

distinct from other lineages. Our morphological cladistic analysis supports the monophyly of *Liquidambar* with *Altingia* as its sister. The discordance between the morphological and the molecular data sets may be due to different rates of morphological evolution as well as convergence in these taxa.

P0794. Floristic changes on the Kem-Ludy islands (Russian White Sea, 1962-2004)

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The lists of flora of Kem-Ludy archipelago (Russian White Sea, near Arctic Circle) produced in years 1962 and 2001-2004 were investigated by different methods of data analysis. The full species list contains 284 species. 27 islands were studied, four new islands were appeared due to the tectonic events. Main dynamic features of islands and island group's floras and of species areas were clarified. Most important factors are island square and openness (accessibility for winds). The close vicinity with species-rich island does not prevent the species disappearance. The presence of forest, ecotops formed by crowberry (*Empetrum* spp.) and *Sphagnum*-bogs are most stabilizing factors whereas riches of rocks play negative role in the floristic stability. Marine birds are most important biological factor for island flora maintenance. Many of effects depend on shoaling of channels between islands and probably on improvement of local climate.

P0795. Origin of the genus *Allium*: place and time.

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The genus *Allium* is currently regarded as a member of the Alliaceae, subfamily *Allioideae*. *Allium* is distributed almost exclusively in the northern hemisphere and 88 % of the 780 species are distributed in Eurasia.

Genus *Allium* is subdivided into 13 subgenera. Most of the subgenera show one center of diversity respectively while subgenus *Amerallium* is distributed in all three continents i.e., North America, Europe and Asia. Current molecular studies (ITS and cpDNA) support the monophyletic origin of the genus *Allium* and it is subdivided into two major clades i.e., subgenera *Nectaroscordum* (x=9), *Amerallium* (x=7) along with monotypic section *Microscordum* (x=8) versus remaining subgenera of genus *Allium* (all x=8). The phylogenetic position of subgenus *Amerallium* as sister to Mediterranean subgenus *Nectaroscordum* and east Asian section *Microscordum* provides evidence for an Old World (x=7,8,9,10) origin of the genus *Allium*.

One conspicuous feature of the ITS data is the unusually large intrageneric genetic distances within *Allium*. These molecular differences together with the distribution area of *Allium* indicate an origin of the genus early in the Tertiary.

P0796. Spatial structure of a willow hybrid complex in European rivers

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The tree forming willow species, *Salix alba* L. (white willow), *Salix fragilis* L. (crack willow) and their hybrid *Salix x rubens* are widely distributed tetraploids across Europe in riparian zones and wetlands. 2000 individual willow trees distributed along major rivers or their tributaries across Europe were analysed with codominant introns of consensus gene families and with dominant ISSRs. The co-dominant markers were ideal markers to identify these *Salix* species, their hybrid and the introgressed hybrids. Much of the ISSR variation is kept within populations of *Salix alba*. Significant relationships between the individual *S. alba* phenotypes based on ISSR markers and their position along a N-S and a W-E gradient in the Western plains and Central Highlands ecoregions were found. For *S. fragilis* a significant relationship was found along a W-E gradient in the Western and Central Highlands ecoregions. Introns and ISSRs could give useful information at different geographical levels.

P0797. The pteridophytic diversity in Yunnan, China

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This paper deals with the diversity of the pteridophytes of Yunnan, China. Yunnan ranks first among China in its number of pteridophytic taxa. There are 60 families, 198 genera and 1500 species of pteridophytes making up 95.2 percent, 85.7 percent and 57.7 percent of the Chinese totals respectively according to Ching's system. There are also many taxa unique to Yunnan/China, *Phlegmariurus yunnanensis*, *Archangiopteris bipinnata* Ching, *Angiopteris esculenta* Ching, *Angiopteris sparsisora* Ching and *Gymnosphaera austro-yunnanensis* (S. G. Lu) S. G. Lu et C. X. Li are examples. While *Christensenia assamica* (Griff.) Ching and *Platyserium wallichii* Hook. belong to families are only occurrence in Yunnan around China. Yunnan has the richest taxa of pteridophytes in China and this area is one of the richest taxa of pteridophytes in the world. The richest taxa of pteridophytes in Yunnan is a combination of long geological history, complicated geographical environment and sustained biotic evolution. Yunnan's pteridoflora vary from tropical to temperate, in the area exist multiple climate types, it is actually an epitome of Eurasia continent's pteridoflora.

P0798. The chloroplast PCR primer database: tools for comprehensive phylogeographic analysis of a whole genome.

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A data base is presented which collects published PCR primer information for chloroplast DNA (<http://bfw.ac.at/200/1859.html>). Chloroplast genes evolve slowly, and many PCR primers have been designed to work across species ('universal primers', Taberlet et al. 1991). Amplicons are either the genes themselves, typically in studies of sequence variation in higher-order phylogeny, or spacers, introns, and intergenic regions in studies of phylogeographic patterns within and among species. The current list of 'generic' primers consists of more than 350 sequences. Our experience shows that many of these primers can be combined into pairs quite freely if 'generic' PCR conditions ('two-step PCR') are applied. With this set of primers it becomes possible to study the whole chloroplast genome for variation in a comprehensive way for many taxa. Efficient methods for analysing polymorphisms are necessary - traditional sequencing may not be an option in large-scale studies. Alternatives are simple PCR-RFLP in gels, or denaturing high-performance liquid chromatography for simultaneous detection and analysis of polymorphisms. Examples will be given.

P0799. Molecular defined migration pathways of rare species of the genera *Lathyrus* and *Oxytropis* (Fabaceae)

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Studies of a large nrDNA data set of the cloned and sequenced ITS region and 5' ETS revealed a detailed insight into intraspecific and intraindividual genetic variability of the morphologically and genetically conserved *Oxytropis pilosa* in contrast to *Lathyrus pannonicus* originally sharing the same Eurasian steppe habitat. The evaluation of the molecular data allowed a defined reconstruction of inter- and postglacial migration patterns. During the westward migration of populations of *L. pannonicus* obviously an ecological shift from xerothermic to wet habitats occurred - inferred by phytosociologic classifications. Numerous mutations characteristic for populations within the disjunct relict habitats could be detected; they are linked to habitat preference and support the assumption that the ecological shift is the driving force for biodiversity. The presently unclear classification of some *L. pannonicus* subspecies due to diffuse morphologic characters and ecologically undefined or intermediate habitat use can now be explained by interpreting such populations as relicts of a transition zone and as a result of repeatedly endured (re-) colonisation.

P0800. Phylogeny and phylogeography of myrmecophytic Macaranga species from the Malaysian region

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Twenty-nine of the about 300 species of the palaeotropical tree genus *Macaranga* (Euphorbiaceae) are obligate ant-plants, or myrmecophytes. We used ITS sequencing and AFLP profiling to