

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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