

**MALE-SPECIFIC MARKERS REVEAL SEX-BIASED DISPERSAL IN ORANG-UTANS (*PONGO* SPP.)**

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Paternally transmitted genetic markers are very useful for investigating sex-biased dispersal and phylogenetic questions, especially when applied in conjunction with maternally transmitted markers. However, polymorphic Y-chromosomal markers are lacking for most mammals and have not been applied to orang-utans. We are the first to investigate phylogenetic patterns and population structure based on several Y chromosome-specific markers (11 microsatellites, 6 single nucleotide polymorphisms, and one insertion-deletion polymorphism). We included 76 wild samples from nine populations of Bornean (*Pongo pygmaeus*) and Sumatran (*P. abelii*) origin, and compared data from Y-chromosomal markers and the hypervariable region I of mitochondrial DNA. On both islands, median-joining networks showed a grouping of similar haplotypes according to geographic origin only for mitochondrial, yet not for Y-chromosomal haplotypes, suggesting that male dispersal occurs over much greater distances than previously thought. Given the massive habitat degradation, this result might have serious ramifications for conservation. Analyses of molecular variance were conducted for seven Bornean populations and showed contrasting patterns. While at 69 %, most of the Y-chromosomal variation was found within populations, only 18 % of the mitochondrial variation was found within populations. These findings support the hypothesis derived from behavioral observations that in orang-utans, dispersal is male-biased (*i.e.* male orang-utans disperse further than females, more frequently, or both). In contrast to chimpanzees and bonobos, dispersal is clearly male-biased in orang-utans, in line with most mammalian species. We will discuss our findings in the context of the correlation between female-biased dispersal and the formation of multimale groups in great apes.

Keywords: Y chromosome, mitochondrial DNA, *Pongo pygmaeus*, *Pongo abelii*