

The role of genetic admixture in ecological diversification of the *Anthriscus sylvestris* complex, a putative ring species

Niche shifts and the source of genetic variation. The evolutionary capacity of a species to adapt to a changing environment or to enter a new ecological niche much depends on its genetic diversity, particularly the presence of beneficial alleles. There is growing evidence for the role of hybridization in adaptive evolution: old genetic variation, previously tested by natural selection may speed up adaptive niche shift. Our aim is to check whether this mechanism is responsible for the diversification of *Anthriscus sylvestris* sensu lato (s.l.), a group of closely related plant species or subspecies exhibiting a remarkable ecological diversity in Europe. Moreover, our preliminary data suggest that this plant group may constitute a ring species around the Mediterranean. A ring species is a rare and interesting example of evolution caught in action: it forms when two waves of migrations surround a barrier (e.g., a sea or mountains) and having met act as two separate species. To check this hypothesis, we will sequence nuclear and chloroplast genomes of *Anthriscus sylvestris* and use them to assemble data from genome skimming of c. 380 plant samples. As chloroplasts are inherited maternally, their phylogenetic tree will help to reconstruct past migrations and to identify the areas of secondary contact between different waves of migration. The gene flow and their role in diversification will be assessed based on nuclear data. Sampling will include herbarium specimens as well as plant collected from the wild, particularly from the areas of highest morphological, ecological and genetical diversity as assessed based on our preliminary data.

***Anthriscus sylvestris* group** (plant family Apiaceae or umbellifers) includes two species in Europe: *A. nitida* and *A. sylvestris*, the latter encompassing at least four subspecies: *sylvestris*, *alpina*, *nemorosa*, and *fumarioides*. *Anthriscus sylvestris* subsp. *sylvestris* usually occurs in lowland secondary habitats, like wet meadows, roadsides, and riparian forests, whereas *A. nitida* inhabits beech-forest belt of mountains of Central Europe. *Anthriscus sylvestris* subsp. *fumarioides* occurs in half-shaded subalpine screes in the mountains of the western part of the Balkan Peninsula, while similar localities in the Alps, Vosges, and possibly Pyrenees constitute the habitat of *A. sylvestris* subsp. *alpina*. This broad ecological spectrum of the *A. sylvestris* complex ranging from lowland to subalpine localities and from open anthropogenic habitats to natural shady forests is unparalleled in any other species or complex of species of umbellifers in Europe. The question is what are the genetic sources of this diversity in Europe. Did European mountainous taxa arise due to selection from widespread (and possibly genetically diversified) lowland *A. sylvestris* subsp. *sylvestris* or did they originate due to genetic admixture from western Asiatic mountainous subsp. *nemorosa*?

Impact of the project. This project will help to understand the *genetic limitations to ecological niche shifts*. If the ecological diversification of *A. sylvestris* s.l. in Europe did not occur with the help of gene flow from distant Asiatic cousins, then its adaptive evolution was most likely constrained (and driven) by ecological opportunity: opening of new habitats and niches during postglacial colonisation. If the diversification occurred due to substantial genetic admixture from older lineages, then it might have been limited by pre-existing variation.