Animals have limited evolutionary capacities to adapt to new conditions. As anthropogenic climate change is one of the greatest challenges we face today, understanding organisms' response to ongoing and future environmental change is crucial to maintain the welfare of current and future generations by meeting conservation management goals. This requires understanding the response to climatic changes of species and species groups in the past. However, particular species can respond differently to climate change; thus, gathering data on individual species is essential. An established way to analyze species-specific responses is by studying their DNA. Unfortunately, errors can occur because different processes may produce similar patterns in genome in modern organisms and in result potentially provide misleading conclusions. Hence, it's key to investigate genetic data obtained from individuals from different periods – so called ancient DNA. The analysis of such data gives a unique opportunity to directly track changes in the genetic diversity of the populations and to reconstruct the processes that shaped it.

Small mammals, such as rodents, are an invaluable asset in reconstructing past climate and its change. On paleontological and zooarchaeological sites they are used as a proxy to describe the past environments. It's possible because they stick to their preferred environment, they breed quickly and so they evolve quickly, they are in the middle of the food chain as they feed on multiple plants and insects and they themselves are prey, and they were not affected by human activity. Those animals are often found at exceptionally high abundances, making them relatively easy to find today, as well as on palaeobiological and archeological sites, with records spanning multiple climate and environmental oscillations. For this project three genera of the subfamily Arvicolinae were selected: water voles (Arvicola), snow voles (Chionomys), and grey voles (Microtus; Figure 1.). They represent various environmental niches, lifestyles, and sizes. All of them showed their evolutionary peculiarities in previous research, yet many mysteries remain unsolved, and new questions arise with each new answer.

The main goal of the project is to investigate the genetic diversity of Arvicolinae in the Caucasus and Middle East. The Caucasus and Middle East are regions important in both human and rodent evolution. They likely functioned as a climatic refugium, offering milder conditions during periods when northern regions were impacted by glaciation, but the dynamics of the Late Pleistocene to Holocene transition was still very much visible in environmental shift here as well. The mosaic character of past and present environments resulted in the high number and diversity of Arvicolinae species found there.

To achieve the goal of the project we will obtain ca. 100 subfossil and modern Arvicolinae samples from multiple locations in the Caucasus and Middle East. We aim to create a dataset with samples as old as 50,000 years. We will use the newest laboratory and *in silico* methods to obtain and analyze ancient and modern DNA. Laboratory work will be performed following strict protocols to reduce the probability of contamination ancient samples with modern DNA. With the obtained data we will reconstruct phylogenetics trees of target groups using mitochondrial DNA, as well as perform multiple advanced demographic analyses on nuclear DNA. The genetic results will be enriched with radiocarbon dating and paleoclimatic data to perform complex interpretations.

We aim to pinpoint the time of gene flow occurring between distant and diverse populations of water voles, to understand population replacements of grey voles south of the Caucasus, as well as explore the region as a hot spot for snow vole diversity. Together we will paint the picture of Arvicolinae diversity over the past thousands of years and both the differences and similarities in their responses to climate change.

Figure 1. Selected representatives of each target genus: Günther's Vole *Microtus guentheri* (left), Snow vole *Chionomys nivalis* (right top), Eurasian water vole *Arvicola amphibius* (right bottom). Source: IUCN (2025).