

**GENETIC DIVERSITY WITHIN AND AMONG REGIONAL POPULATIONS OF LONGTAIL MACAQUES
(*MACACA FASCICULARIS*)**

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Longtail macaques (*Macaca fascicularis*) may soon replace rhesus macaques (*Macaca mulatta*) as the principal animal model for study of human disease. While little attention is given to the geographic origin of longtail macaques employed in biomedical research, the species' wide natural geographic range has exposed its regional populations to different evolutionary forces, which has caused their genetic differentiation. High genetic diversity among longtail macaques selected as subjects in biomedical research can swamp the portion of phenotypic variance contributed by experimental treatment effects, while low genetic diversity reflects the loss of rare genes that influence disease and other phenotypes of interest. We used mitochondrial DNA (mtDNA), microsatellite (STR) loci and single nucleotide polymorphisms (SNPs) to compare 12 regional populations of longtail macaques from Malaysia, Indonesia, Philippines, Mauritius and Indochina. Longtail macaques on the mainland (Indochina) exhibited the highest level of genetic diversity, probably due to admixture with rhesus macaques, and are the most divergent of the regional populations of longtail macaque studied; Mauritian, and less so, the Philippine, longtail macaques exhibited the lowest levels of genetic diversity, probably reflecting strong founder effects during their establishment. The distribution of genetic diversity within and among the four insular populations of longtail macaques reflects Wahlunds effect, with low genetic diversity within populations and high genetic diversity among populations. Mauritian, Philippine and Indochinese longtail macaques were each more similar to Indonesian longtail macaques than to any other regional population, consistent with hypotheses about the founding of these populations, and the species itself, from Indonesian sources. Key Words: mtDNA, STRs, SNPs

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