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# International Organization of Plant Biosystematists

Newsletter

No. 8

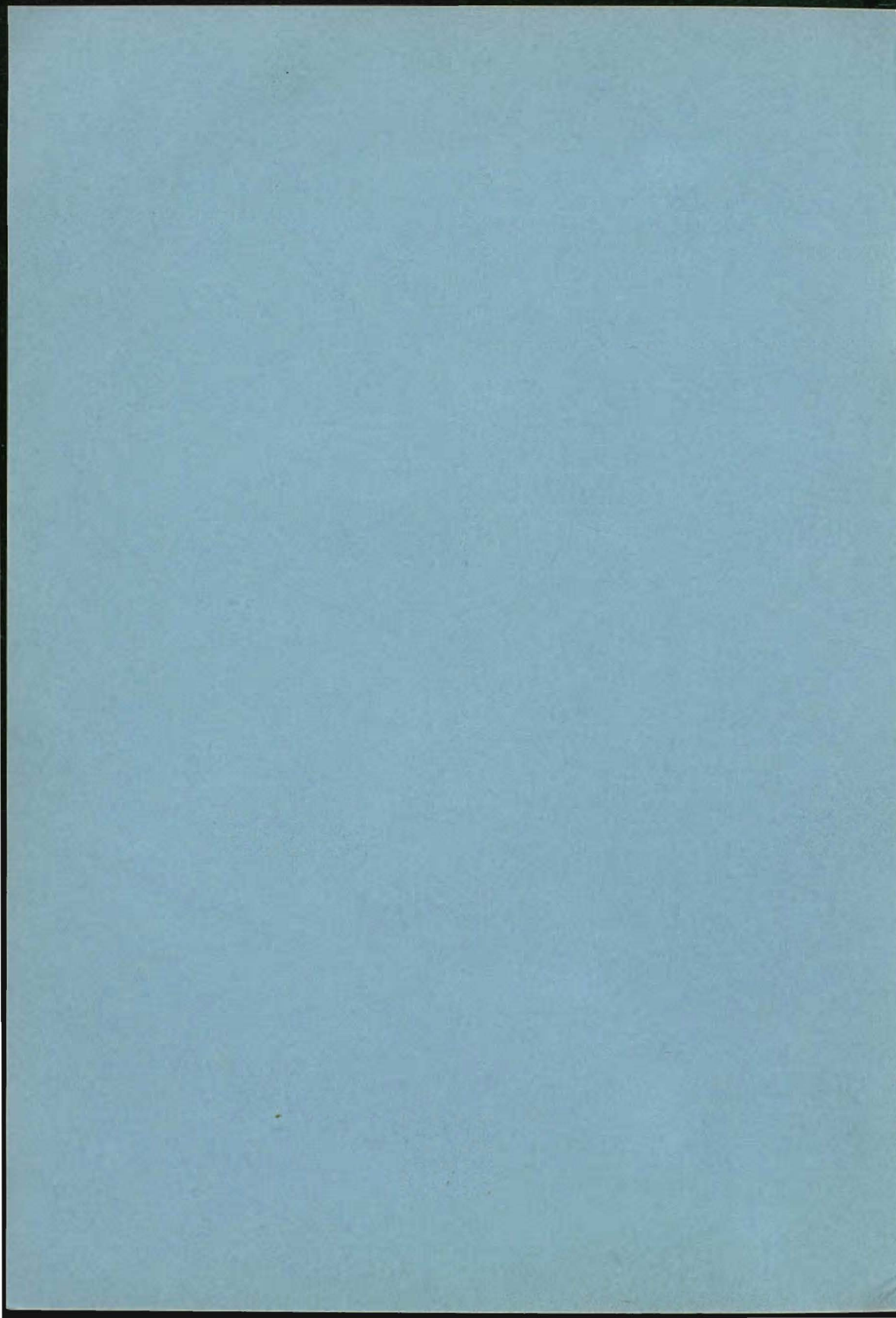
Edited by K. M. Urbanska

**ETH** ZÜRICH

Issued from  
The Department of Geobotany  
Swiss Federal Institute of Technology

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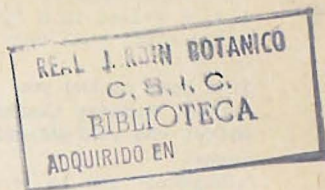
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9 JUL. 1987

INTERNATIONAL ORGANIZATION OF PLANT BIOSYSTEMATISTS

NEWSLETTER No. 8



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Mataselles 1-VII-87

Dear IOPB Members,

Time goes on and you are presented with the summer issue of the Newsletter. Sincere thanks to all contributors and please don't forget your Editor who will be only too glad to receive more material for the next issue.

Dr. Jeff J. Doyle from the Cornell University is the author of our current Lead Article on 'Plant Systematics at the DNA level' (p. 3). Thank you, Jeff, I am happy to have this excellent paper.

Our column 'Profile of a Lab' (p. 7) presents this time the Laboratory of Aquatic Plant Biology in Wuhan. We are thankful to Dr. Chen Jiakuan, who contributed this important information, and hope that the IOPB membership in China will grow.

Only one, but important forthcoming meeting: the IOPB Open Business Meeting will be held during the XIVth International Botanical Congress (see p. 11 for details). We hope to see many IOPB Members and also interested persons who are not (yet?) Members.

First news from the Land of Cherry Blossom concerning the IOPB Symposium 1989 (p. 11). We are looking forward to the Symposium - a scientific event, and a personal pleasure of seeing the old friends and making the new ones. It is time NOW to begin a serious planning of your travelling schedule for 1989 - try to include Japan.

Speaking about the IOPB Symposia: you'll find the last echo of our Zürich Symposium on p. 12 (the column: Publishing News): the Symposium book is soon to appear.

Don't forget to look up the column 'Requests for material and information' (p. 12). Perhaps only YOU can help a fellow scientist.

Data for Newsletter Nr. 9 should arrive here before November 30, 1987.

Have a good field season

The Editor

**NOTE:** Please write in capital letters or use typewriter while preparing your 'Research News' sheet for the Newsletter. You don't want to have some words misspelled in print, do you?

## 2. LEAD ARTICLE

By Dr. Jeff J. Doyle, Assistant Professor of Botany, L.H. Bailey Hortorium, 467 Mann Library, Cornell University, Ithaca, New York 14853-0271, U.S.A.

### Plant systematics at the DNA level: Promises and pitfalls

There is currently great interest among many members of the botanical systematics community for the use of DNA characters. Last summer, for example, at the annual meeting of the Botanical Society of America and American Society of Plant Taxonomists, a session composed almost exclusively of papers dealing with molecular systematics drew a large and enthusiastic audience. In each of the two last years, the prize of the outstanding systematic paper at these meetings has been awarded to a talk dealing with DNA-based systematics. The enthusiasm is certainly warranted, for advances in DNA technology have opened up whole arrays of new characters to the purview of the systematist. With the burgeoning field of plant molecular genetics have come technical advances in the area of DNA isolation, for example, that have had spinoffs for the taxonomist such as our own recent finding that DNA suitable for use in systematic surveys can be extracted from recently-dried plant species (DOYLE and DICKSON 1987).

The complexity of the plant nuclear genome virtually assures that any question of an evolutionary nature, regardless of the taxonomic level, can be addressed with the appropriate DNA sequence. Nuclear ribosomal gene (rDNA) cistrons, for example, certain structural gene regions evolving so slowly as to be useful for investigating questions such as the origins of the angiosperms, while only a few kilobases (kb) away are spacer regions whose length and sequence evolve so rapidly as to differ among - or even within - individual plants. Such variable regions have been used in phylogeny construction (SYTSMA and SCHAAL 1985) and in population studies (SAGHAI-MAROOF et al. 1984). We have used rDNA variation to corroborate the hybrid nature of plants morphologically intermediate between the monotypic genera Tolmiea and Tellima of the Saxifragaceae (DOYLE et al. 1985a) and are currently using rDNA markers to demonstrate hybridization between two morphologically, karyotypically and chemically similar species of Claytonia (Portulacaceae). Though less used in systematic studies, protein-encoding genes may also provide useful characters. The 7S seed storage protein genes of Glycine, for example, contain a large insertion sequence in the first exon that does not occur in Phaseolus, a member of the same tribe (Phaseoleae), or in Pisum, a more distantly related legume (DOYLE et al. 1986). The presence of the insertion appears to be a derived condition, and it explains the size differences among the storage protein subunits in these taxa. This insertion provides a tool for investigating generic relationships within the Phaseoleae, where previous immunological study of 7S proteins has already demonstrated much variation among the many taxa (DOYLE et al. 1985a).

The most widely-used molecular tool, however, is chloroplast DNA (cpDNA), thanks largely to the seminal work of Jeffrey Palmer (Univ. of Michigan, USA). Not only has his work laid the foundation for much of the current progress in this field, but his willingness to distribute his cpDNA recombinant libraries to other researchers has been instrumen-

tal in the rapid growth of the area. A number of structural features make cpDNA a useful systematic tool (reviewed by PALMER, 1985). A molecule of nearly uniform size in all plants (ca. 150 kb), its overall structure and gene arrangement have been strongly conserved among land plants. Furthermore, cpDNA evolves at a relatively slow rate, making it an ideal source of taxonomic characters when assayed for sequence variation using restriction endonucleases. Cladistic analyses of cpDNA data sets have produced phylogenies with great resolution and, perhaps more importantly, minimal homoplasy - a major reason for the excitement such studies have generated. For example, in the most extensive cpDNA phylogenetic study to date, SYTSMAN and GOTTLIEB (1986) produced a tree for nine *Clarkia* species and the monotypic genus *Heterogaura* based on 119 cpDNA characters, with a rate of convergence of only 4.8%. Such results do nothing to diminish the attractiveness of cpDNA for systematists use to struggling with the extensive homoplasy inherent in most morphological studies.

Major arrangements of cpDNA structure occur sporadically throughout the angiosperms and provide characters at higher taxonomic levels (PALMER 1985). Thus, JANSEN and PALMER (1987a) have recently surveyed all of the tribes of Asteraceae, as well as a number of other families in the Asteridae, to determine which groups possess a 22 kb inversion of the cpDNA first discovered in *Lactuca* (JANSEN and PALMER 1987b). Their results indicate that the inversion occurred within the Asteraceae, and have established that all tribes of that family have this mutation, with the exception of some elements of the Mutisieae. The correlations of these results with recent systematic studies of the family and with the many conflicting interpretations of its phylogeny are certain to form the grist of many discussions for years to come. Like the Asteraceae, members of the Leguminosae have been shown to possess the major cpDNA mutations, including a 50 kb inversion and a large deletion (reviewed in PALMER 1985), as well as a second, 75 kb inversion in some taxa (PALMER pers. com.). In collaboration with Jeffrey Palmer, we are beginning a survey of this large family in an effort to establish the extent of these major mutations, and to determine their utility in elucidating relationships among the taxa (some specific questions to be addressed are discussed in DOYLE 1987).

Thus far I have painted a rosy picture of DNA-based plants systematics, and indeed I feel there is a great potential in the field (or I would not, I suppose, be engaging in such research). Nevertheless, problems exist here as anywhere else in taxonomy, and it is well to be aware of the difficulties and pitfalls. First, there are practical problems, of course. True, DNA isolation have been streamlined and improved, and restriction enzymes are not too different in price (in many instances, at least) from the reagents used for isozyme analysis, a methodology already familiar to many systematists. But even so, the isolation and analysis of 200 samples for a study of hybridization, as we have recently done for *Claytonia*, is a major undertaking, and not inexpensive. To a lesser degree the same constraints will exist for any systematist, since we all recognize the need for adequate sampling in any taxonomic study. Furthermore, there is such great variability among plant taxa that the isolation of DNA may be difficult, although this problem has been alleviated by the proliferation of isolation techniques, such that many methods now exist to choose from should one not work.

Next is the problem of finding the proper amount of variation to address the questions at hand. I stated above that it is, in theory at least, possible to find a DNA sequence to answer any problem. But theory is not

always practice, and this can be difficult. For example, we recently were visited by Andrew Henderson, from the New York Botanical Garden, who had arranged to study cpDNA variation among several palm genera in our laboratory. Initially concerned that he would find too much variation to handle, we found, after several weeks and much effort, that there is almost no variation at all among these taxa. This is, certainly, an evolutionary intriguing result, but of little use in answering the taxonomic question at hand. As we know from this and other rather painful recent experiences, not all groups exhibit levels of interspecific variation sufficient for constructing trees that resolve all of the taxa studied. In the genus Solanum, little variation occurs within section Lasiocarpa of subgenus Leptostromonum, while much variation occurs both between that section and a second section of the subgenus, section Torva, as well as between species within Torva (DOYLE et al. in prep.). Is this due to different taxonomic concepts, evolutionary rates, cpDNA divergence rates, or to a malevolent deity? Certainly, results of the sorts described here, combined with the wide differences in the amount of cpDNA variation between related species reported in the literature, has shaken my faith in the often-cited (but fortunately, not yet abused) notion of a cpDNA molecular clock. Our own efforts to calibrate such a clock using Juglandaceae, a family with an excellent fossil record, resulted in our finding that there has been almost no cpDNA divergence between Juglans and the very distinctive Pterocarya, whose fossil records go back to over 40 MY. Look for the data on this group to be published when I convince myself that we are not simply missing something.

More significant than these practical concerns are the hints that DNA phylogenies and taxon genealogies need not be congruent. Introgression of either individual nuclear genes or of the entire cpDNA molecule could certainly perturb the correspondence.

Among the relatively small number of cpDNA phylogenetic studies, there is already one in which a strong suggestion of cpDNA introgression occurs (PALMER et. al. 1983). It is well to recall that although a cpDNA phylogeny may be composed of a hundred or more characters, these characters are all tightly linked in a non-recombining, often uniparentally inherited molecule. No amount of synapomorphic characters will reveal the 'true' relationships among a group of taxa if two of those taxa share a cpDNA genome as a result of introgression. An alternative to introgression as an explanation to incongruence between taxon and molecular phylogenies has recently been discussed by NEIGEL and AVISE (1986), using as an example animal mitochondrial DNA (mtDNA). Their computer simulations demonstrate that sorting of polymorphisms in the ancestral pool during speciation can lead to situations in which derivative taxa will appear para- or polyphyletic with respect to their mtDNA phylogeny. In such cases, lack of knowledge of the degree of variation within taxa could lead to a mistaken assessment of phylogenetic relationships. It is therefore perhaps significant to note how little is known about variation in cpDNA within plant species, or about allele phylogenies of plant nuclear genes. In the latter case, nuclear genes may be expected to show additional levels of complexity due to classic genetic recombinations and the even more arcane processes such as gene conversion that are part of the mysterious fluidity of the eukaryotic genome.

The phylogenetic significance of the major mutations of the chloroplast genome, along with duplications of nuclear genes, must also be interpreted with caution. As JACKSON (1985) has pointed out, the target sites

of the transpositional processes likely to be responsible for duplications may predispose certain regions of the genome to undergo such processes, leading to parallel gain or loss of sequences. Similarly, small repeated sequences in cpDNA may be non-randomly associated with the breakpoints of inversions (BOWMAN and DYER 1986), and could potentially represent hotspots for major rearrangements.

Does this suggest that whole-genome comparisons using DNA-DNA hybridization and thermal stability are better measures of phylogeny than such comparisons involving single molecules or sequences? I think not, given the complexity of the plant genome, its fluidity both with regard to sequence evolution and overall DNA content, the prevalence of hybridization (and particularly allopolyploidy) among plants, and the inherently phenetic nature of such comparisons. Nor do I wish to suggest that more traditional estimates of phylogeny are superior to molecular approaches. After all, morphological characters, to use one example, are likely to be largely determined by genes undergoing the same complex evolutionary processes as those from which we attempt to construct our molecular phylogenies, and in addition are likely to show further layers of complication from interactions of such genes, epigenetic effects, homoeotic mutation, and a host of other processes. At least at the DNA level we may hope to understand the nature of our confusion. What these considerations do suggest is that sweeping statements that a particular molecular phylogeny is 'right' and that more traditional approaches, such as morphology, are 'wrong' when the two do not happen to agree are unwarranted without further investigation. Indeed it is just such instances of incongruence that are likely to lead to major revelations about the evolution of the taxa being studied - or of the molecules being used in the analysis.

In conclusion, then, molecular approaches to plants systematics involving studies at the DNA level are likely to be a major area of investigation for years to come, and this field promises to give us major insights about both taxonomy and evolutionary process. It is my hope that systematists will make every effort to use this powerful tools to good effect, working with a clear understanding of both their potential and their limitations.

#### Literature cited

- BOWMAN C.M. and DYER T.A., 1986: The location of possible evolutionary significance of small dispersed repeats in wheat ctDNA. *Curr.Genet.* 10, 931-941.
- DOYLE J.J., 1987: Variation at the DNA level: uses and potential in legume systematics. In: SIRTON C.H. (ed.), *Advances in legume systematics*. Part 3. Roy.Bot.Gardens, Kew.
- DOYLE J.J. and DICKSON E.E., 1987: Preservation of plant samples for DNA restriction endonuclease analysis. *Taxon* (in press).
- DOYLE J.J., DORN P.S. and SOLTIS D.E., 1985: Ribosomal RNA gene sequence variation: *Tolmiea*, *Tellima*, and their intergeneric hybrid. *Amer.J. Bot.* 72, 1388-1391.
- DOYLE J.J., LADIN B.F. and BEACHY R.N., 1985: Antigenic relationship of legume seed proteins to the 7S seed storage protein of soybean. *Biochem.Syst.Ecol.* 13, 123-132.
- DOYLE J.J., SCHULER M.A., GODDETTE W.D., ZENGER V., BEACHY R.N. and SLIGHTOM J.L., 1986: The glycosylated seed storage proteins of *Glycine max* and *Phaseolus vulgaris*: structural homologies of genes and proteins. *J.Biol.Chem.* 261, 9228-9238.



- JACKSON R.C., 1985: genomic differentiation and its effects on gene flow. *Syst.Bot.* 10, 391-404.
- JANSEN R.K. and PALMER J.D., 1987: A chloroplast DNA inversion marks an ancient evolutionary split in the sunflower family (Asteraceae). *Curr.Gen.* (in press).
- JANSEN R.K. and PALMER J.D., 1987: Chloroplast DNA from lettuce and Barnadesia (Asteraceae): structure, gene localization, and characterization of a large inversion. *Curr.Gen.* (in press).
- NEIGEL J.E. and AVISE K.C., 1986: Phylogenetic relationships of mitochondrial DNA under various demographic models of speciation. In: KARLIN S. and NEVO E. (eds.), *Evolutionary processes and theory.* Acad.Press, Orlando.
- PALMER J.D., 1986: Comparative organization of chloroplast genomes. *Ann. Rev.Genet.* 19, 325-354.
- PALMER J.D., SHIELDS C.R., COHEN D.B. and ORTON T.J., 1983: Chloroplast DNA evolution and the origin of amphidiploid Brassica species. *Theor. Appl.Genet.* 65, 181-189.
- SAGHAI-MAROOF M.A., SOLIMAN K.M., JORGENSEN R.A. and ALLARD R.W., 1984: Ribosomal DNA spacer-length polymorphisms in barley: mendelian inheritance, chromosomal location, and population dynamics. *Proc.Nat. Acad.Sci.USA* 81, 8014-8019.
- SYTSMA K.J. and GOTTLIEB L.D., 1986: Chloroplast DNA evolution and phylogenetic relationships in *Clarkia* sect. *Peripetasma* (Onagraceae). *Evolution* 40, 1248-1261.
- SYTSMA K.J. and SCHAAL B.A., Phylogenetics of the *Lisianthus skinneri* (Gentianaceae) complex in Panama utilizing DNA restriction fragment analysis. *Evolution* 39, 594-608.

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### 3. PROFILE OF A LAB

by Ph.D. CHEN JIKUAN, Laboratory of Aquatic Plant Biology, Department of Biology, Wuhan University, Wuhan, Hubei, China

The laboratory carries out basic research in aquatic plant biology including systematic botany, evolutionary botany, and aquatic plant ecology, with goals of applying the research to practical problems in comprehensive utilization and control of aquatic plants in China. It is housed in the Plant Biology Research centre, and was set up by Wuhan University in 1978. The director, Prof. Sun Xiangshung (Sun Siangchung), is Member of the Standing Committee of the Botanical Society of China, a chief editor of 'Flora Republic Sinicae (8) Helobiae' and 'Journal of Wuhan Botanical Research', and also director of the whole centre. There are three Professors, two lecturers and ten graduate students in the Laboratory now. Three different but complementary groups have been established: a) Systematic Botany: deals with the classification, floristics, distribution, and natural system of aquatic plants (Prof. Sun); b) Evolutionary Botany: research program includes karyological, cross-breeding and phytochemical studies on the Helobiae (Prof. Wang Huiqin, associate director), and investigations on variation and evolution within and among populations of Alismataceae (Dr. Chen); c) Aquatic Plant Ecology

deals with structure, dynamics and control of communities of aquatic plants in the field as well as morphological variations under experimental conditions (Dr. Chen).

The City of Wuhan is situated near the Yangtse River; there are about six hundred fresh lakes in Hubei Province (appropriately named 'Province with Thousand Lakes'). As the aquatic flora is rich, it is an ideal place for studying aquatic plants. Since 1978, ten thousands of specimens have been collected and hundreds Helobiae populations have been investigated. The biosystematic study on genus *Alisma*, *Sagittaria*, *Blyxa*, *Potamogeton*, *Najas*, *Hydrilla* and *Vallisneria* has progressed very much on the different levels (gene, cell, organ, organism, population and community). Morphological, anatomical, cytological, genetical, biochemical and ecological data are important to solve the problems concerning biology of crop and native aquatic plants in China.

The Herbarium of Wuhan University (WH), founded in 1930, is part of the Laboratory and has more than two hundred thousand specimens. All the laboratories: morphological, isoenzyme, aquatic plant biological, numerical taxonomical as well as the aquatic plant experimental garden have been established by the Chinese Government. The scanning and transmission electron microscopy, computer systems and other advanced techniques are currently used. Recently the authorities have agreed to an experimental station for post-doctorate fellow exchange. Three fellows will study aquatic plant biology from 1987 to 1989.

In the area of fundamental research, the Laboratory has concentrated its work on two projects: 1) Cytotaxonomic studies on the major aquatic plants in China (number, structure and behaviour of chromosomes), 2) A study on pollen biology of aquatic plants from the Yangtse Valley (morphological characteristics, structure and pollination mechanisms; relationships between pollen and its environment). These projects are supported by the Chinese Academy of Sciences.

#### Selected recent publications

- CHEN J.K. SUN X.C. and WANG H.Q., 1984: New taxa of *Sagittaria* L. from Hubei. *Bull.Bot.Res.(China)* 4(2), 129-131.
- CHEN J.K. SUN X.C. and WANG H.Q., 1986: A preliminary report on the chromosome numbers of *Sagittaria* in China. *J.Wuhan.Univ., Nat.Sci.Ed.* 4, 108.
- CHEN J.K. SUN X.C. and WANG H.Q., 1986: A preliminary report on populations of *Sagittaria potamogetifolia* - an endemic species in China. *J. Wuhan.Univ., Nat.Sci.Ed.* 4, 119-120.
- CHEN J.K. and WANG H.Q., 1986: The applications of concept and method of population to plant taxonomy. *J.Wuhan.Bot.Res.* 4(4), 377-380.
- CHEN J.K. and GUO Y.H., 1986: The main trends in life science and our counter-measures. *J.Trends in Biology* 4.
- CHEN J.K., 1987: systematic studies on Chinese *Sagittaria*. Ph.D.thesis. Wuhan Univ. (in press).
- CHEN J.K., 1987: Introduction to ecology. Wuhan Univ. 313 pp.
- GUO Y.H., SUN X.C. and WANG H.G., 1985: The geographical distribution and habitats of *Potamogeton* flora in Shaanxi. *J.Wuhan Univ.* 1, 97-104.
- GUO Y.H., SUN X.C. and WANG H.G., 1985: A new species of genus *Potamogeton* L. from in Shaanxi. *Bull.Bot.Res.* 5(2), 133-135.
- GUO Y.H., WANG H.G. and SUN X.C., 1985: Studies on the classification of *Potamogeton* in Shaanxi Province. *Act.Bot.Bor.Occ.Sin.* 4, 291-304.
- HE J.B. and CHEN J.K., 1986: Notes on the investigation in Joucai Bog, Hubei. *Bot.Mag.* 3, 11.

- WANG W.X., 1984: A new species of Potamogeton from Hubei. Act. Phytotax. Sin. 22(6), 490-492.
- WANG Z.Q., SUN X.C. and WANG H.Q., 1986: Karyotypical investigations on *Alisma orientale* (Sam.) Juzep. J. Wuhan Bot. Res. 4(4), 421-423.
- XIONG Z., WANG H.Q. and SUN X.C., 1985: Numerical taxonomic studies on Trapaceae in Hubei (I, II). J. Wuhan Bot. Res. 3(1), 45-53; 3(2), 157-164.
- YOU J., SUN X.C. and WANG H.Q., 1985: Taxonomic studies on *Najas*: A synthetic analysis with evidences on cytology, isozymes and SEM examination. J. Wuhan Univ. 4, 118-119.
- ZHAO Z.C., SUN X.C. and WANG H.Q., 1984: A study on the ecology of the fresh water Hydrocharidaceae in Southern China. Act. Ecol. Sin. 4(4), 355-364.
- ZHAO Z.C., 1987: A study on genus *Blyxa* in China. Ph.D. thesis. Wuhan Univ. (in press).

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#### 4. RESEARCH NEWS

BRUEDERLE Leo, Ph.D., Lehrstuhl für Pflanzensystematik, Universität Bayreuth, Postfach 101251, D-8580 Bayreuth, FRG.

Recent publications:

BRUEDERLE L.P. and FAIRBROTHERS D.E., 1986: Allozyme variation in populations of the *Carex crinita* complex (Cyperaceae). Syst. Bot. 11(4), 583-594.

Projects completed:

Conservation genetics of *Carex mitchelliana* M.A. Curtis (Cyperaceae), a rare sedge.

Projects started:

Allozyme variation in European populations of the *Carex flava* group.

DEN NIJS Jan C.M., Dr., Hugo de Vries Laboratory, University of Amsterdam, Kruislaan 318, 1098 SM Amsterdam.

Recent publication:

DEN NIJS J.C.M., SORGEDRAGER K. and STOOP J., 1985: Biosystematic studies on the *Rumex acetosella* complex. IX. Cyto geography of complex in the Iberian peninsula and taxonomic discussion. Bot. Helv. 95, 141-156.

STERK A.A., DEN NIJS J.C.M. et al. (in prep.): Variation, evolution and utilities of the genus *Dandelion* (*Taraxacum*). (Will be published in Dutch).

Projects completed:

Biosystematics and taxonomy of the *Rumex acetosella* L. complex in Europe.

Projects started:

Analysis of the genetic variation in *Taraxacum* (by allozyme electrophoresis) with respect to the cyto geography and the reproduction strategies, i.e. sexual v. asexual.

Demography and analysis of the genetic variation in (small) populations of some rare and threatened species of the Dutch flora.

FUKUDA Ichiro, Prof., Department of Biology, Rhodes College, 2000 North Parkway, Memphis, Tennessee, U.S.A.

Recent publications:

FUKUDA I., 1986: Allozyme analysis of the Asian *Lycoris*. Sci.Rep. 1986, Tokyo Woman's Christian Univ.

FUKUDA I. and ITOH M., 1986: Mutants in the Japanese *Trillium*. Kushiro Museum Rep. 301, 3-8.

Co-author, 1987 (in press): Plant Genetics. Asakra, Tokyo.

Projects completed:

Comparative studies on the eastern and western *Trillium* in Northern America.

Chromosome variation in *Trillium erectum*.

Population structure and breeding system in *Trillium* populations.

Projects started:

Chromosome variations of the southeastern *Trillium* in Northern America.

Ethnobotanical investigation of the Asian cultivated plants.

FERNANDEZ LOPEZ Carlos, Colegio Universitario "Santa Reino", 24071 Jaén, Spain.

Recent publication:

Blancoana 5 (June 1987): ISSN 0212-8314.

Projects completed:

Revisión de plantas vasculares de la Península Ibérica e Islas Baleares. Un elenco hasta 1986. Blancoana 5, 53-135.

Some results were presented at "I Jornadas de Taxonomía Vegetal," in Sevilla, May 14-17, 1987. Dept. Botánica, Univ. Sevilla.

PINGH-SHENG HSU, Prof., Department of Biology, Fudan University, 220 Handan Lu, Shanghai, People's Republic of China.

Recent publication:

1986:

- Karyotype of *Ormosia henryi* Prain. Trop.Forest.Sci.and Techn. 2, 14-17.
- An evaluation of the interspecific relationships of *Lycoris* based on pollen viability and rate of seed-set after crossing. Acta Genet.Sin. 13(5), 369-376.
- The variation pattern of *Rorippa indica* populations in response to different environments. Acta Bot.Yunnan. 8(4), 421-428.
- The recognition of *Camellia octopetala* Hu based on morphological and karyological evidences, Gihaiia 6(4), 253-259.
- Patterns of karyotype differentiation of some geographical races of *Cunninghamia lanceolata*. J.Wuhan Bot.Res. 4(4), 347-352.
- The role of hybridization in plant evolution and methods of recognizing and naming hybrids. J.Wuhan Bot.Res. 4(4), 385-397.
- Interspecific hybridization between *Lycoris sprengeri* and *L. chinensis*. Acta Hort.Sin. 13(4), 283-284.

1987:

- Chromosome numbers in *Leonurus japonicus* Houtt. (Labiatae). Acta Phytotax.Sin. 25(1), 73-76.
- Progress in plant taxonomy in the past two decades. J.Wuhan Bot.Res. 5(1), 77-92.
- Karyotype analysis in *Atractylodes macrocephala*. Acta Bot.Yunnan. 9(1), 116-118.
- Biosystematics, then and now. Acta Bot.Bot.-Occ.Sin. 7(1), 65-72.
- The current situation of cytotaxonomy. Refer.Mat.Biol.Sci., Sci.Press, Fasc. 22, 1-14.
- An analysis of the variation patterns of infra- and interpopulations of *Rhododendron ovatum*. Bull.Bot.Res. 7(2), 81-94.

5. 1989 IOPB INTERNATIONAL SYMPOSIUM, JAPAN

Writes Professor S. Kawano: The organization of the IOPB Symposium in Japan has begun. The Symposium will be held at Kyoto-Kaikan, in the City of Kyoto. It is tentatively scheduled for the first week of July, 1989.

Supporting organizations:

The Society for the Study of Species Biology  
The Japan Society of Plant Taxonomists  
The Weed Science Society of Japan  
The Japan Academy (under request)  
The Japan Society for Promotion of Science (under request)

Members of the local organizing committee:

CHIHARA Mitsuo, Univ. of Tsukuba  
HORI Yoshimishi, Ibaragi Univ.  
HOTTA Mitsuru, Kyoto Univ.  
INOUE Ken, Akikusa Gakuen Junior College  
ISHIZUKA Kouzou, Univ. of Tsukuba  
ITO Misako, Kyoto Univ.  
IWATSUKI Kuniô, The Univ. of Tokyo  
IWATSUKI Zennosuke, Hiroshima Univ.  
KACHI Naoki, The National Institute for Environmental Studies  
KASUYA Hiroyuki, National Science Museum  
KAWANO Shoichi, Kyoto Univ.  
KIMATA Mikio, Tokyo Gakugei Univ.  
KOBAYASHI Hisao, Kyoto Univ.  
MASUYAMA Mikio, Tokyo Women's Univ.  
MATSUNAKA Shoichi, Kobe Univ.  
MIYAHARA Masuji, Agricultural Research Centre  
MORISHIMA Keiko, National Institute of Genetics  
NAKANISHI Minoru, Hiroshima Univ.  
SUZUKI Kazuo, Tokyo Metropolitan Univ.  
SAKAMOTO Sadao, Kyoto Univ.  
TOBE Hiroshi, Kyoto Univ.  
UEKI Kunikazu, Kyoto Univ.  
WATANABE Kuniaki, Kobe Univ.  
WATANABE Makoto, The National Institute for Environmental Studies  
YAHARA Tetsukazu, The University of Tokyo

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6. MEETINGS

The IOPB will held Business Meeting during the XIVth International Botanical Congress in Berlin. The meeting, open to all Members and interested persons is scheduled for July 27, during the lunch break at 12:30. The conference room number will be given in the Congress Programme and/or announced at the Congress Registration Desk. Among the items on the agenda are: report on the preparatory work for the IOPB Symposium 1989 in Japan, report on publication of the book based on Invited Papers of the IOPB Symposium 1986, announcement concerning the elections of the

elections of the new Vice-President and the Council of the IOBP.

The Editor's note: Grab your sandwich and try to come early, you may have problems with finding a seat that is not yet taken.....

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#### 7. PUBLISHING NEWS

'evolutionary trends in plants', the new international journal charting the best in current research, will soon appear.

etp accepts research contributions across the spectrum of plant evolutionary studies. Emphasis will be given to papers increasing our understanding of the processes of evolution rather than purely observational results, and a rapid publication schedule brings you the developments as they happen.

etp is devoted to botanical research and therefore is essential to students of that discipline. It is also a forum for news, debate and general features which are not catered for in other titles. This feature affords etp a unique role among publications currently on offer.

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'Differentiation Patterns in Higher Plants', a book based upon the Invited Papers presented at the IOBP Symposium 1986 in Zürich will be published by Academic Press, London, presumably in September 1987. The corrected proofs are now returned to the Publisher. A clean bound proof copy will be presented at the IOBP stand during the XIVth International Botanical Congress in Berlin.

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#### 8. REQUESTS FOR MATERIAL AND INFORMATION

DEN NIJS Jan C.M., Dr., Hugo de Vries Laboratory, University of Amsterdam, Kruislaan 318, 1098 SM Amsterdam, would appreciate herbarium material of *Taraxacum* section *Taraxacum* (= *Vulgaria*), the common dandelion, from eastern and southern European countries. The material will be used to complete the cytogeographical study of the section.

FUKUDA Ichiro, Prof., Department of Biology, Rhodes College, 2000 North Parkway, Memphis, Tennessee, U.S.A., would appreciate *Trillium* and *Paris* (rhizomes) from all over the world.

THOMPSON Sue A., Collection Manager, Carnegie Museum of Natural History, Section of Botany, 4400 Forbes Avenue, Pittsburgh, PA 15213, U.S.A.,

would appreciate specimens of Acorus (Araceae) from Asia and Europe.

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9. MISCELLANEOUS NOTES

Change of address:

Dr. Randall Bayer, University of Windsor, Windsor, Ontario, Canada N9B 3P4, from the end of June 1987 will be Professor at the Botany Department, University of Alberta, Edmonton, Alta, Canada.

DEN NIJS Jan C.M., Dr., Hugo de Vries Laboratory, University of Amsterdam, Kruislaan 318, 1098 SM Amsterdam. (New adress since the end of 1986).

Temporary change of address:

FUKUDA Ichiro, Prof., is Visiting Professor from September 1986 to August 1987 at Rhodes College, Department of Biology, 2000 North Parkway, Memphis, Tennessee, U.S.A.

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INTERNATIONAL ORGANIZATION OF PLANT BIOSYSTEMATISTS

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