position of them, possibly due to the recent evolution of this Alpine taxon. The application of the NewHybrids software to AFLP datasets suggested that *S. lantoscana* derived from hybridization events between *S. callosa* subsp. *callosa* and *S. cochlearis* Reichenb., living toghether in Maritime Alps. Introgression of genetic traits was confirmed by cpDNA markers, a simple and quick method based on length variation in cpDNA sequences.

P0837. Tracking the origin and evolution of high polyploids in *Cerastium* (Caryophyllaceae) from non-coding regions of the RNA polymerase genes

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The Arctic is one of the most polyploid-rich areas, in particular of high-level and recently evolved polyploids. The Cerastium alpinum group is a mature polyploid complex, with high ploidal levels dominating and no diploid progenitors known. Previous studies on morphology, isozymes, and DNA fingerprints have identified several evolutionary lineages, and the low level of cpDNA variation observed suggests recent origins and recurrent episodes of range expansions and contractions during the Quaternary glaciations. Non-coding regions of the RNA polymerase genes are now being used to identify progenitor lineages. Results from RPB2 suggest that only one functional paralogue exists in tetraploid Cerastium taxa. Arctic high-polyploid taxa appear to have European origins, with the tetraploid C. semidecandrum representing the maternal lineage and tetraploid taxa from the central and south-eastern European mountains representing different paternal lineages. However, the patterns of reticulate evolution are complicated and other putatively independent nuclear regions are needed to conclude on the origin of several individual taxa.

P0838. AFROALP - Phylogeography, glacial refugia, and conservation of the unique afroalpine ecosystem: a new project

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The unique afroalpine environment occurs in the scattered high mountains of tropical Africa like islands in a sea of lowlands. The afroalpine plants have their closest relatives not in the surrounding lowlands but in remote areas, even in the northern hemisphere. Where did their ancestors come from, how, and when? In the main part of this new project, we investigate the phylogeographic history and population genetics of 6-8 afroalpine ecological key species without obvious mechanisms for long-distance dispersal. Three populations per species have been collected in the 12 highest mountain systems of East Africa and Ethiopia, as well as from other areas. Using AFLP fingerprinting, sequencing of chloroplast DNA, phylogeographic analyses, and assignment statistics, we will determine migration rates among mountain systems, the number and location of glacial refugia, possible secondary contacts between differentiated glacial gene pools, and infraspecific diversity hotspots. In other subprojects, we address the deeper history of some afroalpine plant groups including speciation, phylogeny, and biogeography.

P0839. Phylogeography of Arabis alpina: What do populations from the distribution edges tell us about its evolutionary history?

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Arabis alpina is widely distributed in northern hemispheric alpine habitats and the arctic regions. Its distribution range spans an area from Central Asia to E Africa, from the Canary Islands and N Africa to Iceland and Scandinavia. We analysed 200 accessions from the whole distribution range using DNA sequence data of the nuclear ITS and the plastidic trnL-trnF region. Both data sets are mostly in congruence with each other and favour the recognition of two major lineages: 1) Central Asia, Arabian Peninsula, East African hight mountains 2) All remaining areas.

DNA sequence commparisons of some selected alleles of the chalcone synthase and Ks-derived distance analysis revealed that both lineages have been separated since approximately 500.000 my. Consequently, Arabis alpina is not a tertiary relict in the East African mountains or the Canary Islands as hypothesized in the past, but has been greatly influenced by pleistocenic glaciation and deglaciation cycles. However, continously distributed genetic diversity in its southern distribution area indicates fragmentation processes rather than migration.

P0840. Plant evolution on the small islands of the Russian White Sea

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Small islands and islets in the Kandalaksha Bay of the Russian White Sea are now rising. Thus, new islands are continuously appearing, these islands are settling from scratch and it is relatively easy to estimate the age of an island. We tried to find plant species that are polymorphic enough to show the differences between the mainland and island populations and the populations from the different islands. These differences could be the result of population bottleneck or even the evolutionary process on the isolated islands. Species of Carex (C. salina and C. aquatilis groups), Euphrasia, Achillea, Rhodiola, Atriplex and Parnassia were chosen for preliminary morphological analysis (~ 2200 plants were measured). In addition, geometric morphometrics methods were used for Rhodiola and Atriplex leaf shapes. We found that at least three groups show significant differences between mainland and insular populations. Some of our results are useful for the adjustment of the taxonomic boundaries in several taxonomically `critical" groups.

P0841. Biodiversity of alpine flora of Iran

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Except the interior deserts and lowlands along the Caspian Sea, Persian Gulf, c. half of Iran composed of high mountains. The Alborz along the Northern, Zagros along the Western parts of Iran and several other mountains in Khorassan and Baluchestan provide diverse mountainous ecosystems. The flora and vegetation of Iranian alpine zones are not well known. A first evaluation of vascular flora show that 675 species belonging to 205 genera and 40 families are known in alpine zones (mostly above 3000m) of Iran. Asteraceae with 119 species ranks first, followed by Fabaceae (74), Poaceae (57), Caryophylaceae (54), Labiatae (48), Apiaceae (38), Brassicaceae (34) and Rosaceae with 32 species, respectively. Astragalus with 41, Cousinia with 20, Nepeta with 19, Silene with 18, Oxytropis and Potentilla each with 16 species are the largest alpine genera in Iran. The hemicryptophytic life form dominates in alpine zone with 73 % in Iran. The thorny cushion species are mostly dominate in the subalpine-zone. In spite of their dominancy in the alpine zone their absolute number of species with 41 species is not very high. The alpine flora of Iran consisted of 53% endemics and subendemics.

P0842. Historical and contemporary processes of *Gentiana ligustica*: toward evolutionary conservation at a regional hotspot scale.

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Gentiana ligustica is a submountain neoendemic species located in the Maritime and Ligurian regional hotspot (France and Italy). A phylogeographic analysis was performed using AFLPs in 270 individuals and 28 populations. A spatial genetic structure appears in congruence with the location of the five presumed glacial microrefugia distributed along valleys. High mountains on either side of valleys correspond to contact areas between groups and constitute the major barriers to gene flows. Among the five groups of populations identified, the central group exhibit the highest Shannon diversity. The high levels of AFLP variation observed among populations and among groups, together with the lower