

# Mitochondrial control region sequence variation within the argali wild sheep (*Ovis ammon*): evolution and conservation relevance

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## SUMMARY

The phylogenetic relationship of several subspecies of *Ovis ammon* were analyzed by comparing DNA sequences within the entire mitochondrial D-loop region. Five putative subspecies of *ammon* (*dalai-lamae*, *darwini*, *hodgsoni*, *saiensis* and *adametzi*) were sampled from four provinces in China [Xinjiang, Qinghai, Gansu and Xizang (Tibet)] and two (*severtzovi* and *nigrimontana*) from Uzbekistan. The argalis sampled represent most of the currently recognized putative subspecies of argali. Analysis of mtDNA sequences revealed high variability within *ammon* (7.7%), ranging from 2.4 to 11.5%. Maximum-Parsimony tree indicated that *nigrimontana* from Uzbekistan diverged first, followed by *severtzovi* from Uzbekistan. The dispersal of argalis into China gave rise to three clades, suggesting that the argali originated in Western Asia and then dispersed throughout the central Asian highlands on a southeasterly course. Among the Chinese argalis, mtDNA analysis places *dalai-lamae* genetically closer to *hodgsoni* than to *darwini*. *Severtzovi* and *nigrimontana* are two separate subspecies and genetically distinct from the Chinese argali.

## KEY WORDS

Argali (*Ovis ammon*),  
mtDNA,  
control region,  
phylogenetic relationship.