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POPULATION GENETICS IN HUMANS AND NON-HUMAN PRIMATES: HOW ARE WE DIVERSE?

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How many human-specific biological traits have been driven by adaptive evolution is a challenging but tantalizing issue in a human evolutionary biology study. The theory of population genetics predicts that the effect of weak natural selection is less pronounced in a small population, indicating more slightly deleterious alleles might be segregating and become fixed in the human population. A characteristic feature in humans is low genetic diversity compared with other non-human primates. Here I show the genetic diversity of macaque monkeys revealed by resequencing of 54 autosomal loci in 24 *M. fascicularis* and 3 *M. mulatta*. The results showed that the within-species genetic diversities of both macaque species are 4-5 times larger than extant humans, even if they sampled from a single country. Previous studies also showed larger population size in other great apes than that in humans.

Looking at a large human polymorphism data, we observed an excess of non-synonymous polymorphisms in human genomes. We also have observed higher non-synonymous substitution rate in the human lineage than the other non-human primate lineages. Although some human-specific traits have been driven by adaptive evolution, we have to consider the smaller population size of humans and its effect on the human evolution.

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