Yafei Mao

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Education:

Okinawa Institute of Science and Technology Graduate University Japan

Ph.D., Evolutionary Genomics Sep 2014 - Apr 2019

(Advisors: Dr. Noriyuki Satoh and Dr. Evan Economo)

Nanjing University China

B.Sc., Life Sciences, GPA: 4.5/5.0, Ranking: 2/77 Sep 2010 - Jun 2014

Other training:

Princeton University USA

Visiting student (Advisor: <u>Dr. Ricardo Mallarino</u>) May 2018 - Oct 2018

Hong Kong University of Science and Technology Hongkong, China

Visiting student (Advisor: <u>Dr. Mingjie Zhang</u>) Oct 2013 - Mar 2014

Professional Experience:

University of Washington USA

Postdoctoral Fellow (Advisor: <u>Dr. Evan Eichler</u>) Jun 2019 – present

Okinawa Institute of Science and Technology Graduate University Japan

Junior Researcher Apr 2019 - Jun 2019

(Advisors: <u>Dr. Noriyuki Satoh</u> and <u>Dr. Evan Economo</u>)

Awards:

Japan Society for the Promotion of Science (JSPS) Fellow, DC1

Outstanding Graduates of Nanjing University

2014

Gold medal of iGEM

Cyrus Tang Scholarship

2010 - 2012

National Scholarship

2012

Workshops and Conferences:

Conferences:

Bold Predictions for Human Genomics by 2030		Virtual Meeting	2021
T2T/HPRC Symposium		Virtual Meeting	2020
The Use of Big Data in Quantitative Genetics		Lucca, Italy	2019
The 1st AsiaEvo Conference, (Invited speaker)		Shenzhen, China	2018
Agricultural Genomics 2017		Wuhan, China	2017
Speciation (Selected for Oral Poster Presentation)		Lucca, Italy	2017
Workshops			
Machine Learning		Princeton, USA	2018
Population and Speciation Genomics	Český Krum	nlov, Czech Republic	2016
Molecular Evolution Workshop		Woods Hole, USA	2015

Publications:

Mao, Y., Catacchio, R. C., ... & Eichler, E. E. (2021). A high-quality bonobo genome refines the analysis of hominid evolution. *Nature*. (Accepted, co-first author)

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.

Mao, Y.* (2020). Genomic insights into hybridization of reef corals. *Coral Reefs*, 39(1), 61-67.

Mao, Y.*, & Satoh, N. (2019). A likely ancient genome duplication in the speciose reef-building coral genus, *Acropora*. *Iscience*, 13, 20-32.

Mao, Y.* (2019). GenoDup Pipeline: a tool to detect genome duplication using the dS-based method. *PeerJ*, 7, e6303.

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.

Logsdon, G. A., Vollger, M. R., Hsieh, P., **Mao, Y.**, Liskovykh, M. A., Koren, S., ... & Eichler, E. E. (2020). The structure, function, and evolution of a complete human chromosome 8. *Nature*, (in press).

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).

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.

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.

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