

Climate and environmental changes have a huge impact on the distribution and evolution of many species. However, particular species can differently response to the climate changes. Thus, generalisations of the climate influence can be incorrect and gathering data on individual species is essential. By examining how species have behaved in response to these changes in the past, we can understand how animals and plants will behave in the face of current climate change. Therefore, a great help in this study can be provided by ancient DNA (aDNA), which is obtained from extinct organisms. One of interesting species in this context is the European snow vole *Chionomys nivalis* (Martins, 1842), a small rodent, which is a glacial relict with a fragmented distribution in mountainous parts of south-eastern Europe as well as south-western Asia (Fig. 1). In the past, this species was much more diversified and its many morpho-species were described. Due to specific rocky habitats occupied by *C. nivalis* associated with colder and arid conditions, it will be interesting to check if alterations in Pleistocene climate are also reflected in genetic variation recorded in fossil remains.



**Fig. 1**  
Geographic range of the European snow vole. According to IUCN (International Union for Conservation of Nature) 2008. The IUCN Red List of Threatened Species. Version 2019-2.

The main goal of this project is to investigate the genetic variation of the Pleistocene *C. nivalis* to reconstruct its origin, population dynamics, migration routes and extinction events in relation to climatic changes during the last 50,000 years. Analysis of fossil samples can help to verify if the present discontinuity in the geographic distribution of the snow vole resulted from a recent fragmentation of one big population accompanied by geographical isolation or these particular populations originated separately from already diversified groups, e.g. in small refugia, much earlier during the Last Glacial Maximum.

To achieve these goals, we will study sequences of mitochondrial genomes and selected nuclear markers obtained from fossil as well as contemporary specimens with the broad geographical range. The genetic results will be compared with radiocarbon dating, palaeoclimatic data and ecological niche modelling. We will perform advanced phylogeographic analyses and verify if the genetic and morphological variations are associated with the climatic and environmental changes.

The intraspecific morphological variation in this rodent coincides with its phylogeographic structure based on genetics. It indicates a concordance between the morphological and molecular evolution, which is not common in other species. Thus, analyses of *C. nivalis* offer a promising opportunity to compare directly the morphological and genetic variation. Examination of aDNA can also help to assess validity of fossil subspecies determined solely on the morphology and provide the most versatile way to reconstruct evolutionary history of this species. The result will have consequences on interpretation of other rodent fossils, which are dominated component of the Pleistocene fauna.

Many studies attempted to answer the question whether the extinction of large mammals at the end of last glaciation was caused by human hunting or climate changes. Small mammals are more susceptible to climate changes, and direct impact of humans on their populations is negligible, thus they are a superior subject for studying the influence of climate changes on demographic processes. Obtained results can be a good reference point and working model for other mammals, which were widespread in the Pleistocene and survived to the present as glacial relicts. The study can be helpful in research of present species that are also subjected to drastic changes of climate and environment. *C. nivalis* is especially interesting because its habitats lie in rocky areas in high mountains, which are most vulnerable to global warming. Accordingly, this species occurred very useful as an appropriate bioindicator in monitoring and understanding the environmental impact in mountain areas.

This project focus on the species inhabiting the high mountains, which is essential part of the whole network of interactions between species on different trophic levels and occupying different ecological niches within one ecosystem. Our study will provide a complete picture of the relationship between climate change and populations dynamics over thousands of years. The project is an interdisciplinary approach that will involve a fruitful integration of various disciplines: genetics, palaeontology and palaeoecology.