

DNA Barcoding of the Sri Lankan Slender Loris (*Loris tardigradus* or *Loris lydekkerianus?*) –  
A preliminary report

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*Loris* is the common name for the primates of the subfamily Lorinae in the family lorisidae. *Loris* is a genus in this subfamily and represents all slender lorises. The slender lorises are two species of loris native to India and Sri Lanka. They are found in the highlands as well as lowland dry zones of Sri Lanka. The two species of slender loris are *Loris tardigradus* (red slender loris) and *Loris lydekkerianus* (grey slender loris). While the *Loris lydekkerianus* species was used to be considered as *Loris tardigradus*, *Loris tardigradus* is now classified as a separate species found primarily in Sri Lanka. This species has been divided into several geographically separated subspecies. However at present there is still much doubt on the taxonomic distribution of these loris species in Sri Lanka. There is also very little genetic data available on lorises in Sri Lanka or in other parts of the globe, to help resolve these issues. The database of the Consortium for the Barcode of Life (CBOL) as well as genbank (NCBI) contains the mitochondrial DNA sequence of only two specimens of loris.

Analyses of the individuals of the species is based on DNA sequencing of a 648 base pair region of the mitochondrial cytochrome oxidase I (COI) gene region, a short standardised gene region known as a DNA barcode. DNA barcodes are used not only as a species identification tool, but also to promote further biological studies on taxonomy and identification of ambiguous and endemic species.

In this context this study was undertaken to generate DNA barcodes for the Slender Loris species found in Sri Lanka. We have at present obtained DNA barcode data for a total of 12 lorises (2 from the Knuckles region, 6 from Dambulla and 4 from Mihintale). This preliminary data was generated with the hope of expanding to lorises found within all the ecozones of Sri Lanka, in order to help resolve the taxonomic issues hampering a better understanding of the loris species. From the sequence data obtained thus far, the pairwise genetic distance obtained ranged from 0.00 to 0.047. This range is acceptable for intraspecific taxa. The phylogenetic tree generated showed a very close relationship between all loris sequences obtained. Extending the number of specimens and their geographical range would enhance the genetic information that can be derived from DNA barcoding of the lorises. This is a preliminary report of an ongoing study.

Keywords: DNA barcoding, Cytochrome oxidase I, *Slender loris*, Sri Lanka