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## Geographic and genetic boundaries of brown bear (*Ursus arctos*) population in the Caucasus

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### KEYWORDS

Caucasus • genetic distance • Georgia • least-cost distance • microsatellites • mtDNA • *Ursus arctos*

### ABSTRACT

The taxonomic status of brown bears in the Caucasus remains unclear. Several morphs or subspecies have been identified from the morphological (craniological) data, but the status of each of these subspecies has never been verified by molecular genetic methods. We analysed mitochondrial DNA sequences (control region) to reveal phylogenetic relationships and infer divergence time between brown bear subpopulations in the Caucasus. We estimated migration and gene flow from both mitochondrial DNA and microsatellite allele frequencies, and identified possible barriers to gene flow among the subpopulations. Our suggestion is that all Caucasian bears belong to the nominal subspecies of *Ursus arctos*. Our results revealed two genetically and geographically distinct maternal haplogroups: one from the Lesser Caucasus and the other one from the Greater Caucasus. The genetic divergence between these haplogroups dates as far back as the beginning of human colonization of the Caucasus. Our analysis of the least-cost distances between the subpopulations suggests humans as a major barrier to gene flow. The low genetic differentiation inferred from microsatellite allele frequencies indicates that gene flow between the two populations in the Caucasus is maintained through the movements of male brown bears. The Likhi Ridge that connects the Greater and Lesser Caucasus mountains is the most likely corridor for this migration.

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