The evolutionary history, phylogenetic and ecology of moose is much less studied in comparison with other contemporary large ungulates of the northern hemisphere such as red deer (*Cervus elaphus*) or rare and endangered European bison (*Bison bonansus*). Especially, there are not many data concerning the ecology, phylogeography and genetic diversity of moose inhabiting Asia although the species evolved there. The aims of the project are: recognition of the genetic diversity, identification of habitats of occurrence and reconstruction of changes in the range of moose (*Alces alces*) in Eurasia in the time period of the last 50 000 years using various interdisciplinary methods. Recognition of the phylogeographic pattern of different mtDNA clades of Eurasian moose since the Late Pleistocene until recent times will be based on the analyses of mtDNA extracted from bones and teeth of this species. Obtained genetic data will be used to estimate the divergence time of different mtDNA clades, reconstruction of the Last Glacial Maximum (LGM) refugia, postglacial colonization routes and changes of the effective population size of moose in Eurasia. The habitats occupied by the species in the past by will be identified based on the analyses of stable isotopes of carbon and nitrogen extracted from bones and teeth of the studied individuals. In the final step, the changes in the range, occupied habitats, effective population size and the genetic diversity of moose will be compared with the climatic oscillations and the changes in ranges of different vegetation types since the Late Pleistocene.

We suppose that the genetic diversity of moose was higher and the Eurasian population of the species was more homogenous in the past. We hypothesize that the range of moose, their effective population size and genetic diversity have been changing in time with climatic oscillations, namely decreasing in warmer periods. The moose survived the LGM in larger area than it was previously thought and responded differently than other species of Eurasian large mammals to climate changes. In the Holocene the range of moose shrunk significantly and the Eurasian population disappeared from some of its LGM refugial areas, but probably survived in large continuous range in the eastern part of Europe and in some areas in Asia. In addition to climate oscillations also humans had significant impact on the distribution and genetic diversity of moose, especially in Europe.

The study will be performed using novel research method such as analyses of the whole mtDNA genomes of moose, analyses of the carbon (^{13}C) and nitrogen (^{15}N) stable isotope compositions in bone collagen, AMS radiocarbon dating and spatial analyses using Geographic Information Systems (GIS). Majority of contemporary samples of Eurasian moose planned to use in this study (in total 150 samples) will come from the large collection of tissue samples deposited in the Mammal Research Institute PAS in Białowieża. Additionally, new materials will be collected from the Ural Mountains and Siberia where genetic diversity of the contemporary population is the highest. The fossil materials for this studies (about 250-300 samples) will be collected from different zoological collections and archaeological excavations in Europe and Asia. In the frame of this project we will study the moose population inhabiting Eurasia during the last 50 000 years, since the Late Pleistocene until modern times. About 120 selected samples will be dated using ^{14}C AMS method. In the final step of the project we will check how the genetic diversity parameters, phylogeographic pattern and inhabited habitats of moose had been changing in time in relation to climate oscillations. In the end we will test different demographic and ecological models and choose these, which in the best way explain the history of evolution and changes in distribution and genetic diversity of moose in Eurasia.

To our best knowledge there is no many studies which present such complex data in spatial and temporal scale of Eurasia for one species. As a common species inhabiting different habitats moose is a good model species for identification of the suitable habitats for other boreal and temperate mammal species which occurred in Eurasia during the last 50 000 BP, especially in time of the LGM. The results of this study will also help to predict the response of these species to the contemporary climate changes. Obtained data will have also significant impact on the development of evolutionary biology and will also asses the human impact on the populations of large ungulates in large spatial and temporal scale.