat, M.*, VanCampen, J., Nevonen, K. A., ... **Mao, Y.** ... & Carbone, L.* (2023). TAD Evolutionary and functional characterization reveals diversity in mammalian TAD boundary properties and function. ***Nature Communications***, 14(1), 8111.
18. Yang, X., **Mao, Y.**, Wang, X., …, Li, Z.*, Takahashi, E.* & Li, W.* (2023). Population genetics of marmosets in Asian primate research centers and loci associated with epileptic risk revealed by whole-genome sequencing. ***Zoological Research***, 44(5), 837–847.
17. Li, Z.*, Liu, X., Wang, C., ... **Mao, Y.** ... & Chen, Y.* (2023). The pig pangenome provides insights into the roles of coding structural variations in genetic diversity and adaptation. ***Genome Research***, 33(10), 1833-1847.
16. Yang, C., Zhou, Y., Song, Y., ... **Mao, Y.** ... & Zhang, G.* (2023). The complete and fully-phased diploid genome of a male Han Chinese. ***Cell Research***, 1-17.

15. **Mao, Y.***, Zhang, G.* (2022) A complete, telomere-to-telomere human genome sequence presents new opportunities for evolutionary genomics. ***Nature Methods***, 19, 635–638.

Before SJTU

14. Wang, T.*, Kim, C. N., Bakken, T. E., Gillentine, M. A., Henning, B., **Mao, Y.**, ... & Eichler, E. E.* (2022). Integrated gene analyses of de novo variants from 46,612 trios with autism and developmental disorders. ***Proceedings of the National Academy of Sciences***, 119(46), e2203491119.
13. Ebler, J., Ebert, P., Clarke, W. E., Rausch, T., Audano, P. A., Houwaart, T., ... **Mao, Y.** ... & Marschall, T.* (2022). Pangenome-based genome inference allows efficient and accurate genotyping across a wide spectrum of variant classes. ***Nature Genetics***, 54(4), 518-525.
12. **Mao, Y.**, Catacchio, C.R., Hillier, L.W., Porubsky, D., Li, R., Sulovari, A., ... & Eichler, E.E.* (2021). A high-quality bonobo genome refines the analysis of hominid evolution. ***Nature***, 594(7861), 77-81.
11. Logsdon, G.A., Vollger, M.R., Hsieh, P., **Mao, Y.**, Liskovykh, M.A., Koren, S., ... & Eichler, E.E.* (2021). The structure, function and evolution of a complete human chromosome 8. ***Nature***, 593(7857), 101-107.
10. Hsieh, P.*, Dang, V., Vollger, M.R., **Mao, Y.**, Huang, T.H., Dishuck, P.C., ... & Eichler, E.E.* (2021). Evidence for opposing selective forces operating on human-specific duplicated TCAF genes in Neanderthals and humans. ***Nature Communications***, 12(1), 1-14.
9. **Mao, Y.***, Hou, S., Shi, J., & Economo, E.P. (2020). TREEasy: an automated workflow to infer gene trees, species trees, and phylogenetic networks from multilocus data. ***Molecular Ecology Resources***, 20:832–840.
8. **Mao, Y.*** (2020). Genomic insights into hybridization of reef corals. ***Coral Reefs***, 39(1), 61-67.
7. Warren, W.C.*, Harris, R.A., Haukness, M., … **Mao, Y.** ... Rogers, J.* & Eichler, E.E.* (2020). Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. ***Science***, 370(6523).
6. Cantsilieris, S., Sunkin, S.M., Johnson, M.E., Anaclerio, F., Huddleston, J., Baker, C., … **Mao, Y.**, ... & Eichler, E.E.* (2020). An evolutionary driver of interspersed segmental duplications in primates. ***Genome Biology***, 21(1), 1-35.
5. Maggiolini, F.A.M., Sanders, A.D., Shew, C.J., Sulovari, A., **Mao, Y.**, Puig, M., ... & Antonacci, F.* (2020). Single-cell strand sequencing of a macaque genome reveals multiple nested inversions and breakpoint reuse during primate evolution. ***Genome Research***, 30(11), 1680-1693.
4. **Mao, Y.***, & Satoh, N. (2019). A likely ancient genome duplication in the speciose reef-building coral genus, *Acropora*. ***iScience***, 13, 20-32.
3. **Mao, Y.*** (2019). GenoDup Pipeline: a tool to detect genome duplication using the dS-based method. ***PeerJ***, 7, e6303.

2. **Mao, Y.***, Economo, E.P.*, & Satoh, N.* (2018). The roles of introgression and climate change in the rise to dominance of *Acropora* corals. ***Current Biology***, 28(21), 3373-3382.
1. Zhang, Y., Shao, Z., Yang, L., Sun, X., **Mao, Y.**, Chen, J.* & Wang, B.* (2013). Non-random arrangement of synonymous codons in archaea coding sequences. ***Genomics***, 101(6), 362-367.

NOTE: *Corresponding author

PRESENTATIONS

2024	Shanghai Genetic Society and Center for Evolutionary Biology of Fudan University - 2024 Annual meeting (Invited speaker)	Shanghai, China
2024	the International Symposium on Primate Phenotypes and Genetics (ISPPG) (Invited speaker)	Kunming, China
2024	Chinese Society of Genetics - 2024 National Academic Symposium (Invited speaker)	Changsha, China
2024	CSHA: Computational Biology of the Genome (Oral talk)	Suzhou, China
2024	Shanghai Bioinformatics Society - 2024 Academic Annual Meeting (Invited speaker)	Shanghai, China
2024	School of Life Sciences, Fudan University (Invited speaker)	Shanghai, China
2024	Capital Institute of Pediatrics (Invited speaker)	Beijing, China
2024	Human Genetics and Genomics: maximizing power to address complexity and human health (Flash talk)	Beijing, China
2024	CSHA: DNA Metabolism, Genomic Stability and Human Disease (Oral talk)	Suzhou, China
2024	Frontiers of Biotechnology Forum (Invited speaker)	Shenzhen, China
2024	China Primatological Society Conference 2024 (Invited speaker)	Zhengzhou, China
2024	National Genome Informatics Conference (Invited speaker)	Wuhan, China
2023	The 3rd AsiaEvo Conference (Oral talk)	Singapore
2023	International Symposium on Human Cultural and Genetic Diversity in Southeast Asia and Southwest China (Invited speaker)	Kunming, China
2023	GSC2023 (Invited speaker)	Wuhan, China
2023	The Innovation Webinar No.66 (Invited speaker)	Virtual Meeting
2023	School of Life Sciences, Southwest University (Invited speaker)	Chongqing, China
2023	Chengdu Institute of Biology, Chinese Academy of Sciences	Chengdu, China
2023	School of Life Sciences, Southern University of Science and Technology (Invited speaker)	Shenzhen, China
2023	School of Life Sciences, Nanjing University (Invited speaker)	Nanjing, China

2023	Neuroscience Research Institute, Peking University (Invited speaker)	Virtual Meeting
2022	Institute of Neuroscience, Chinese Academy of Sciences Center for Excellence in Brain Science and Intelligence Technology, Chinese Academy of Sciences (Invited speaker)	Shanghai, China
2022	Department of Anthropology and Human Genetics, Fudan University (Invited speaker)	Shanghai, China
2022	Structural Variants and DNA Repeats	Virtual Meeting
2022	School of Medicine, Zhejiang University (Invited speaker)	Hangzhou, China
2022	CAS, Kunming Institute of Zoology (Invited speaker)	Kunming, China
2021	Biodiversity Genomics 2021 (Invited speaker)	Virtual Meeting
2021	Structural Variants and DNA Repeats	Virtual Meeting
2021	Bold Predictions for Human Genomics by 2030	Virtual Meeting
2020	T2T/HPRC Symposium	Virtual Meeting
2019	The Use of Big Data in Quantitative Genetics	Lucca, Italy
2018	The 1st AsiaEvo Conference (Invited speaker)	Shenzhen, China
2017	Agricultural Genomics 2017	Wuhan, China
2017	Speciation (Selected for Oral Presentation)	Lucca, Italy

GRANTS AND FELLOWSHIPS

2024	Outstanding Scholar Program of Natural Science Foundation of Chongqing, China
2024	General Program of National Natural Science Foundation of China
2024	National Natural Science Fund for Excellent Young Scientists Fund Program (Overseas)
2022	Shanghai Pujiang Program (A-type)
2022	Shanghai Jiao Tong University 2030 Program (C-type, continuous support)
2022	Opening research fund from Shanghai Key Laboratory of Stomatology, Shanghai Ninth People’s Hospital
2017	Japan Society for the Promotion of Science (JSPS) Fellow, DC1

AWARDS AND HONORS

2024	Shanghai Science & Technology 35 Under 35
2024	Excellent Young Researcher of Shanghai Jiao Tong University
2023	Shanghai Young Talent Program

2022	CUHK Vice-Chancellor Assistant Professorship (withdraw)
2014	Outstanding Graduates of Nanjing University
2013	Gold Medal of iGEM (team leader)
2010, 2011, 2012	Cyrus Tang Scholarship
2012	National Scholarship
2011, 2013	National Motivational Scholarships
2011	Outstanding Students of Nanjing University

MENTORSHIP

Shanghai Jiao Tong University

Xiangyu Yang
Kaiyue Ma
Shilong Zhang
Xinrui Jiang
Da Lian
Jieyi Chen
Xuankai Wang
Lianting Fu
Junmin Han
Feifei Zhou

Nanjing University

Shuke Xiao
Kun Lv
Yuanyuan Wang
Jianchen Yang

ACADEMIC SERVICE

Society Memberships

Society for Molecular Biology & Evolution
Human Pangenome Reference Consortium
Chinese Society of Biotechnology
Genetics Society of China

Associate Editor/Review Editor

2025-present	*Zoological Research*
2024-present	*Genome Biology*
2022-present	*BMC Biology*
2021-present	*eLife (Early-Career Reviewers Pool)*

Peer Reviewer

Cell Genomics, *Cell Reports*, *eLife*, *Genome Research*, *Nature Communications*, *PLoS Genetics*, *Science Bulletin* and others

Grant Review

National Natural Science Foundation of China
Ministry of Education of the People's Republic of China
Research Grants Council (RGC) of Hong Kong: The General Research Fund (GRF)

REFERENCES

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