

**DISENTANGLING THE COMPLEX POPULATION HISTORY OF ORANGUTANS**

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Conflicting scenarios of orangutan population history have been proposed in recent genetic studies. This is most likely due to limited geographical coverage plus unreliable provenance of samples in previous studies. Such limitations lead to an incomplete picture of population structure. We have reconstructed the phylogeography of orangutans based on the most comprehensive collection of samples available to date. Additionally to seven Bornean sites, we were able to include samples from five Sumatran sites. Using Bayesian frameworks on mtDNA data (HVRI, 16SrDNA, CYTB, and ND3), we show that Sumatran and Bornean orangutans have been strictly separated for at least 1.5 million years. In contrast to previous studies, we did not find evidence of recent gene flow between the islands. Unexpectedly, the southernmost Sumatran population of Batang Toru is clearly separated from all other Sumatran sites and basal to all Bornean populations. Sumatran orangutans show a clear structuring into four geographical clusters with much deeper divergence compared to Bornean orangutans. Autosomal microsatellite data confirm the occurrence of high genetic differentiation across Sumatra ( $F_{ST} = 0.085$ ,  $P < 0.01$ ). X- and Y-chromosomal markers confirm strict separation between Borneo and Sumatra, but indicate a more recent divergence. Yet, both marker systems do not recover any geographical structure within each island compared to mtDNA. We attribute these findings to the occurrence of strong female philopatry and wide-ranging male-mediated gene flow. We discuss our findings within the framework of an orangutan colonization scenario for Sundaland, and elaborate on the consequences for species taxonomy and conservation management.

**Keywords:** *Pongo* spp., phylogeography, population structure, Sundaland