Two African Origins and Extremely Weak Population Structure in Donkeys Revealed by Mitochondrial DNA Sequencing

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Introduction

Often considered the poor man’s back and legs, the donkey is today the most threatened domestic species 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 donkeys 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. However, still be controversial which was the precise wild progenitor, been most probably the African wild ass (Equus africanus) synonymous of backwardness, underdevelopment and low status. 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?

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 domesticisation is the fact that domestication centres retain higher genetic diversity. Therefore, we estimated and compared the gene diversity (H) between hypothetical centres of domestication.

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

<table>
<thead>
<tr>
<th>Taxon</th>
<th>Within populations</th>
<th>Among populations within groups</th>
<th>Among continental groups of populations</th>
</tr>
</thead>
<tbody>
<tr>
<td>Donkey</td>
<td>0.28</td>
<td>5.08</td>
<td>0.05 (Africa/Eastern Africa/ Western Europe)</td>
</tr>
<tr>
<td>Donkey</td>
<td>5.14</td>
<td>2.88</td>
<td>0.08 (Africa/Eastern Europe)</td>
</tr>
<tr>
<td>Donkey</td>
<td>0.26</td>
<td>7.94</td>
<td>0.08 (Africa/Eastern Europe)</td>
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<tr>
<td>Horse</td>
<td>0.18</td>
<td>16.64</td>
<td>1.49 (Africa/Eastern Europe)</td>
</tr>
<tr>
<td>Goat</td>
<td>0.70</td>
<td>12.21</td>
<td>1.13 (Africa/Eastern Europe)</td>
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<tr>
<td>Cattle</td>
<td>0.25</td>
<td>1.75</td>
<td>0.85 (Africa/Asia/Europe)</td>
</tr>
</tbody>
</table>

Acknowledgements

The authors thank C. Miquel and L. Gidly for help with laboratory analysis, C. Vilà and T. Jansen for providing mtDNA sequence datasets from horses, and to the following who kindly provided or helped in the collection of samples: M. Abu, T. Tsedev, P.. A.B.P. is supported by a research grant from Fundação para a Ciência e a Tecnologia (FCT/POCTI/FEDER/27443/2001) through the Graduate Program in Areas of Basic and Applied Biology from University of Porto (GABA). Participation in this congress was possible with the support from: FCT Fundação para a Ciência e a Tecnologia.

References