

GENETIC STRUCTURE OF GUINEA BABOONS IN GUINEA BISSAU (WEST-AFRICA)

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Hunting pressure can have an impact in the genetic diversity and patterns of relatedness between individuals within social groups. Here we present a descriptive analysis of the mitochondrial and nuclear genetic diversity of a social group of Guinea-Bissau baboons, a population thought to be declining due to hunting pressure since the 1980's. Twenty faecal samples were collected in Cantanhez National Park (Guinea-Bissau) in 2008 after observation of the group. The extracted DNA was amplified and sequenced for a D-loop (HVR I) 387bp fragment of mitochondrial DNA (mtDNA) and samples were genotyped for 11 autosomal microsatellite loci (D21S1442, D14S306, D4S243, D3S1766, D21S1442, D1S533, D3S1768, D5S1457, D7S503, D10S611, D13S159). For mtDNA, we found eight different haplotypes, with 4.96 average nucleotide differences. The nucleotide diversity estimate ($0,015 \pm 0,0038$) is relatively low when compared with other baboons; however, the number of haplotypes is high when compared with social groups of kinda, gray-footed and yellow baboons (data from Burrell 2008), which may suggest a different dispersal pattern for guinea baboons. For nuclear DNA diversity, the observed heterozygosity (H_o) found ranged between 0,05-0,7 (mean=0,46) with an average of 4 alleles across loci. These preliminary results point to a lower genetic diversity for Guinea-baboons. Further work will compare the genetic diversity patterns, relatedness and dispersal levels in social groups of Guinea-Bissau baboons with different hunting pressures. This project is funded by *Fundação para a Ciência e Tecnologia* (SFRH/BD/37417/2007).

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