

CHARACTERIZATION OF GENETIC DIVERSITY AND STRUCTURE OF CAPTIVE COLONIES OF MACAQUES

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Primate research Institute, Kyoto University (KUPRI) maintains breeding colonies of Japanese (*Macaca fuscata*) and rhesus (*M. mulatta*) macaques for various biological research. Since these macaques in wild are known to have genetic characteristics of their localities of origin, the breeding colonies are considered to hold such genetic diversity. This study aims to characterize genetic diversity and structure of KUPRI macaque colonies as the first step of genetic management. We genotyped 15 loci of autosomal microsatellite DNA and quantified population genetic parameters for Takahama (n=51), Wakasa A (n=26) and B (n=38), and Arashiyama (n=41) groups of *M. fuscata*, and Indian (n=47) and Chinese (n=48) groups of *M. mulatta*. Mean heterozygosity (H) was estimated to be 0.598 to 0.657 and 0.606 to 0.706 for the groups of *M. fuscata* and *M. mulatta*, respectively. Comparing this to previous studies using similar set of markers, the level of H for the group of *M. fuscata* at KUPRI was comparable to the wild troops of this species (0.559-0.646; Shotake and Yamane 2002). For the rhesus, we performed genotyping of the standardized microsatellite marker set (Kanthaswamy et al. 2006) and sequenced mtDNA HSV1 to compare genetic diversity of rhesus colonies in USA. The KUPRI *M. mulatta* groups (approx. 0.60-0.70 in H) showed slightly lower diversity than the colonies of USA (approx. 0.70-0.77). Phylogenetic analysis of mtDNA revealed that animals from different localities of origin formed the KUPRI rhesus colonies. Characterization and monitoring of genetic diversity is necessary for captive populations in order to detect inbreeding.

Keywords: macaques, genetic diversity, microsatellite DNA, captive population