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## Introduction

Often considered the poor man's back and legs, **the donkey is today the most threatened domestic specie in Europe**. In spite of the important role played by the donkey, their use has been regarded as synonymous of backwardness, underdevelopment and low status. Carrying wood, water or short distance riding donkey become a crucial help to survive in desert areas. The oldest archaeological evidence of domestic donkeys was found in Sudan and Egypt and dated from 5000 years ago<sup>1,2</sup>. However still be controversial which was the precise wild progenitor, been most probably the African wild ass (*Equus africanus*)<sup>1,3</sup>, since is exceedingly difficult to distinguish bone and teeth remains of domestic asses from those of wild asses<sup>4</sup>. Presently, the remaining populations of African wild asses are often divided in two subspecies: the *E. a. africanus* or Nubian ass and the *E. a. somaliensis* or Somali ass.

## Objectives

1. Study the current phylogeography of the domestic donkey across the old world
2. Identify possible centres of domestication.

Southwest Asia or/and Africa?

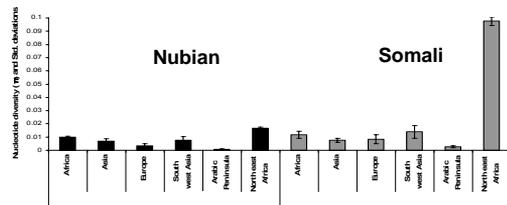


Fig. 2. The nucleotide diversity ( $\pi$ ) for each mtDNA lineage, for each continent and each hypothetical domestication centre. Nucleotide diversity was computed using the ARLEQUIN (S. Schenider, D. Roessli, L. Excoffier, Arlequin Ver. 2000: A software for population genetics data analysis, Genetics and Biometrics Laboratory, University of Geneva, Switzerland), Northeast Africa (NEA: Egypt, Sudan, Ethiopia and Eritrea); Arabic Peninsula (AP: Saudi Arabia, Yemen, and Oman); Southwest Asia (SWA: Turkey, Syria, Jordan, Lebanon, Israel and Iraq).

## Results & discussion

Phylogenetic analyses (building neighbor-joining, UPGMA and maximum likelihood trees)<sup>7</sup> identified two divergent maternal lineages (Fig.3). The average sequence divergence between these two lineages is 15.73  $\pm$  0.61 substitutions (3.29  $\pm$  0.01%) with a maximum divergence of 27 substitutions (5.64  $\pm$  0.01%). This high level of divergence suggests:

> **Two origins for domestic donkeys**, one from each of two divergent wild progenitor populations.

> **Both lineages showed significantly higher ( $P < 0.01$ ) nucleotide diversity in the domestic donkeys from North-eastern Africa (NEA)** (Egypt, Sudan, Ethiopia and Eritrea; Fig. 2). The large nucleotide diversity value in NEA makes it highly likely that domestication occurred within this region. If this is true, it represents the only known example of an ungulate solely domesticated in Africa.

> **Donkeys have the lowest degree of population structuring** of any livestock species, consistent with its unique and important role throughout history in transportation, trade and warfare.

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Past



Present

## Material & Methods

We analysed the genetic variation in 478 base pairs (bp) from the control region of mtDNA in 200 domestic donkeys from across the old world and found that all diversity is divided in two maternal lineages. To pinpoint the geographic region of donkey domestication we considered current and historical location of the wild progenitors (Northeast Africa), and genetic diversity. A frequent justification used to place domestication is the fact that domestication centres retain higher genetic diversity. Therefore, we estimated and compared the gene diversity ( $\pi$ ) between hypothetical centres of domestication.

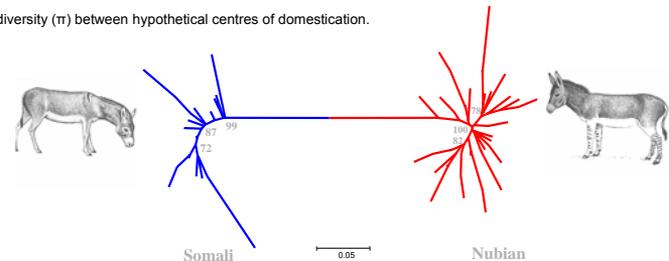


Fig. 2. Unrooted NJ network of all domestic donkey haplotypes. Two clades (somali and Nubian) of donkey haplotypes are indicated. Branch lengths are according to the indicated scale. The nucleotide substitution model (HKY+G) for our data set was optimized using a hierarchical maximum likelihood (ML) approach<sup>8</sup>. A starting tree was calculated under the HKY +G model using the neighbour-joining method and further searched by 116 tree bisection and reconnection (TBR) iterations under the minimum evolution criteria<sup>9</sup>.

Table 1. Hierarchical distribution of mtDNA (HVI) diversity within and among populations (and continental groups of breeds) for donkey, horse, goat, sheep, and cattle as computed under the AMOVA framework. The continental groups in donkeys were chosen for comparison with published AMOVA values from other livestock species having the same geographic population groupings (Africa, Asia and Europe). 'Populations' refer to breeds or local populations for the livestock species.

Taxon	Distribution of sequence variation (% of total)		
	Within populations	Among populations within groups	Among continental groups of populations
Donkey	92.08	5.98	1.94* (Donkey Southern Africa/ Northern Africa/ Western Africa/ Eastern Africa/Near East/ Middle East/ Far East/ Eastern Europe/ Western Europe)
Donkey (Clade I)	97.14	2.88	0.00 (Africa/Asia/Europe)
Donkey (Clade II)	92.24	7.94	0.00 (Africa/Asia/Europe)
Horse	82.18	16.43	1.40* (Africa/Asia/Europe)
Goat	72.70	12.21	13.9 (Africa/Asia/Europe) <sup>9</sup>
Cattle	33.22	1.75	65.03 (Africa /Asia/Europe) <sup>10</sup>

\* ( $P < 0.05$ )

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