Original Article

Ancestry, Plasmodium cynomolgi prevalence and rhesus macaque admixture in cynomolgus macaques (Macaca fascicularis) bred for export in Chinese breeding farms

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Abstract

Background: Most cynomolgus macaques (Macaca fascicularis) used in the United States as animal models are imported from Chinese breeding farms without documented ancestry. Cynomolgus macaques with varying rhesus macaque ancestry proportions may exhibit differences, such as susceptibility to malaria, that affect their suitability as a research model.

Methods: DNA of 400 cynomolgus macaques from 10 Chinese breeding farms was genotyped to characterize their regional origin and rhesus ancestry proportion. A nested PCR assay was used to detect Plasmodium cynomolgi infection in sampled individuals.

Results: All populations exhibited high levels of genetic heterogeneity and low levels of inbreeding and genetic subdivision. Almost all individuals exhibited an Indochinese origin and a rhesus ancestry proportion of 5%-48%. The incidence of P. cynomolgi infection in cynomolgus macaques is strongly associated with proportion of rhesus ancestry.

Conclusions: The varying amount of rhesus ancestry in cynomolgus macaques underscores the importance of monitoring their genetic similarity in malaria research.

Keywords
admixture, ancestry, Macaca fascicularis, Macaca mulatta, Plasmodium cynomolgi