

History, Evolution & Future of Arctic & Alpine Flora

- Botanical Society of Scotland Symposium, St Andrews University, Scotland, 25-27 June 2007

Poster Abstracts

1. Speciation on the Balkan Peninsula - examples from *Veronica* (Plantaginaceae)

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The Balkan Peninsula is richer in plant species than any comparable area in Europe; presumably because of its role as a refugial area during the ice ages. Despite this, the Balkan Peninsula was a place for further diversification and formation of new species given its richness in endemic species. Until now, our knowledge of the phylogeographic history of plant taxa of the Balkan Peninsula is predominantly based on studies of tree species. However, most of its species richness is due to herbaceous species such as the genus *Veronica*. We focus on species from three different subgenera: *Stenocarpon* – growing in alpine habitats – *Pseudolysimachion* – occurring on open meadows – and *Chamaedrys* – mainly inhabiting forests. Using genome size estimation, AFLP fingerprints, cpDNA markers and nuclear low-copy DNA sequence data we address the following main questions: 1) Which taxa form well-defined taxonomic units? 2) How are the phylogeographical patterns of these taxa on the Balkan Peninsula? 3) What are the differences between ecologically different (alpine vs. open meadow vs. forest) taxa? Genome size estimation reveals that diploid as well as tetraploid cytotypes are present in the investigated taxa, not always with clear geographical separation from each other.

2. Early Holocene forest dynamics from Eastern Brandenburg, Germany.

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Small forest hollows allow for reconstruction of forest dynamics at stand scale, in contrast to more conventional regional studies from lakes or peat bogs. This poster presents work in progress from a small forest hollow in Eastern Brandenburg, Germany. A 150 cm core was analysed for pollen, plant macrofossils, charcoal and organic content. This allowed for detailed reconstruction of Early Holocene vegetation dynamics close to the coring site. The data presented show the colonisation and expansion phase for the forest taxa *Alnus*, *Quercus*, *Tilia* and *Ulmus*. The charcoal record gives a rare insight into early Holocene fire regime and provides evidence for continual burning, but with periods of clear charcoal maxima from the period under study. The forest hollow site is close to Grosser Treppelsee which has been subject to a Late Glacial and Holocene pollen study recording regional vegetation dynamics. Comparison between the two sites suggest that the small hollow covers a short period during the early Holocene with taxa of local importance being *Pinus*, *Betula*, *Corylus*, Cyperaceae and Graminaceae.

3. Population genetic studies in the alpine apomict *Ranunculus kuepferi* (*Ranunculaceae*)

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The alpine plant *Ranunculus kuepferi* has three ploidy levels ($2n= 2x, 3x$ and $4x$), the diploids are sexual and the tetraploids are known to be apomictic (flowers, pollen and fruit irregular). The species is distributed along the Alps, south Corsica and the north of Apennine. Diploids occur only in the Alps Maritimes, whereas the tetraploid apomicts are more widespread and occur also in previously glaciated areas. This general phenomenon, known as geographical parthenogenesis, is being studied on population samples out of the range of the species. In the mixed area, the putative hybrid origin of triploids and amount of introgression of apomixis into sexuals will be analyzed. Using molecular markers like AFLPs, we study the biogeographical patterns related to its ploidy level which is assessed by flow cytometry. Preliminary AFLPs results show less genetic variation within the tetraploids compared to the diploids, but considerable variation is distributed among populations. A decreasing gradient of genetic variation is observed from the diploid area in the Alps Maritimes towards the Eastern Alps, Corsica and the Apennine supporting a hypothesis that the pattern is caused by re-colonization events and superior colonizing abilities of apomicts.

4. Hybrid speciation in coastal sedges. Evolutionary opportunities in dynamic habitats?

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The fascination of arctic environments to biologists is primarily due to the effects of harsh winter conditions and short growing season. However, arctic coastal habitats are also notably different from those in temperate zones. The presence of sea ice movement creates open dynamic habitats, classic conditions for hybrid speciation. Such evolutionary flux is found in *Carex* section *Phacocystis* (Cyperaceae) where one northern coastal species, *Carex paleacea* Wahlenb., has supposedly hybridized with several close relatives. This has produced four hybrid species all found on the coast, presumably utilising different niches. The majority of these species have an amphi-atlantic distribution. The hybrids are found within the range of the parental species although there is evidence that some are extending their range beyond that of their parents. Preliminary work on leaf surfaces supports the evolutionary origin of one species, *Carex recta* Boott. The aim of the research is to extend this approach to other species in the group, augmented also by evidence from molecular markers to address the taxonomic problems and evolutionary origin of these species.

5. Bipolar disjunctions in *Carex*: long distance dispersal, vicariance or parallel evolution?

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Carex maritima, *C. macloviana*, *C. capitata*, *C. canescens*, *C. magellanica* and *C. microglochin* are the unique six species of *Carex* with a strict bipolar distribution. The principal aims of this study are to establish: 1) the origin of these disjunctions (long distance dispersal, vicariance or parallel evolution; and 2) in case of dispersal, its direction. To this purpose we have analyzed sequence variation of plastid (*rps16* intron) and nuclear DNA (ITS) and phylogenetic reconstructions with Bayesian Inference were also conducted. The analysis of sequence variation lead us to propose mountain hopping (long distance dispersal) as the primarily cause of bipolar disjunctions discarding vicariance as a plausible explanation. In addition, in the case of *C. canescens* and *C. magellanica*, we propose N America as the origin of the current disjunction. *Carex microglochin* seems to present a more complicated evolutionary scenario. In this case, parallel evolution may be considered as this species is not monophyletic.

6. Reticulate phylogenetics and phytogeographical structure of *Heliosperma* (*Sileneae*, Caryophyllaceae) inferred from chloroplast and nuclear DNA sequences

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We used nuclear ribosomal ITS sequences and intron sequences of the chloroplast gene *rps16* to examine phylogenetic and biogeographical patterns within the genus *Heliosperma*, which has its main diversity at the Balkan Peninsula. Three strongly supported clades are found in both data sets, corresponding to *Heliosperma alpestre*, *H. macranthum* and the *H. pusillum* clade, including all other taxa. The interrelationships among these three differ between the nuclear and the plastid data sets. Hierarchical relationships within the *H. pusillum* clade are poorly resolved by the ITS data, but the *rps16* intron sequences form two well-supported clades which are geographically, rather than taxonomically, correlated. A similar geographical structure is found in the ITS data, when analyzed with the NeighbourNet method. The apparent rate of change within *Heliosperma* is slightly higher for *rps16* as compared to ITS. In contrast, in the *Sileneae* outgroup, ITS substitution rates are more than twice as high as those for *rps16*. Unlike most other *Sileneae* ITS sequences, the *H. pusillum* group sequences display extensive polymorphism. A possible explanation to these patterns is extensive hybridization and gene flow within *Heliosperma*, which together with concerted evolution may have eradicated the ancient divergence suggested by the *rps16* data.

7. Future of alpine flora in a changing climate: the Global Observation Research Initiative in Alpine Environments

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A long-term observation network has been established to study the impacts of changes in the alpine flora and vegetation world-wide. Rooting zone temperature on alpine summits is logged continuously in permanent plots, whose species composition and cover is recorded periodically. We present (1) details on the network, (2) some results on floristic richness and temperature relationships in the European alpine ranges, and (3) predictions on how the future species richness of alpine summits may be shaped by rising temperature.

8. Molecular phylogeny and biogeography of *Euphrasia* (Orobanchaceae)

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Euphrasia (Orobanchaceae) are perennial or annual green parasitic plants with a disjunct bipolar distribution, except for one transtropical connection across the high mountains of Oceania. This disjunction together with the strikingly contrasting patterns of morphological diversity in the southern and northern hemispheres make the genus an exciting model to study processes of evolutionary diversification which shaped present floras. We used a molecular phylogenetic framework to address long-debated questions in *Euphrasia* systematics and biogeography. We inferred the relationships among 51 species representing 14 of the 15 sections based on nrDNA ITS and cpDNA trnL-trnF, atpB-rbcL intergenic spacer and trnL intron sequences. Maximum parsimony and Bayesian inference support monophyly of the genus and of several intrageneric groups characterized by morphology, ploidy level, and geographic range. Phylogenetic dating suggests that the earliest *Euphrasia* radiations occurred minimum 10–8 Mya. Dispersal-vicariance analysis supports Eurasia as an ancestral area for the genus. Both long-distance dispersal and across land vicariance can be invoked to explain the diversification in the genus, which experienced rapid radiations driven by new ecological opportunities in the late Pliocene and Pleistocene but also retained a set of endemic or relict species of an earlier origin.

9. Observations on east Greenland flora

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(i) Northern limits of British species in east Greenland: Of the 452 vascular plants in Greenland 205 occur in Britain. A few of these occur throughout Greenland where vegetation is present, from 60°–82°N. These are wide-ranging hardy arctic species such as *Saxifraga oppositifolia*, *Cerastium arcticum*, *Pericaria vivipara* and *Oxyria digyna*. However most occur in southern Greenland and disappear progressively northwards, particularly at the transition from the low arctic to high arctic (70°–72°N). Examples include *Alchemilla glomerulans*, *Gnaphalium supinum* and *Woodsia ilvensis*. By contrast a few species, notably *Minuartia stricta*, *Saxifraga hirculus*, *Kobresia simpliciuscula* and *Alopecurus borealis*, are restricted to the high arctic. This is surprising in view of their occurrence far to the south in Britain, e.g. in the north Pennines. It is feasible that in the very different climate prevailing in Britain these southern populations represent different physiological ecotypes.

(ii) A Greenland endemic: The only really convincing endemic in the Greenland flora is *Saxifraga nathorstii*, which occurs over a range of 500 km in north-east Greenland. It is a fertile, stable amphidiploid of the two diploid parents *S. oppositifolia* and *S. aizoides*. Although both species have arctic-alpine distributions with considerable overlap in Europe and the western Arctic the pronounced difference in flowering time appears to have been sufficient to prevent hybridisation except in the brief high arctic summer. *Saxifraga nathorstii* has salmon-pink flowers, compared with the deep pink and yellow of the parent species. Plants occasionally occur with petals intermediate between *S. nathorstii* and the parents. These may represent backcrosses.

(iii) Disjunct distributions of two Greenland plants: *Draba sibirica* and *Potentilla stipularis* are two vascular plants which feature prominently in discussions on per-glacial survival in Greenland. Both are restricted in Greenland to the east coast, the *Draba* being relatively frequent over a limited area on the north side of Scoresby Sund (72°N) while the *Potentilla* is known from only six sites between Scoresby Sund and Kuhn Ø, 400 km to the north. Both are quite different from other Greenland members of their genera, the *Draba* having a creeping habit and the *Potentilla* having palmate leaves with 7–11 leaflets, like a lupin. Both are Asiatic arctic-alpine species with a gap of some 2600 km between their western limits in the northern Urals and east Greenland.

10. Reticulation processes, taxonomic delimitation and geographical patterns in *Carex flava* complex in Europe.

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Five taxa constitute the *Carex flava* group (sect. *Ceratocystis*) in Europe (*C. demissa*, *C. flava*, *C. lepidocarpa*, *C. nevadensis* and *C. viridula*). This group is extremely peculiar within the subgenus *Carex* because of its short life cycles and the extensive hybridization. The analyses of molecular regions have been widely used for taxonomic delimitation and inferring geographical patterns. In this study we have sequenced the regions ITS (nuclear) and rps16 (plastid) of European *C. flava* group taxa with special emphasis in Mediterranean ranges. Four independent groups of plants can be established based on plastid haplotypes, namely: (1) *C. lepidocarpa* and Iberian allies, (2) *C. demissa* and *C. viridula* group, (3) *C. flava* and (4) divergent haplotypes from the Alps and Filabres range (SE Spain). Patterns of additive polymorphic sites (APS) found in ITS sequences are mostly in agreement with traditional taxonomic division of the group. All the three sources of data analysed (molecular sequences, morphology, cytogenetic) revealed the Pyrenees and Cantabrian range could be an extensive hybridization area for at least *C. lepidocarpa* and *C. flava*. The boreoalpine *C. flava* in its south western limit seems to be suffering an introgressive dissolution into the more temperate *C. lepidocarpa*.

11. *Arabidopsis thaliana*'s wild relatives: an updated overview on systematics, taxonomy and evolution.

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Arabidopsis thaliana is one of the most intensively studied plant species. More recently, information is accumulating about its closest relatives, the former genus *Cardaminopsis*. *Arabidopsis thaliana* diverged from these relatives, actually treated within three major lineages (*Arabidopsis lyrata*, *A. halleri*, *A. arenosa*) approximately 5 million years ago. Significant karyotype evolution in *Arabidopsis thaliana* with base chromosome number reduction from $x=8$ to $x=5$ might indicate and favour effective genetic isolation from these other species, although hybrids are occurring naturally and have been also constituted under controlled conditions. We tested the evolutionary significance to separate the $x=5$ from the $x=8$ lineage using DNA sequence data from the plastome and the nuclear ribosomal DNA based on an extensive, representative worldwide sampling of nearly all taxonomic entities. We conclude that (i) *Arabidopsis thaliana* is clearly separated phylogenetically from the $x=8$ lineage, (ii) five major lineages outside *A. thaliana* can be identified (*A. lyrata*, *A. arenosa*, *A. halleri*, *A. croatica*, *A. pedemontana* together with *A. cebennensis*, and (iii) centres of genetic and morphological diversity are mostly in congruence and are located close to the Balkans in Austria and Slovakia outside glaciated and permafrost regions with few notable exceptions. We also define selected gaps in knowledge to focus and stimulate future research activities and present some first results for the phylogeography of the arctic-subarctic *A. lyrata* species complex from outside Europe.

12. Project for a modern Circumarctic Flora and an Arctic Vegetation database

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Of all the global biomes, the Circumpolar Arctic Tundra Biome is the only one that has its entire known list of plants, including vascular plants, mosses and lichens, documented in up-to-date floras of the entire biome. These checklists are an essential first step in understanding the relationship of the flora and plant communities to climate and other geographical variables and how these might change under altered climate regimes. Our proposed project will use these pan-Arctic floras to make three interlinked databases that are needed for circumpolar studies of plant ecology and vegetation (1) the web-accessible *Flora Arctica* database containing the taxonomic, ecological, genetic, and geographic information as well as images, line drawings, and maps for all Arctic plant species, (2) the Arctic Vegetation Database hosting and standardizing all available relevé data and associated header data and (3) the Arctic Prodromus, i.e. an annotated list of all described plant communities in the Arctic. We will furthermore analyze the content of the databases to determine trends with respect to key physical and biotic variables, provide the first complete biodiversity assessment and gap analysis for Arctic plants, and integrate the results as educational tools in the Arctic Geobotanical Atlas. We invite scientists with an interest or focus on Arctic botany (systematics, vegetation description and analysis, phylogeography, biodiversity, ethnobotany, global change modeling, education, and/or species databases) to contribute and comment on this collaborative circumarctic project.

13. Conservation of genetic diversity in *Trollius europaeus*

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Genetic diversity is likely to be important for maintaining the sustainability of populations across a species range. For example, loss of genetic diversity may affect population viability and reduce the potential to adapt to environmental change. The main function of designated sites for conservation, such as National Nature Reserves and Sites of Special Scientific Interest, is to conserve biodiversity. Whilst conservation effort is predominantly focused at the level of species diversity, it is less clear how effective designated areas are at conserving intraspecific diversity. Conservation of genetic diversity is likely to be increasingly important towards the range-edge of a species where populations are likely to be genetically differentiated and subject to different environmental pressures than core populations. I have investigated the effectiveness of designated sites as a network to conserve species' genetic diversity by examining genetic data from across the distributional range of *Trollius europaeus* in the UK.

14. Phylogeography of *Cardamine resedifolia* and *C. alpina* in Europe.

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The present study aims to explore phylogeographic history of two diploid species, *Cardamine resedifolia* and *C. alpina* (Brassicaceae), growing on siliceous bedrock in alpine belts across several European mountain ranges. The distribution area of the former species covers the Sierra Nevada Mts., Corse, the Pyrenees, Alps and Southern Carpathians; the species usually grows on moist screes. *Cardamine alpina*, in contrast, is a typical plant of snow beds and is confined to the Pyrenees and Alps. Genetic variation is inferred on the basis of AFLP markers. Due to the small genome size of the studied species, the standard AFLP protocol was modified so that *MseI*-selective primers had only two selective nucleotides. Data evaluation is under progress. We intend to assess patterns of genetic variation in order to identify potential glacial refugia and to track postglacial colonization routes. Even if the species apparently differ in their ecological demands, they can be found growing close each other. Based on the nrDNA ITS sequences, a few morphologically suspected plants found both in the Alps and Pyrenees were proven to be hybrids. Therefore, another task of the present study is to explore the extent of hybridization between these two species in more detail.

15. ENSCONET, the European Native Seed Conservation Network

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ENSCONET, the network headed by the Millennium Seed Bank (Royal Botanic Gardens, Kew), is composed of 24 institutes from 17 European countries and two associate members, covering 9 of 10 major bio-geographical regions of Europe (Alpine, Arctic, Atlantic, Black Sea, Boreal, Continental, Macaronesian, Mediterranean and Pannonian). It is a Co-ordination Action funded under the European Union's 6th Framework Programme. Its purpose is the improved quality, coordination and integration of European seed conservation practice, policy and research for native plant species, and to assist EU conservation policy and its obligations to the Convention on Biological Diversity and its Global Strategy for Plant Conservation.

ENSCONET co-ordinates and enhances activities of several European seed banks, botanical gardens or institutes interested in seed conservation, in order to reduce duplicated efforts in establishing and improving technologies for seed collecting, curation and data management. That is being achieved through creating common high standard protocols for collection and curation, compiling data on species held in European seed banks. At this moment, a virtual seed bank is being created for European native plants. The 24 partners are establishing priority species lists for new seed collection in each of the 9 bio-geographical regions.

16. The impact of glaciations in the phylogeography of the mountain endemic *Reseda* section *Glaucoseseda*

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Reseda section *Glaucoseseda* is composed of 5 endemics to the high mountain ranges and plateaus of the Iberian Peninsula and Morocco. It is a well-supported monophyletic group, as revealed by a previous molecular phylogenetic reconstruction (ITS, *trnL-F*). However, poor internal resolution of sect. *Glaucoseseda* was revealed by these markers, mostly due to low level of sequence divergence. Phylogeographic patterns within this section were studied by means of AFLPs, nuclear ITS and plastid *trnL-F* and *rps16* sequences. Incongruence found between nuclear and cpDNA data sets may reveal the intervention of biological processes like hybridization and/or lineage sorting. In this case, geographic distribution of haplotypes may be indicative of differential lineage sorting of ancestral polymorphisms rather than recent hybridization. Our data suggests a vicariant hypothesis in which an ancestral widespread polymorphic species could have suffered polyploidization, followed by fragmentation caused by Quaternary glaciations. Afterwards, allopatric speciation of the resulting isolated populations confined to different ranges may have occurred, leading to current endemics. Higher differentiation detected in northern (Pyrenean populations of *R. glauca*) and southern (*R. battandieri*) limits of section's range could be explained by longer term of isolation.

17. The Botanical Society of the British Isles: The leading Society for amateur and professional botanists in Britain & Ireland

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The poster very briefly sets out who the Botanical Society of the British Isles (BSBI) is and what we do. The BSBI is one of the world's largest contributors of biological records, providing over 9 million records to date, which form the bedrock of plant conservation work in Britain and Ireland. Our 3,000 members are responsible for this activity, coordinated by staff, volunteers and 157 Vice County Recorders across Britain and Ireland. In addition to our main role of collecting, checking and curating plant records, we undertake national surveys and publish our data in books and on the web. We also publish journals, newsletters and expert identification guides. In addition, we hold field meetings, workshops and conferences; promote research, education and training and provide expert advice on botanical issues. We warmly welcome all those with an interest in the flora of Britain and Ireland and would encourage them to join.

18. The history of the bipolar genus *Empetrum* L. (Ericaceae) inferred from plastid and nuclear low copy DNA

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Empetrum is a taxonomically complex genus with up to 18 taxa accepted at the species/subspecies level. The genus has a highly disjunct bipolar distribution. It is circumpolar in the northern hemisphere but restricted to southern South America and the Tristan da Cunha and Gough islands in the southern hemisphere. Both di- and tetraploids are found in the north, whereas only diploids are found in the south. We present preliminary results from a phylogenetic/phylogeographic study using non-coding nucleotide sequences from the plastid *trnS-trnfM* and *trnS-trnG* regions and the nuclear low-copy regions *RPB2* and *RPC2*. The phylogeny inferred from the plastid DNA data placed an East Canadian diploid, morphologically corresponding to *E. eamesii*, as sister to all other *Empetrum* accessions. A South Alaskan diploid, morphologically corresponding to *E. nigrum* s. lat., was placed as sister to the southern hemisphere accessions (*E. rubrum*). The nuclear data, however, indicate a more complex history involving multiple polyploidization events and relatively recent gene flow between the southern and northern hemispheres.

19. Phylogeography of the arcto-alpine species *Hieracium alpinum* s.str. (Asteraceae)

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Hieracium alpinum L. s.str. is an arcto-alpine, diploid-triploid species. While diploid populations occur only in the Southern and Eastern Carpathians, triploids occupy the rest of distribution area from the Western Carpathians, the Alps and the Sudeten Mts to Fennoscandia, Scotland and the northern Urals. Isolated exclaves of triploids are in the Vosges Mts, Harz Mts and Vranica Plateau. Diploids are strictly allogamous, while triploids reproduce via diplosporous agamospermy. A survey of AFLP and nuclear ITS variation revealed no clear phylogeographic structure. However, there was a tendency for plants from Fennoscandia and Scotland to group together with some populations or plants from the Western Alps and several plants from the Western Carpathians. Generally, Fennoscandian, Scottish and some mainly Western Alpine populations are much less variable than populations from other regions. Surprisingly, the level of intrapopulation genetic diversity of many apomictic triploid populations is comparable with that found in sexual diploid populations. We suppose that recent genetic variation of triploids might be derived from ancestral divergent diploid populations. Another possibility could be recent occasional gene flow among triploids. However, direct proof of facultative apomixis in triploids is still lacking. The complex geographic pattern of genetic variation suggests the existence of a large periglacial refugium between the Alps and Scandinavian Ice sheet from where plants colonized deglaciated areas when ice-sheets retreated.

20. Genetic structure of the Spanish endemic species *Senecio boissieri*

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Senecio boissieri is an endemic Spanish species distributed over three geographically disjunct mountain ranges – Sierra Nevada, Sierra Guadarrama and Picos de Europa. In this study, 9 populations were examined. High genetic diversity was revealed within populations and significant variation among populations with RAPD analysis. Populations from the south (Sierra Nevada) and central mountains (Sierra Guadarrama) were shown by Principal Coordinate analysis and UPGMA clustering to be more similar to each other than to populations from the north (Picos de Europa). Genetic distance among all populations (in terms of F_{ST}) was not related to geographical distance. The results suggest that since the last glacial maximum, when this species may have had a more continuous distribution in Spain, populations from the south and central mountain ranges remained in contact for a longer period than was the case for these populations and those located in the Picos de Europa. This might be explained by the presence of high mountains connecting the southern and central mountain ranges. A survey of chloroplast DNA diversity in the species has so far resolved very little diversity. Only one out of 53 cpDNA microsatellites has been shown to be polymorphic, while PCR-RFLP analysis of 4 conserved regions using 4 different digest enzymes yielded no variation.

21. The contribution of the *Silene ajanensis* (sect. *Physolychnis*, *Caryophyllaceae*) group to the formation of Arctic and Siberian polyploids

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The diploid *Silene ajanensis* group, which comprises about four taxa distributed in North/Northeast Asia, has been involved in the formation of both tetraploid and hexaploid Arctic *Silene*. Using sequence data from chloroplast DNA, nuclear ribosomal DNA and a region from the low copy nuclear RNA polymerase (RNAP), we have studied its relation to three polyploid derivative taxa, as well as to two taxa of unknown ploidy level (*S. sachalinensis* and *S. tolmachevii*), occurring in the Arctic and in Northeast Russia. Several genetic variants of the RNAP introns were found and many of these can be explained by allopolyploidy, but there are two indications of independent gene duplications. This emphasizes the need to study multiple unlinked regions to discriminate between different evolutionary processes. A close relationship between two members of the *S. ajanensis* group and two hexaploids is suggested. Allotetraploid origins of *S. sachalinensis* and *S. tolmachevii* are strongly supported, with the *S. ajanensis* stem group as paternal lineage. *S. sachalinensis* is likely to stem from a diploid member of the *S. uralensis* lineage on the maternal side, whereas the maternal lineage of *S. tolmachevii* is to be sought in the stem group of a more inclusive group, including *S. uralensis*.

22. Phylogeography of *Saxifraga oppositifolia* (Saxifragaceae) in Svalbard

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Phylogeography combines investigations on the genealogical relationships and geographical distributions of organisms. The choice of appropriate molecular markers is vital when reconstructing genealogical histories. In the present study, we analyzed sequence variation in the nuclear ribosomal DNA region, ITS1-5.8S rRNA-ITS2 in the purple saxifrage (*Saxifraga oppositifolia*) from 10 localities in the Svalbard Archipelago (Spizbergen), altogether 24 individuals. In addition, we sequenced the ITS region from five individuals from mainland Norway. Ten additional ITS sequences available in GenBank were included in the phylogenetic analysis. Considerable polymorphism was detected. The phylogenetic analysis revealed the presence of the following three clades: 1) The main clade, 2) a clade including Alaska and northern Norway, and 3) a clade including the remote Kinnvika area and a sample from Longyearbyen. The plants from the distant Biscayerhuken region appeared to be of mixed origin. The climate history, sea currents and partly dispersal by vectors, such as humans and birds, may explain the present phylogeographic pattern of *S. oppositifolia*. To complement the phylogeographic knowledge of *S. oppositifolia* in the Arctic, we will conduct precise analyses of population genetic structures, genetic variability and mating systems. Such population-level analyses will be carried out using microsatellite markers, which we have recently developed for *S. oppositifolia*.

23. Phylogeography in the genus *Melampodium* – a case study

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Melampodium (Asteraceae, Heliantheae) comprises 39 species distributed throughout Mexico, Central America and the southwestern US. All species have yellow rays except for three shrubby, xerophytic taxa of the southwestern US and adjacent Mexico: *M. argophyllum*, *M. cinereum* (with three varieties), and *M. leucanthum* all of which have white-rays and form the so-called white-rayed complex. Three different ploidy levels have been reported for this complex: diploid, tetraploid (with occasional triploidy) and hexaploid. While *M. argophyllum* is uniformly hexaploid, both diploid and tetraploids cytotypes have been reported in *M. leucanthum* and *M. cinereum*. In both of these species, diploid and tetraploid cytotypes prevail in the western and eastern parts of their distribution areas, respectively. All species and varieties are well supported both in AFLPs and chloroplast haplotype analyses. A previously hypothesized origin of the white-rayed complex from yellow-rayed ancestors further south is not fully supported either by molecular phylogenetic analyses of the whole genus (using nuclear and chloroplast markers) or by AFLP and cp haplotype analyses.

24. Approaching biogeography of arctic-alpine fungi

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Macrofungi, being ecologically confined to arctic-alpine plants by mycorrhiza or specific saprotrophic links, belong to important elements of arctic-alpine ecosystems. This group is still insufficiently known worldwide. Most probably, the majority of species are widespread in most arctic and alpine areas. There are also, however, species reported only from the Arctic so far. It could be hypothesized that in fungi, like in plants, the arctic-alpine element comprises subcategories. A systematic survey of the arctic-alpine fungi in all important areas of Europe is indispensable to deal with such questions as: degree of specificity of arctic-alpine fungi and role of these areas in fungal speciation, and relationship between isolated arctic and alpine sites. We initiated a project, where we attempt to: 1) prepare a synthesis of available knowledge on biogeography of arctic-alpine fungi; 2) gather a possibly broad data set from important areas scarcely studied so far (Carpathians, Iberian and Balkan Peninsulas); 3) initiate a phylogeographical survey of selected arctic-alpine taxa to compare their patterns with those of plant hosts and verify whether traces of past co-migrations could be detected or recurrent long-distant spore transport cause constant redistributions of propagules and gene flow over arctic-alpine areas. We will discuss the first results of this project.

25. Phylogeography of alpine plants in the mountains of Central Europe: a preliminary view.

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Alpine zone forms a discontinuous system in Central Europe, involving several distinct mountain ranges (mainly including the Carpathians, part of the Alps, the Sudetes, the northern Balkan ranges). Potential gene and species exchange among presently isolated mountain ranges was linked in the past with the Quaternary glacial periods. Few detailed phylogeographical studies addressed the history and level of intraspecific differentiation in disjunct distribution areas of Central European alpine plants so far, but recently several intraspecific data sets covering partial or total distributions have become available, allowing new insights into these questions. Most data sets showed significant phylogeographic structures, revealing various histories, but with some repeated tendencies. Relatively high differentiation among populations from isolated mountain ranges was found in several species and observation of several genetic breaks indicated presence of many refugial areas and long-term isolation rather than wide glacial or postglacial range expansion in the late Quaternary. However, also examples of probable recent (re)colonization from currently isolated areas were observed. In the Carpathians, the major mountain range of Central Europe, main genetic break supported by most taxa separated Western and South-Eastern Carpathians, following the well-known phytogeographical boundary. Preliminary analyses of exemplary species will be presented and discussed on the poster.

26. Glacial survival in and recent long-distance dispersal to the Iberian mountains: phylogeographic history of *Artemisia umbelliformis* (*A. mutellina*, Asteraceae) inferred from AFLP fingerprinting

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Artemisia umbelliformis Lam. is an alpine perennial with disjunct distribution in the central and western part of the European Alpine system (Sierra Nevada, Cantabrian Mountains, Pyrenees, Alps). In order to unravel the history of its immigration into the Iberian mountains and to explore the large-scale phylogeographical structure we applied AFLPs to 142 individuals (19 populations) covering the whole distribution area. Non-hierarchical AMOVA attributed 93 % of the overall genetic variation to variation among populations. Neighbour joining and PCO analyses revealed three genetically highly differentiated groups: (a) Alps, Apennines and Sierra Nevada, (b) Central Pyrenees and Cantabrian Mountains and (c) Western and Eastern Pyrenees. The Cantabrian Mountains and the central Pyrenees populations harboured the highest number of private AFLP fragments whereas in the Sierra Nevada population no private fragments were found. Altogether, our results suggests *in situ* long-term survival in the central Pyrenees and the Cantabrian Mountains and a fairly recent long-distant dispersal event (LDD) from the Alps to the Sierra Nevada. Consequently, the disjunction of *A. umbelliformis* within the Iberian Peninsula could be explained by both vicariance and LDD events that gave rise to the geographically strongly isolated populations on the western and southern limits of the species' distribution range.

27. Loss of genetic diversity in isolated populations of the alpine diploid species *Pilosella ullepitschii* (Asteraceae, Lactuceae)

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Distribution of *Pilosella ullepitschii*, a diploid and strictly self-incompatible endemic taxon of the Carpathians, has a strongly disjunctive character. It is a species of primarily alpine and subalpine meadows on acid bedrock with contiguous range in the Vysoké and Západné Tatry Mts (Western Carpathians, Slovakia and Poland). Extremely rare and isolated populations of *P. ullepitschii* are known from the Eastern and Southern Carpathians (Romania), where the species often occurs at human-influenced habitats (e.g. secondary formed pastures in the spruce belt). This disjunctive pattern of distribution may be either due to a fragmentation of populations of previously continuous range of distribution or an incidental (recent?) long-distance dispersal. In our study, we tried to test both hypotheses using co-dominant allozyme

markers. Genetic diversity was estimated for 7 Slovak and 3 Romanian populations (145 plants altogether). In total 12 alleles representing 6 loci were scored. Romanian populations display significantly lower values of both allelic and genotypic variation in comparison with those from the Western Carpathians. This obvious loss of genetic diversity, in the disjunctive and less numerous Romanian populations suggests a likely bottleneck *via* recent long-distance dispersal rather than long-term vicariance. However, it remains a question whether this dispersal was natural or caused by an unintentional introduction by human activities.

28. Did vascular plants and bryophytes survive the last ice age in Scandinavia?

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Glacial survival versus postglacial immigration of the Scandinavian alpine flora has been debated for more than 100 years, and has recently received increased attention with the development of molecular tools. Many vascular plant species occur disjunctly on both sides of the North Atlantic Ocean, but are lacking from areas east- and westwards. A subset also absent from the Alps, the so-called 'West-arctic' species, has been considered to provide the strongest evidence for local survival in Scandinavia throughout the entire Quaternary, or at least through the last glaciation. Bryophytes have never attained weight in this discussion, even though many of them are exceptionally hardy and therefore more likely as nunatak survivors. In this project, we will carry out a comparative phylogeographic analysis of about 10 species of amphi-Atlantic vascular plants and bryophytes to test whether the Scandinavian populations originate from recent (post-glacial) cross-oceanic dispersal from the west, and/or whether they descend from long-term glacial in-situ survivors. The results for *Saxifraga rivularis* ssp. *rivularis* (AFLPs: 268 samples, 45 polymorphic markers) shows that survival in the arctic archipelago of Svalbard during the last glacial maximum cannot be excluded, but samples from Novaya Zemlya and/or Frans Josef Land are required to confirm this.

29. Plant colonization of the Werenskiöld glacier forefield (W. Spitsbergen)

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The Werenskiöld glacier forefield is situated on the south part of Spitsbergen, on Wedel Jarlsberg Land (77°05'N, 15°20'W). The recession rate of Werenskiöld glacier since the first half of the 20th century is about 20-25 m/year. The first colonizers of bare bottom moraine were cyanobacteria and mosses followed by vascular plants. The first two groups of organisms were found at a distance of 10-20 m from the front of glacier, whereas vascular plants were found at a distance of 60-70 m. In the parts of forefield nearest the front of glacier, single plants occurred and the cover of the soil is very low (<1%). Occasional Bryophyta of a few species were found in the moist shade of larger stones. Among the vascular plants, *Saxifraga oppositifolia* was the earliest colonizer and this species played the most important role in the plant assemblages during the vegetation succession in the investigated area. Cyanobacteria contributed little to the process of colonization and total ground cover. In the front of glacier *Chroococcus turgidus* and *Merismopodia* sp. were found, whereas small colonies of *Noctoc commune* and *N. punctiforme* with admixture of *Gloeocapsa kutzingiana*, *G. sanguinea*, *G. punctata*, *Letolyngbya* sp. div., *Microcoleus vaginatus*, *Carothrix gypsiphila*, *Shizothrix* sp. div., *Tolypothrix tenuis*, *Scytonema* sp. appeared later in the succession of vegetation, forming a cyanobacterial crust.

30. GIS-modelling of population connectivity in highly structured alpine landscape, the case of myrmecochore *Melampyrum sylvaticum* L.

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The processes acting within and between populations at a landscape scale are the basis for most evolutionary events in nature. They shape the genetic structure of populations, affect local adaptations to microhabitats and the development of ecotypes and subspecies. Populations are the functional units on which natural selection acts as well as the targets of nature conservation and of plant genetic resources management efforts. Understanding the dynamic processes acting on natural populations at a landscape scale is therefore a prerequisite to understand mechanisms of microevolution. *Melampyrum sylvaticum* L. is a species widely distributed throughout the Alps, it is annual, pollinated by bumble bees but predominantly selfing, and its seeds are dispersed by ants (myrmecochory). Thus gene-flow is supposed to be very limited. In addition, it shows clear altitudinal preferences, and the investigation area, the region of Trentino/Alto Adige (Südtirol), is characterised by extensive altitudinal differences. A lack of connectivity and low gene-flow between populations is

expected in such highly structured alpine landscapes, as a result of the presence of potentially severe distribution barriers such as valleys or ridges, unsuitable for this species. Comparison of the regional genetic structure of populations obtained by neutral markers (AFLP) with geographic distances, should provide an insight about the relevance of such barriers. In order to calculate more realistic estimates for population connectivity and potential gene-flow than simple straight-line distances, we developed a GIS-model describing the suitability of the landscape for *M. sylvaticum*. Data from the local floristic mapping project was used to assess the altitudinal distribution of the populations and mapped onto a digital elevation model (DEM). Assuming that the number of population records in a certain elevation range reflects the density of populations within that range, which is further considered to be positively correlated with potential gene-flow, an estimate of population connectivity was assigned to each range. Taking these values, for each pair of grid points, a map of population connectivity was calculated as well as least-cost paths between populations. Both a potential species distribution map and an example of a population connectivity map are shown on the poster. A correlation analysis comparing pairwise least-cost distances of different populations, with pairwise genetic distances was performed resulting in significant correlations up to $r=0.75$.