



Abb. 10: *Pulsatilla vernalis*

isolated parts of species distribution (Pyrenees, Central Massif, Alps, Rila Mts., Western Carpathians, northern Poland lowlands, Finland lowlands, Norway lowlands and mountains – Jotunheimen massif).

Basing on appropriate molecular AFLP markers, genetic variability of species will be estimated and a molecular variability pattern will be established. Research should permit a verification of several hypotheses concerning: (1) the primary centre of the species' origin; (2) probable routes of its migration and presumable history of the forming of its present range; (3) relations between single mountain parts of the distribution area; (4) history of the lowland part of the total range.

Circumpolar cpDNA phylogeography of the diploid *Cassiope tetragona* – a new project Anne-Cathrine Scheen¹, Ulf Molau², Inger Nordal³ and Christian Brochmann¹

The diploid, woody perennial *Cassiope tetragona* has a circumpolar distribution. The species is an important component of arctic vegetation and has been investigated in global change programs in connection with the International Tundra Experiment (ITEX), by experimental manipulations as well as by retrospective analyses. We presently initiate a study of molecular variation in *C. tetragona* on a circumpolar scale. Silica-dried leaf material has so far been collected from arctic Canada (extensive sampling made possible by participation in the Swedish Tundra Northwest 99 expedition), Greenland, Svalbard, Scandinavia, and one site in arctic Russia; additional field-collections as well as herbarium material will be used to cover the entire geographic distribution of the species. We plan to do (1) initial, complete sequencing of a series of non-coding cpDNA regions of a few field-collected plants from different geographic main regions, in order to identify small parts (<300 bp) with high level of variation and with sufficiently conserved flanking regions to allow for design of new internal primer pairs; and (2) full analysis of all material including partly degraded DNA from herbarium specimens, based on complete sequencing of small regions and/or fragment analysis to identify particular single- or few-nucleotide polymorphisms. Preliminary results will be presented.

Phylogeography of the high alpine cushion-plant *Androsace alpina* (Primulaceae) in the Alps Peter Schönswitter and Andreas Tribsch

Androsace alpina is a perennial cushion plant endemic to high alpine to nival habitats in siliceous mountain ranges of the European Alps where it ascends up to 4200 m. The plant can be found in major portions of the Alps, but although the distribution is rather continuous, *A. alpina* does not occur in postulated major refugial areas in the Southwestern Alps or the Eastern Alps. This distribution pattern might be interpreted as an indication for in situ survival on nunataks during the ice ages. To test this hypothesis, we investigated 259 individuals from 53 populations covering the entire distribution area of *A. alpina* using AFLP-fingerprinting. With three primer combinations used, 218 unambiguously scorable fragments were generated, 177 of which (81.2%) were polymorphic. The *FST*-value under the random-mating-hypothesis among all populations was 0.8 (95% C.I. 0.45–0.51), the Shannon-Index ranged from 4.26–4.50. Both a UPGMA clustering of the populations and a Principal Coordinate Analysis between pairs of individuals revealed a relatively high geographical structuring between groups of populations. An AMOVA conducted on those groups partitioned the overall variation into 57.7% variation within populations, 19.7% among populations and the comparatively high value of 22.6% among regions.

Five geographic regions were clearly separable: (1) the south-western-most part of the distribution area (Cottic and Grajic Alps), (2) the Western Alps from Mont Blanc to Splügenpass, (3) the southern part of the middle Alps from Splügenpass to the Dolomites, (4) the Eastern Alps ± east of Mt. Grossglockner and (5) one population in the Dolomites (Pordoi). The northern part of the



Abb. 11: *Androsace alpina*

middle Alps (6), Silvretta to Kitzsteinhorn, is intermediate between (3) and (4). Mantel tests were used to assess the goodness-of-fit between our grouping and the genetic distance matrix and gave congruent results.

Our results suggest, that *A. alpina* survived the last glaciations in at least four regions (1–4). There is no evidence for nunatak survival in the western part of the main chain of the Eastern Alps (6). In fact, it was colonised from refugia to the south (3) and to the east (4). Within regions (1)–(4) no contributions to the nunatak-debate can be derived from our data: due to the overall weak structuring within regions, it is not possible to decide, whether plant populations within the well-defined regions survived on nunataks or outside the ice-shield.

Immigration AND in situ glacial survival in the lowalpine *Erinus alpinus*? Ivana Stehlík¹, J. Jakob Schneller¹ and Konrad Bachmann²

It was hypothesised that *Erinus alpinus* survived in south-west peripheral refugia during glaciation. Its present-day, mainly sub-alpine distribution is nearly continuous in a south-west to north-eastern direction along the Alps. Nevertheless, *E. alpinus* is also known from proposed glacial refugia in the northern Prealps. Twelve plants each from 22 populations covering the proposed postglacial immigration route from possible southern French refugia along the north-western edge of the Alps were collected, including several populations from northern alpine refugia. High genetic variation was detected by AFLP, but no variation was found in PCR-RFLP of cpDNA. Hence, interpretations were mainly based on AFLP data. Using cluster analyses, several Mantel tests and AMOVAs, three basic groups could be discriminated. One contained all populations from Central Switzerland, one all individuals from the Rigi mountain and one all other populations (west-eastern group). While the two south-western most populations, sampled as potential refugial sources, were not genetically distinct of the west-eastern group, there was a clear genetic isolation between Rigi and Central Switzerland. Over all, west-eastern individuals showed slightly higher numbers of fragments than individuals from Central Switzerland and Rigi, while there was a decline in the number of fragments within the west-eastern group from West to East (lowest number at the eastern distribution edge of *E. alpinus*). No individual was genetically intermediate between the west-eastern, the Central Swiss and Rigi individuals, pointing to a lack of gene flow.

The present investigation demonstrates how two genetically contrasting processes acted at distant timespans. The genetic pattern in Central Switzerland and Rigi pointed to an in situ survival on nunataks in the northern Prealps (possibly dating back to 60–28 ky AD), whereas the west-eastern gene-pool immigrated postglacially from southern France through the prealpine lowlands (after the retreat of glaciers, 14.6 ky AD), leaving out the colonisation of Central Switzerland. In many cases, potentially different historical genetic patterns have possibly been swamped by immigrating genotypes. Nearly lacking gene flow among central Swiss and west-eastern populations and the geographic remoteness of the Rigi mountain (lakes on three sides) enable that this old genetic pattern is still detectable in *E. alpinus*.

Comparative phylogeography of alpine plants Pierre Taberlet, Ludovic Gielly and Philippe Choler

In a previous comparative study, we compared the intraspecific phylogeographic structure of ten taxa across Europe, including mammals, amphibians, insects, and plants. The most striking result was the considerable dissimilarity among European-wide phylogeographic patterns. It seems that each taxon has responded independently to Quaternary cold periods. As a consequence, assemblages of plants comprising particular communities might be not stable over time, an observation consistent with previous findings based mainly on fossil pollen data.

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