

Yafei Mao, Ph.D.

Associate Professor
Evo-Geno-Disease Lab (<https://yafmao.org/>)

Shanghai, 200030
CHINA

+86-(021)-62932151
yafmao@sjtu.edu.cn

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

14. **Mao, Y.**, Zhang, G. A complete, telomere-to-telomere human genome sequence presents new opportunities for evolutionary genomics. *Nature Methods* 19, 635–638 (2022).
13. Ebler, J., Ebert, P., Clarke, W. E., Rausch, T., Audano, P. A., Houwaart, T., ... & 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.**, Liskovych, 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 Resource*, 2020;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., Fiddes, I.T., Murali, S.C., Fernandes, J.,... **Mao, Y.** ... & 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. Maggolini, 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.M., Shao, Z.Q., Yang, L.T., Sun, X.Q., **Mao, Y.F.**, Chen, J.Q., & Wang, B. (2013). Non-random arrangement of synonymous codons in archaea coding sequences. *Genomics*, 101(6), 362-367.

NOTE: *Corresponding author

PRESENTATIONS

2022 Zhejiang University, School of Medicine (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

2017 Japan Society for the Promotion of Science (JSPS) Fellow, DC1 (\$25,000)

AWARDS AND HONORS

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

Dan Meng
Xuankai Wang
Yawen Zou

Nanjing University

Shuke Xiao
Kun Lv
Yuanyuan Wang
Jianchen Yang

ACADEMIC SERVICE

Society Memberships

Society for Molecular Biology & Evolution

Subject/Associate Editor/Review Editor

2022-present *Frontiers in Genetics*

2022-present *BMC Biology*

2021-present *eLife (Early-Career Reviewers Pool)*

Peer Reviewer

GigaScience, Scientific reports, Frontier in Plant Science, eLife, Frontiers in Marine Science

REFERENCES

Evan P. Economo

Professor
Biodiversity and Biocomplexity Unit
Okinawa Institute of Science and
Technology Graduate University
+1 (617) 386-6669 (US)
+81 (098) 982-3328 (JP)
economo@oist.jp

Evan E. Eichler

Principal Investigator
Professor of Genome Sciences
Department of Genome Sciences,
University of Washington
(206) 543-9526
eee@gs.washington.edu

Douglas E. Soltis

Distinguished Professor
Florida Museum of Natural History
Department of Biology
University of Florida
(352) 273-1963
dsoltis@ufl.edu