

Chloroplast and nuclear DNA variation on a circumpolar scale: migration history of the clonal *Saxifraga cernua* Pernille Bronken¹, Pierre Taberlet², Ludovic Gielly³ 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.

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

Address of the authors:

¹Natural History Museums and Botanical Garden, University of Oslo
Sarsgate 1, 0562 Oslo/Norway
pernildb@bio.uio.no

²Laboratoire de Biologie des Populations d'Altitude
UMR 5553 UJF-CNRS
et Station Alpine du Lautaret
Université de Grenoble
38041 Grenoble Cedex 9/France



Abb. 5: *Saxifraga cernua*

Address of the authors:

Laboratoire de Biologie des Populations d'Altitude, UMR 5553 UJF-CNRS et Station Alpine du Lautaret, Université de Grenoble
38041 Grenoble Cedex 9/France
philippe.choler@ujf-grenoble.fr

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that post-glacial recolonization of high altitude habitats has probably been achieved separately by each ecotype.

Tests of Pleistocene speciation among alpine and montane species of *Globularia* (Globulariaceae) from the European high mountains Hans Peter Comes and Joachim W. Kadereit

Address of the authors:

Institut für Spezielle Botanik und
Botanischer Garten
Johannes-Gutenberg-Universität,
Saarstraße 21
55099 Mainz / Germany
comes@mail.uni-mainz.de

There has been a resurgence of debate among zoologists on whether the Pleistocene glaciations inhibited speciation. Here we test the hypothesis of Pleistocene speciation by focusing on the phylogenetic relationships and divergence times of various alpine and montane plant species of the genus *Globularia* L. from the European high mountains.

Parsimony analyses of nrDNA (ITS) sequences for the entire genus suggest a near simultaneous origin of altogether three alpine/montane clades, and two Mediterranean clades, all of which form a basal polytomy in the strict consensus tree. Such a branching pattern would be expected if these clades arose from the fragmentation of a widespread – most likely Mediterranean – ancestor. Under this hypothesis the three European alpine/montane lineages identified [(i) *G. nudicaulis*, *G. gracilis*; (ii) *G. neapolitana*, *G. stygia*, *G. cordifolia*, *G. repens*; and (iii) *G. punctata*, *G. trichosantha*] arose independently, most likely in the western, central, and eastern parts of the Mediterranean region, respectively.

All these European high mountain species appear to have originated within the Pleistocene. In general, sequence divergence among species *within* lineages is less than 1.9%, corresponding to divergence times less than 2.4 million years ago (assuming a conservative divergence rate of 0.79% per Myr). However, comparisons of sequence divergence across lineages or sister taxa suggest that speciation events were associated with different glacial-interglacial cycles.

The three European alpine/montane lineages identified (i-iii) are rather ancient and differ in their ecological requirements, growth form and/or chromosome number. In accordance with one of the major criteria for adaptive radiation, they «pass the test of sympatry» in areas of range overlap. Contrastingly, sister species *within* lineages, with their recent Pleistocene origins, are ecologically and morphologically very similar, differing primarily in leaf shape and minute floral characteristics, or – rarely – ploidy level (only *G. cordifolia*/*G. repens*). In view of the pronounced vicariant pattern of distribution within lineages, it is posited that morphological character differences simply accumulated as a consequence of geographic isolation and allopatric divergence among sister species maintaining similar ecological niches.

Despite periodic glacial cycles, associated distributional shifts of taxon ranges, and possibly ample opportunities for population mixing, the dynamic history of the Pleistocene apparently did not preclude speciation within *Globularia*. Rather, by fostering geographic isolation, these climatic fluctuations may have increased the initiation of species. This is in accordance with our recent molecular-systematic studies on other European high mountain taxa (e.g., *Gentiana* sect. *Ciminalis*, *Soldanella*, *Primula* sect. *Auricula*).

Genetic diversity, biogeography, and evolution of apomixis in North American *Arabis holboellii* Hornem. and *Arabis drummondii* Gray (Brassicaceae). Experimental approach. Christoph Dobeš and Marcus Koch

Taxa of North American *Arabis*, treated as genus *Boechera*, are of a Pleistocene origin. They are not related to Eurasian *Arabis* or taxa such as *A. glabra*, *A. pauciflora* or *A. turrita*. The genus *Boechera* consists of more than 70 species. Polyploidy and even aneuploidy is widespread, and apomixis is thought to represent one major force which is driving the evolution of the species complex.

Arabis holboellii in several respects is a remarkable species. (1) The species is highly polymorphic, consisting of a number of varieties or microspecies with various chromosome numbers. (2) It has a disrupted range, being an American-

Address of the authors:

Institut für Botanik
Universität für Bodenkultur Wien
Gregor-Mendel-Strasse 33
1180 Wien/Austria
koch@edv1.boku.ac.at