Molecular Phylogenetics and Evolution 83 (2015) 242–249

Contents lists available at ScienceDirect

Molecular Phylogenetics and Evolution

journal homepage: www.elsevier.com/locate/ympev

Complete mitochondrial DNA sequence of the endangered giant sable antelope (*Hippotragus niger variani*): Insights into conservation and taxonomy

Gonçalo Espregueira Themudo [a,*,1], Ana C. Rufino [b], Paula F. Campos [c,a,*]

[a] CIMAR/CIIMAR, Centro Interdisciplinar de Investigação Marinha e Ambiental, Universidade do Porto, Rua dos Bragas 177, 4050-123 Porto, Portugal
[b] Museu da Ciência, Universidade de Coimbra, Laboratorio Chimico, Largo Marquês de Pombal, 3000-272 Coimbra, Portugal
[c] Centre for Geogenetics, Natural History Museum Denmark, University of Copenhagen, Østervoldgade 5-7, 1350 Copenhagen, Denmark

ARTICLE INFO

Article history:
Received 25 June 2014
Revised 4 December 2014
Accepted 6 December 2014
Available online 17 December 2014

Keywords:
Giant sable antelope
Mitogenome
Conservation
Divergence time

ABSTRACT

The giant sable antelope is one of the most endangered African bovids. Populations of this iconic animal, the national symbol of Angola, were recently rediscovered, after many decades of presumed extinction. Even so, their numbers are scarce and hence conservation plans are essential. However, fundamental information such as its taxonomic position, time of divergence and degree of genetic variation are still lacking. Here, we used a museum preserved horn as a source of DNA to describe, for the first time, the complete mitochondrial genome of the giant sable antelope, and provide insights into its evolutionary history. Reads generated by shotgun sequencing were mapped against the mitochondrial genome of common sable antelope and the nuclear genomes of cow and sheep. Phylogenetic reconstruction and divergence time estimate give support to the monophyly of the giant sable and a maximum divergence time of 170 thousand years to the closest subspecies. About 7% of the nuclear genome was mapped against the reference. The genetic resources reported here are now available for future work in the field of conservation genetics and phylogeny, in this and related species.

1. Introduction

Not long ago, the sable antelope (*Hippotragus niger*) occurred widely in the savannah woodlands of southern and eastern Africa with an isolated population in Central Angola, between the Cuanza and Luando rivers. Nowadays, there are four recognized subspecies (Matthee and Robinson, 1999): *H. niger roosevelti* (east Africa), *H. niger niger* (South Africa, Zimbabwe), *H. niger kirkii* (Zambia, Malawi) and *H. niger variani* (Angola, Fig. 1). As for many other antelope species, the validity and precise distribution of most of the described subspecies are uncertain (IUCN SSC Antelope Specialist Group, 2008a).

H. niger variani, Thomas, 1916, the giant sable antelope, is endemic to the Malanje province in central Angola. It is a national symbol of Angola and has been officially protected since the 1930s due to its popularity among hunters and the uniqueness of its large horns, kept as trophies (Frade and Sieiro, 1960). In the 1950s, despite the protection of the government, only around 300 individuals remained (Frade and Sieiro, 1960). During the late 1990s, it was thought to be extinct after almost three decades of civil war in the country. However, comparisons of mitochondrial DNA extracted from dung pellets collected in Cangandala National Park and Luando Integral Nature Reserve and from old museum specimens of certain provenance, provided evidence that indeed this subspecies had survived (Pitra et al., 2006). Before that, the last accepted sights of the subspecies dated from 1982 (Estes, 1983). Although it survived thirty years of intense poaching and armed conflict, its numbers are still very low (IUCN SSC Antelope Specialist Group, 2008b). The subspecies is now listed as critically endangered on the IUCN's Red List and is included on CITES Appendix 1 (IUCN SSC Antelope Specialist Group, 2008b). Its rarity, isolation and impressive horns, one of the biggest in the family Bovidae (Bro-Jørgensen, 2007; Pitra et al., 2006), along with its uncertain taxonomic placement makes it one of the most enigmatic of the African mammals. Little is known about the giant sable's population biology or ecology. The habitat of this subspecies is within the Angolan miombo ecosystem associated with natural salt licks

* Corresponding authors at: Centre for Geogenetics, Natural History Museum Denmark, University of Copenhagen, Østervoldgade 5-7, 1350 Copenhagen, Denmark (P.F. Campos).
E-mail addresses: gethemudo@gmail.com (G. Espregueira Themudo), campos.f.paula@gmail.com (P.F. Campos).
[1] Current address: Section of Forensic Genetics, Department of Forensic Medicine, Faculty of Health Sciences, University of Copenhagen, Copenhagen, Denmark.

http://dx.doi.org/10.1016/j.ympev.2014.12.001
1055-7903/

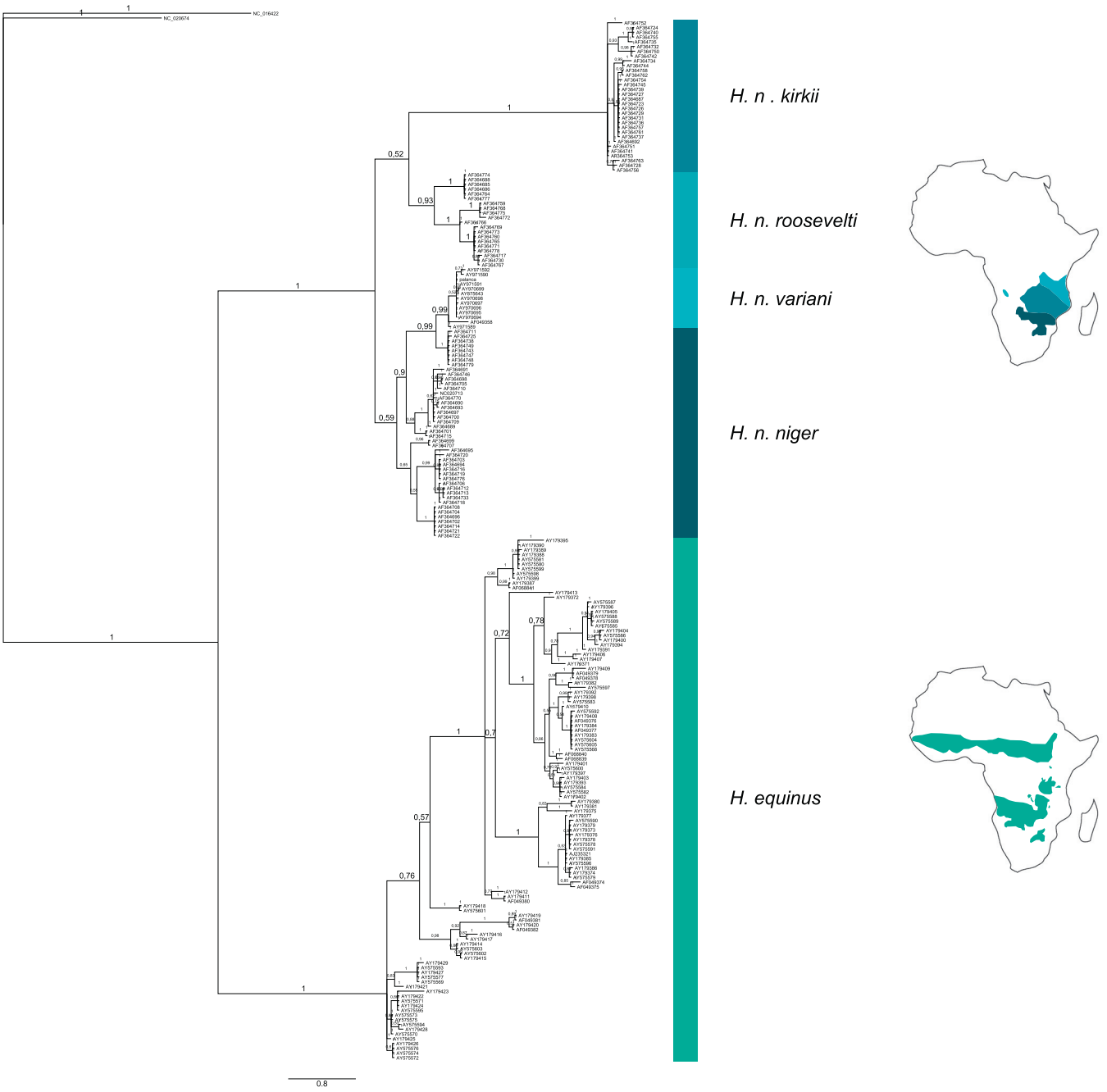

Fig. 1. Bayesian phylogenetic reconstruction based on complete D-loop of 93 *Hippotragus*. Sequences of *Addax nasomaculatus* (NC_020674) and *Oryx gazella* (NC_016422) were included as outgroups. Values above branches indicate posterior probability support. Colored bars and maps indicate the different subspecies of *H. niger*. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

that are found around the natural parks. As these woodlands are nutrient poor, these licks are of vital importance as nutrient hotspots (FAO, 2005).

Habitat modification, increased human pressure, and introgression with roan antelope (Vaz Pinto, 2006) have certainly played a role in the evolutionary and demographic history of the giant sable antelope. The two extant species, roan and sable antelope, are among the largest of the African plains antelopes and are often found in sympatry. Hybridization between sable and roan antelope has been described before in Kruger Park, South Africa. In 2006, Pedro Vaz Pinto reported its repeated occurrence in Cangandala National Park. In the absence of mature sable antelope males, females were systematically mating with males of the congeneric species *H. equinus*. The unusually long and floppy ears and uncharacteristic facial marks present in a few sable individuals gave the suspicion but camera trapping recordings of a male roan antelope leading a herd of female sable antelopes confirmed it. The very unbalanced group composition clearly suggests a decline in population size (Vaz Pinto, 2006).

The occurrence of introgression and hybridization with the sister species *H. equinus* highlights the importance of defining CUs (conservation units) or ESUs (Evolutionary Significant Units; Moritz, 1994). To do so it is important to obtain DNA information from a true giant sable antelope and not a hybrid. In these circumstances, historical museum specimens of *H. niger variani* play an important role.

Museum specimens have been largely used, in the recent past, to uncover past genetic diversity, domestication or taxonomic placement of extinct species (e.g. Campos et al., 2010; Gilbert