Abstract

The mountain bongo antelope *Tragelaphus eurycerus isaaci* has rapidly declined in recent decades, due to a combination of hunting, habitat degradation and disease. Endemic to Kenya, mountain bongo populations have shrunk to approximately 100 individuals now mainly confined to the Aberdares mountain ranges. Indirect observation of bongo signs (e.g. tracks, dung) can be misleading, thus methods to ensure reliable species identification, such as DNA-based techniques, are necessary to effectively study and monitor this species. We assessed bongo presence in four mountain habitats in Kenya (Mount Kenya National Park, Aberdare National Park, Eburu and Mau forests) and carried out a preliminary analysis of genetic variation by examining 466 bp of the first domain of the mtDNA control region using DNA extracted from faecal samples. Of the 201 dung samples collected in the field, 102 samples were molecularly identified as bongo, 97 as waterbuck, one as African buffalo and one as Aders' duiker. Overall species-identification accuracy by experienced trackers was 64%, with very high error of commission when identifying bongo sign (37%), and high error of omission for waterbuck sign (82%), suggesting that the two species' signs are easily confused. Despite high variation in the mtDNA control region in most antelope species, our results suggest low genetic variation in mountain bongo as only two haplotypes were detected in 102 samples analyzed. In contrast, the analysis of 63 waterbuck samples from the same sites revealed 21 haplotypes. Nevertheless, further examination using nuclear DNA markers (e.g. microsatellites) in a multi-locus approach is still required, especially because the use of mitochondrial DNA can result in population overestimation as distinct dung samples can potentially be originated from the same individual.