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**Original Research Article** 

# Relatedness and genetic variation in wild and captive populations of Mountain Bongo in Kenya obtained from genome-wide single-nucleotide polymorphism (SNP) data

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### ABSTRACT

To assess the relatedness and amount of genetic variation of wild and captive Mountain Bongo Tragelaphus eurycerus ssp. isaaci, both non-invasive and invasive samples were efficiently analyzed using SNP's. Mountain Bongo is estimated to remain in Kenyan forest with less than 96 individuals, possibly as low as 73 individuals, split in five subpopulations whereof four populations are isolated from each other. The genetic diversity of wild animals was studied using fecal samples, and using tissue samples from the 62 animals presently held captive at the Mount Kenya Wildlife Conservancy. In strategic conservation of the wild Mountain Bongo, the captive animals constitute a potential genetic input to wild populations. Our study shows there is still genetic variation in the wild population and that the subpopulations are to some extent genetically differentiated. This leads to an overall effective population size of around 14 in the wild population, which is good relative to the small population, but dangerously small for long-term, or even short-term, survival. Most individuals in the wild population were unrelated, while in the captive population most individuals were related at the level of half-sibs. The captive population still host genetic variation and is differentiated slightly to the wild population. Careful restocking from the captive populations could be an effective means to enhance the genetic variation in the wild, but most importantly make the dwindling population less vulnerable to stochastic events.

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#### 1. Introduction

Global decrease in biodiversity strikes hard on numerous wild mammals and in several cases dwindling wild populations are smaller than captive populations. Conservation strategies may then imply re-stocking of protected wild populations with

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captive animals, however, the genetic and evolutionary impact from such anthropogenic conservation will consequently be in focus. Ideally, relatedness or genetic health should be investigated before action is taken, but practical problems may come into account. To evaluate the relatedness in populations targeted for applied strategic conservation we have chosen a modern genomic methodology to obtain genetic variation data, using both non-invasive and invasive sampling techniques, suitable for undersized wild and captive populations of a critically endangered mammal.

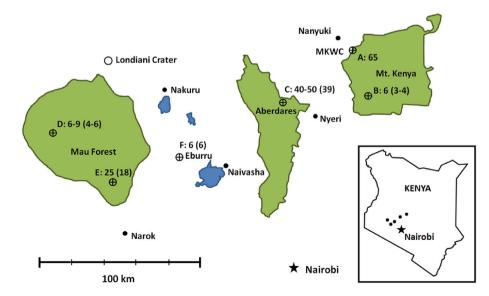
The Mountain Bongo *Tragelaphus eurycerus* ssp. *isaaci*, also referred to as the Eastern Bongo, is endemic to Kenya and classified as critically endangered (CR C2a(i) ver 3.1.). In an assessment made 2008 by IUCN was the wild population estimated to a total of 75–140 individual animals composed of four different subpopulations (IUCN, 2008). The mountain Bongo is a large size forest ungulate ( $\$ \le 276$  kg;  $\eth \le 405$  kg) with a complex social behavior. At a sexual maturity of 2 years of age, one offspring may be born after a gestation time of 38 weeks (Kingdon, 2015). Disturbance from human activities may have significant impact on the breeding success of this species (Prettejohn, 2017).

At present, there are five known wild subpopulations with an uneven population distribution, accounting for an estimated total population of 96 animals based on information from camera traps in combination with experience from several years of surveillance in the forests. However, evidence based solely on camera trap identification results in 73 individuals only (see Fig. 1; Prettejohn, 2017; Shears, 2015). The smaller population size would qualify for classification as critically endangered with criteria D as it is likely that less than 50 individuals are mature (IUCN, 2001).

The five wild subpopulations are not managed actively, thus natural genetic exchange between the present subpopulations may only occur within Mau forest, see Fig. 1. Consequently, inbreeding is an imminent problem and conservation strategies improving genetic diversity have been raised (Mallon, 2013; CBSG, 2010).

Historically, the Kenyan subpopulations of mountain Bongo have been described in Cherengani Hills, Londiani forest and crater, Mau highland forest, Aberdare mountain range, the mountain area of Ol Doniyo Eburru and Mt Kenya commonly habituated in mountainous forest between 2100 m–3000 m altitude (Kingdon, 2015; Ralls, 1978; Price, 1969). Before human exploitation of the land, animals could possibly be able to pass between these locations and thus there were possibilities of gene flow. The habitat at these highland forest areas in Kenya, and likely some few more highlands in the region, is in total a relatively small area thus could not host a large total population of animals. This becomes further obvious in relation to the species relative, the Low Land Bongo Tragelaphus eurycerus ssp. eurycerus, also called the Western Bongo, inhabiting a vast area stretching from Sierra Leone in the west, to Southern Sudan in the east, the Congo Basin and to northern Angola in the south (Kingdon, 2015; Ralls, 1978). Therefore, it can be expected that the genetic diversity of the mountain Bongo has been severely reduced, and thus it is of interest with regard to the present status of the species and the conservation strategy for sustainable population growth.

The Mount Kenya Wildlife Conservancy (MKWC) is located on the slopes of Mt. Kenya bordering the Mt. Kenya Forest, a UNESCO world heritage site (Fig. 1). At present, 63 Mountain Bongo (25 bulls, 38 cows) are ranging in an enclosure of 60 ha mostly comprised of natural forest and grassland. The land has further been subdivided into 4 breeding groups, 3 bachelor groups and 2 nursery groups. A majority of these animals would not survive in the wild because they have to some extend lost their natural instincts, for example to fend or evade predators, or they may not be able to meet their nutritional



**Fig. 1.** Map showing the present Bongo populations and sizes in Kenya. Estimates are based on information from camera traps in combination with experience from several years of surveillance in the forests. Population size solely by evidence from camera trap identification is presented within parenthesis. The captive population is found at Mt. Kenya Wildlife Conservancy (A) and the wild populations are Ragati at Mt. Kenya (B), Honi-Salient in the Aberdares (C), South West Mau (D) and Maasai Mau (E) in the Mau Forest and Eburru (F) in Mau Eburru.

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