

Chloroplast and nuclear DNA variation on a circumpolar scale: migration history of the clonal *Saxifraga cernua* Pernille Bronken¹, Pierre Taberlet², Ludovic Gielly² and Christian Brochmann¹

Vast areas of the Arctic were covered by ice during the Quaternary glaciations. Plant populations were repeatedly fragmented into refugia and differentiated genetically for long periods of time, followed by large-scale expansion from refugia during each of the short-term interglacials. The present geographical structuring of their organellar and nuclear genomes may thus reflect where the plants survived and the migration routes followed during postglacial expansion. *Saxifraga cernua* is an arctic-alpine, perennial polyploid with efficient vegetative reproduction via bulbils. It is distributed almost ubiquitously throughout the Arctic and has isolated occurrences in more southern mountain areas. We examined molecular diversity in *S. cernua* on a circumpolar scale using a combination of nuclear (AFLP) and organellar markers (fragment analysis of single- and few-nucleotide polymorphisms in several non-coding cpDNA regions). Samples have so far been analysed from most main geographic regions (AFLP: 100 plants from 43 populations; cpDNA: 274 plants from 71 populations), but there is still a major gap in the central Siberian Arctic and the Central Asian mountains. Although the level of cpDNA variation was too low to allow for cladistic analysis, three major groups of haplotypes could tentatively be recognised: (1) an American-Beringian lineage (easternmost Siberia, Alaska, Canada), (2) an Amphi-Atlantic lineage (Greenland, Iceland, Scotland, Scandinavia, Svalbard, and Novaja Zemlja), and (3) an eastern/southern Eurasian lineage (Ural Mts., the Alps, and partly NE Scandinavia). The American-Beringian and the Amphi-Atlantic lineages were also recognised in analyses of the mainly nuclear AFLP data (no plants of group 3 analysed). The combined molecular data further suggest that Greenland, Svalbard, and north-eastern Scandinavia are postglacial meeting points for these three lineages, which probably expanded from different refugia after the last glaciation.

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Abb. 5: *Saxifraga cernua*

An AFLP analysis of genetic diversity within and between the ecotypes of the alpine sedge *Carex curvula* s.l. Philippe Choler, Ludovic Gielly and Pierre Taberlet

The alpine sedge *Carex curvula* is the dominant species of most European alpine tundra. It exhibits a calcifuge ecotype (*C. curvula* ssp. *curvula*) and a calcicole ecotype (*C. curvula* ssp. *rosae*). Extensive data set on the geographical distribution, morpho-anatomy and ecology of these two ecotypes provides a unique framework for assessing the genetical basis of this ecotypic differentiation.

In this study, we investigated the genetic relatedness of 20 *C. curvula* s.l. populations coming from 10 distant localities in the Alps. In each site, we collected leaves from calcicole and calcifuge populations and used AFLP technique to investigate the level of genetic diversity within and among these populations. In the 192 individuals analysed, we scored the presence or absence of 214 unambiguous polymorphic markers (200 to 500 bp long) obtained with three primer pairs.

With phenotypic frequencies, we calculated Shannon's index of diversity. On average, most of the diversity was found within population, with 88% of the variation being within and 12% being between populations. UPGMA dendrogram of Nei's unbiased genetic distance and Principal Component Analysis plot of AFLP data both revealed a clear distinction between the two ecotypes. Further, several DNA fragments were found to be specific of each ecotype. Three populations included individuals with intermediate AFLP profiles, suggesting that these individuals might represent different levels of introgression between both ecotypes.

Based on these preliminary results, we hypothesised that the calcicole-calcifuge ecotypic differentiation in *C. curvula* s.l. is probably an old event and

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