

During the last Ice Age in the Pleistocene, the huge area in Eurasia and North America was covered by steppe-tundra, which was inhabited by cold-adapted species, e.g. mammoths and rhinoceros. A substantial component of this faunal complex was a small steppe antelope, saiga (*Saiga tatarica*), which survived to modern times (Fig. 1). Therefore, knowledge about this species can provide important information about the development and disappearance of this past ecosystem as well as verify the concept about different response of individual species to climatic and environmental changes. Its characteristic feature is a short proboscis, which filter out dust and cool the animal's blood in summer, while in winter, it heats up and moistens the frigid and dry air. This trait made the saiga adapted to the Pleistocene environment, when this species was widely distributed in the central and northern Eurasia up to North America. However, this relic of the Ice Age is now critically endangered and it is restricted to only five populations: one in Russia, three in Kazakhstan and one in Mongolia (Fig. 2). Its size is still decreasing due to diseases, poaching pressure for the illegal trade in horns as well as changes in climate and environment, so its studies are a priority.

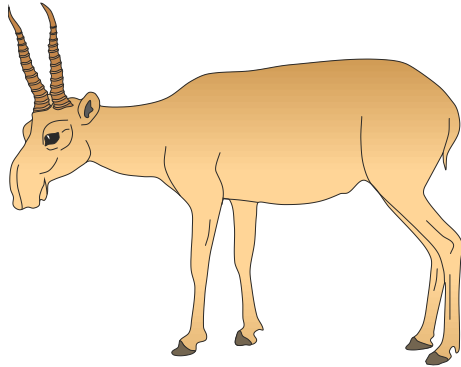


Fig. 1. Male of *Saiga tatarica*.

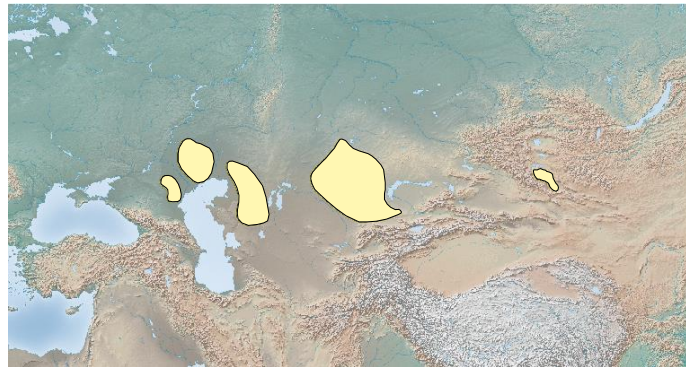


Fig. 2. Current distribution of saiga populations.

The past geographic range of saiga probably contracted and expanded many times depending on the climatic conditions. However, the details about the migration routes of this mammal are still unclear. Another important problem which is still not solved concerns the number of Pleistocene forms of saiga and their taxonomic levels. Many authors classify analysed remains to the different taxa changing their taxonomic level. In consequence, evolutionary history and taxonomic status of saiga are still hotly debated.

The best way to solve these questions is the analysis of ancient DNA from fossil remains. Therefore, to reliably solve these issues, we will analyse the sequences of the entire mitochondrial and nuclear genomes acquired not only from modern species but mainly fossil remains from sites across the whole Eurasia and dated to the Pleistocene and the Holocene. We will perform advanced phylogenetic, phylogeographic and demographic analyses to determine the evolution and genetic variation of saiga in time and space.

The results of the genetic analyses will be compared with morphometric studies. Thanks to that we will be able to verify if the morphologically established forms are justified on the genetic basis. These forms might represent ecotypes or morphotypes resulted from local biogeographical differentiation of the saiga populations widely widespread in the Pleistocene. Alternatively, they may be separately evolving and genetically isolated lineages. The other aim of our project is reconstruction of migration routes including expansions and local extinctions of saiga populations. The saiga is an especially good taxon to analyse migrations because it is a nomadic herding species that migrates seasonally looking for areas with better food availability. We are going to determine if the saiga colonized Europe in several waves from distant refugia or if European saigas were descendants of local populations survived in cryptic refugia.

The genetic data will be compared with dated fossils and oxygen isotopic records, which are a good proxy of climatic conditions in the past. Thus we verify if the emergence and extinction of saiga lineages as well as the migration routes were linked with the climatic and environmental changes. For example, migrations could be intensified during periods of continental climate and restricted when the climate got warmer and humid. Since there are many common factors influencing the saiga in the past and nowadays, the results of this project can help in the prediction of future fate of saiga populations and their protection. Our results will be important for the initiative of Pleistocene Park in Siberia, whose aim is to restore and study the steppe-grassland ecosystem from the glacial period. Saiga will be a crucial herbivore in it.

The results of the project can be a good reference point and working model for other members of the Pleistocene megafauna and can be helpful in research of modern species that are also subjected to drastic changes in climate and environment. The project is an interdisciplinary approach that show a fruitful integration of different disciplines: molecular and population genetics, palaeontology and palaeoecology.