

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/polyploidisation events in the group. Populations of all taxa are presently investigated using RAPDs, and additional molecular methods will be used.

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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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Genetic diversity was found to be lower in the mitochondrial than in the chloroplast genome, which corroborates earlier findings on their mutation rates. As expected, the maternally transmitted mtDNA marker showed a markedly higher degree of genetic population differentiation than did the cpDNA markers. This pattern is in accordance with the dispersal abilities of the vectors of the two marker types. Whereas the mtDNA marker illustrates seed dispersal over limited distances, the cpDNA SSRs mainly reflect anemochorous pollen dispersal. Both marker types revealed a clear trend of reduced genetic diversity in the western compared with eastern Alpine populations.

We thus infer that Norway spruce re-immigrated from eastern European glacial refugia, assumed in the Carpathian mountains and on the Balkan peninsula, as had been postulated by studies on fossil pollen records. We suggest that the northern and western Alpine populations were predominantly founded by immigrants originating from the Carpathian mountains, while the southern Alpine range appears to have been mainly colonized by individuals arriving from the Balkans. Furthermore, Norway spruce possibly encountered a severe founder effect during its postglacial re-colonization of the Alps, which led to the considerable loss of genetic diversity detected in the western Alps.

Does glacial survival really not matter? The Pleistocene fate of *Saxifraga oppositifolia* in the European Alps Rolf Holderegger^{1, 2}, Ivana Stehlik³ and Richard J. Abbott²

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The outbreeding *Saxifraga oppositifolia* is one of those arctic-alpine plant species that are best studied with molecular methods. A recent survey of cpDNA haplotypes in the Holarctic found Pleistocene refugia of *S. oppositifolia* both in the Arctic and at more southern latitudes. However, in situ glacial survival of this species was not detected in a RAPD study in Northern Europe and Svalbard. It was concluded that local glacial refugia were of no relevance in these latter areas because in situ surviving genotypes were swamped by massive immigration of periglacial genotypes after glaciation. So far, no specific phylogeographic analysis on the purple saxifrage across the Alps has been carried out. The present study tested whether it is possible to refer to the Pleistocene fate of a common mountain species, whose ecology and distribution hardly allow any prediction on where it survived the ice age by using molecular methods and complemented the phylogeographic work on *S. oppositifolia* done in the Arctic with an investigation of 15 populations sampled in potential Nunatak areas of the central chains and outer chains of the middle part of the Alps. To enable direct comparison with former phylogeographic studies on *S. oppositifolia*, their molecular protocols were followed as close as possible. Southern hybridisation and PCR-RFLPs of cpDNA showed that two common European haplotypes occurred in varying frequencies throughout the Alps. Nevertheless, three individuals from three different locations exhibited two additional rare haplotypes. Hence, cpDNA analysis gave weak evidence for in situ glacial survival of *S. oppositifolia* in the Alps. Analysis of mainly nuclear RAPD markers confirmed the results of former genetic studies on *S. oppositifolia*: high within, but low among population diversity with no distinct geographic clustering of the populations. RAPD data did thus not point at glacial in situ survival of *S. oppositifolia* in the Alps. *Saxifraga oppositifolia* thus had a comparable glacial fate in the Alps as it had in Northern Europe and Svalbard. Although some populations, nowadays harbouring distinct cpDNA genotypes, could have survived in situ, they were swamped by common immigrating genotypes, now found throughout the Alps, after glaciation. This re-immigration probably took place out of periglacial refugia in the alpine forelands, as it is suggested by fossil record.



Abb. 8: *Saxifraga oppositifolia*