

The Late Pleistocene (approximately 130–11,7 thousand years ago) was marked by sudden and rapid climatic changes, including successive phases of climate cooling and warming. These changes had a huge impact on the population dynamics of many animal species. In Europe, they led to the extinction and emergence of new species. Climatic cycles and associated environmental changes forced species to either migrate to more suitable habitats, expand or shrink their ranges, or cause their local extinctions and subsequent recolonizations. Mammals such as voles provide an excellent model for studying the effects of climate change on fauna - they are abundant, reproduce quickly, and respond rapidly to environmental changes. In addition, their remains are often found at archaeological and paleontological sites, providing numerous materials for analysis.

The goal of this project is to reconstruct some aspects of the evolutionary history of pine voles (subgenus *Terricola*, genus *Microtus*) from Southern Europe from the Late Pleistocene to modern times. Current knowledge of the *Terricola* subgenus's past is fragmentary - many species are difficult to distinguish based on morphology, and genetic data is very limited. The Pine voles also show low genetic diversity, which has made it difficult to establish their exact phylogenetic relationships. Currently, 15 species are distinguished, which significantly differ in their ranges. For example, the European pine vole (*M. subterraneus*) occupies almost all of Europe (from France through Central Europe, the Balkans, and Northern Turkey to Russia), while the Tatra pine vole (*M. tatricus*) only the area of the Carpathian Mountains (fig 1.).

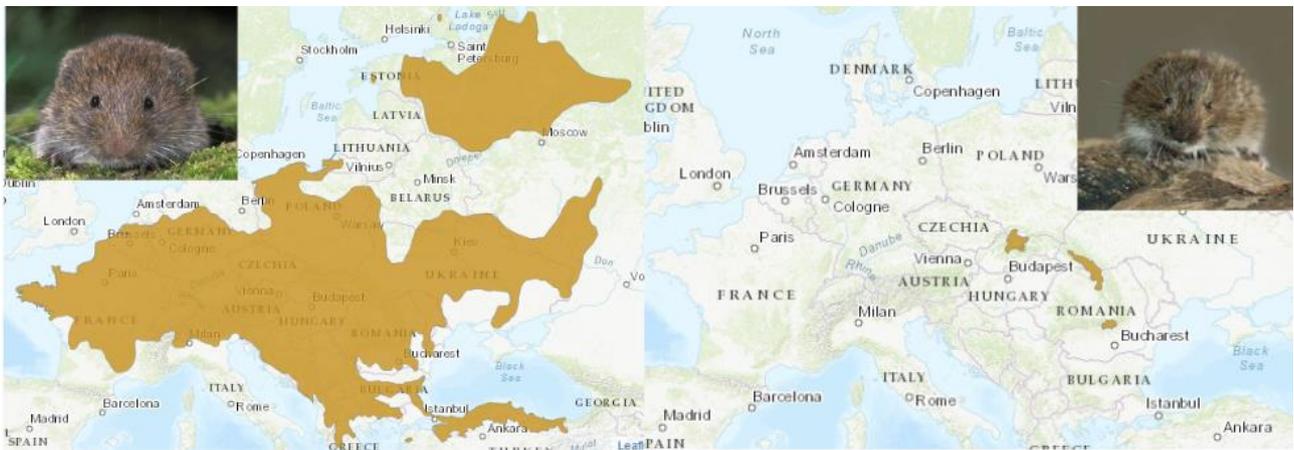


Figure 1. Geographic range and a photo of a representative of *M. subterraneus* (left) and *M. tatricus* (right) according to the IUCN International Union for Conservation of Nature (Version 2025).

We plan to obtain subfossil teeth of about 80 voles from a number of paleontological sites in Southern Europe, representing different periods, and a dozen modern samples, especially in the area of Northern Italy and the Balkans. DNA will be isolated and sequenced using protocols optimised for highly degraded DNA. We will focus on the analysis of mitochondrial DNA, which is most easily recovered from subfossil material. The analysis of ancient DNA will enable the assignment of paleontological samples to species and thus trace changes in their ranges over time. We also plan to analyse the nuclear genomes of selected modern individuals. This will allow us to reconstruct changes in the effective population size of the *Terricola* species over time and relate it to changes in ranges derived from the analysis of subfossil samples.

Reconstruction of phylogenetic trees of individuals from different periods and analysis of the history of effective population size will allow us to assess the dynamics of population changes over time, such as the emergence of new lineages, their spread, and extinction under the influence of the changing climate. Previous studies of other vole species have documented high population dynamics in Central and Western Europe. Interstadials, short warm episodes when forest ecosystems emerged in parts of Europe dominated by treeless tundra ecosystems throughout most of the last glacial, have been identified as the main cause of these dynamics. In this project, we want to check if similar dynamics can be observed in the southern part of the continent, where environmental changes were milder.

Through the proposed project, we will gain new insights into the evolutionary dynamics of these rodents in Southern Europe, which will contribute to a better understanding of the impact of climate change on biodiversity over long-time scales across Europe.