I am currently a principal investigator at Shanghai Jiao Tong University, where I have been since May 2022. I completed my Ph.D. at the Okinawa Institute of Science and Technology Graduate University (OIST) in the Spring of 2019 and did my postdoctoral training at the University of Washington. My research employs a combination of experimental and computational approaches to study the basic theory/mechanisms of evolution and genomics for understanding the origins of species and human genetic diseases.

A major goal of ecological and evolutionary biology is to understand the origins of species. Understanding speciation, divergence, and diversification could help us to acknowledge not only biodiversity on our planet but also the origins of human genetic disease.

Reef-building corals support one of the most productive and diverse ecosystems on the planet, but they are increasingly threatened due to anthropogenic stressors (e.g., global warming). Yet, it still is a long-standing question of how reef-building corals are under fast speciation and diversification. I used the latest genomic approaches and self-developed tools to understand the speciation of reef-building corals. Modern Indo-Pacific reefs are dominated by species of the staghorn coral genus *Acropora* (Anthozoa: *Acroporidae*), one of the most diverse genera with close to 150 species, but the evolutionary and ecological factors associated with their diversification are unclear. I used *Acropora* genomes to discover an ancient genome duplication event in the most recent common ancestor of *Acropora* and different functional clusters of duplicated genes that lead to the divergence of gene expression during development. Moreover, I identified a major introgression event in *Acropora* and found that the introgressed genes evolve faster, indicating that adaptive introgression shapes coral genome evolution. This coincided with a population expansion event that likely provides an ecological opportunity for the diversification of *Acropora* (Mao et al., 2018, *Current Biology*; Mao et al., 2019, *iScience*; Mao, 2019, *PeerJ*; Mao et al., 2020, *Molecular Ecology Resources*). Collectively, these studies explain the origin and diversification of *Acropora* while providing genomic evidence and relevant historical context to understand the current and future challenges to coral reefs.

Primates are highly adaptive and well studied with episodic bursts of genetic duplication and chromosomal rearrangement. Importantly, these genetic duplication and rearrangement are always associated with human adaptive traits (e.g., larger brain) and human genetic diseases (e.g., autism). Therefore, I aim to address a fundamental question in primate evolution—"what makes us uniquely human?". I would like to illustrate how we humans evolve more adaptively rather than other primates as well as why we humans have genetic diseases in our populations. I systematically characterized and genotyped lineage-specific SVs in primate populations using the latest long-read approaches. My analysis

suggests that fixed SVs contribute to phenotypic or functional differences in primates. For example, *RGPD* is a human-specific gene family expansion, and recent duplicate copies provide a substrate for inversion and microdeletion of *NPHP1* in human populations, which is known to be associated with Joubert syndrome in humans (unpublished). Beyond the unique genetic variants in each lineage, I am also interested in shared variants (e.g., ILS) in primates and have performed a comprehensive ILS analysis of primates to discover that >50% of ape genomes arose via ILS. Importantly, I demonstrated that ~21% of ILS clusters non-randomly, and exons associated with these regions show accelerated amino acid replacement and are more likely enriched in immunity-related functions. These results suggest that relaxed/positive selection drives ILS in primate evolution. My findings are consistent with both long-term balancing selection and background/purifying selection. These findings not only systematically characterize the genetic changes in primates but also expand our understanding of the role of ILs in evolution (Mao et al., 2022, *Nature Methods*; Mao et al., 2021, *Nature* and unpublished).

As I witness the establishment and continuingly successful operation of the MIT Technology Review—China, I become increasingly excited about the potential to win the Innovators Under 35 China and join an interdisciplinary group of talents. On the one hand, I expect to collaborate with other winners to make my work industrialization. On the other hand, I would like to build a unique perspective (evolution-genomics-disease) to understand the human genetic disease for future molecular diagnosis and gene therapy. Together, my experience and my interdisciplinary training prepare me well for collaborating with outstanding talents and contributing myself to the Chinese social community.

I believe that my track record as an ambitious, productive, innovative, and independent researcher with broad interests makes me a uniquely strong choice for this award.

Thank you for your consideration.