Summary

Pleistocene climatic changes had a great impact on distribution and genetic structure of many populations. It is generally accepted that warm adapted species were restricted to refugia during colder events and recolonized previously inhabited area during climate amelioration. A genetic diversity observed today within many species is a result of repeated changes in distribution and isolation in refugia. Red deer (*Cervus elaphus*) is the most widespread deer species in the world. Analyses of contemporary populations revealed that geographic distribution of the red deer mtDNA lineages were caused by isolation in refugia and subsequent postglacial migrations. On the other hand, as an important game species, red deer was affected by humans since the prehistoric times by translocations, introductions and habitat alteration. Human influence could therefore blur natural phylogenetic patterns. The aim of this study was to investigate the Eurasian red deer population history and to determine to what extent climate changes and humans affected the distribution and genetic diversity of this species in the late Quaternary.

Analysis of a fossil record showed that the ice sheet evolution and paleovegetation in the Late Pleistocene had a major impact on the red deer distribution. During the Last Glacial Maximum (LGM) the species range was contracted to southern Europe. Afterwards, due to deglaciation and climate amelioration, at about 15 thousand years ago the red deer started to expand to the northern part of Europe.

Genetic analyses of 353 red deer subfossils from European and Asian sites resulted in obtaining the cytochrome *b* sequences from 151 individuals. Phylogenetic analyses revealed that Eurasian populations belonged to seven mtDNA lineages and allowed, together with sample dating to reconstruct phylogeographic structure during the last 50 thousand years. In MIS 3 there were many contact zones of different haplogroups, for example in the Urals and the Crimean Peninsula. Those results indicate a lack of phylogeographic patterns before LGM, although they are present in contemporary populations. Haplogroup distribution started to change after LGM, during a postglacial recolonization. Divergence time estimation suggested that most of the mtDNA genetic diversity was formed at the end of the Pleistocene. A comparison of the haplogroup distribution in few time periods allowed to establish that despite many translocations, humans did not blurred the natural red deer phylogeographic patterns, although affected the populations locally.
The obtained results confirmed the hypothesis about the origin of populations inhabiting the islands of Sardinia and Corsica. Red deer were translocated from the source population in the Apennine Peninsula to the Tyrrhenian islands.

Very interesting results were obtained for the Crimean samples. ABC analyses showed that at least two events of extinction and recolonization happened in the peninsula. The first event was correlated with climate deterioration during LGM and the second one with activities of Greeks. These results suggest that Crimea has not been a glacial refugium for the red deer.