

# Phylogenetic relationships and molecular dating of the main evolutionary events within Caprini tribe inferred by mtDNA and globin genes sequence

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The Caprini tribe consists of sheep, goats and related species that display a uniquely old-world distribution. The phylogenetic relationships among these species are one of the much controversial issues for paleontologists, zoologists and molecular biologists because of the complexity in their evolutionary mechanisms. Very few paleontological data are available because their preferred mountainous habitats are not favourable for fossil preservation [1]. Consequently, the evolutionary history of Caprini species is poorly understood. Phylogenies have been proposed based on morphological, behavioral, ecological and some molecular comparisons including nuclear (n) and mitochondrial (mt) DNA sequences. Considerable progress has been made during the past few years with the sequencing of *Ovis aries*, *Capra hircus* and *Ammotragus lervia* mitogenomes [2-4]. According to recent taxonomic propositions inferred by mtDNA analysis, the tribe includes 35 species, which can be classified into 14 genera [5]. In this report we examined the phylogeny of the Caprini tribe by analyzing two mitochondrial (Cyt *b* gene and D-loop region) and one nuclear (adult  $\beta$ -globin gene) molecular marker of wild and domestic species from North Africa, Mediterranean area and South Asia, representing most of the taxonomic diversity of the group. Total DNA was extracted from whole blood samples of Barbary sheep (*A. lervia*), argali (*O. ammon*), urial (*O. vignei*), bighorn (*O. canadensis*), European and Asian domestic sheep (*O. aries*), wild Corsico-Sardinian (*O. a. musimon*) and Cyprus mouflon (*O. a. ophion*) and domestic goat (*Capra hircus*). Gene targets were amplified and analyzed by automated capillary sequencing. The three genetic markers were studied separately and also combined to benefit from the maximum number of molecular characters. Data sequences were analyzed using Maximum Likelihood (ML) and Neighbor Joining (NJ) methods for the tree reconstructions. Phylogenetic analyses based on mtDNA sequences indicated that the Caprini species descend from a common ancestor from which two well-separate mtDNA lineages evolved. One clusters *A. lervia*, *Capra*, *Hemitragus* and *Pseudois*, while *Ovis* is placed in a distinct clade. Within *Ovis* species, bighorn was found more closed to *O. dalli* than to

urial and argali which were grouped in a separate cluster including muoflons, wild and domestic sheeps. The Cyprian mouflon shares a common ancestor with the European species. The tree topology provides strong evidence that the Cyprian mouflon constitutes a unique evolutionary lineage in the Caprini radiation. Monophyly of Caprini tribe is not supported. Sequence comparisons of the adult  $\beta$ -globin gene suggested that caprines share a common ancestor carrying the triplicated A-haplotype and that a recent deletion of a gene set gave rise to the duplicated cluster (B-haplotype) containing the HBBB locus found in sheep of the Hb B type and Cypriot mouflon, which evolved independently. Data also suggests that the *Ammotragus*  $\beta$ -globin gene is older and indicates it followed an independent evolution after separating from species having the same HBBA locus. Molecular dating pointed on a common ancestor first appeared about 6-7 MYBP during the Pliocene. The divergence ancestor/caprines of the A-haplotype and  $\beta$ -haplotype have been dated 1.8 MYBP and 1.5 MYBP, respectively.

## References

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