Structure of mitochondrial DNA control region and genetic diversity of *Moschus berezovskii* populations in Shaanxi Province

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**ABSTRACT.** In China, *Moschus berezovskii* (forest musk deer), a first-class national protected animal, was earlier widely distributed. However, wild populations of the forest musk deer have declined because of human activity and habitat loss. In order to gather useful information for its conservation and management, we investigated the genetic diversity and population structure of this species by analyzing a 632-bp fragment of mitochondrial DNA (mtDNA) control region in three wild populations in Shaanxi Province, China. The average A+T content (64.1%) of mtDNA was higher than that of G+C (35.9%). A total of 178 variable sites (about 28.03% of the total nucleotides in the sequence) were detected in 71 individuals. The nucleotide diversity \((P)\) in the 71 individuals was 0.04688, and the average nucleotide differences \((K)\) were 21.238. The 71 individuals belonged to 33 haplotypes according to the determined sequences. The average genetic distance \((P)\) among the haplotypes of the species was 0.169. The phylogenetic tree constructed using the neighbor-joining method revealed that these individuals were clustered into three groups, but the individual distribution in those groups was disordered. These data indicated the variation and rich genetic diversity in the three populations of
M. berezovskii. Compared to the wild population in Longxian, those in Liuba and Fengxian had a close kinship. The present results indicated no signs of inbreeding or a decline in genetic diversity in the wild M. berezovskii population.

**Key words:** Moschus berezovskii; Mitochondrial DNA; Genetic diversity; Control region