

Pan-European phylogeography of the European roe deer (*Capreolus capreolus*)

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Abstract

To provide the most comprehensive picture of species phylogeny and phylogeography of European roe deer (*Capreolus capreolus*), we analysed mtDNA control region (610 bp) of 1469 samples of roe deer from Central and Eastern Europe and included into the analyses additional 1541 mtDNA sequences from GenBank from other regions of the continent. We detected two mtDNA lineages of the species: European and Siberian one (an introgression of *C. pygargus* mtDNA into *C. capreolus*). The Siberian lineage was most frequent in eastern part of the continent and declined towards Central Europe. The European lineage contained three clades (Central, Eastern and Western) composed of 2 to 8 subclades, many of which were separated in space. The Western clade appeared to have a discontinuous range from Portugal to Russia. Most of the subclades in the Central and the Eastern clades were under expansion during the Weichselian glacial period before the Last Glacial Maximum (LGM), while the expansion time of the Western clade overlapped with the Eemian interglacial. High genetic diversity of extant roe deer is the result of their survival during the LGM in a large, contiguous range spanning from the Iberian Peninsula to the Caucasus Mts. and in two northern refugia.

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