middle Alps (6), Silvretta to Kitzsteinhorn, is intermediate between (3) and (4). Mantel tests were used to asses 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 Stehlik[1], J. Jakob Schneller[1] and Konrad Bachmann[2]

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*.

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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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DOI: https:// doi.org/10.12685/bauhinia.2182

In order to test the persistence of plant communities over time, we decided to compare the intraspecific phylogeographies of five plants from the same community (*Cardamine* gr. *bellidifolia* L., *Cerastium cerastoides* (L.) Britton, *Omalotheca supina* (L.) DC., *Salix herbacea* L., *Sibbaldia procumbens* L., *Veronica alpina* L.). Ten individuals of these six plant species were sampled in three localities in Scandinavia, three localities in the Alps, and two localities in the Pyrenees. The intraspecific phylogeography will be assessed using the AFLP technique. We expect to find concordant phylogeographic patterns if plant communities are stable over time.

Patterns of populational differentiation in *Hypochaeris* (Asteraceae) of the southern Andes Karin Tremetsberger[1], Yan-Ping Guo[2], Alexandra Müllner[1], Rosabelle Samuel[1] and Tod Stuessy[1]

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Less is known about effects of ice ages in southern South America than in Europe and North America. The Andes in southern Chile (south of Temuco) were completely glaciated, whereas only descent of local glaciers occurred throughout other Andean regions. Species of South American *Hypochaeris* sect. *Achyrophorus* are members of the high-Andean flora (Chile and Argentina) and serve to test hypotheses of biogeographic effects of ice ages in this region. We have analyzed three species that differ in ecology and reproductive modes: *H. tenuifolia*, a perennial allogamous pioneer on exposed lava slopes, and *H. acaulis* and *H. palustris*, both inbreeders localized in moist seeps along small arroyos.

Two hypotheses were tested: (1) regional patterns of genetic partitioning north of the glacial boundary do not correlate with isolation by distance and (2) genetic variation within glaciated southern regions is reduced in comparison to populations further north.

AFLP markers provide an estimate of genetic variation within and among populations. In *Hypochaeris tenuifolia*, three primer-combinations were analyzed yielding 206 fragments of which 186 (90%) were polymorphic. *Hypochaeris tenuifolia* has high dispersal and colonizing abilities. Genetic similarities exist between pioneer populations on ash slopes of Volcán Lonquimay (that erupted in 1988) and those more than 100 kilometers away. The distance class correlogram among populations throughout the species also indicates genetic correlations between populations up to 130 kilometers distant. This value is similar to those documented in other alpine species (Alps, Scandinavia). Absence of deep gaps in the infraspecific phylogeny also indicates lack of older historical separations. Isolation by distance may be the main factor responsible for these observed patterns, with past and present long distance gene flow via wind-dispersed seeds swamping effects of Pleistocene differentiation. The only suggestion of ice age isolation may be seen in characteristic fragments that show a slight regional geographic pattern of allelic differentiation characterizing northern, central, and southern parts of the range.

Hypochaeris acaulis and *H. palustris* are small herbs with limited dispersal capabilities and isolated to subalpine seeps. Genetic data reveal patterns of phylogeographic differentiation in these taxa, suggesting impacts from inbreeding as well as local Pleistocene glaciation. Reduction in genetic variation within and between populations is observed in the southern glaciated areas in contrast to northern parts of the range.

Several peripheral Pleistocene refugia for the alpinecushion plant *Saponaria pumila* (Caryophyllaceae) Andreas Tribsch and Peter Schönswetter

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Saponaria pumila (Caryophyllaceae) occurs in the Eastern Alps and in the southern parts of the Eastern Carpathians. Within the Alps its distribution shows strong affinities to presumptive Pleistocene refugial areas for the flora of the siliceous Alps (eastern-most Alps, Dolomites), but also extends to central parts (Hohe Tauern, Deferegger Alpen, Presanella, Sarntaler Alpen). Popu-