Molecular Phylogeny Confirms The Subspecies Delineation Of The Malayan Siamang (Symphalangus Syndactylus Continentis) And The Sumatran Siamang (Symphalangus Syndactylus Syndactylus) Based On The Hypervariable Region Of Mitochondrial Dna

ABSTRACT

Siamangs (Symphalangus syndactylus) are native to Peninsular Malaysia, Sumatra and southern Thailand and their taxonomical classification at subspecies level remains unclear. Morphologically, two subspecies were proposed as early as 1908 by Thomas namely *Symphalangus s. syndactylus and Symphalangus s. continentis.* Thus, this study aims to clarify the Siamang subspecies status, based on mtDNA D-loop sequences. Faecal samples were collected from wild Siamang populations at different localities in Peninsular Malaysia. A 600bp sequence of the mitochondrial D-loop region was amplified from faecal DNA extracts and analysed along with GenBank sequences representing Symphalangus sp., Nomascus sp., Hylobates sp., Hoolock sp. and outgroups (Pongo pygmaeus, Macaca fascicularis and Papio papio). The molecular phylogenetic analysis in this study revealed two distinct clades formed by S. s. syndactylus and S. s. continentis which supports the previous morphological delineation of the existence of two subspecies. Biogeographical analysis indicated that the Sumatran population lineage was split from the Peninsular Malaysian population lineage and a diversification occurred in the Pliocene era (~ 3.12 MYA) through southward expansion. This postulation was supported by the molecular clock, which illustrated that the Peninsular Malaysian population (~ 1.92 MYA) diverged earlier than the Sumatran population (~ 1.85 MYA). This is the first study to use a molecular approach to validate the subspecies statuses of S. s. syndactylus and S. s. continentis. This finding will be useful for conservation management, for example, during Siamang translocation and investigations into illegal pet trade and forensics involving Malayan and Sumatran Siamangs.