

**Genetic diversity, biogeography, and evolution of apomixis in North American
Arabis holboellii HORNEM. and *A. drummondii* GRAY (Brassicaceae)**

Marcus Koch and Christoph Dobeš

Apomixis is a trait that has greatly attracted the interest of numerous botanists for decades. It is widely distributed among flowering plants, and it has been shown for monocots that the responsible genetic background might involve only one or a few genes. Among dicots apomixis has been analysed mostly on a descriptive level, and less attention has been paid on the evolution of this trait. The dicot model plant for molecular biologists, *Arabidopsis thaliana*, does not show this trait. However, apomixis is widespread among North American *Arabis* species and has been described to occur there even on the diploid level. Although the genus *Arabis* is not a monophyletic group and North American *Arabis* should be renamed to genus *Boechera*, *Arabis* sensu lato is closely related to *Arabidopsis thaliana*. North American *Arabis* consists of more than 50 species depending on the underlying species concept. More than 10% of these taxa are known only as triploids, and apomixis is the assumed way of seed production. An additional 20% are known as diploids as well as triploids, which might indicate varying breeding systems within a single taxon. Therefore, apomixis played a major role as a mechanism of population differentiation and speciation within North American *Arabis*. The occurrence and evolution of this trait should be reflected by distribution patterns and the evolution of the species itself.

In this project the genetic diversity of *Arabis holboellii* and the closely related *A. drummondii* should be analysed on the molecular level with the help of DNA sequences (plastid and nuclear DNA) and microsatellites for several purposes. First, the degree of apomixis within a population has a great impact on the distribution of its total genetic variation. Therefore, populational genetic diversity and the intra-populational degree of apomixis should be analysed using molecular markers and cytological investigations. Second, genetic variation on the populational level should be used to estimate interpopulational genetic distances and to infer a phylogenetic network of *Arabis* populations. As a third step, correlations between geographic distribution of molecular variation, apomixis and genetic distances between populations should help to elucidate the degree of apomictic variation within and between populations.

In general, the aims of this project are (1) to analyse postglacial speciation and biogeography of *A. holboellii* and the related *A. drummondii* and its trait apomixis and (2) to provide information and material for future genetic work on the trait apomixis among cruciferous plants.

**Glacial survival of European mountain plants: evidence for the long-lived
Anthyllis montana L. (Fabaceae) inferred from AFLP fingerprint data**

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As part of a project illuminating the historical biogeography of European mountain taxa AFLP variation within *Anthyllis montana* L. was investigated. 16 populations from throughout its distribution range and single individuals of *Anthyllis aurea*, *A. barba-jovis* and *A. tejedensis* as outgroup taxa were included. Altogether 74 individuals were analysed using four AFLP primer combinations. A total of 1211 AFLP fragments were detected. There were twelve monomorphic markers (= 0.99%) within *A. montana*. The remaining 1199 fragments could discriminate all individuals as non-clonal samples.

Neighbour-joining analysis resolved *A. montana* as a monophyletic group with *A. barba-jovis* as sister species. One well-supported group was recognised within *A. montana* representing the western part of the distribution range. The other group containing samples from the eastern range showed a substructure: Two populations from north-western Italy (Liguria, Alpi Apuani) and two populations from the peripheral south-east (Greece, Balkan Mountains) formed well-supported geographical clusters, respectively.

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PCO analysis confirmed the general west-eastern differentiation within *A. montana*. Furthermore AMOVA indicated a large variance component among these two regions (west/east; 14.4%) and populations (32.1%). Regression analysis of pairwise F_{ST} values among populations on geographical distance showed a significant positive relationship (i.e., isolation by distance). A PCO analysis based on F_{ST} values among populations discriminated both regions with an intermediate position of the Ligurian population and clearly separated peripheral south-eastern populations.

Genetic differentiation within *A. montana* mainly reflects a west-eastern separation which can be explained historically. During the last ice ages montane/subalpine species like *A. montana* probably retreated into southern refugia. Within *A. montana*, (1) the comparison of genetic, morphological, and geographical information indicates a contact zone in Liguria (south-western Alps) reflecting the main west-eastern pattern. Furthermore, (2) this west-eastern pattern and the geographically and genetically rather isolated position of the south-eastern populations are strongly suggestive of at least three refugial areas: (i) the Iberian Peninsula, (ii) the central part of the species' range and (iii) the Balkan Peninsula. Thus the perennial *A. montana* shows a biogeographical pattern with three main refugial areas in Europe so far only known from tree species like *Abies alba* or *Quercus robur*. Isolation by distance relationships within the central part of the distribution range are non-significant. This may indicate that this area was not re-colonised from one southern refuge but rather contained multiple refugia. Refugial areas are known in periglacial regions where *A. montana* may have persisted close to the Alps.

Genetic variation in central and peripheral populations of the alpine plant *Dianthus glacialis* revealed by RAPD and allozyme markers Daniela J. Lang¹, Patrizia Glauser¹, Felix Gugerli² and J. Jakob Schneller¹

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Dianthus glacialis is an alpine plant with a prevalent distribution in the Eastern Alps. The western boundary of the species' range is situated in south-eastern Switzerland, where *D. glacialis* is a rare species, whereas the main distribution range is in Austria. We used this species to test the central-marginal model. In accordance to this model, populations near the centre of a species' distribution range usually are continuously distributed, occur at high density, and display high levels of genetic and phenotypic variation, while populations at the margin are sparse and isolated, show reduced genetic variation and increased population differentiation. Therefore, we compared the genetic pattern of allozyme and RAPD variation in four marginal and four central populations with a set of total 240 individuals (30 per population). Eight of 19 allozyme loci were polymorphic, which displayed 19 alleles and resulted in 53 multilocus genotypes, while four RAPD primers revealed 17 polymorphic markers out of 24 and presented 53 RAPD-phenotypes. The regions differed in allozyme diversity as well as RAPD variation: Austrian populations exhibited more internal allozyme diversity than Swiss populations. The same tendency was valid for RAPD variation comparing central populations with peripheral populations. To investigate the partitioning of genetic variation for allozyme and RAPD data, we calculated an AMOVA. A qualitatively similar pattern was revealed in finding a large proportion of variance between the regions (41.15% for allozymes vs. 63.35% for RAPDs). The distribution of the variance among population within regions and of the variance within population, however, showed a contrasting pattern in relation of these two methods. Analyses of the separate regional data sets revealed larger population differences within Austrian populations for allozymes than for RAPDs (61.20% for allozymes vs. 27.27% for RAPDs), while Swiss populations did not differ so extremely in allozymes than in RAPDs (25.37% vs. 97.67%). The RAPD data supported the central-marginal model, but the allozymes revealed a contrary pattern. The quantitative comparison of the F_{ST} values exhibited no differences between paired samples and a positive correlation between all samples. These results show us that it is difficult to compare these two very different methods.

Abb. 9: *Dianthus glacialis*

Foto: D. Lang

