

Abstract

The Kenyan mountain bongo (*Tragelaphus eurycerus isaaci*) is an endangered Tragelaphine antelope sub-species endemic to Mt. Kenya- Aberdare ecosystems. This antelope has currently been reduced to pockets of small populations in forest patches (mainly in the Aberdares) exacerbated primarily by habitat fragmentation due to anthropogenic and disease factors. The conservation and survival of these species needs vital empirical data on critical factors such as genetic processes that might affect their fitness and geographical distribution. The current study examines the population genetics of the mountain bongo in Kenya using mtDNA control region sequences. A total of 212 bongo dung samples derived from 4 populations representing Mt. Kenya, Aberdares, Eburu and Mau were collected following track signs at designated bongo ecological home ranges. Total genomic DNA was extracted and a 500bp mtDNA control region amplified by polymerase chain reaction (PCR) using MT4 and B161811 primers. 112 representing 53% of the samples analyzed were bongo, 98 representing 46% were waterbuck, a single buffalo and a duiker. Samples collected from Eburu and Mau forests were also identified as bongo in spite of anecdotal evidence pointing to non existence of the species in these areas. Only two mtDNA haplotypes were detected in the 112 bongo samples identified. The haplotype and nucleotide diversities were 0.442 and 0.095 respectively estimated using Nei's method as implemented in DnaSP. Genetic differentiation of the bongo subpopulations due to the geographical isolation as estimated by NcIs UST was 0.075 indicating very little differentiation. The current study confirmed presence of bongo in all areas studied and detected very little genetic variation. This information is crucial in guiding the reintroduction initiative of the bongo back to their native habitats in Kenya. Breeding strategies aimed at increasing the mountain bongo's genetic variation such as out breeding need to be put in place to prevent the adverse consequences associated with low genetic variation in the animals.