

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*