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Intra- and inter-species genetic diversity is strongly associated with the reproducibility of clinical trials and animal experiments. In the post-genomic era, we wish to overcome these problems using the information of individual genomes. Many studies have shown that, on average, humans have the genetic diversity of 0.07% at the single nucleotide polymorphisms (SNP) level. On the other hand, little is known about the genetic diversity at the SNP level within and between experimental animals, especially for laboratory non-human primates. Here I would like to discuss the intra- and inter-species genetic diversity of *Macaca fascicularis* (cynomolgus macaque) and *M. mulatta* (rhesus macaque). Genus *Macaca* includes 19 species and mainly distributed throughout Asia. Among them, *M. fascicularis* and *M. mulatta* are two of the most popular animals that have been used for medical research.

Human and macaque genomes differ at the nucleotide level by about 5~7%, but more changes in gene expression and genomic structure are observed. The genetic diversity of *M. fascicularis* was about 0.3~0.4%, indicating that they have 4~5 times higher genetic diversity than humans. Between *M. fascicularis* and *M. mulatta*, substantial nucleotide differences were observed in CYP genes, probably owing to natural selection on the drug-metabolizing genes. Considering these effects on pre-clinical studies or laboratory experiments would become important to future biomedical studies.