

Publication

Genetic diversity, genetic structure and diet of ancient and contemporary red deer (Cervus elaphus L.) from north-eastern France

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In north-eastern France, red deer (Cervus elaphus L.) populations were rebuilt from a few hundred individuals, which have subsisted in remote valleys of the Vosges mountains, and to a lesser extent from individuals escaped from private enclosures; at present times, this species occupies large areas, mainly in the Vosges Mountains. In this study, we examined the population dynamics of red deer in the Vosges Mountains using ancient and contemporary mitochondrial DNA (mtDNA) from 140 samples (23 ancient + 117 modern) spanning the last 7'000 years. In addition, we reconstructed the feeding habits and the habitat of red deer since the beginning of agriculture applying isotopic analyses in order to establish a basis for current environmental management strategies. We show that past and present red deer in the Vosges Mountains belong to mtDNA haplogroup A, suggesting that they originated from the Iberian refugium after the last glacial maximum (LGM). Palaeogenetic analysis of ancient bone material revealed the presence of two distinct haplotypes with different temporal distributions. Individuals belonging to the two haplotype groups apparently occupied two different habitats over at least 7'000 years. AM6 correlates with an ecological type that feeds in densely forested mountain landscapes, while AM235 correlates with feeding in lowland landscapes, composed of a mixture of meadows and riverine, herb-rich woodlands. Our results suggest that red deer of north-eastern France was able to adapt, over the long term, to these different habitat types, possibly due to efficient ethological barriers. Modern haplotype patterns support the historical record that red deer has been exposed to strong anthropogenic influences as a major game species.

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