

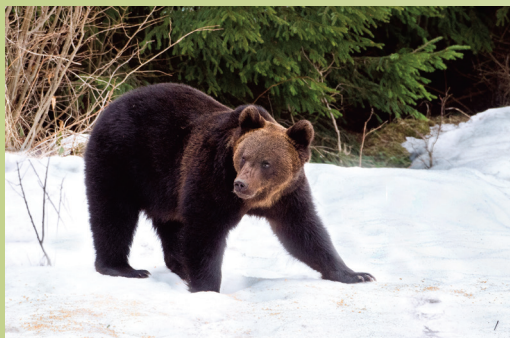
36th Congress of International Union of Game Biologists



Quo vadis wildlife management?

The future of wildlife management in the
evolving social and environmental realities

August 28–31, 2023 Warsaw, Poland



Phylogeography and distribution of moose (*Alces alces*) in Eurasia during the last 50 000 years

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Keywords: expansion, extinction, genetic diversity, mitochondrial DNA, recolonization, stable isotopes, cold-adapted species

We analysed the range, habitat and mitochondrial DNA variability of moose (*Alces alces*) in relation to environmental changes in Eurasia since the Late Pleistocene. In our study, we analysed both contemporary and radiocarbon-dated moose samples, their whole mitochondrial DNA (mtDNA) genomes as well as stable carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) isotope composition in bone collagen extracted from selected samples. The range of moose and their genetic diversity were larger in the Late Pleistocene and the Early Holocene than today, and they have changed as a result of climatic oscillations and human impact. After surviving in several refugia during the Last Glacial Maximum (LGM), moose rapidly recolonised more northerly located areas that were released by the glacier. By the Early Holocene, moose was found almost everywhere in Europe, except the southernmost areas. Then the moose's range began to decline. The most dramatic contraction occurred in the last few hundred years, probably due to intensive over-hunting by humans. Some of the genetic variants of the species have not survived to modern times. Today we have three mtDNA clades of moose in Europe. Two of them, the Western and the Central ones, have suffered the most because of range contraction during the Holocene.