Illustrations:
Wagner, H. (1871): Illustrierte Deutsche Flora
Primula elatior (L.) Hill
Tragopogon pratensis L.
Heracleum sphondylium L.

Tadeáš Hájek z Hájku (1562): Matthioli, Herbář jinak bylinář velmi užitečný
Anemone sylvestris L.
Pulsatilla lutea L.

Saxifraga oppositifolia L.

Cover illustration: Juncus conglomeratus L.

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IOPB NEWSLETTER NO. 33

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A note from the president

Three years have passed since the 1998 symposium in Amsterdam, and we are looking forward to the 2001 Symposium which will be held in Albuquerque, New Mexico, USA, in conjunction with the annual meetings of the Botanical Society of America (BSA), American Bryological and Lichenological Society (ABLS), American Fern Society (AFS), and American Society of Plant Taxonomists (ASPT) at Botany 2001, August 12-16, 2001, Albuquerque Convention Center. You can reach information on the Botany 2001 meetings via our web page. We are very grateful to Scott D. Russell for designing and maintaining this very attractive web page of IOPB at http://www.iopb.org/. This page gets a surprisingly large number of hits, and is a very valuable new way to make us known world-wide. If you have not done so already, do have a look at it. Of course, our web page offers a chance to post information in addition to that published in the Newsletter. If you have some item of interest to the membership of IOPB, send it on to me and I shall see that it gets published or posted.

As usual, in addition to the Chromosome Data, the newsletter features ongoing projects from several labs in the "Profiles" section. This section and the "Research Notes" describe work in progress, ideas that are being pursued, and methods that are applied. It is supposed to be an international forum for the exchange of information of interest to plant biosystematists. This time, a wide range of topics is covered by contributions from 5 countries in 3 continents. We should aim at contributions from all six continents in each Newsletter.

Two of the profiles introduce the work of two of the four new candidates for positions on the IOPB council. At the business meeting in Albuquerque, council and executive for the period from 2001 to 2004 will be nominated. Together with the approval of the 2004 meeting site, we shall nominate the president elect and the executive. A ballot for the council is included. Please send your vote (check ten of the twelve candidates) to me as soon as possible. I want to thank the four new candidates for council positions, who have been nominated and agreed to be candidates. Two members of the council, Liv Borgen and Shoichi Kawano, are not standing for election again. We shall acknowledge their contributions to IOPB at the meeting. Both Liv Borgen and Shoichi Kawano have worked hard for IOPB. I had to miss the legendary 1989 IOPB symposium organized by Shoichi Kawano in Kyoto but was lucky enough to be a guest of Dr. Kawano's at a later date. I understand why the symposium, both the scientific and the social parts, were fondly remembered by the participants for years afterwards. I attended the 1995 IOPB symposium organized by Bengt Jonsell and Liv Borgen in Tromsö, Norway, a completely different setting from Kyoto, but with just as many fond memories of interesting science, a lovely setting with a remarkable flora, and long, light nordic summer nights. In Tromsö, Bengt Jonsell and Liv Borgen took over for three years as editors of the Newsletter from Krystyna Urbanska who set the standards by which every president and newsletter editor of IOPB will forever be measured. That they continued the tradition in style must be counted as a major accomplishment. Both Liv Borgen and Shoichi Kawano made IOPB history, and we hope they will continue their active association with IOPB.

Konrad Bachmann
Program for the symposium in Albuquerque, which forms part of „Botany 2001“

MONDAY AFTERNOON, 13 AUGUST

1:30-4:45 PM SESSION

SYMPOSIUM: IOPB - Origin and biology of desert flora

Organized by: TIMOTHY K. LOWREY, Department of Biology, University of New Mexico, Albuquerque, NM 87131. Tele: (505)277-2604 E-mail: tlowrey@unm.edu

Presiding: TIMOTHY K. LOWREY, University of New Mexico, Albuquerque.

1:30 CROZIER, BONNIE* and ROBERT K. JANSEN. University of Texas, Austin. Historical relationships in the American desert plant family Cactaceae.


2:30 LANDRUM, VIC. Washburn University, Topeka, KS. Four families and 40 million years of evolution and adaptation to xeric environments.

3:00 BREAK

3:15 MULDAVIN, ESTEBAN H. University of New Mexico, Albuquerque. Some floristic characteristics of the northern Chihuahuan Desert: a search for its northern boundary.

3:45 VERBOOM, G. ANTHONY*, WILLIAM D. STOCK, and H. PETER LINDER. University of Cape Town, Rondebosch, South Africa. Phylogenetics of the Cape grass genus Ehrharta (Ehrharteae): evidence for diversification in a summer-arid system.

4:15 DISCUSSION.

5:30-7 PM RECEPTION/MIXER: IOPB (Ticketed event)

Presiding: KONRAD BACHMANN, Institut für Pflanzengenetik und Kulturpflanzenforschung, IPK Gatersleben, D-06466 Gatersleben, Germany
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WEDNESDAY AFTERNOON, 15 AUGUST

4:30-5:45 PM BUSINESS MEETING: IOPB

Presiding: KONRAD BACHMANN, Gatersleben, Germany.
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Profiles

Plant Molecular Systematics lab at the Institute for Systematic Botany and Botanical Garden, University of Zürich, Switzerland:

Elena Conti’s research group

As a newly appointed professor at the University of Zürich (starting date: March 1, 2000), I would like to share with the IOPB community the main research projects that I am already actively engaged in (see points 1, 2, and 3 below) or that I am planning to continue in my lab (see point 4 below):

1) PHYLOGENY AND EVOLUTION OF BREEDING SYSTEMS IN Primula L.

Collaborators: John Richards (Prof., University of Newcastle); Sylvia Kelso (Prof., Colorado College); Austin Mast (Dr., Post-doctoral researcher; University of Zürich); Sky Feller (project assistant, University of Zürich); Daniela Lang (Lab assistant, University of Zürich).

My research on Primula strives to integrate a phylogenetic approach with the study of evolutionary ecological processes. The starting questions in this research included: 1) What are the evolutionary relationships between homostyly and distyly in Primula, and how many origins can we infer for each breeding system? 2) What are the evolutionary relationships between breeding system, ploidy level, and biogeography in sect. Aleuritopsis. Specifically, do the phylogenetic trees identify a Eurasian and a North American clade, thus lending support to proposed hypotheses of repeated biogeographic patterns shaped by recent climate changes (i.e., Pleistocene glaciations)? 3) Do molecular phylogenies support the detailed sets of species relationships that have been proposed on the basis of morphological, cytological, and biogeographic considerations? 4) What are the taxonomic implications of the phylogenetic results? 5) How does floral development of homostyloid flowers compare with floral development of heterostyloid flowers?

These questions represent the starting point for a long-term project aimed at elucidating the phylogeny and evolution of breeding systems in the entire genus Primula. By enabling us to shed light on the order of character assembly pertaining to the morphological and physiological components of distyly, a detailed phylogeny of the genus Primula will ultimately allow us to discriminate between competing models for the evolution of this reproductive syndrome. This research will also provide the necessary phylogenetic framework for undertaking future microevolutionary studies on distyloid/homostyloid sister species of Primula and for elucidating the molecular evolution of incompatibility genes in Primula, thus building on similar studies in other groups of flowering plants.

Currently, over 150 species (30 of 37 sections) of Primula are represented in our collection of leaf tissue, flowers, seeds, and live plants. We have sequenced the nuclear ribosomal ITS DNA from over 50 Primula species [see Conti et al., 2000, 2000 (abstract), and 1999 (abstract)] and the trnL and rpl16 introns of the chloroplast DNA from 91 Primula species [see Mast et al., 2001 (submitted), and 2001 (abstract)]. Phylogenetic analysis of these regions has provided an important evolutionary framework for our study of the group’s ecological and biogeographical diversification. It has also allowed us to reassess the utility of characters historically deemed to be of taxonomic importance in the genus, including hetero-/homostyly, chromosome base number, leaf vernation, and pollen shape. Currently, we are sampling single-low-copy nuclear regions to provide a complementary phylogenetic hypothesis for members of the genus. Once this is completed, we plan to make broad generic and subgeneric realignments in Primula, Dionysia, Dodecatheon, Cortusa, and Sredinskya.
Key words: Primula, distyly, homostyly, breeding systems, molecular phylogeny, nuclear DNA, chloroplast DNA, floral development, character evolution, biogeography, ploidy level, Pleistocene glaciations.

2) PHYLOGENY OF CRYPTERONIACEAE and RELATED GONDWANAN FAMILIES: IMPLICATIONS FOR MORPHOLOGY AND BIOGEOGRAPHY.

Collaborators: David Baum (Prof., Harvard University); Ken Sytsma (Prof., University of Wisconsin); Juerg Schoenenberger (Dr., Postdoctoral researcher, University of Zürich); Daniela Lang (Lab assistant, University of Zürich).

The Asian family Crypteroniaceae (Sri Lanka and south-east Asia) shares with Myrtales the two wood anatomical synapomorphies that define the order. However, as the numerous taxonomic changes of the last 100 years suggest, the circumscription and evolutionary affinities of the family are less well defined. The main goals of this research project are to elucidate the circumscription and detailed phylogenetic relationships of Crypteroniaceae and related Gondwanan families by using evidence from DNA sequences of the chloroplast and nuclear genomes. The phylogenetic tree obtained from analyses of rbcL sequences strongly supported the sister relationship between Crypteroniaceae and a clade comprising the monotypic south American family Alzateaceae plus three small families endemic to southern Africa (Oliniaceae, Penaeaceae, and Rhynchocalyceae) [see Conti et al., 1999 (abstract)]. Further analyses are focusing on faster evolving cpDNA regions and nuclear genes [see Schoenenberger and Conti, 2001 (abstract)]. The resulting phylogenies will be used as a framework for re-evaluating the evolution of floral development and biogeographic history in this clade. The working hypothesis is that India served as a raft for carrying the stem lineage of Crypteroniaceae to Asia. We intend to expand testing the hypothesis of India as Noah's Ark to other plant groups.

Key words: phylogeny, biogeography, vicariance, character evolution, nuclear DNA, chloroplast DNA, India.

3) PHYLOGENETIC RELATIONSHIPS OF THE RARE ALASKAN PLANT Oxytropis arctica var. barnebyana

Collaborators: Kent Schwaegerle (Prof., University of Alaska); Jane Jorgensen (Master's student, University of Alaska)

We examined the systematic relationships of the rare Alaskan plant, Oxytropis arctica var. barnebyana to other closely related Beringian species with molecular tools. Both nuclear sequences and population level random markers were employed to resolve phylogenetic relationships among these morphologically and taxonomically confusing taxa. A pilot study was conducted by amplifying the nuclear Internal Transcribed Spacer (ITS) region and the External Transcribed Spacer (ETS) region in order to reconstruct phylogenetic relationships among Alaskan plants in the Oxytropis genus. Relationships among O. arctica and O. campestris populations were poorly resolved for both nuclear regions. Most taxa formed a polytomy indicating highly unresolved phylogenetic relationships. Because of the low phylogenetic signal of ITS and ETS, Randomly Amplified Polymorphic DNA (RAPD) markers were used to further determine congeneric relationships. Results of this population-level marker also point towards little genetic differentiation among these arctic populations. Lack of distinct morphological characters separating the taxa corroborates the molecular results. The conserved ITS and ETS regions, along with little variation in RAPD patterns among these arctic Oxytropes suggest recent isolation of these populations. Results of this research contribute to the understanding of the current taxonomy of a rare Alaskan plant. This study represents an integration of molecular biological and conservation genetic approaches to the problem of management of rare plants in Alaskan plant (see Jorgensen et al., 2001, in prep.).
Key words: rare plants, conservation, molecular phylogeny, RAPDs, ITS, ETS, Alaska.

4) PHYLOGENETIC RELATIONSHIPS OF THE RARE PLANT SPECIES Saxifraga florulenta Moretti (Saxifragaceae)

Collaborators: Douglas Soltis (Prof., Washington State University)

The rare plant species Saxifraga florulenta Moretti, an arctotertiary relict which earned such distinctive names as "Ancient King" and "Glory of the Maritime Alps", is restricted to a small area (less than 100 km²) of the Southwestern Alps. The low numbers of populations and individuals per population justified the inclusion of this endemic species in the IUCN Red Data book. S. florulenta is characterized by monocarpic (semelparous) reproductive behaviour, whereby each individual remains in the vegetative stage for several years, then it blooms and dies. The distinctive life history of S. florulenta, coupled with its occurrence at very high elevations and human encroachment resulting from tourism, contributes to the challenge of establishing sound conservation plans for this species. Global warming trends further threaten the survival of S. florulenta, which already occurs on mountains summits, between 2500 and 3500 m. The elucidation of phylogenetic relationships of rare species is essential for the establishment of long-term conservation plans. Parsimony and maximum likelihood analyses of the nuclear ribosomal ITS region of S. florulenta and allied species reveal that S. florulenta belongs to sect. Porphyrodes, rather than sect. Ligulatae, as proposed by previous taxonomic studies. Furthermore, our analyses suggest that monocarpic evolved independently three times in the European saxifrages, possibly in response to dryer climatic conditions associated with glacial peaks of the Pleistocene glaciations. This information provides the essential phylogenetic framework for comparative studies of floral development and for AFLP-based studies aimed at comparing genetic variation within and among populations of S. florulenta and closely related species. (see Conti et al., 1999, and Conti, in prep.)

Key words: rare plants, conservation, management, alpine biogeography, Pleistocene glaciations, semelparity, monocarp, molecular phylogeny.

FACILITIES: The Plant Molecular Systematics lab is endowed with cutting-edge equipment, for example a Perkin Elmer ABI 377 automated Sequencer, 4 PCR machines (including a thermal gradient apparatus), several gel electrophoresis apparatuses, a new gel-imaging system, a number of Macintosh and PC computers, the most up-to-date software for DNA sequence and phylogenetic analysis, and a soon-to-be purchased flow cytometer. This outstanding facility is at the service of all research groups in our Institute of Systematic Botany, which include: 1) The biogeography and monocot evolution group, led by Prof. Peter Linder, the new Institute's director; 2) The floral development and evolution group, led by Prof. Peter Endress; 3) The microevolution and fern biosystematics group, led by Professor Jakob Schneller; 4) The plant structure and morphology group, led by Prof. Rolf Rutishauser; 5) The Algae taxonomy and evolution group, led by Prof. Hans Ruedi-Preising; 6) The mosses taxonomy and evolution group, led by Dr. Edi Urmi. Furthermore, researchers in our Institute can count on the professional skills of highly trained gardeners in our outstanding garden and greenhouse facilities. A herbarium with over 3.5 million specimens and a library with the most important books and journals in plant sciences complete the remarkable facilities at the service of researchers and students from all over the world. Check out the home page of our Institute at http://www.unizh.ch/bguz/Pages/Home.html

RECENT PUBLICATIONS:


In preparation:


Conti, E., Phylogenetic relationships of the rare plant Saxifraga florulenta Mottriti.

QUESTIONS?

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Pulsatilla lutea
Biosystematics and molecular phylogenetics. New approaches to genome evolution in polyploids.

J. Chris Pires

Polyploidy is a major evolutionary force in plants. Because elucidating the causes and consequences of polyploid evolution is central to understanding the diversification of many plants, the study of polyploidy has recently exploded. My primary research interest in polyploid plants is focused on the integration of biosystematic and phylogenetic studies. Integrating biosystematics (the experimental study of biological aspects of organismal variation, diversity, and diversification) and phylogenetics (the study of genealogical relationships of organisms) has been a promising avenue for evolutionary and ecological investigations because phylogenies provide a meaningful historical context for biosystematic comparisons. However, biosystematic data (e.g., chromosome number) is often merely mapped onto given phylogenies, which effectively privileges phylogenetics over biosystematics. My long term goal is to provide a more general approach to bridge biosystematics and phylogenetics by using molecular cytogenetic techniques and DNA microarrays.

Molecular Phylogenetics of Themidaceae and related illioid monocots. Over the past few years I studied plant systematics and evolutionary biology at the University of Wisconsin-Madison under the direction of Ken Sytsma. My PhD thesis dealt with the 12 genera and 61 species of the resurrected plant family Themidaceae. These genera, formerly recognized as tribe Brodiaeae in the Alliaceae, have been previously divided into two complexes: the *Milla* complex centered in Mexico and the the *Brodiaea* complex centered in the western Unites States. Brodiaea s.l. has been a classic example of evolutionary radiation in floral diversity, habitat specialization, and chromosome number. However, other genera of the *Brodiaea* complex have been little studied. While writing treatments for most of these genera as part of the Flora of North America project, I also sequenced three regions of the chloroplast genome (*ndhF, trnL-F, and rpl16*) and internal transcribed spacer regions of nuclear ribosomal RNA (ITS). I found that the *Milla* complex was embedded in the *Brodiaea* complex, and that morphological characters (e.g., presence of a perianth tube) that have been used to circumscribe the genera have evolved independently at least twice. In addition, common biogeographical distribution patterns (e.g., *Brodiaea* and *Triteleia* having centers of diversity in northern California and the Pacific Northwest) appear to be the result of separate evolutionary radiations. I have continued doing phylogenetic work at the Royal Botanic Gardens, Kew, in collaboration with Mark Chase and others on a multiple gene tree of the monocots.

Molecular Cytogenetics and Chromosome Evolution in Allotetraploid Tragopogon (Asteraceae). Currently, I am an NSF-NATO Postdoctoral Fellow studying chromosome evolution at the Royal Botanic Gardens, Kew, under the direction of Michael Bennett and Ilia Leitch. I am working on *Tragopogon* in collaboration with Douglas and Pamela Soltis who are visiting scientists on sabbatical leave at Kew. Previous molecular studies indicate that *T. mirus* may have evolved 12 times and *T. miscellus* may have formed 20 times within the past 70 years. We are evaluating the two allotetraploids, *T. mirus* and *T. miscellus*, relative to their three diploid progenitors using molecular cytogenetic and phylogenetic approaches. Fluorescent in situ hybridization (FISH) is being used to identify several loci on individual chromosomes to detect chromosomal evolution. Probes for the 18S-5.8S-26S array, 5S array, and other repeats are being evaluated in diploids and recurrent polyploids for number of loci and activation. Nucleolar dominance is a common feature in many allotetraploids, presumably only when the units have not homogenized and remain clearly related to the diploid progenitors. Thus, the rDNA unit structure data predicts that nucleolar dominance may be a feature of *Tragopogon* allotetraploids. Also, phylogenetic studies of nrDNA show perfect additivity (no interlocus homogenization) in that all cloned ITS
sequences from *Tragopogon* polyploids give sequences from the progenitor diploids. However, Southern hybridization to the diploids reveals that all units of the 18S units of an array are similar, yet there are clearly population differences amongst the diploids, showing that intralocus gene conversion (homogenizing the entire array) must be occurring. Integrating molecular cytogenetics and phylogenetics is proving a powerful approach in assessing the complex histories of these dynamic polyploid genomes.

**DNA Microarrays: Structural and Functional Genomics of Brassica.** Over the next two years I will be working with Tom Osborn at the University of Wisconsin as a postdoctoral researcher and program manager on a multi-institutional NSF Plant Genome Grant. The purpose of the project is to assess separate lineages of resynthesized polyploids and hybrids of *Arabidopsis, Brassica*, and corn using genetic mapping techniques and DNA Microarrays.

Ultimately, I hope to integrate biosystematics and phylogenetics studies more thoroughly.

Molecular cytogenetics in particular is a promising tool in this integration. Although changes in chromosome number have been mapped onto phylogenies to determine the direction of change, few studies have been done to investigate the kinds of chromosomal change (e.g., translocations) that can serve as isolating mechanisms in speciation processes. Thus, FISH-generated chromosomal characters may be phylogenetically informative in themselves.

FISH can be combined with southern hybridization data or comparative genetic mapping data to help determine the number and locations of individual loci. Significantly, this enables one to demonstrate orthology of low copy nuclear sequences before phylogenetic analyses, understand concerted evolution in rDNA and its implications for ITS-based phylogenies, and confront the problems of incongruent phylogenies inherent in polyploid organisms.

**PUBLICATIONS:**


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Molecular phylogeography of the European Alps at the University of Zürich, Switzerland

Ivana Stehlik

There is a long-lasting debate about the fate of the mountain flora of the European Alps during the Quaternary ice ages. Two opposing views about glacial survival of alpine plants have been proposed: the nunatak and the tabula rasa hypotheses. According to the former, species survived in situ on small 'islands in a sea of ice' (nunataks), whereas the tabula rasa (Latin for 'empty table') hypothesis assumes that species had to colonize vacant Alpine regions from peripheral refugia after the retreat of the glaciers. There was a first flush of investigations in this field of alpine biogeography at the beginning of the 20th century. These works mainly relied on distribution patterns of alpine plants. Locations of glacial survival on nunataks, peripheral refugia and corresponding migration routes into the Central Alps were documented as precisely as possible at that time (Stehlik 2000). In combination with molecular methods, this background offers fascinating options to re-evaluate the questions asked by the pioneers of alpine biogeographical research and to address them with a modern approach. Another reason for the recent popularity of alpine phylogeography is that the Alps offer an especially suitable stage for investigations of evolutionary mechanisms at the species level, because their geological and climatic history is well known and because their spatial dimensions are relatively limited. This interest in alpine (and arctic) plants was reflected by the 1995 symposium of the IOPB in Tromsø, Norway (Borgen and Jonsell 1997), and only recently again by the "First Joint Botanical Mountain Phylogeography Meeting", June 1-3, 2001, at the Institute of Systematic Botany of the University of Zürich in Switzerland (Stehlik, Tribsch, and Schönswetter 2001). The aim of my present research which I conduct in collaboration with J. Jakob Schneller (Systematic Botany, Zürich), Konrad Bachmann and Frank Blattner (Institute of Plant Genetics and Crop Plant Research, IPK, Gatersleben, Germany), and Rolf Holderegger (Swiss Federal Research Institute, WSL, Birmensdorf, Switzerland), is to test explicit phylogeographic hypotheses on plant species of the European Alps with distinctly different ecological demands and distribution patterns (Stehlik et al. 2000). Four species are being investigated using molecular techniques (AFLP, PCR-RFLP of cpDNA, Southern hybridization, RAPDs) for which clear biogeographic hypotheses of glacial survival were given in the literature. (1) In situ glacial survival on nunataks of the Central Alps in the high-alpine Eririchium nanum (Boraginaceae); (2) Pleistocene extinction within the Alps and postglacial recolonization from southern refugia of the low-alpine Erinus alpinus (Scrophulariaceae), and (3) immigration from eastern refugia or eastern pre-alpine nunataks for the snowbed species Rumex nivalis (Polygonaceae; work in progress). (4) Saxifraga oppositifolia (Saxifragaceae) has been chosen to investigate whether it is possible to deduce the biogeographic history of a widespread, common alpine species exhibiting no particular geographic characteristic (as opposed to the former three species) that would suggest any specific, likely hypothesis on its dispersal history.

By investigating 20 populations of the Alpine endemic Eririchium nanum of potential nunatak and peripheral refugial regions with AFLPs, considerable genetic differences between populations from the Central Alps and populations from peripheral refugia were detected (Stehlik, Schneller, and Bachmann 2001). Hence, the latter probably did not serve as a source for the recolonization of the Central Alps after the ice ages. Within the Central Alps, where glaciation was most intense, three genetically distinct regional groups of populations could be distinguished. This result pointed to survival in at least three independent nunatak areas. However, a considerable level of recent or historical random gene flow among the populations prevented the identification of the exact mountain ranges of in situ survival of E. nanum. The investigation of chloroplast DNA haplotypes from a larger sample of populations covering the entire range of the species promises to provide additional information (Stehlik et al., in preparation).
The species chosen to test the tabula rasa hypothesis, the mainly sub-alpine Erinus alpinus, is also known from suggested nunataks in the northern Prealps, where it might have survived glaciation. Nevertheless, postglacial re-immigration from southern refugia is much more likely. PCR-RFLP of its cpDNA revealed no variation in the entire sample set, whereas AFLPs suggest a very peculiar pattern of a massive wave of recolonization from outside the Alps that skirted a northern pre-alpine nunatak region. Interestingly, there is no convincing evidence of gene flow between immigrant and nunatak derived plants (Stehlik, Schneller, and Bachmann, submitted).

As for the widespread Saxifraga oppositifolia, the results based on Southern hybridization of cpDNA and RAPD were not decisive. We only found a very low number of cpDNA haplotypes as compared to E. alpinus. This included two common, widely distributed ones and two very rare ones. Hence, some support for in situ nunatak survival was found, as the rare haplotypes occurred in these regions, where in situ survival was detected in E. nanum. On the other hand, no strong grouping of genotypes could be detected in the RAPD analysis in contrast to the AFLP results in E. nanum. Additionally, the result of no isolation by distance principally supported postglacial immigration of S. oppositifolia to the Alps. Therefore, it is a question of subjectively weighting the results in S. oppositifolia whether in situ glacial survival in the Alps is accepted or denied (Holderegger, Stehlik and Abbott, in preparation).

One of the most remarkable results of the above studies is the variety of specific biogeographic histories that have been found in the Alps, a situation apparently quite different from that in western North America. Apart from a general feature such as the genetic hot spot area in the Central Alps exemplified by E. nanum and S. oppositifolia, each species has its own distinct history. The differences in genetic structure may be influenced by various breeding systems, dispersal abilities, ecological amplitudes, or they may be historical accident.

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Genome analysis in mulberry (*Morus* sp.): DNA profiling of germplasm using molecular markers and development of mapping populations at the Central Sericultural Research and Training Institute (CSRandTI), Srirampura, Mysore, India

Modal Venkateswarlu

The success and efficiency of the varietal improvement programme depends on the selection of the right parents which carry desirable traits and rich genetic variability to give desirable recombinants. This assumes significance in mulberry, having rich diversity, but where little is known about its genetic basis. This makes it necessary to understand the genetic structure and relationships for their use in improvement programmes. Mulberry breeding efforts are severely restricted due to multiple problems. Mulberries are highly heterozygous due to outcrossing, there is virtually no information on their genetics and inheritance patterns, they are trees with a long generation cycle, and the absence of efficient selection strategies make conventional breeding difficult. Hence, the vast potential offered by DNA marker technology should be utilized to solve some of the above mentioned problems.

Mulberry is a hardy perennial tree, belonging to the Moraceae. Under suitable cultivation, it is grown as bush by repeated pruning. It is a fast growing plant, from which leaves are harvested several times a year. Mulberry in India is mainly propagated commercially through stem cuttings. From seed sowing to flowering it takes 2-3 years. Normally mulberry flowers in the months of January through April, but flowers can be induced at any time by mechanical injury like pruning. Mulberry is mostly dioecious; a few monoecious genotypes are also known. To support breeding programmes CSRandTI, Mysore is maintaining a germplasm stock of 450 genotypes which have been collected from different agro-ecological zones of India and abroad.

Mulberry breeding efforts are underway to develop varieties having various desirable traits like: a) quick sprouting and good rooting ability with a high root proliferation rate to suit the climatic conditions; b) higher leaf yield per unit area, high moisture percentage and long moisture retention capability of leaves; c) fast growth with high photosynthetic efficiency, good quality with high carbohydrates in young leaves and more proteins in mature leaves; d) tolerance to biotic and abiotic stresses; e) thick succulent leaves. To achieve these goals, various conventional and non-conventional approaches are pursued at Central Silk Board, Bangalore under its constituent Institutions.

Objectives:

1. To characterize the overall genetic variation in the mulberry germplasm using DNA markers.
2. To develop specific molecular descriptors/DNA fingerprints of selected elite mulberry genotypes/varieties, for their individualization and use as molecular ID in the context of IPR/patent protection/plant breeder rights.
3. To develop mapping populations of mulberry using elite parental materials, as a first step towards development of molecular linkage map of mulberry.

For molecular characterization, the DNA samples from 50 selected genotypes will be analyzed using three types of DNA markers which exploit different types of variation in the genomic DNA and thus are expected to provide a better evaluation of the whole genome. The types of DNA markers that are to be used are AFLP, RAPD, and ISSR markers. DNA has been extracted and purified, and RAPD analysis has been carried out, which is showing high a level of polymorphism.

For developing mapping populations, suitable plant materials having contrasting characters will be identified from among the elite varieties such as V1, Mysore Local, Bilidevalaya, S36, Sujanpur-5 etc. The selected genotypes will be used to generate
F1 hybrid populations that will make the base material for developing a molecular linkage map. Progress: Mysore Local and V1 genotypes where a majority of contrasting traits are available were selected for crossing (pseudo test cross). The cross has been made and 15000 seeds were obtained, sown in nursery beds and about 10,000 seedlings are growing. Under the Bulked Segregant Analysis (BSA) method two contrasting traits were selected viz. leaf shape and size (Mysore Local x V1; Bilidevalaya x V1) and rooting (S36 x V1), approximately 10,000 seeds sown and 6000 F1 seedlings were developed. (Funded by Department of Biotechnology, New Delhi and in collaboration with Centre for Cellular and Molecular Biology, Hyderabad)

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My laboratory is a research unit composed of a professor (myself), an associate professor (entomologist), two assistant professors (ornithologist and mammalogist), 16 graduate students, and 6 post docs. I believe our unit is unique in that we are trying to integrate evolutionary studies of sexual systems both in plants and in animals. My "botanical" view on animals successfully contributed to our recent findings on maternal control of sex ratio in a frog (1) and female control of paternity in feral cats (2). These are zoological versions of labile sexuality and inbreeding avoidance commonly found in plants. We are also enjoying interactions of botanists and entomologists in elucidating pollinator behaviours on flowers (3, 4). One of our key ideas is that memory limitation of pollinators enhances inter-plant movements of pollinators. A simple model based on this idea could explain surprisingly well how long a bumble bee stays on a plant with a particular number of flowers. We are also interested in the evolution of nocturnal flowering (5, 6). We are now studying introgressive hybridization of nocturnal and diurnal species of *Hemerocallis*, and also examining genetic basis of flowering time, flower color, floral odors and other traits associated with pollination syndromes of these two species by studying the genetic segregation of these characters relative to that of molecular markers in appropriate hybrids. Another ongoing project is exclusively on a plant, focusing on cytoplasmic male sterility in wild radish. Using PCR primers designed for a mitochondrial MS gene and a nuclear restorer gene, we are tracing population dynamics in field populations under the well-known intergenomic conflict.

While I am supervising graduate students working on the above projects, I myself am working on the evolution of agamospermy in *Eupatorium* and *Stevia* (Asteraceae, Eupatorieae) in collaboration with Dr. Watanabe (Kobe University), Dr. Soejima (Osaka Prefecture University) and others.
**Eupatorium** s. str. consists of 22 East Asian, 23 eastern North American and a single European species, and agamospermous polyploids are common in East Asia and North America (7). The evolutionary history of the genus is inferred from sequence data of the nrDNA ITS region and cpDNA RFLP. The genus originated in North America and then migrated to East Asia and Europe (8). Among East Asian species, *Eupatorium chinense* s. lat. includes sexual and agamospermous populations, and the incidence of geminivirus infection is much higher in agamospermous populations (9). Geminivirus infection reduces host viability through destruction of photosynthetic properties (10) and causes epidemics and rapid local extinction of agamospermous populations (11). Geminiviruses isolated from *Eupatorium* leaves are genetically highly diverged (12) and amino acid replacements in host-range determinant genes are more frequent in sexual host populations than in agamospermous populations (13). These findings support the parasite "Red Queen model" for the evolution of sex. To further test this model, we are now comparing molecular evolution of NBS-LRR type R-genes (pathogen resistance genes) between sexual and agamospermous populations. We determined *Eupatorium* sequences of the 5' part of the R-gene homologues that show approximately 50% amino acid homology with previously known sequences of *Arabidopsis* and other plants. We are now trying to determine the 3' parts of the sequences that include the LRR region probably responsible for gene-for-gene relationships. Molecular biological evidence has suggested that specificities in R-genes often evolved through interlocus recombination. If interlocus recombination mainly occurs in meiosis, agamospermous populations would be inferior in their ability of evolving new specificities against rapidly evolving parasites. We think our *Eupatorium-geminivirus* system provides an excellent opportunity to test this idea.

Another project of mine concerns taxonomic, phylogenetic and evolutionary studies on Mexican *Stevia*. As a result of 6-year field expeditions, we recognized 99 species including 14 new ones (14). Among them, 42 species include agamospermous polyploid populations (15, 16). Usually agamospermous populations are more widespread and sexual populations are restricted to narrow areas. In *Stevia origanoides*, however, both sexual and agamospermous populations are common. In some areas, two morphologically and ecologically distinct sexual forms are coexisting with agamospermous forms. It seems that the evolution of agamospermous forms caused disruptive selection on sexual populations and enhanced sympatric speciation. We are looking for molecular markers suitable to test this idea.

Finally, I have been responsible for editing Red Data Book of Japanese Vascular Plants. We developed extensive data base of current population size and recent decline trend for approximately 2,000 candidate taxa in collaboration with about 450 botanists. Using this data base, we carried out computer simulations to quantitatively assess extinction risk of these taxa (17). The Red Data Book was published last year by the Environment Agency of the Japanese Government. Unfortunately, 24% of our vascular flora had to be listed in the Red Data Book. We are now working to prepare hot spot maps using some hot spot coefficients developed for quantifying relative importance of an area based on the above data base.

**REFERENCES**


Research Note

*Arabidopsis thaliana* as a tool for biosystematics: studies in molecular phylogeography

Matthias H. Hoffmann and Heike Schmuths

Recently, several studies have been published that deal with the molecular diversity in relation to biogeography of the "model plant", *Arabidopsis thaliana* (L.) Heynh. Implicit to these studies is the hope to find a correlation between the geographical origin of the accessions and molecular data. Such correlations can be of three kinds: there can be an overall relationship between geographic and genetic distance, there may be an infraspecific cladistic pattern reflecting the history of dispersal, or there can be correlations between specific molecular markers and environmental parameters suggesting selection during local adaptation. Almost all of the studies to date finish with the conclusion that geographical correlations cannot be detected. Alonso-Blanco and Koornneef (2000) realize that in *Arabidopsis* research the term "ecotype" is improperly used because the *Arabidopsis* "ecotypes" simply denote different accessions. The term "ecotype" has a precise genetic connotation and should be used to designate subspecific taxa that are demonstrably adapted to their specific habitats (see e.g. Langlet 1971).

Investigations of ecotypic differentiation of populations have a long tradition in Biosystematics (Hagen, 1983). Considering the immense amount of genetic information and the general interest in *Arabidopsis thaliana*, a thorough biosystematic investigation seems appropriate. Many groups are working in this highly interesting field (see, for example, http://vanilla.ice.mpg.de/departments/Gen/ESF/esf.htm).

Here, we want to review briefly recent molecular biogeographical publications dealing with *A. thaliana*. A set of 19 recent publications addressing this topic have been selected and compared (tab. 1). These studies make use of widely varying numbers of accessions, ranging from 7 (Hanslingl et al. 1994, sequencing part of the paper) to 360 (Adam et al. 1999) out of currently more than 1100 accessions from the wild stored in the Nottingham Arabidopsis Stock Center (NASC, http://nasc.nott.ac.uk/). This poses the problem of comparability among the studies. There is apparently no single accession that has been used in all studies, unless the various Columbia "ecotypes" are treated as one. Similarly divers are the markers, methods and analytical tools applied in these surveys. It appears that virtually the whole spectrum of DNA markers and methods currently used in population genetics have been applied, e.g. AFLP, RFLP, CAPS, microsatellites, and DNA sequencing. The data are evaluated using phylogenetic methods and similarity methods such as cluster analysis and principal component analysis. The different methods of data analysis raise an additional problem of comparability between the studies. Nevertheless, even if comparability between these surveys is restricted, some common conclusion can be drawn.

**Genetic variability within "populations"**

Plants collected at a site are sometimes genetically more distantly related than plants from geographically more remote sites (e.g. Abbott and Gomes 1989, Purugganan and Suddith 1999). Such plants are separated by accessions from other sources in the diagrams or dendrograms. This picture may become more complicated in single-gene comparisons. For example, Lisse-1 and Lisse-2 from the Netherlands are quite similar in the nucleotide sequence of the *APETALA3* alleles, whereas the *PISTILLATA* alleles are different, separating the accessions in the cladogram (Purugganan and Suddith 1999). This pattern is not very surprising because of the high degree of inbreeding of *A. thaliana*, which may result in fixation of different genotypes at the same place after chance dispersal. Similarly complicated is the picture emerging from investigations of the transposable element *Tag1* content in different accessions (Frank et al. 1998). Plants from the same place may have a varying number of these
elements suggesting that either seeds from different provenances have been dispersed to this particular location and are now growing together, or the transposable elements have partially and recently been lost from parts of the population. These observations point to the fact that great caution is required when dealing with single-plant accessions from various sites.

**Correlation between genetic polymorphisms and geographical location**

Sharbel et al. (2000, AFLPs) found a significant correlation of genetic distance between accessions with increasing geographic distance but no "ecotype" phylogeny. Kuittinen et al. (1997) in a study of Scandinavian populations observed variability only in the southern populations. All other studies failed to find geographic correlations in their data. The published analyses, beside the limited comparability, point to another problem than a mere failure of finding geographical correlations. It can be observed that accessions have different positions in the dendrograms or cladograms. Two examples, one from nucleotide sequence analysis, and one from a microsatellite survey shall illustrate this problem. (1) Nucleotide sequences of the CHI gene (Kuittinen and Aguadé 2000) and the APETALA3 gene (Purugganan and Suddith 1999) show a different arrangement of the four shared accessions in the dendrograms. In the AP3 gene Ler (laboratory strain Landsberg erecta) and Cvi-0 (Cape Verde Islands) are very closely arranged on the same branch whereas the basal split in the diagram separates them in the CHI-tree. (2) Nine accessions and 8 out of total 27 microsatellite loci are shared in the studies of Innan et al. (1997) and Vander Zwan et al. (2000). The shared accessions have completely different positions in the various trees. For example, Kas-1 (Kashmir, India) and Es-0 (Espoo, Finland) are to be found on the same branch in the neighbour-joining tree (Innan et al. 1997), whereas in the unrooted tree of the absolute differences between alleles they appear on the most distant branches (Vander Zwan et al. 2000). Three of these nine accessions have also been used by Kuittinen and Aguadé (2000).

However, these accessions are too widely dispersed over the trees to draw conclusions about comparability between molecular methods addressing geographical variation of *A. thaliana*.

**Hypotheses concerning the absence of correlations between geography and genetic variation**

The most frequently stressed and favoured explanation for the absence of a correlation between geography and genetic variation is that the postglacial dispersal in Western Eurasia was chaotic and strongly influenced by man. However, the survey of Sharbel et al. (2000) indicates that there is a distinct historical component, i.e. traces of migration and isolation to be observed in the molecular data of *A. thaliana*. The northern, Central European accessions appear to be genetically less diverse than the accessions from the Iberian Peninsula and Asia. This decrease in diversity from their putative Pleistocene refugia northwards did, however, not explain the absence of geographic correlations in the other marker systems. Therefore, it may be argued that no appropriate markers have been applied to find the correlations. This would suggest that most of the previously used molecular markers are ecologically neutral and are not of ecological or biogeographical significance.

A close study of the distribution range of *A. thaliana* and climatic range modelling (M.H.H., in prep., see also Hoffmann 2000) revealed that the species occurs in a very wide ecological and climatic range. *Arabidopsis thaliana* covers a range of mean January temperatures from about -20°C to +16°C and from 4°C to 30°C in July, respectively. Due to its short life cycle, the species may also occupy hot and very summer-dry areas (e.g. the Mediterranean region, Middle Asia) as well as oceanic humid and cool regions (e.g. western Scandinavia). However, plants are not to be found in most parts of Siberia and Central Asia (e.g. Mongolia, Northern China). In spite of the short life cycle of *A. thaliana*, distinct limitations in the capability to cope with certain climatic conditions become apparent.
These observations raise a basic question: to which degree is this wide tolerance to different growth conditions a reflection of genetically different true "ecotypes", and to which is it the result of plastic responses of an "all purpose genotype" which could be expected for a plant that seems to be spreading as a result of anthropogenic dispersal. Much relevant variation in various traits reported by Alonso-Blanco and Koornneef (2000) has a genetic basis, either as mendelian or as quantitative loci. Does this play a significant role in local adaptation in nature? A biosystematic investigation of this aspect can make use of an unusually wide choice of resources. In turn, the results of this study will connect the laboratory analysis of *A. thaliana* with the survival of the plant in its natural environment.

REFERENCES


Kuittinen, H. & Aguadé, M. (2000): Nucleotide variation at the *CHALCONE ISOMERASE* locus in


Tab. 1. Selected publications addressing the problem of molecular biogeography of A. thaliana.

<table>
<thead>
<tr>
<th>Method and molecular marker</th>
<th>Authors</th>
<th>Number of accessions</th>
<th>Method of data analysis and presentation</th>
<th>Geographical correlation</th>
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<tr>
<td>Nucleotide sequences, AP3 and PI genes</td>
<td>Purugganan and Suddith 1999</td>
<td>16</td>
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<td>Nucleotide sequences, CAL gene</td>
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<td>Adam et al. 1999</td>
<td>360</td>
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IOPB Chromosome Data 17

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Please send contributions to Professor Stace at the above address (preferably by email with the contribution in WORD 98 or earlier, or in RTF, but failing that on a 3.5 inch microdisc with text in ASCII-file and a printed copy) using the exact layout of the present list. Neither proofs nor reprints will be made available, but the editor will acknowledge receipt of contributions and raise queries with authors if necessary.

Reports by:

Matthias Baltisberger and Anna-Barbara Utelli, Geobotanical Institute, Swiss Federal Institute of Technology, Zollikerstrasse 107, CH-8008 Zürich, Switzerland. Vouchers in ZJZT (voucher numbers of cultivated plants in brackets).


RANUNCULACEAE


Llano, Sierra Nevada, 2450m, 10.8.1997, P. Senn and A.-B. Utelli, 14451.

Switzerland: Les Places, near Arolla, S of Sion, canton Valais, 2050m, 7.7.1995, M. Baltisberger and M. Soliva, 13042; Sagentobel, Stettbach in Zürich, canton Zürich, 500m, 25.5.1995, A.-B. Utelli, 14401 (13706); Muswinkel, Glattrub, canton Zürich, 420m, 25.5.1995, A.-B. Utelli, 14402; Stierenbergli, near Kandersteg, canton Berne, 1720m, 12.7.1995, A.-B. Utelli, 14403 (13709); between ChantBrella and the hut Heidi, near S1. Moritz, canton Grisons, 2020m, 2.9.1995, P. Senn and A.-B. Utelli, 14424 (13600); Gamsalp, near Wildhaus, canton St. Gall, 1750m, 22.9.1995, B. Gautschi and A.-B. Utelli, 14425 (13596); Rigi-First, mountain Rigi, canton Schwyz, 1410m, 24.9.1995, B. and M.A. Gautschi, 14427 (13597); between Vicosoprano and Soglio, Bergell, canton Grisons, 1170m, 14.10.1995, A.-B. Utelli, 14429 (13598); between Louche and Arolla, S of Sion, canton Valais, 2200m, 12.7.1996, B. Gautschi and A.-B. Utelli, 14432; between Grellingen and Seewen, canton Baselland, 450m, 4.6.1997, A.-B. Utelli, 14436 (13713); All’Acqua, Val Bedretto, canton Ticino, 1590m, 11.9.1997, A.-B. Utelli, 14462.


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SALICACEAE

Salix setchelliana C. Ball. n=19, 2n=38.

United States: Alaska: Knik River, south side of river, 1.5 miles east of bridge to Palmer on Old Glenn Highway, Argus 13903 (voucher at CAN).

Salix floridana Chapman. n=19, 2n=38.

United States: Florida: Mormon Branch of Juniper Creek, Ocala National Forest, Marion County, Miller and Buechler 0010 1801 (voucher at SRP). 2n = 38.

Georgia: Chattahoochee River, ca. 4 miles SW of Hilton, Early County, James R. Allison 12400 (voucher at GA).

C. Favarger, Institut de Botanique, Université de Neuchâtel, Rue Émile-Argand 11, CH-2007 NEUCHÂTEL, Switzerland

BRASSICACEAE


M.E. Mansanares, E.R. Forni-Martins and J. Semir, Departamento de Botanica, Instituto de Biologia, Unicamp, Caixa Postal 6109, 13083-970 Campinas, SP, Brazil. Localities in Brazil, Minas Gerais. Vouchers in UEC and SPF. First author abbreviated to MEM.

ASTERACEAE

Lychnophora canadelbrum Sch.Bip. 2n=36.

MG: Gouveia, MEM et al. 27.

L. cipoensis Semir and Leitao. n=19, 2n=38.

MG: Serra do Cipo, Feres et al. 98/39; Diamantina, MEM and Aona 10.

L. diamantiniana Coile and S.B.Jones. n=17, 2n=34. MG: Milho Verde, Feres et al. 98/56; Diamantina, Feres et al. 98/66.

L. ericooides Mart. 2n=34: MG: Furnas, Serra da Canastra, Lopes NPL-128a; Furnas, Serra da Canastra, NPL-128b; Delfinopolis, Serra da Canastra, NPL-123; Babilonia, Serra da Canastra, NPL-157.

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Michael G. Pimenov, Tatyana V. Alexeeva, and Eugene V. Kljuykov, Botanical Garden of Moscow State University, Moscow 119899, Russia. E-mail: pimenov@2.botgard.bio.msu.ru. Vouchers in MW. All localities in Central Nepal (E Himalaya). Collectors: M.G.Pimenov and E.V.Kljuykov. The investigations were supported by grants of the Russian Foundation of Fundamental Investigations (RFFI).

**APIACEAE**


*Angelica cyclophalcarpa* (C. Norman) Cannon. 2n=22. Southern slopes of Annapurna mountain massif, valley of Modi Khola, right bank, between Doban (Dovan) and Himalaya Hotel, 28°28'N, 83°52'E, 2700-3000m, 22.10.1999, N 11.

*Bupleurum dalhollseianum* (e.B. Clarke) Koso-Pol. 2n = 16. Langtang National Park, basin of Trisuli Khola, between Cholang Pati and Lauribina Yak, 28°05'N, 85°25'E, 3300m, 1.11.1999, N 47.


*Chaerophyllum villosum* DC. 2n=22. Southern slopes of Annapurna mountain massif, valley of Modi Chola, right bank, between Chhomrong and Dovan, 28°27'N, 83°51'E, 2000-2300m, 23.10.1999, N 23.

*Coriaria depressa* (D. Don) C. Norman. 2n=22. Southern slopes of Annapurna mountain massif, valley of Modi Chola, right bank, between Machhapuchhare Base Camp and Annapurna Base Camp, 28°30'N, 83°51'E, 3900m, 23.10.1999, N 23; Langtang National Park, basin of Trisuli Khola, between Lauribina Yak and Gossainkunda, 28°04'N, 85°26'E, 4500m, 1.11.1999, N 52.
**Heracleum nepalense** D. Don. 2n=44. Southern slopes of Annapurna mountain massif, valley of Modi Chola, right bank, between Chhomrong and Dovan, 28°27'N, 83°51'E, 2000-2300m, 21.10.1999, N10.

**Heracleum sublineare** C.B. Clarke. 2n=22. Langtang National Park, basin of Trisuli Khola, between Sing Gompa and Cholang Pa-ti, 28°07'N, 85°20'E, 3100m, 31.10.1999, N 37.

**Hymenidium apiolens** (C.B. Clarke) Pimenov et Kljuykov. 2n=22. Langtang National Park, basin of Trisuli Khola, between Sing Gompa and Cholang Pati, 28°05'N, 85°25'E, 3700m, 1.11.1999, N 22.

**Lalldhwoja staintonii** Farille. 2n=22. Langtang National Park, basin of Trisuli Khola, between Dhunche and Cholang Pati, 28°07'N, 85°20'E, 3300m, 2.11.1999, N 53.

**Ligusticopsis wallichiana** (DC.) Pimenov et Kljuykov (Selinium wallichianum (DC.) Raizada et Saxena). 2n=22. Southern slopes of Annapurna mountain massif, valley of Modi Khola, right bank, between Himalaya Hotel and Deorali (Deurali), 28°28'N, 83°52'E, 3250m, 22.10.1999, N 19.


**Oenanthe thomsonii** C.B. Clarke. 2n=18. Southern slopes of Annapurna mountain massif, Pothana, moist places in dense forest, 28°18'N, 83°52'E, 1900m, 19.10.1999, N 3.


**Physospermopsis mukinathensis** Farille et Malla. 2n=18. Southern slopes of Annapurna mountain massif, valley of Modi Khola, right bank, between Deorali (Deurali) and Machahapuchhare Base Camp, 28°30'N, 83°52'E, 3350m, 23.10.1999, N 22.

**Pimpinella pimplinisimulacrum** (Farille et Malla) Farille. 2n=20. Langtang National Park, basin of Trisuli Khola, between Cholang Pati and Lauribina Yak, 28°05'N, 85°25'E, 3700m, 1.11.1999, N 44.

S. Dominic Rajkumar, SPK Centre for Environmental Sciences, Manonmaniam Sundaranar University, Alwarkurichi 627 412, Tamil Nadu, India. Vouchers in herbarium of SPK Centre for Environmental Sciences (SPKCES). The author gratefully acknowledges the financial assistance received from the Department Science and Technology through the Young Scientist award scheme (HR/SX/B- 21/97).

**ACIENPTERIDACEAE**

Actiniopteris radiata (Swartz) Link. n=87. India: Mahendragiri hills, Tamil Nadu, 800m, 2-7-1999, SPKCES 132.

**ADIANTACEAE**

Adiantum radianum Presl. n=58. India: Anamalai, Tamil Nadu, 800m, 7-3-2000, SPKCES 207.

**ANGIOPTERIDACEAE**

Angiopteris evecta (Forst.) Hoffm. n=80. India: Ponmudi hills, Kerala, 1500m, 1-5-2000, SPKCES 242.

**ASPLENIACEAE**

Asplenium aethiopicum (Burm.) Becherer. n=144. India: Ponmudi hills, Kerala, 1000m, 1-5-2000, SPKCES 249.
ATHYRIACEAE
*Diplazium poly podioïdes* Bl. n=82. India: Mahendragiri hills, Tamil Nadu, 800m, 2-7-1999, SPKCES 155.

DROOPTERIDACEAE
*Tectaria paradoxa* (Fée) Sledge. n=82. India: Ponmudi hills, Kerala, 1000m, 1-5-2000, SPKCES 244.

PTERIDACEAE
*Pteris biaurita* L. n=87. India: Nilgiri hills, Tamil Nadu, 1800m, 4-10-1999, SPKCES 173.
*Pteris cretica* L. n=87. India: Mahendragiri hills, Tamil Nadu, 900m, 2-7-1999, SPKCES 143.
*Pteris longipes* Don. n=58. India: Waynad hills, Kerala, 700m, 4-8-2000, SPKCES 350.
*Pteris vittata* L. n=58. India: Anamalai, Tamil Nadu, 1300m, 7-3-2000, SPKCES 202.

THELYPTERIDACEAE
*Christella parasitica* (L.) Lev. n=72. India: Anamalai, Tamil Nadu, 1200m, 8-3-2000, SPKCES 220.
*Christella dentata* (Forsk.) Brownsey et Jermy. n=72. India: Mahendragiri hills, Tamil Nadu, 700m, 3-7-1999, SPKCES 157.
*Pseudocyclosorus ochthodes* (Kunze) Holtt. n=35. India: Waynad hills, Kerala, 700m, 4-8-2000, SPKCES 361
*Sphaerostephanos subtruncatus* (Bory) Holtt. n=36. India: Palani hills, Tamil Nadu, 1800m, 4-4-1999, SPKCES 123.
*Trigonospora caudipinna* (Ching) Sledge. n=72. India: Waynad hills, Kerala, 700m, 4-8-2000, SPKCES 364.

F. M. Vázquez, S. Ramos, E. Doncel, J. Blanco and E. Balbuena, Department of Forest Production, Service of Investigation and Technological Development, Council of Agricultural and Environment, P. O. Box 22, E-06080 Badajoz, Spain. Vouchers in Herbario del Servicio de Investigación Agraria, Badajoz, Spain (HSIA).

ASTERACEAE
*Chamaemelum fuscatum* (Brot.) Vasc. 2n=18. Spain: Badajoz: near Badajoz city, 38°90'N, 6°95'W, 180m, 31.6.1996, C., I., and F.M. Vázquez, HSIA 1873.

FABACEAE

PAPAVERACEAE

SCROPHULARIACEAE

Heracleum sphondylium
Carpo-anatomical data on clarification of *Cnicus benedictus* L. position within the subtribe Centaureinae (Asteraceae).

The monotypic genus *Cnicus* L. is one of numerous small genera within *Centaureinae* that are disputed and difficult from the taxonomic point of view. According to some investigators the majority of genera from this group, including *Cnicus*, morphologically is closer to *Centaurea* L. representatives. As the features of achene microstructure are reliably diagnostic, we investigated achene envelope microstructure of *Cnicus benedictus* L. for clarification of relationships between these genera. The results were compared with the published data for *Centaurea* representatives (Mouradian, 1999). The comparative analysis revealed similarity only in spermoderm structure (well expressed testepiderm with radially elongated macrosclereids, well preserved parenchotesta, remains of endosperm, etc.). However representatives of these genera distinctly differ by pericarp structure. Thus *C. benedictus* has pericarp with 19-20 rather large, closely settled ribs with well-developed mechanical tissue, and pericarp domination. These features are not at all characteristic for *Centaurea* representatives and, in our opinion, it is a convincing argument for confirmation of the independence of the genus *Cnicus*.

Current projects:
Carpological revision of *Centaurea* L. and related genera. Micro- and macrostructure of the achenes of the subtribe Carduinae representatives.

Preparation of the seventh volume in the series "Comparative anatomy of seeds", containing information about family Compositae. Carpological data in the systematic position of the tribes Eupatorieae and Heliantheae.

Project completed:
The identification of extreme growth conditions by morpho-anatomical indices of endemic species of barley.

Publications:


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Project Started:
Systematics of Leyland Cypress
7

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and should have arrived on the 3rd of August 2001 at the latest, or be handed in during registration in Albuquerque.

Saxifraga oppositifolia
New Candidates:

Elena Conti, Switzerland

J. Chris Pires, USA

Tod Stuessy, Austria
B.S., DePauw University, Greencastle, Indiana, 1965; Ph.D., University of Texas at Austin, 1968. Postdoc Harvard University, 1971-72. 1968-74, Assistant Professor, 1974-79, Associate Professor, 1979-1995, Professor, Ohio State University, Columbus. Also at Ohio State, Director of Herbarium 1980-95, Director of Museum of Biological Diversity, 1991-94; Deputy Director for Research and Collections, Los Angeles County Natural History Museum, 1995-97; Professor, Head of Department of Higher Plant Systematics and Evolution, Director of Botanical Garden, Institute of Botany, University of Vienna, 1997-present. Associate Program Director, Systematic Biology Program, NSF, Washington, D.C., 1977-78. Secretary-Treasurer, IAPT and Editor-in-Chief, Taxon, 1999-present. ASA Gray Award from ASPT, 1999; Gleason Award from New York Botanical Garden, 1990; Corresponding Member, Austrian Academy of Sciences, 1999-present. Published 7 books and more than 170 papers. Research interests: (1) Island biology, especially in the Robinson Crusoe Islands; (2) Biogeography of southern South America; (3) Systematics of Compositae; and (4) Concepts and methods of biological classification.

Tetsukazu Yahara, Japan

Cut off and send to K. Bachmann (the above address), please.

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Peter Hoch (Regional Treasurer for the USA)
Jan Kirschner (Editor of the Newsletter)
Clive Stace (editor of Chromosome numbers)

Council (one vote each for one to ten of the candidates)

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O Pilar Catalan, Spain
O Chengxin Fu, P.R. China
O Elena Conti, Switzerland, NEW CANDIDATE
O Jorge Crisci, Argentina
O Elsbieta Kuta, Poland
O John Murray, USA
O Hans den Nijs, The Netherlands
O J. Chris Pires, USA, NEW CANDIDATE
O Tod Stuessy, Austria, NEW CANDIDATE
O Suzanne Warwick, Canada
O Tetsukazu Yahara, Japan, NEW CANDIDATE
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PROJECTS STARTED

REQUESTS FOR RESEARCH MATERIAL AND INFORMATION

Articles and reports should be attached!

In capital letters or e-mail!

Please select three titles and add the remainder as e.g. "seven further papers"!

To be sent to

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