

Patterns of genetic diversity and migration in increasingly fragmented and declining orang-utan (*Pongo pygmaeus*) populations from Sabah, Malaysia

Abstract

We investigated the genetic structure within and among Bornean orang-utans (*Pongo pygmaeus*) in forest fragments of the Lower Kinabatangan flood plain in Sabah, Malaysia. DNA was extracted from hair and faecal samples for 200 wild individuals collected during boat surveys on the Kinabatangan River. Fourteen microsatellite loci were used to characterize patterns of genetic diversity. We found that genetic diversity was high in the set of samples (mean H-E = 0.74) and that genetic differentiation was significant between the samples (average F-ST = 0.04, $P < 0.001$) with F-ST values ranging from low (0.01) to moderately large (0.12) values. Pairwise F-ST values were significantly higher across the Kinabatangan River than between samples from the same river side, thereby confirming the role of the river as a natural barrier to gene flow. The correlation between genetic and geographical distance was tested by means of a series of Mantel tests based on different measures of geographical distance. We used a Bayesian method to estimate immigration rates. The results indicate that migration is unlikely across the river but cannot be completely ruled out because of the limited F-ST values. Assignment tests confirm the overall picture that gene flow is limited across the river. We found that migration between samples from the same side of the river had a high probability indicating that orang-utans used to move relatively freely between neighbouring areas. This strongly suggests that there is a need to maintain migration between isolated forest fragments. This could be done by restoring forest corridors alongside the river banks and between patches.