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Genetic variation of Caucasian pit viper (*Gloydius halys*) populations in Iran using mtDNA marker

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The concept of genetic variation is a vital factor to investigate the effect of evolutionary process on genus *Gloydius*' populations. Having a vast distribution in many parts of Asia, genus *Gloydius* (Serpentes: Crotalinae) is from the venomous group of snakes, and consists of thirteen species. Caucasian Pitviper (*Gloydius halys*) is scattered from Northwest to Northeast Iran in wide variety of terrestrial and mountainous, forestal and bush-lands habitats. This study aims to analyze biodiversity, genetic variation and genetic structure among the Caucasian Pitviper populations in Alborz habitats. For this purpose, 18 individuals representing two populations (northern and northeastern Alborz) were captured, and, some ventral scale specimens were collected. Polymorphism of a mitochondrial gene *Cytb*, was investigated in these samples. For this purpose, using PCR, a segment of this gene with 1067 base pair length was amplified and the amplified sequence was then subjected to sequencing. The genealogy analysis was conducted to determine the best evolutionary model using Bayesian and maximum likelihood approaches. Our results revealed that the Alborz populations were separated by 0.99 and 95.34 posterior probability and bootstrap values, respectively. Besides, 13 unique haplotypes out of 18 sequenced individuals (7 from northern and 6 from northeastern population), were analyzed and consequently a considerable distinction was detected between north and northeastern population haplotypes by 17 mutational steps. Also, a significantly high genetic variation ($Fst>0.25$, $p<0.01$) was found between populations in the north and northeast Alborz through the Analysis of Molecular Variance (AMOVA). On the other hand, using neutrality tests, the incidence of spontaneous expansion was determined in north and northeast populations. As a conclusion, we believe that the genetic distance between these two populations is due to their local adaptability. Hence, they can be considered as two distinct conservational units in terms of biodiversity conservational plans.

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Relative abundance, prey preference and niche partitioning of snow leopard (*Uncia uncia*) and Tibetan wolf (*Canis lupus chanku*) in Karakoram Pamir mountains

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Reliable information about predator's abundance, their feeding habits, potential habitats and niches is imperative to understand the ecological interactions among herders, herbivores and carnivores on shared habitats. Therefore, the present study endeavors to fill knowledge gaps for the sustainable conservation and management of the remaining lot of endangered Snow leopard and Tibetan wolf in Khunjerab National Park (KNP) in Pakistan and Taxkorgan National Nature Reserve (TKNR) in China. Our results revealed that the Tibetan wolf and Snow leopard as the major predators in KNP, with an estimated population size of 30-35 with 0.006 Snow leopards in per km^{-2}. Also, out of estimated total 822.7 kg km^{-2} (animal's km^{-2}) biomass, it was found that that livestock and ungulates offered around 66% and 34% diet for Snow leopard and Tibetan wolf collectively. Through scat analysis, results showed that both these predators rely heavily on livestock to fulfill food requirements. Moreover, Tibetan wolf was found having a large niche separation with Snow leopard, whereas, Snow leopard was found comparatively having greater niche than the Tibetan wolf. In the same vein, considering the large biomass needs of the carnivores and the low availability of wild prey, human-wildlife conflict is therefore an inevitable and critical issue in the region. Trans-boundary efforts are necessary to develop conservation management schemes that protect threatened wildlife species as well as provide support and benefits to the local communities living adjacent to KNP and TNR in the Karakoram and Pamir mountains of China and Pakistan.

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