



A revised phylogeny of Antilopini (Bovidae, Artiodactyla) using combined mitochondrial and nuclear genes

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ABSTRACT

Antilopini (gazelles and their allies) are one of the most diverse but phylogenetically controversial groups of bovids. Here we provide a molecular phylogeny of this poorly understood taxon using combined analyses of mitochondrial (CYTB, COIII, 12S, 16S) and nuclear (KCAS, SPTBN1, PRKCI, MC1R, THYR) genes. We explore the influence of data partitioning and different analytical methods, including Bayesian inference, maximum likelihood and maximum parsimony, on the inferred relationships within Antilopini. We achieve increased resolution and support compared to previous analyses especially in the two most problematic parts of their tree. First, taxa commonly referred to as “gazelles” are recovered as paraphyletic, as the genus *Gazella* appears more closely related to the Indian blackbuck (*Antilope cervicapra*) than to the other two gazelle genera (*Nanger* and *Eudorcas*). Second, we recovered a strongly supported sister relationship between one of the dwarf antelopes (*Ourebia*) and the Antilopini subgroup Antilopina (*Saiga*, *Gerenuk*, *Springbok*, *Blackbuck* and *gazelles*). The assessment of the influence of taxon sampling, outgroup rooting, and data partitioning in Bayesian analyses helps explain the contradictory results of previous studies.

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1. Introduction

Antilopini (gazelles and their allies) has been described as one of the least understood groups of bovids (Rebholz and Harley, 1999; Hernández Fernández and Vrba, 2005). The tribe Antilopini belongs to the subfamily Antilopinae, a group that also includes goats and most African antelopes (e.g., Wildebeests, Sable antelope, Duikers, Impala, Waterbucks). The sister taxon of Antilopinae is Bovinae, comprising mostly cattle and spiral-horned antelopes (e.g., Kudus). Both groups comprise the artiodactyl family Bovidae. Antilopini is a very speciose group of great biological and economic importance. The earliest fossil bovids that are clearly attributable to one of the living clades (early Middle Miocene gazelles from Fort Ternan) belong to Antilopini (Bibi et al., 2009). However, their phylogenetic relationships (e.g., if they belong to the stem- or crown-group of Antilopini) are not known, in part because of the unresolved relationships of living antilopines themselves.

In the last decade, many researchers have worked on bovid phylogenies that included a large number of species in Antilopini (Gatesy et al., 1997; Gatesy and Arctander, 2000; Groves, 2000; Vrba and Schaller, 2000; Kuznetsova and Kholodova, 2003; Lei

et al., 2003; Marcot, 2007; Agnarsson and May-Collado, 2008; Ropiquet et al., 2009), and a consensus has emerged on the taxonomic composition of this clade (Table 1). The most recent work by Hassanin et al. (2012) introduced new names for four subgroups of Antilopini: Antilopina, based on the genus *Antilope*, consists of *Antilope cervicapra*, *Gazella* spp., *Nanger* spp., *Eudorcas* spp., *Antidorcas marsupialis*, *Ammodorcas clarkei*, *Litocranius walleri*, and *Saiga tatarica*; Procaphrina, based on the genus *Procaphra*, includes the three living *Procaphra* species; Ourebina, based on the genus *Ourebia*, is monotypic and includes only *Ourebia ourebi*; Raphicerina, based on the genus *Raphicerus*, includes *Raphicerus* spp., *Dorcatragus megalotis*, and *Madoqua* spp. Historically, *Ourebia* and *Raphicerina* have been united with other small-bodied and short-horned species, i.e., *Neotragus* spp. and *Oreotragus oreotragus*, to form the group “Neotragini”. This group, however, is now known to be polyphyletic as *Neotragus* and *Oreotragus* are not closely related to Antilopini (Gentry, 1992; Matthee and Robinson, 1999; Matthee and Davis, 2001; Kuznetsova and Kholodova, 2002, 2003; Hassanin and Douzery, 1999; Marcot, 2007; Agnarsson and May-Collado, 2008; Ropiquet et al., 2009; Hassanin et al., 2012).

Within the last 6 years, three studies on Antilopini phylogenetics were published with near-complete taxon sampling at genus level based on multiple genes (Marcot, 2007; Ropiquet et al., 2009; Hassanin et al., 2012; see Fig. 1). Comparisons of these studies

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Bovid species included in this study and their taxonomic affiliations. Species marked with an asterisk were included in the reduced-taxon set. % mol. data = percentage of available data compared to the total alignment length of 7793 nucleotides. The term “CHA-clade” is used for the taxon composed of Caprini, Hippotragini and Alcelaphini.

Twenty-eight species of Antilopini form the ingroup in this analysis. Twelve species from all other major bovid groups were

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