

The general goal of this project is to use genetic and morphological data obtained from subfossil and contemporary specimens to investigate population dynamics, migrations and extinctions of three small mammal species during the Late Pleistocene and Holocene and to assess the impact of climate changes onto those events. These species, the bank vole (*Clethrionomys glareolus*), the narrow-headed vole (*Microtus gregalis*) and the root vole (*Microtus oeconomus*), were selected to represent different adaptations and environmental requirements and we assume that their evolutionary histories were different. Analyses of samples from broad temporal and geographical range will allow us to answer several important questions regarding history of the species among others, was Carpathian area a glacial refugium for bank vole? Were evolutionary histories of studied species different at high and low latitudes? Were abrupt climate changes at the end of last glaciation more harmful than gradual cooling during the Last Glacial Maximum? It will be also interesting to investigate whether molecular and morphological analyses will produce different signals of population history.

To achieve these goals we plan to obtain mtDNA sequences from 150 subfossil and 50 contemporary specimens of each species and to examine their tooth morphology. Earlier studies showed that this is the most versatile approach to investigate past species histories. However, analysis of DNA from fossil paleontological samples is full of obstacles. Typically there is only a minute amounts of highly fragmented DNA molecules. Moreover, endogenous DNA constitute usually less than 1% of the total extracted DNA while majority comes from microorganisms. To overcome these problems we will take advantage of targeted enrichment procedure. This method allows for even hundred-fold increase of amount of targeted DNA molecules in DNA extracts and coupled with high throughput sequencing enables reconstruction of mtDNA sequences. Paleontological materials will be selected from numerous sites in Europe dated to last 50,000 years. Reconstructed mtDNA sequences will be used to infer phylogenies of each species, which depicts relations between populations. To infer species histories, beside molecular and morphometric data, information about the age of specimens is needed. We plan to use radiocarbon dating method to estimate age of 60 samples. Distribution of mtDNA lineages in space and time will allow us to infer migrations, population turnovers, demographic expansions and declines.

In recent years, there is a growing number of studies that use paleogenetic approach to investigate species responses to climate changes. However, most of these studies focus on large mammals like mammoths, cave bears or musk ox. Studies of small mammals, that are important components of all ecosystems, are still rare. Moreover, most of the studies deal with single species only, while reactions of species to changing environments depends on combination of their individual adaptations and interactions with other species occupying the same ecosystem. In this project we will use the most up to date molecular and morphological techniques to investigate evolutionary histories of three small mammal species. We believe that such approach will provide not only valuable information on species-specific responses to climate changes but will be the first step towards the community-wide reconstructions.