



Research Article

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

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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 600-bp 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.

Keywords

Symphalangus syndactylus, siamang, small ape, Hylobatidae, phylogenetic

Introduction

The Siamang (*Symphalangus syndactylus*) is a small ape species with declining numbers and, thus, it has been classified as an endangered species and is included in the Red List of the International Union for Conservation of Nature (Nijman et al. 2020). The Siamang (Fig. 1) is distributed in Peninsular Malaysia and Sumatra, Indonesia (Brandon-Jones et al. 2004, Roos et al. 2014, Md-Zain et al. 2021,

Md-Zain et al. 2022), with a few populations living in the central and western parts of the Bala Forest of southern Thailand (Thong-aree 2000). It was once classified as a subgenus of *Hylobates* (Kloss 1929) until it was elevated to the full genus level under the name *Symphalangus*. Later, gibbons comprise two genera, namely, *Symphalangus* and *Hylobates* (Napier and Napier 1967). Primatologists recognise the following four genera of Hylobatidae using morphological (Groves 2001), behavioural (Geissmann 2002) and molecular criteria (Chivers 2013, Roos 2016): *Hoolock*, *Symphalangus*, *Hylobates* and *Nomascus*. *Symphalangus syndactylus*, first described in 1821, is the sole representative of the genus *Symphalangus* (Raffles 1821). Subsequently, two subspecies of Siamangs, namely, the Sumatran Siamang and Peninsular Malaysian Siamang, were described by Thomas (1908) on the basis of their skull appearance. The classification gained support from other researchers (Hooijer 1960, Frisch 1967), who provided more detailed