

# Phylogeography of the Sunda pangolin, *Manis javanica*: implications for taxonomy, conservation management and wildlife forensics

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## Abstract

**Aim:** The Sunda pangolin (*Manis javanica*) is the most widely distributed Asian pangolin species. It is one of the most trafficked mammals in the world, which not only negatively impacts wild Sunda pangolin populations, but also poses a potential disease risk to other species, including humans and livestock. Despite the imminent threat to the species' survival and its prevalence in the wildlife trade, the phylogeography and evolution of the Sunda pangolin is not well understood. We aimed to investigate the species' phylogeography across its distribution to improve our understanding of the species' evolutionary history, elucidate any taxonomic uncertainties and enhance the species' conservation genetic management and wildlife forensics applications. **Location:** Southeast Asia and southern China. **Methods:** We sequenced mtDNA genomes from 23 wild Sunda pangolins from Borneo and Peninsular Malaysia. We used these data in conjunction with previous generated mtDNA and nuclear datasets from across the species' range to perform various phylogenetic and population genetic analyses. **Results:** We identified an evolutionarily distinct mtDNA lineage in north Borneo, which was estimated to be ~1.6 million years divergent from lineages in west/south Borneo and the mainland, comparable to the divergence time of the Palawan pangolin. There appeared to be mitonuclear discordance, with no apparent genetic structure across Borneo based on analysis of nuclear SNPs. **Main conclusions:** These findings are consistent with the 'out of Borneo hypothesis', whereby Sunda pangolins diversified in Borneo before subsequently migrating throughout Sundaland, and/or a secondary contact scenario between mainland and Borneo. We have elucidated possible taxonomic issues in the Sunda/Palawan pangolin complex, and highlight the critical need for additional georeferenced samples to accurately apportion its range-wide genetic variation into appropriate taxonomic and conservation units. Additionally, these data have improved forensic species identification testing involving these species and permit the implementation of geographic provenance testing in some scenarios.

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