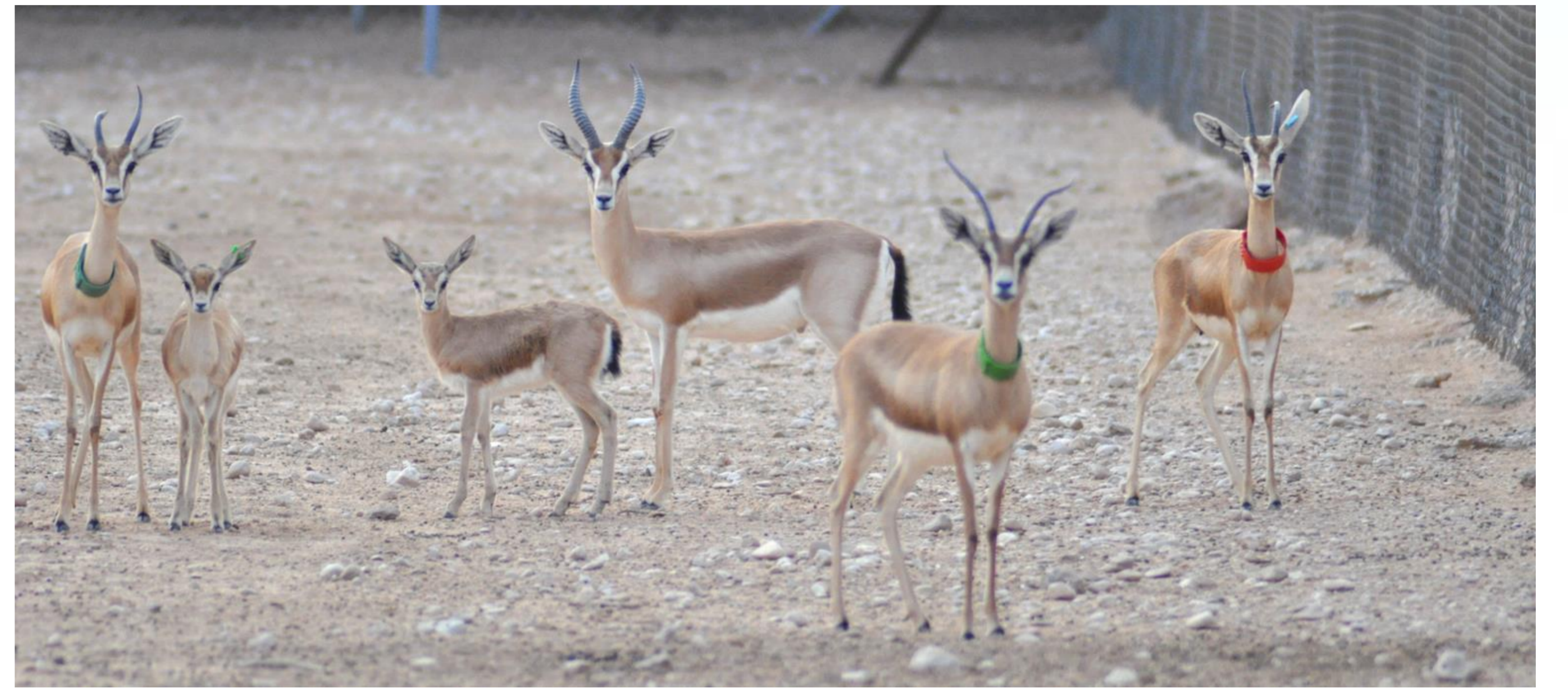


Phylogenetic and phylogeographic analyses of African and Arabian Dorcas gazelles (*Gazella dorcas*)

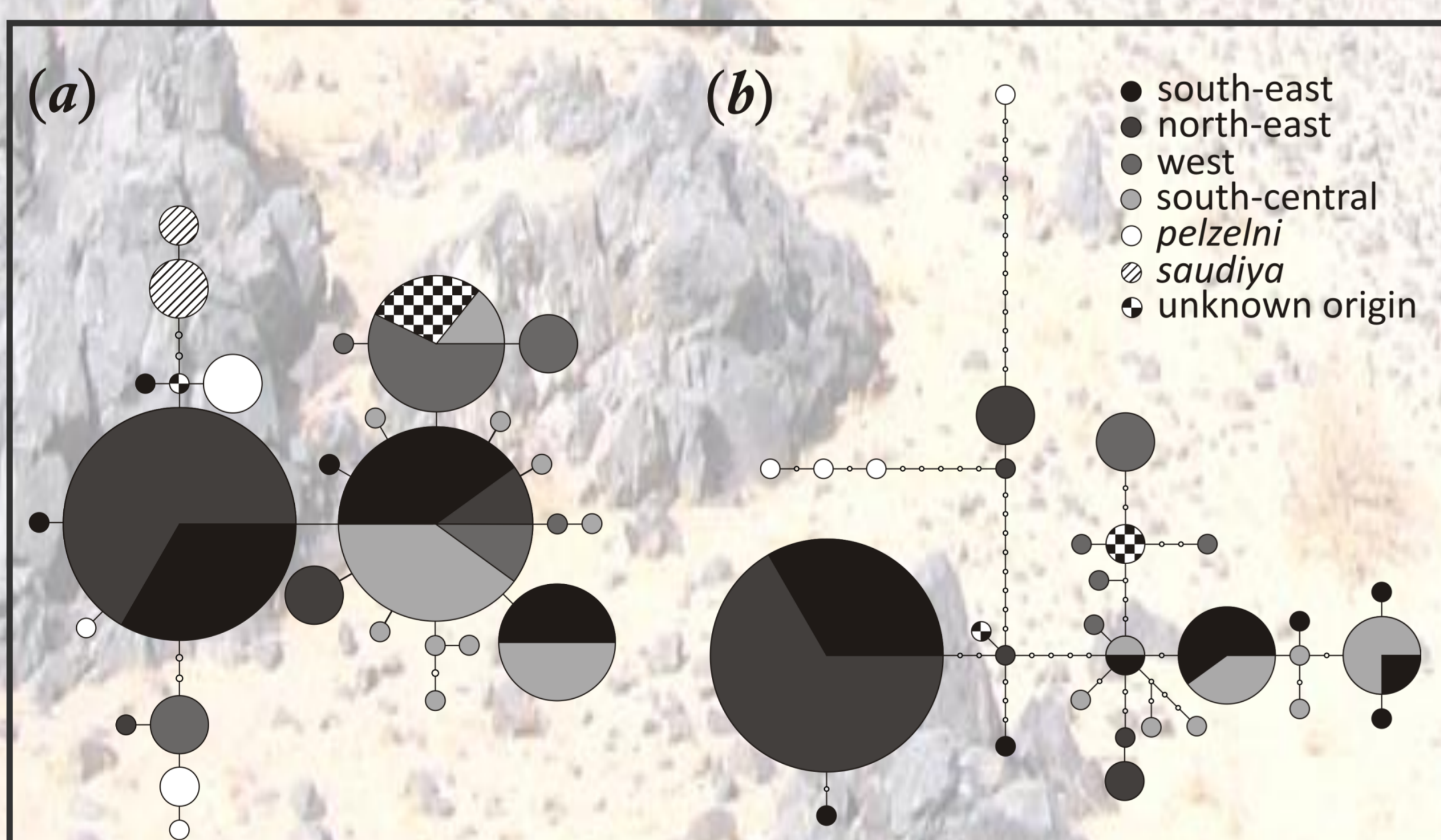
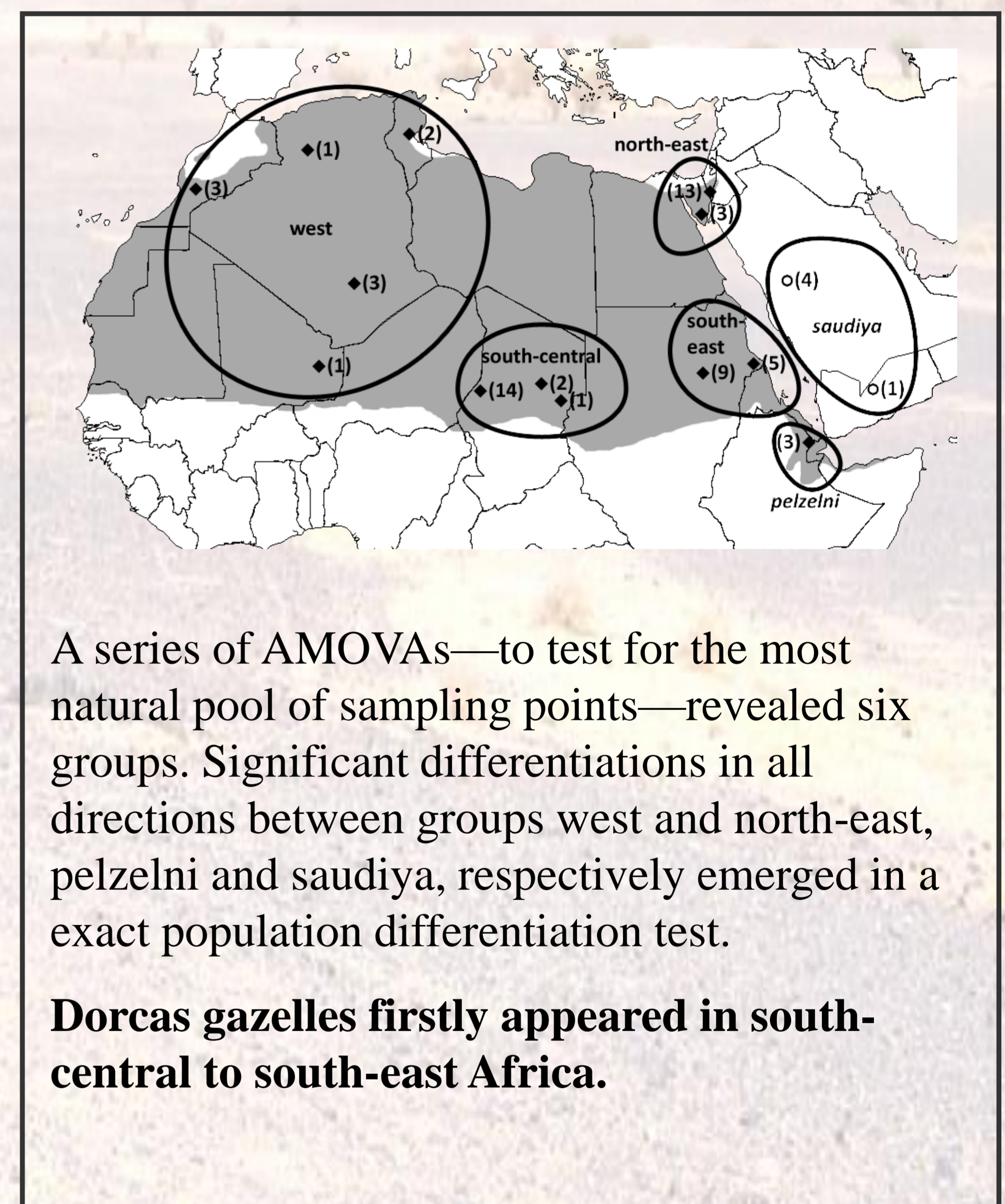
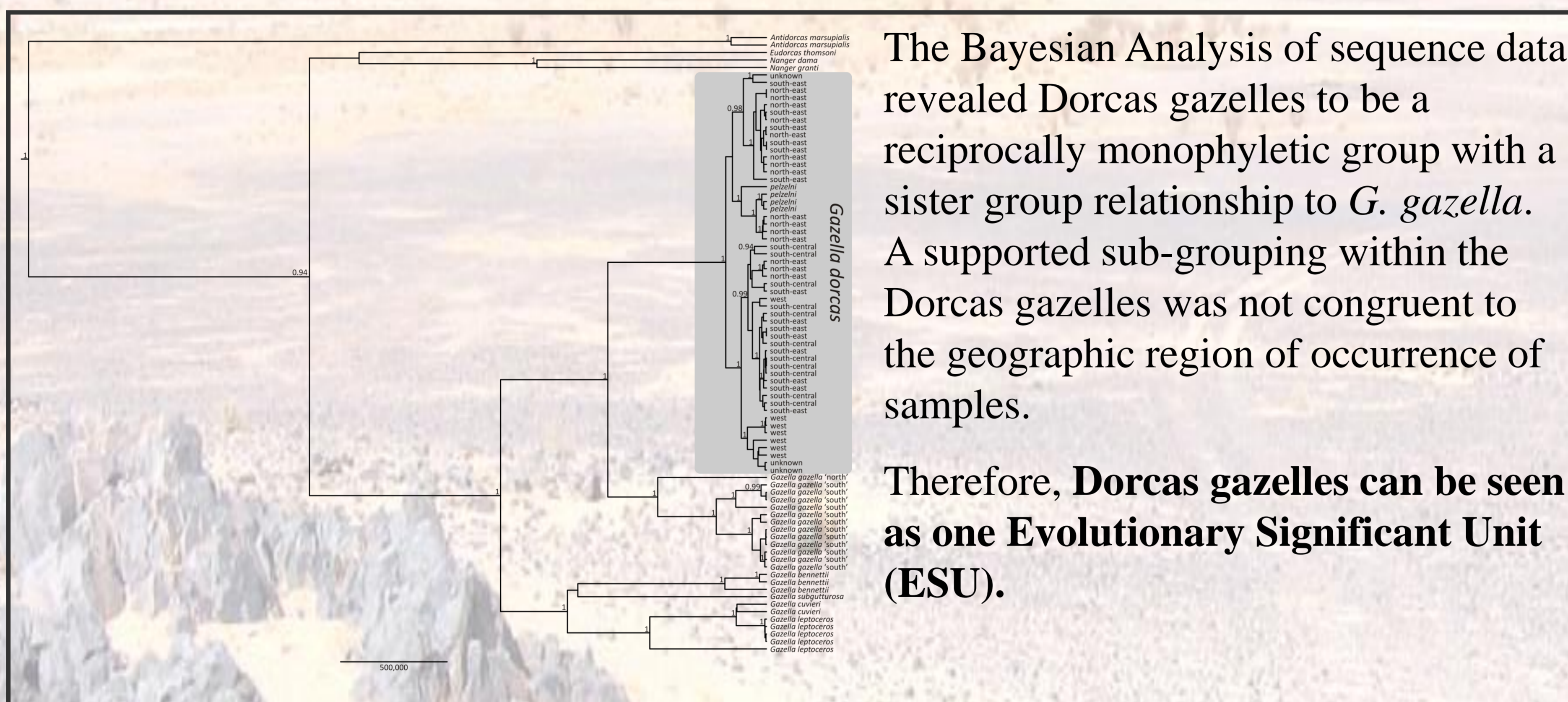
Hannes Lerp¹, Martin Plath¹, Markus Pfenninger² and Torsten Wronski^{3,4}

Background

Once common throughout the entire Sahelo-Saharan region, population sizes of Dorcas gazelles (*Gazella dorcas*) are nowadays decreasing dramatically. The uncertain taxonomy of this species—with a variety of described subspecies without validated status—hampers conservation efforts. In this situation, phylogenetic and phylogeographic investigations using molecular techniques are highly warranted conservation tools. Here, we investigate sequence variation of the mitochondrial cytochrome b gene and control region of 73 dorcas (*G. dorcas*) and Saudi gazelles (*G. saudiya*) throughout the entire distribution range.

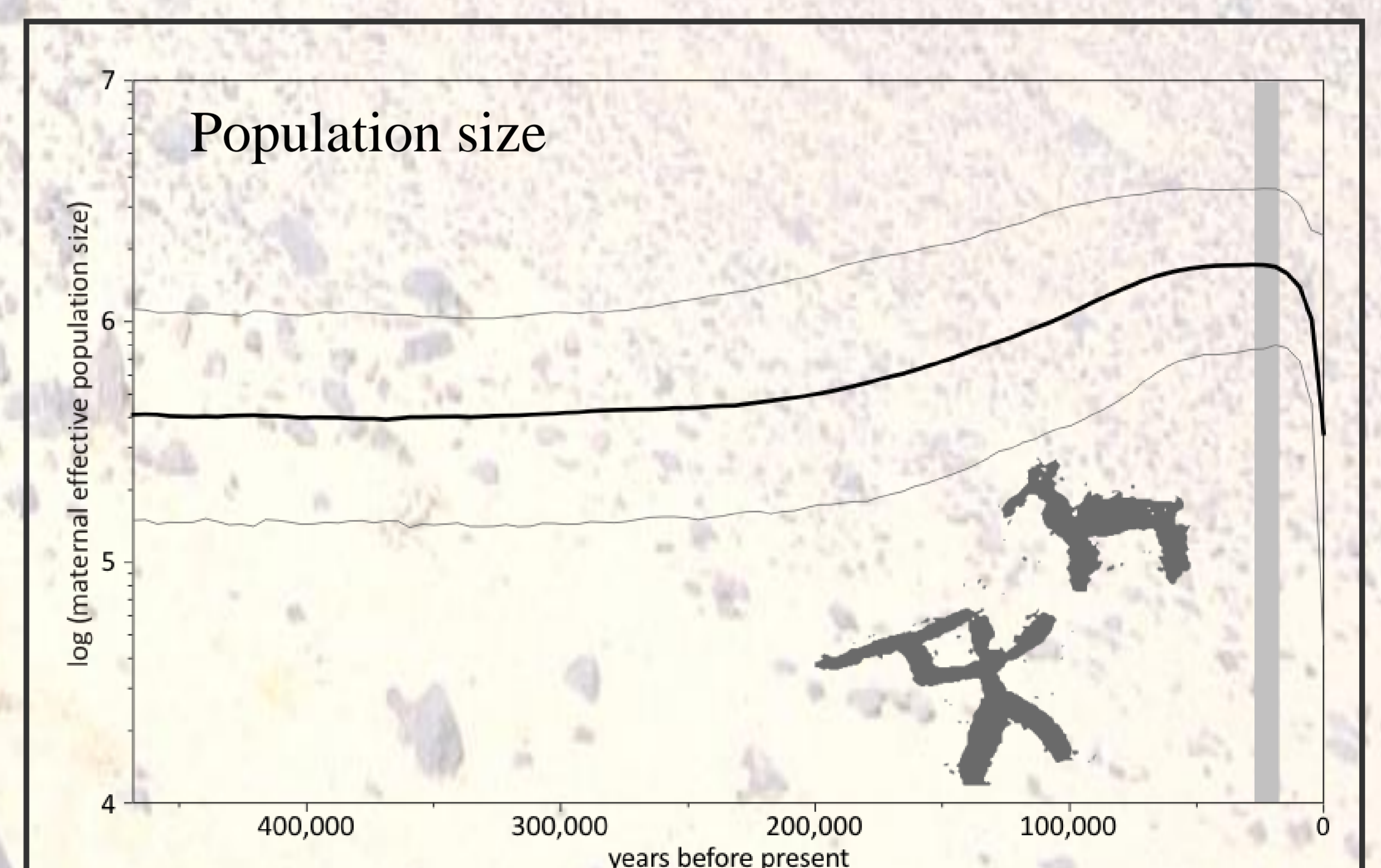


Results and Discussion



Reintroductions of Dorcas gazelles into suitable habitats can be undertaken notwithstanding the origin of founder animals.

In both cladograms (*a* comprises more animals with less sequence data and *b* vice versa) we found haplotypes with geographically mixed distribution, especially between the groups of south-central and south-east Africa. In the case of Saudi gazelle (*G. saudiya*) we found two different haplotypes (*a*), which are distinct from all other samples.



The hunting of Dorcas gazelles started in ancient times and goes on until now.

The past population demography shows a step population decline started about 25,000 years before present (grey shaded area). This date coincide with first fossils records of long-range hunting weaponry.