Polytopic autopolyploidy and post-glacial recolonisation of

*Biscutella laevigata* in the Western Alps:
a cpDNA phylogeographic study.

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Past climatic changes have had a great impact on both the distribution and the genetic composition of plant populations (Hewitt, 2000). The autopolyploid *Biscutella laevigata*, a representative species of alpine meadows, is a classical example of polyploidy linked to glaciations (Manton, 1937) and is thus an interesting model to explore migration and speciation driven by climate changes. New chromosome counts indicate that diploids (2n = 2x = 18) survived the last glacial maximum (LGM) in some ice free parts of the Alps, as well as deglaciated areas outside the alpine chain. Tetraploids (2n = 4x = 36) are clearly dominant in the central parts of the Alps and thus interpreted as having recolonised this area from refugia (Parisod et al. *in prep*). Previous range-wide study failed to identify the diploid parent(s) of the present tetraploids and was unable to precisely determine the polyploidisation mechanism. Classically, tetraploids were thought to be derived from the German lowland diploid taxon (sub-sp. varia), but a new one (*B. prealpina*) has been recently described in Italy and questioned as a putative ancestor of the polyploids (Tremetsberger et al., 2002). The aim of this study is to highlight the phylogeographic relationships (i.e. in space and time) of maternal lineages in the Western Alps.

Using *trnSG* and *trnL-intron* plastidic sequences together with highly polymorphic cpDNA-SSR markers in 60 populations densely sampled throughout the study area, as well as outgroup individuals sampled outside the Alps, phylogenetic relationships were assessed using Median-Joining Network and phylogeographic pattern is viewed through Gst/Nst comparison.

While some diploid haplotypes present in local refugia seem not to have expended, Western Alps tetraploids are phylogenetically linked to several diploid taxa: the german varia sub-species, the *B. prealpina* taxon, as well as diploids found in the Western Alps. They display haplotypes belonging to different lineages. The northern and the southern parts of the Western Alps are inhabited by tetraploids lineages derived from different diploid taxa. Polytopic autopolyploidy out of refugia is thus apparent at the study scale (figure 1). Furthermore, *in situ* survival on Nunatacks seems probable in the central Alps as shown by the presence of a third unrelated haplotype in the Val d’Anniviers.

No obvious isolation by distance is detectable and Gst = Nst at the Western Alps scale, suggesting that the species had a recent and rapid radiation, mainly along recolonisation routes postulated by De-
larze (1987). Furthermore, when comparing such patterns in formerly refugial vs. glaciated areas, Gst is greater than Nst in refugia. Such a pattern indicates that phylogenetically unrelated haplotypes tend to co-occur in populations of refugia. Such a pattern should be explained by the LGM contraction of unrelated lineages in refugia, followed by the expansion of a few haplotypes during recolonisation.

Figure 1. Haplotype found in the Western Alps: The frequent one (mid grey) probably originated and expanded from the northern Prealpine refugia, while the southern one (light grey) is indicated as originated from Italy by the phylogenetic analysis. A third haplotype (dark grey) is ancestral and shows a restricted expansion in the central areas were nunatck have been postulated. Relationships among populations in space and time can be further discussed to depict recolonisation routes out of the last glacial refugias.

REFERENCES


Parisod, C., Jurt, D. & Brüssow, F. (In Prep.) Cytogeography of the autoploid complex *Biscutella laevigata* (Brassicaceae) in the Western Alps: insights from ecology, chromosome counts and taxonomy to the late Pleistocene history.