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Sable antelope nuclear genetic diversity and origin

The Molecular Zoology Laboratory (MolZooLab, University of Johannesburg) and the Research Centre in Biodiversity and Genetic Resources (CIBIO, University of Porto, Portugal) developed a methodological approach for the molecular assignment of sable antelope (*Hippotragus niger*) samples to original populations distributed throughout Africa. To this end, more than 350 samples from across the distribution range were included; these samples were all obtained from wild animals unaffected by human intervention or human-facilitated translocations. The new development is based on nuclear DNA and essentially extends the work done on the mitochondrial markers. A world-class suite of microsatellite markers (57 independent autosomal microsatellites loci) were developed for this purpose; the largest microsatellite library developed to date for any mammal species. The development of these markers is the result of a large international collaboration between research lab in Portugal, Denmark, Angola and South Africa; the results have been published in an international peer-reviewed journal, and have received wide-spread recognition (Vaz Pinto *et al*. *European Journal of Wildlife Research*, 2015, 61: 313-317). Further publications detailing the findings from our collaborative research is currently being prepared.

The nuclear DNA, being inherited from both parents, allows us to determine the purity of individuals and to trace mixing between different populations. Nuclear DNA essentially provides information about specific individuals whereas the mitochondrial DNA, which is maternally inherited, provides information about the evolutionary origin of specific lineages without indication of paternal contribution. These two markers therefore provide complementary information about the evolutionary origin of lineages (mitochondrial DNA) as well as migration between / mixing of different populations (nuclear markers).

The spatial distribution of genetic variation based on the nuclear microsatellite markers complements and to a large extent mirrors the mitochondrial results; this would indicate limited movement of wild sable populations. In broad terms, the same geographic barriers identified using mitochondrial markers has influenced the spatial distribution of nuclear variation.

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Five population groups are clearly distinguished for sable antelope based on genetic data; these are shown in Figure 1. From here onwards, we will use these population groups for assignment of animals on game farms:

i) **Eastern sable** from Kenya to Northern Mozambique (indicated in orange)
ii) **West Tanzanian sable** (indicated in blue)
iii) **Angolan sable** (indicated in purple)
iv) **Zambian sable** (indicated in bright green)
v) **Southern sable** (indicated in grey-green)

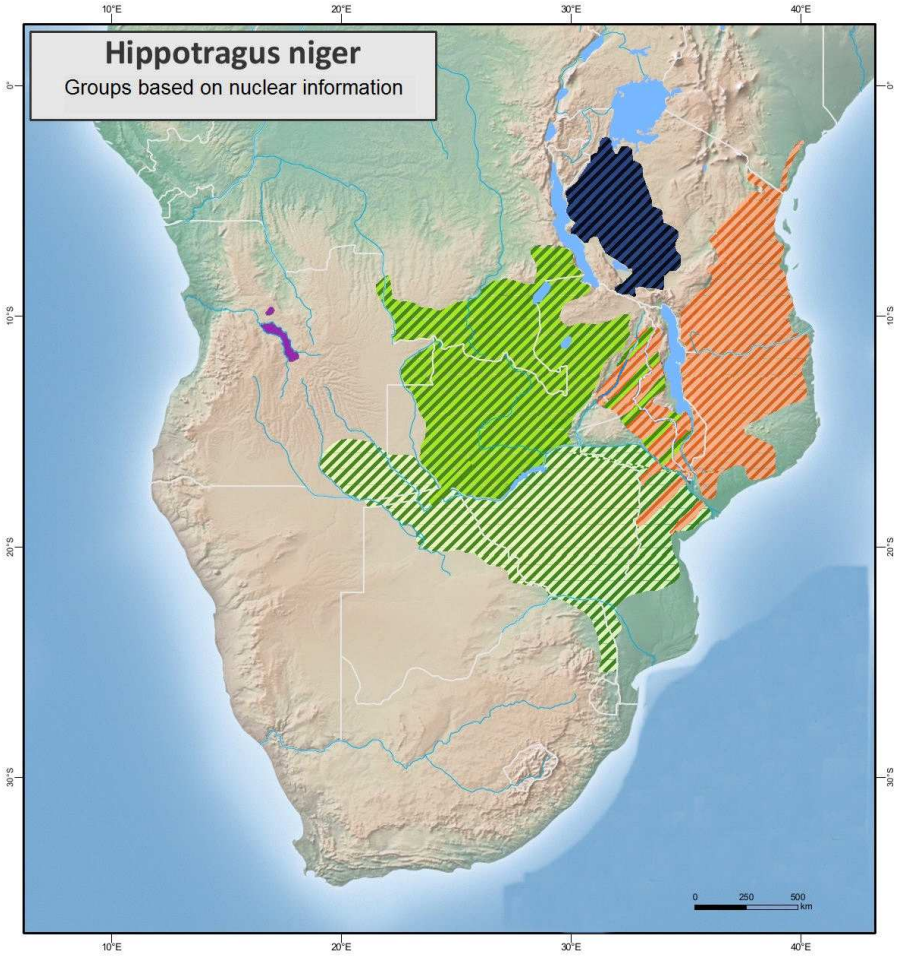

Figure 1. Distribution area of the five sable genetic groups is based on the analyses of 57 nuclear markers.

1. Methodology

DNA extractions are performed for all samples by standard laboratory methodology. Individual genetic profiles are achieved by genotyping the 57 autosomal microsatellite loci (following Vaz Pinto *et al*. 2015). Individual genotypes are analysed by conducting Bayesian assignment procedures implemented in the STRUCTURE software. Prior information on the origin of the wild dataset is used to assist clustering and maximize the power of the analyses. Analyses are implemented allowing five populations as was found for sable antelope across their range (refer to Figure 1). This essentially means that each individual can have their genome probabilistically assigned to each of these clusters (as a percentage membership).

2. Results

In addition to the mitochondrial results, samples that are successfully analysed for the suite of nuclear loci are then assigned to the different groups. The results are presented in table format, indicating the membership of an individual to each group. An example of the format in which results are reported on is given in Table 2.

Table 2 Individual assignment of sable samples to five wild population clusters (K=5) based on the analyses of the microsatellite markers. Nuclear results are based on ten (10) independent Bayesian runs of 1,000,000 generations each. Individual assignments above 95% can be confidently considered as pure. Results are given as percentages (%).

	Individual assignment to sable populations				
	Eastern	W Tanzanian	Angolan	Zambian	Southern
Sample 1	8%	-	-	92%	
Sample 2	-	-	-	-	98%
Sample 3	-	-	-	99%	-
Sample 4	-	-	-	40%	60%
Sample 5	6%	-	-	14.0%	80%

3. Interpretation of the Results

The results presented in Table 2 should be interpreted as follows:

- Animals with individual assignment above 95% to one population can be considered as pure animals;
- Animals with individual assignment between 90 and 95% may still be pure sable from one population, or may contain residual contribution from other populations as result of past mixing;
- All remaining animals can confidently be considered the result of mixing of different populations, the degree of mixing is given as a percentage membership to the different populations.

Sincerely yours,

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