Mitochondrial control region and population genetic patterns of Nycticebus bengalensis and N. pygmaeus

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Abstract: Bengal slow lorises (Nycticebus bengalensis) and pygmy slow lorises (Nycticebus pygmaeus) are nocturnal which creates difficulties to study them in the field. There is a scarcity of data on them and their population genetics are poorly understood. We sequenced and analyzed a partial fragment in the first hypervariable region of the mitochondrial control region or D-loop HVRI of 21 Nycticebus bengalensis and 119 N. pygmaeus from the boundary between China and Vietnam where they are sympatric. Though the sample size for Nycticebus pygmaeus is much larger, the polymorphism level is much lower than that of N. bengalensis, possibly because of (1) external gene flow from other habitats of N. bengalensis, (2) gene ingression from Sunda slow lorises (N. coucang coucang) to N. bengalensis, (3) a skewed birth sex ratio in N. pygmaeus, and (4) a possible low survival rate of infant N. pygmaeus. Based on genetic comparisons to Nycticebus bengalensis, we propose that N. pygmaeus in southern China and northern Vietnam might have migrated from middle or southern Vietnam recently. ?? 2007 Springer Science+Business Media, LLC.

Author Keywords: Bengal slow loris; Mitochondrial control region; Population genetics; Pygmy slow loris
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