

DIVERSITY AND MOLECULAR PHYLOGENY OF MITOCHONDRIAL DNAs OF RHESUS MACAQUES IN BANGLADESH

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We studied the mitochondrial DNA variations in the populations of rhesus macaques (*Macaca mulatta*) of Bangladesh. Recent phylogenetic study of this species revealed remarkable diversity between India and Myanmar/China populations (Smith & McDonough 2005; AJP 65:1-25). As Bangladesh is a transitional zone of those areas, we investigated evolutionary and biological features of the populations of this species in Bangladesh. Partial sequence (476 bps) of the mitochondrial DNA (mtDNA) control region, including hyper variable region 1 (HVR1), was analyzed for 63 fecal samples which were collected from 21 rhesus populations in Bangladesh between March 2008 and February 2009. Twenty-one haplotypes were detected, where 41 substitution changes were observed without repeat polymorphism and insertion/deletion. Most of substitution changes were transitions (97.5%) and the estimate of gene diversity was 0.908 ± 0.023 for the total population. Clustering results on the HVR1 sequences suggested differentiation of the southernmost population (Chunati) from others. Conspicuously, an isolated population in the southwestern area (Sundarbans) showed proximity to the central and northeastern populations and correlation between geographical and genetic distances was significantly positive but weak. The topology of the obtained phylogenetic tree was less supported in the statistical analysis. Those features may result from recent isolation of populations to each other. Comparison with deposited sequence data revealed monophyletic origin of Bangladesh rhesus and separation from a major cluster of Indian and China-Vietnam rhesus by forming a single outside cluster.

Keywords: rhesus macaques, mtDNA, HVR 1, Bangladesh.