

GENETIC EVIDENCE FOR RECENT CONTRACTION AND EXPANSION OF BORNEAN ORANGUTAN POPULATIONS

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Compared to other great apes, the evolutionary history of orangutan populations is poorly understood. Their genetic structure remains unresolved, largely due to the limited number of localities sampled across their distribution, small sample sizes and problems with provenance. To date, studies of one subspecies of Bornean orangutan, have detected high population differentiation across the Kinabatangan river, highlighting the role of impassable rivers as barriers to gene flow. This study examines the population history of Bornean orangutans more broadly and capitalizes on the inclusion of a large number of non-invasively collected samples from 5 additional locales across Borneo (Tuanan $n = 31$, Sungai Lading $n = 26$, Sabangau $n = 29$, Gunung Palung $n = 19$, Danum Valley $n = 18$), separated by various rivers. We used autosomal data from 12-26 microsatellite loci as well as control region mtDNA haplotypes. Both microsatellites and mtDNA point to high population differentiation between locales, but simultaneously indicate a recent radiation within Borneo, consistent with the presence of one or more refugia during the Pleistocene but not with a recent recolonization from Sumatra. In addition, mtDNA haplotypes show at least 6 geographical clusters, with previously undescribed substructuring found within the *P.p. wurmbii* subspecies. We also provide evidence for higher genetic diversity in peat swamp locations, with possible recent microcolonisations from these regions to dryer areas. We discuss these results in the context of Pleistocene climatic changes and human disturbances leading to population contractions and expansions, with a view to clarifying Bornean taxonomy and providing guidelines for future conservation management.

Keywords: evolutionary history, *Pongo*, genetic structure, refugia