

Greenlandic species with its main distribution in West America. It is absent from arctic Northeast America, but is found on the Gulf of St. Lawrence, which might indicate periglacial survival. (3) Apomixis is wide-spread. In contrast, *A. drummondii* is clearly defined morphologically. Its distribution area matches those of *A. holboellii*, and, throughout the sympatric range of both species the putative hybrid *A. ×divaricarpa* occurs more frequently.

The hybrid status of some *A. ×divaricarpa* accessions have been demonstrated by ITS sequence analysis. Chloroplast DNA sequences (*trnL* intron and *trnL-F* spacer) should provide information about the distribution and spatial transmission of maternal inherited genetic variation within *A. holboellii*, within *A. drummondii*, within *A. ×divaricarpa* and between these taxa. Sequencing of the ITS region will provide additional information about multiple hybridisation and reticulation.

The analysis of ITS sequences is biased by a mechanism called concerted evolution. In order to analyse an independent, biparentally inherited marker, microsatellites will be analysed. The information of the total *Arabidopsis* genome sequence has been successfully used to identify numerous *Arabidopsis* microsatellite loci with defined genomic positions (in *Arabidopsis*). Using a synteny approach microsatellites will be selected covering the total genome. This procedure should provide additional information about «genom-wide» genetic differentiation. The initial study is based on approximately 800 specimens covering the total distribution area and morphological variation. To get further information about the ploidy levels of the specimen, pollen size measurements have been tested as indicator.



Abb. 6: *Arabis ×divaricarpa*

Do refugial populations exhibit greater genetic diversity? René Füchter, Alex Widmer and Matthias Baltisberger

The genetic consequences of the survival of plant populations in glacial refugia are contradictory. Many authors suggest that putative refugial populations harbour higher levels of genetic diversity relative to their likely descendant populations. Others assume a massive loss of allelic variability in refugial populations through inbreeding, founder events and population bottlenecks, at least if refugial areas and population sizes are small.

Considering the glacial refugia of tree species the situation appears to be clear: a decline in the number of haplotypes with increasing distance from a refugium is consistent with theoretical models of postglacial migration in species undergoing leptocurtic dispersal. However, much less is known about alpine plants where the situation may be different (e.g. generally smaller refugial areas and a fragmented distribution even during interglacial stages).

In order to formulate hypotheses concerning the distribution of genetic diversity in refugial versus non-refugial populations, the mode of preglacial retreat and postglacial re-dispersal needs to be considered. Many authors imply that plant populations contract into small refugial areas, which suggests an active retreat from the forward pushing glaciers. In this case, refugial populations might harbour great genetic diversity. Alternatively, one may assume that only plants which were already growing in a later refugial area were able to survive the ice age in situ, which implies a loss of most of the diversity at the beginning of the ice age. In this case, the initial genetic diversity of the refugial population is restricted. Depending on the mode of postglacial colonisation, non-refugial populations may show higher diversity today if recolonisation from several refugia has occurred.

With regard to postglacial expansion, it is crucial to consider the widely differing abilities of taxa for dispersal and gene flow, factors which depend on traits such as the mode of seed dispersal and the pollination system. These are likely to have an impact on the genetic diversity of the descendent populations and therefore influence our ability to detect differences between refugial and non-refugial populations.

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