

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

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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.

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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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