# Genetic Diversity in Oryx Dammah of North Africa

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## Introduction

Captive breeding is seen to play an increasingly important role in the conservation of threatened species. Several species such as the scimitar-horned oryx (Oryx dammah), have been successfully retained in captivity after extinction in the wild. This trend is likely to continue in the future since thousands of threatened species are thought to require captive breeding over the next few hundred years in order to prevent them from going extinct (Tudge 1995). Regional and international programs now exist for many endangered species in captivity where coordinated breeding and management is practised. Efforts are made to preserve the genetic variation of the wild population from which founders were drawn, to minimize loss of this initial diversity as a consequence of inbreeding, and to produce appropriate animals for reintroduction to the species' former range (Russello & Amato 2004).

The scimitar-horned oryx (SHO) belongs to the Hippotragini tribe within the Antilopinae subfamily of Bovidae. During the middle ages, SHO is known to have spanned right across North Africa, from Mauritania on the Atlantic coast to Sudan on the Red Sea, along the interface between true desert and the less arid 'North Saharan/Mediterranean' habitat and the 'Sahelian' habitat (region bordering the Sahara to the south and varying in width from several hundred kilometres to over 1000 km) (Newby 1978, 1980). Populations on the northern fringe of the Sahara are thought to have disappeared by the beginning of the 20th century, with the southern Sahelian range remaining almost continuous until the 1960s. Continued fragmentation eventually led to the extermination of the species from across this region, with the last confirmed sightings made in Chad in the mid-1980s (Newby 1988). Reasons for the decline include drought, loss of habitat, over-hunting, and competition with domestic livestock (Jackson 1978; Newby 1988; Dixon et al . 1991). SHO is now officially classified as extinct in the wild (IUCN 2006) but exists in large numbers in captivity, and there may be as many as 6000 animals held in zoos, private collections, and ranches worldwide (Gilbert 2005). Although there are records from the 1930s of a small number of individuals that may have contributed to the modern captive groups, the vast majority of founders were captured in Chad in the 1960s (Wakefield et al . 2004) (figure1).

In order to preserve and better manage this population of Oryx, the objective of this study was to establish an inventory of different kinds of oryx existing and study their genetic diversity.

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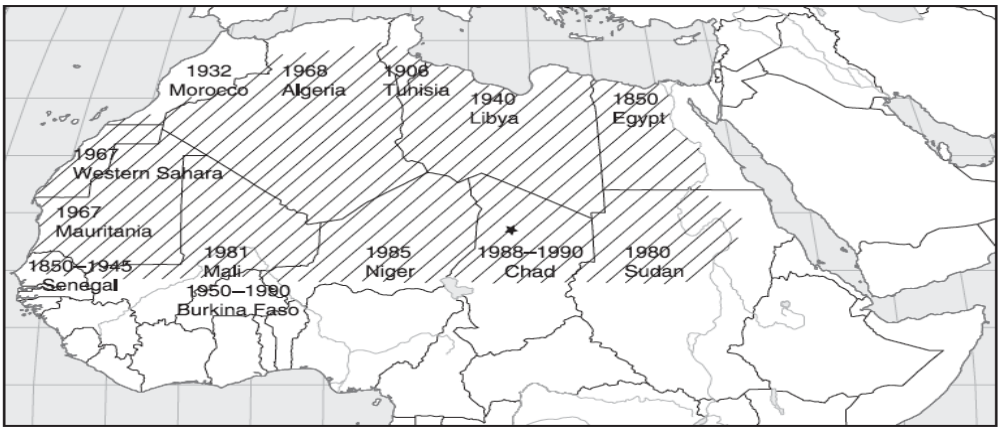


Figure. 1 Historical distribution of SHO across North Africa with approximate extinction times within regions. The star in Chad indicates the approximate location of the base camp in 1967 from which SHO were captured within a 200-km radius. Outline map obtained from BYU Geography Department (www.geog.byu.edu/outlinemaps.dhtml). Information obtained from Wakefield et al. (2004).

## Material and methods

**Study of biodiversity of Oryx Dammah of North Africa.** Oryx Dammah was present at least until the Roman period in the Mediterrraneo-Saharan zone of Tunisia, but there 'was no subsequent data, with the exception of a few catches in the early twentieth century could refer to animals erratic from southern regions (the probable extinction in 1906). The species has been reintroduced in Tunisia (National Park of Bouhedma) in 1985 in a suitable environment steppe and woodlands Accacia Raddiana. A total of fifty hair and ten blood samples was collected in two wild reserves of Oryx in Tunisia (Bou hedma and Tozeur) in order to investigate the genetic diversity created from two subpopulations initiated from 5 females and 5 males re-introduced in Tunisia since 1985. The population reached a total population size of 107 individuals in 2009. Five microsatellites were used for genotyping.
A set of five microsatellite loci previously described insheep (MAF46, MAF50, OarFCB304, OarAE119, OarCP26) and found to amplify polymorphic alleles in Arabian oryx (Marshall et al . 1999) was used. Polymerase chain reactions (PCR) were carried out in a 15- µ L volume containing 2 µ L template, 1 × PCR buffer (ABgene, 75 m m Tris-HCl, pH 8.8, 20 m M (NH4 ) 2 SO 4 , 0.01% (v/v) Tween 20), 1.0–3.0 m M MgCl 2 , 12 µ g BSA (Roche), 200 µ m each dNTP, 200 n m each primer and 0.4 U DNA polymerase (ABgene). Amplification conditions consisted of initial denaturation for 4 min, followed by 30–45 cycles (blood and faecal DNA, respectively) at 94 °C for 30 s, 54– 62 ° C annealing temperature for 30 s, and 72 ° C for 30 s, followed by a final extension at 72 °C for 10 min.

**Statistical analyses.** Allelic richness (Na), Hetrozygosity in the total population, Hetrozygosity per locus and per population (Ho, Hnb), Indice of fixation (Fis, Fit and Fst) and Genetic distance between the two populations. Data analysis is done by software that is GenALEX6.2.

## Results and discussion

Estimates of genetic parameters are shown in table 1. Main results showed a total of 52 alleles. The average number of alleles (Na) was 6.7, the average number of alleles by locus varied from 5 to 7.5. The observed heterozygosity was 0.28 and the unbaised heterozygosity was 0.71. Values for Fis and Fit varied from 0.38 to 1 and from 0.45 to 1 respectively. The average Fis value is equal to 0.59 and the average Fst was 0.15 showing that total variability is due to individual variability.

**Table 1: Estimates of genetic parameters of Oryx in the two wild reserves (Bou hedma et Tozeur)**

| Locus | Na | Ho | Hnb | Fis | Fit | Fst |
|---|---|---|---|---|---|---|
| MAF46 | 5.5 | 0.32 | 0.71 | 0.53 | 0.56 | 0.08 |
| OARAE119 | 9 | 0.45 | 0.76 | 0.38 | 0.45 | 0.12 |
| OARCP26 | 7.5 | 0.41 | 0.74 | 0.41 | 0.50 | 0.16 |
| OARFCB304 | 5 | 0.20 | 0.54 | 0.60 | 0.73 | 0.31 |
| MAF50 | 6.5 | 0.00 | 0.82 | 1.00 | 1.00 | 0.08 |
| Mean | 6.7 | 0.28 | 0.71 | 0.58 | 0.65 | 0.15 |

The lack of strong evidence for population genetic structure using microsatellites could be a result of the small number of loci used in this study since Evanno et al. (2005) have reported a drop in detection of signal of population genetic structure with five loci in comparison to 10 loci. However, other studies have successfully detected evidence for population structure using just five microsatellite loci (Pritchard et al. 2000; Hufbauer et al. 2004). Consequently, we interpret our finding of a lack of population structure as being a result of very large numbers of SHO existing largely in panmixia within the Sahelian region after the early Holocene pluvial episode. SHO are thought to have been highly nomadic, travelling vast distances on a regular basis (Newby 1988; Wacher 1988). Mean observed microsatellite heterozygosity in SHO across all groups was identical to that seen in wild populations of roan (42%, Alpers et al. 2004), and values seen within the Tozeur and Bou hedma groups (42% and 13.9%) were very similar to that seen in captive populations of Arabian oryx (54% across six loci, four of which were the same as those used in this study) (Marshall et al. 1999).

## Conclusion

This first molecular study of the population of Oryx in Tunisia, and exactly at the two national parks of BouHedma and Tozeur, shows a genetic difference between individuals that is not accompanied by morphological differences. This genetic difference despite the common origin of both populations can be explained by a non-breeding flocks when they were all in the park of Bou Hedma.

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