

Nunataks as glacial refugia? A molecular phylogeographic case study with *Draba aizoides* René Füchter, Alex Widmer and Matthias Baltisberger

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Foto: R. Füchter

Abb. 7: *Draba aizoides*

Where have alpine plants survived the ice ages? The nunatak-hypothesis states that they survived on single mountain tops surmounting the general ice-level (nunataks). In contrast, according to the tabula-rasa-hypothesis, all alpine populations became extinct during the Last Glacial Maximum, and those that survived in peripheral refugia re-immigrated after the retreat of the glaciers.

Draba aizoides L. (Brassicaceae) is a yellow flowered, perennial alpine rosette plant. It was chosen as a model species as it shows extensive intraspecific cpDNA sequence variation (*trnL* intron and *trnL*-F spacer) which exceeds interspecific variation among other, closely related *Draba* species. A PCR-RFLP test was designed in order to distinguish seven groups of haplotypes (out of a total of eleven detected haplotypes). Their frequency and distribution was assessed for 19 populations distributed over large areas of the Swiss Alps. In addition, horizontal starch gel electrophoresis of isozymes was conducted for a subset of populations to gain information on the nuclear genetic constitution of populations and for comparison to the chloroplast genome data.

No effect of isolation by distance was found for the isozyme loci. This suggests that postglacial recolonisation history has had a strong impact on the genetic constitution of extant populations. By comparing pairs of populations, each pair including a population from a presumed nunatak and one from a non-nunatak area, genetic variability (numbers of alleles and observed heterozygosities) observed in nunatak areas was not found to be consistently higher.

The geographical distribution of cpDNA haplotypes revealed an extremely low haplotypic diversity in the Northern Alps. Only the three presumed nunataks Stockhorn, Faulhorn and Säntis harboured haplotypes that were unusual for this region. Hence, these areas could be confirmed as glacial refugia. In addition, the Dent de Mörtsch in the Lower Rhone valley most probably also acted as a glacial refugium.

Generally, higher levels of diversity were observed in the Central Alps. This, combined with the fact that three rare haplotypes were found only there, strongly suggests that Central Alpine glacial refugia of *D. aizoides* existed. Accordingly, the tabula-rasa-hypothesis was not supported by the available data.

***Gentianella* Moench sect. *Gentianella* – a model of Quaternary evolution**

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The small gentians (*Gentianella* Moench sect. *Gentianella*) exhibit biological and biogeographical features which make them a model group for studying evolutionary processes in the European flora during the Quaternary as the section comprises widespread taxa occurring nearly all over Europe as well as narrowly distributed endemics concentrated in or nearby refugial areas around the Alps. So far, by applying isozymes we found some evidence for higher genetic diversity in *G. austriaca* populations of refugial areas than in those of presumably recolonised areas in higher parts of the north-eastern Alps. In some contact zones between widespread taxa and the endemics introgressive or hybridisational processes might have taken place as can be judged from morphology. The differentiation into seasonal (ecological) vicariads in some taxa very likely is caused by postglacial disruptive selection due to human impact. Molecular and morphological evidence point to a polytopic origin of the widespread taxa *G. germanica* and *G. amarella*. And finally, all the European taxa are polyploids with evidence for allopolyploidy in *G. austriaca*. So far, the diploid level is known only from the Caucasus region.

Currently we are examining evolutionary processes and relationships in European *Gentianella* sect. *Gentianella* by applying different molecular methods, cytogenetic analyses and a re-evaluation of morphological characters. This research focuses on the reconstruction of how the European polyploids have formed, a process that might have taken place recurrently. We investigate the

relations of these processes to glaciation events and the role of the latter in establishing reticulate relationships. Altogether, the patterns of relations and distributions in *Gentianella* can contribute to a better understanding of evolutionary processes in the Quaternary, the impact of the ice ages as well as the impact by historical human land-use. The section *Gentianella* certainly is one of few groups of closely related organisms, which are an outstanding mirror of these processes.

Quaternary history of the circumpolar *Draba lactea* complex Hanne H. Grundt, Liv Borgen, Reidar Elven and Christian Brochmann

The hexaploid *Draba lactea* belongs to a taxonomically intricate species group. It is one of the comparatively few arctic allopolyploids for which putative diploid progenitors still are extant, facilitating the study of its evolutionary and migrational history. Crossing barriers have previously been documented within one of the diploid species, further contributing to the complexity in this group. We collected populations of *D. lactea* and the diploids *D. nivalis*, *D. fladnizensis*, and *D. subcapitata* on a circumpolar scale: more locally distributed species such as *D. lonchocarpa* and *D. palanderiana* were also collected. A few species were also collected from more southern mountain ranges (the Alps, the Altai Mts., and the Canadian Rocky Mts.). Our main aims are to (1) estimate the number and geographic distribution of sibling species within individual diploid taxonomic species, (2) identify the diploid progenitors and number of origins of *D. lactea*, and (3) produce taxonomic revisions. This presentation includes preliminary results. Conspecific populations of the diploids *D. nivalis* and *D. fladnizensis* were crossed, revealing frequent and high degrees of intersterility even between some geographically neighbouring populations. So far we have not detected any distinct geographical pattern; it thus appears that sterility barriers evolve rapidly within these species. The existence of sibling diploids opens for the possibility that different diploid populations may hybridise to give rise to taxonomically autopolyploid, but genetically allopolyploid species. Flow cytometry analysis have also revealed some tetraploid populations, indicating ongoing hybridisation/polyplodisation events in the group. Populations of all taxa are presently investigated using RAPDs, and additional molecular methods will be used.

Mitochondrial and chloroplast haplotype variation in Norway spruce (*Picea abies*) indicate a marked founder effect during postglacial re-colonisation of the Alps Felix Gugerli¹, Giovanni G. Vendramin², Maria Anzidei², Josef Senn¹ and Christoph Sperisen¹

Organelle genomes provide suitable molecular markers to elucidate migration pathways because they are uniparentally inherited. Recombination is merely absent, and effective population size is lower than that of nuclear loci. In most conifers, cytoplasmic organelles are differentially inherited: mitochondrial (mt) DNA is maternally transferred as in most angiosperms, whereas paternal inheritance is the rule rather than the exception for chloroplast (cp) DNA. As a consequence, mtDNA markers are dispersed through seed only, whereas cpDNA markers are spread through pollen and through seed. This differentially affects the geographic patterns of genetic variation derived from molecular markers of either of the two genomes and thus influences the detected degrees of population differentiation.

Present-day geographic patterns of genetic variation in the organelle genomes of forest trees are basically shaped by the routes of postglacial re-immigration from refugial areas. In order to elucidate the postglacial history of Norway spruce (*Picea abies*) in the Alps, we analyzed autochthonous populations from the natural Alpine range using both mtDNA and cpDNA markers. The mitochondrial marker was mainly characterized by two tandemly repeated segments of varying copy numbers, whereas three single-nucleotide simple sequence repeats (SSRs) were studied in the chloroplast genome.

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