

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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DOI: <https://doi.org/10.12685/bauhinia.2171>

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