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Gene flow patterns in West African baboons

Gene flow is one of the main determinants of genetic structure and thus directly influences the evolutionary fate of populations. Behavioural patterns, ecological factors and landscape characteristics, demographic history, and phylogenetic relationships are major contributors that shape gene flow within and between species. In this study we investigate gene flow patterns over the whole distribution of West African Guinea baboons (*Papio papio*). For well over 350 non-invasively collected samples we analysed sequence data of the mitochondrial hypervariable region I (d-loop) and up to 25 nuclear microsatellite markers. We specifically tested how gene flow patterns in this species are affected by features of their social system (i.e. sex-biased dispersal patterns), its recent demographic history, and its interaction with its neighbouring congeneric, the olive baboon (*P. anubis*). Our results reveal discordances in gene flow patterns between mitochondrial and nuclear markers that are best explained by female-biased dispersal. Moreover, characteristic patterns of genetic structuring at the fringes of their distribution point to a recent range expansion in this species. This probably led to asymmetric gene flow between Guinea and olive baboons, shaping the distribution of genetic variation in the contact zones.