

Several factors such as history, gene flow or genetic drift shape the genetic structure of a species. Especially the climatic changes of the Quaternary had important impacts on recent phylogeographic and population genetic structures of organisms. So far, phylogeographic studies that focused on the Quaternary history, refugial areas and (re-)colonization routes in Europe have been clearly dominated by highly mobile taxa (seed of plants, vertebrates, flying insects). Comparative phylogeographic analyses focusing on distantly related but co-distributed species with proposed different dispersal abilities are an approved strategy to infer the effect of historical and/or contemporaneous processes driving species diversification. The present proposal is a pilot study that shall provide first insights into local- and large-scale phylogeographic patterns by comparing several co-distributed arboreal oribatid mite species with (presumed) different dispersal modes (phoretic versus non-phoretic behavior) in Europe. The use of “traditional” molecular techniques, plus modern next-generation sequencing (NGS) - a new application for population genetics and phylogeography in arachnids – will allow for illuminating recent (gene flow, genetic drift) and past (bottlenecks) evolutionary processes as far as population contractions/expansion and colonization routes, which had important impacts on contemporary intraspecific diversity of species that overlap in time and space. The following three main hypotheses could be formulated and shall be tested in the framework of the project by the use of landscape genetic approaches, standard population genetics, clustering methods and correlation analyses: i) higher dispersal ability overrules the effect of historical processes on phylogeographic/population genetic structure, ii) apparent low levels of host specificity and Palaearctic distributions are due to unrecognized cryptic diversity and iii) different underlying bio-geographical traits determined the varying responses of co-distributed species to Pleistocene glaciation events. The integration of species distribution models can further contribute to the exploration of the impact of global climate change on small organisms with different dispersal modes inhabiting specific habitats. Several direct and indirect effects (as e.g. climate change, habitat fragmentation, agricultural work, urbanization or deforestation) are responsible for shaping large-scale distribution of species. Given that most of the included study species are specialized to life on trees, insights into ecology, structure and dispersal modes/rates should serve as a basis for acquiring knowledge about the effects of human activities on micro- and mesofauna of specific habitats.