# IS-MPMI
# REPORTER

International Society for Molecular Plant-Microbe Interactions

**- December 1999 -**

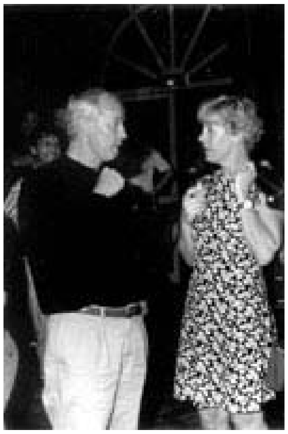
**IN THIS ISSUE:**

## Report on Amsterdam Meeting

The IS-MPMI meeting at the RAI in Amsterdam was a roaring success! In attendance were 1041 scientists representing 43 countries. We owe a great debt of gratitude to the organizers: Pierre de Wit, Tom Bisselling, Dr. Willem Stiekema, Maria Augustijn, Els de Wit, Ria Fonteijn-Boele, and Ali Ormel. The organization and facilities were superb. The quality of the abstract book and circulars was first rate. And the scientific program was truly outstanding. This will be a difficult act to follow!!

Working locally, these individuals were instrumental to the success of the meeting.
Left to Right: Maria Augustijn, Dr. Pierre de Wit, Els de Wit, Ria Fonteijn-Boele, Ali Ormel

Dr. Pierre de Wit
Chairman of the Local Organizing Committee



Dr. W. J. Stiekema, Treasurer of the Local Organizing Committee talking to his wife, Nel.

Dr. A. H. J. Bisseling
Secretary of the Local Organizing Committee

**Scientists attended from the following countries:**

Argentina • Australia • Austria • Belgium • Brazil • Canada • Chile • China • Colombia
Denmark • Egypt • Estonia • Finland • France • Germany • Greece • India • Ireland • Israel • Italy
Japan • Latvia • Luxemburg • Mexico • New Zealand • Norway • Poland • Portugal • Russia
Sierra Leone • Singapore • Slovenia • South Africa • South Korea • Spain • Sudan • Sweden
Switzerland • Taiwan • The Netherlands • Ukraine • United Kingdom • United States of America

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## RESEARCH ON MOLECULAR PLANT-MICROBE INTERACTIONS IN THE "NEUE LAENDER" IN GERMANY

Over the past eight years since the German re-unification in 1990 a number of new university departments and research groups studying aspects of plant-microbe interactions using molecular genetic tools have been established in the "Neue Laender." These groups are financially supported (renovated or new labs, new equipment, etc.) by the Federal as well as the local ("Land") governments. As there is a strong focus on molecular plant genetics and plant microbes at the University of Halle where I am located, as well as the independent research institutes nearby, I will begin my report with these institutions before discussing those in Dresden and Jena.

### Martin-Luther University in Halle

The university (approx. 14,000 students) was founded almost 500 years ago and is one of the oldest in Germany. Research on microbes is

performed in several institutes. The Department of Microbiology (head: Jan Andreesen, J.Andreesen@mikrobiologie.uni-halle.de) is interested in trace metal ions needed for enzymatic reactions and works with the anaerobic gram-positive bacterium *Eubacterium acidominophilum,* which expresses a number of genes coding for interesting seleno-proteins. The group on Ecological and Technical Microbiology(head: Dietrich Nies, d.nies@mikrobiologie.uni-halle.de) studies homoeostasis of heavy metal ions in *Alcaligenes eutrophus.* Transcription regulation in yeast is the main research topic of the Department of Molecular Genetics in the Institute of Genetics (head: Karin Breunig, breunig@genetik.uni-halle.de).

**Several departments are devoted to plant-microbe interactions:** Research in the Department of Phytopathology and Plant Protection (head: Holger Deising, http://www.landw.uni-halle. de/lfak/inst/pzps/pbppp.htm; e-mail: deising@landw.uni-halle.de) is focused on molecular fungal-plant interactions. Fungal cell wall biogenesis and modification of cell wall polymers is studied in *Colletotrichum graminicola.* The role of several chitin synthase genes in infection structure differentiation and chitin deacetylation during the process of fungal penetration of and establishment in the plant cell are main projects. In addition, mechanisms of salycilate-induced resistance in broad bean against fungal pathogens are being investigated. One focus is the cloning and study of the regulation of salicylate-responsive genes.

Plant pathogenic bacteria and their interactions with plants are studied at the molecular and genetic level (in both the bacterium and the plant) in the Department of Plant Genetics at the Institute of Genetics (head: Ulla Bonas, http://www.biologie.uni-halle.de/Genetics/index.html; e-mail: bonas@genetik.uni-halle.de). The interaction between *Xanthomonas campestris pv. vesicatoria* and its host plants (pepper and tomato) is used as a model system. Current research projects are focused on the analysis of the bacterial Hrp type III protein secretion system and the avirulence gene *avrBs3,* and on plant resistance genes. The AvrBs3 protein is probably injected into the plant cell where it acts as a trigger of the specific cell death reaction in the corresponding resistant pepper line. To unravel the initial signaling events, the Department is currently isolating plant proteins interacting with AvrBs3 in the yeast-two hybrid system. In addition, the Department has initiated a map-based cloning approach to isolate resistance genes from pepper and tomato genetically interacting with *avrBs3* and the homolog *avrBs3-2.*

### Institute of Plant Biochemistry (IPB) in Halle

Studies on plant-microbe interactions are also among the central research topics at the Leibniz Institute of Plant Biochemistry (IPB, home page: http://www.ipb.uni-halle.de) in Halle. The IPB is a non-university research institute with basic funding from the Federal and Land governments. In the IPB Department of Stress and Developmental Biology (head: Dierk Scheel, dscheel@ipb.uni-halle.de) non-host resistance of plants against fungal and bacterial pathogens is investigated using several experimental systems. Plant plasma membrane receptors apparently recognize typical microbial or plant cell wall constituents released during early stages of pathogen attack. Upon binding of these elicitors to their receptors, signal transduction processes are initiated that activate a multicomponent defense response. The molecular mechanisms of pathogen recognition and local as well as systemic signaling events are analyzed in *Arabidopsis,* tobacco, potato and parsley using different *Phytophthora* and plant-pathogenic *Pseudomonas* species. The IPB Department of Secondary Metabolism (Head: Dieter Strack) studies the symbioses between obligatory biotrophic fungi (e.g. *Glomus intraradices*) and the roots of terrestrial plants (e.g. barley, wheat, maize, tobacco, tomato). The arbuscular mycorrhizal fungi promote growth of the host plant, which in turn supplies carbohydrates to the fungus. Current research in the Department focuses on fungus-induced expression of the non-mevalonate plastidic methyl-erythritol-phosphate (MEP) pathway of carotenoid biosynthesis and the accumulation of apocarotenoids (C14-acyclic polyene esters and C13-cyclohexenone derivatives) in mycorrhizal roots. Fungal induction of carotenoid metabolism is accompanied by transient accumulation of phenolics (hydroxycinnamic acid amides) and jasmonic acid. One of the major goals is to understand the role of jasmonic acid and the involvement of phenolics and carotenoid metabolites in the developmental program of the fungus and functional maintenance of the symbiotic plant-fungus relationship.

### Institute of Plant Genetics and Crop Plant Research in Gatersleben

Another Leibniz-Institute is located approximately 60 miles from Halle, in Gatersleben: the Institute of Plant Genetics and Crop Plant Research (IPK, http://www.ipk-gatersleben.de/englisch/home-uk.htm). The IPK, formerly Zentral-Institut für Genetik und Kulturpflanzenforschung of the GDR, was founded in 1992. The Institute's objective is to carry out basic and applied research in the field of crop plant genetics as well as the conservation and evaluation of the genetic variation of crop plants, their progenitors and relatives. Among the interdisciplinary approaches, the following are relevant for plant-microbe interactions: the IPK harbors a well-known gene bank (contact: A. Boerner, e-mail: boerner@ipk-gatersleben.de), with a collection of approximately 100,000 accessions of many different plant species, a number of which have been tested for the presence of disease resistance genes. Two research groups are involved in map-based isolation of disease resistance genes. The Molecular Genetics of Cereals group (head: Andreas Graner, e-mail: a_graner@IPK-Gatersleben.de) is focused on molecular mapping of genes in barley conferring resistance to various fungal and viral pathogens and on the development of corresponding, selectable markers to be assayed by PCR-techniques. In addition, a comparative map of rice chromosome 1 and barley chromosome 3 was constructed to possibly exploit synteny for gene isolation. The main goal of the Gene and Genome Mapping research group (head: Martin Ganal, e-mail: ganal@IPK-Gatersleben.de) is the genetic mapping and molecular isolation of agronomically important traits in tomato, barley and wheat. One of the tomato projects deals with mapping and isolation of disease resistance genes, e. g., the gene Hero, conferring broad spectrum resistance against *Globodera rostochiensis.* The work on cereals is focused on the two most important crop plants in Germany, wheat and barley. For barley, techniques are being developed for the map-based cloning of resistance gene *Rh2* against scald (*Rhynchosporium secalis*).

There are a number of interactions and cooperations between the research groups in Halle (university and IPB) and the IPK Gatersleben. One example is a research network (Sonderforschungsbereich;SFB 363) funded by a grant by the Deutsche Forschungsgemeinschaft. The overall theme of the SFB 363 (http://www.sfb363.uni-halle.de/) is Plant Cell Biology (head: Ulla Bonas). Funding is for 3-year periods (up to a total of 12 years if evaluations are positive) and is granted to basic research projects on the basis of novelty and cooperation. The SFB 363 was founded 7 years ago and currently consists of 17 research groups.

### Technical University of Dresden

In the new Faculty of Biology, the Department of Molecular Genetics (Head: Michael Göttfert, e-mail: mgoettfe@rcs.urz.tu-dresden.de; http://www.phy.tu-dresden.de/bio/genetik/gen-home.html) studies the genetic basis of the interaction between *Bradyrhizobium japonicum* and legumes with a focus on transcriptional regulation of the bacterial genes involved. In addition, a physical map of the *B. japonicum* chromosome has been established, and part of the genome has been sequenced.

### University of Jena

The Institute of Microbiology in Jena houses a fungal collection of roughly 8,000 isolates, mainly zygomycete and ascomycete plant pathogens. This Fungal Reference Centre (head: Kerstin Voigt, e-mail: b5kevo@rz.uni-jena.de) together with the General Microbiology and Microbial Genetics group is involved in research programs on molecular phylogeny of fungi based on protein-coding genes and on development of molecular probes for a variety of plant pathogens.

There are three departments working on various aspects of prokaryotic and eukaryotic microbes. The Department of Applied and Environmental Microbiology (head: Gabriele Diekert, e-mail:

b8diga@uni-jena.de; http://www.uni-jena.de/biologie/tech_mikrobio/) concentrates on biochemistry and physiology of degradative capacities of anaerobic prokaryotes (methyltransferases, dehalorepiration). The Department of Microbial Phytopathology (head: Erika Kothe, e-mail: ekothe@pmail.hki-jena.de) studies ectomycorrhizal relationships between *Tricholoma* species and their host plants pine and spruce, as well as on mating type differentiation and the characterization of MAT loci in the basidiomycete *Schizophyllum commune.* The Department of General Microbiology and Microbial Genetics (head: Johannes Wöstemeyer, e-mail: b5wojo@rz.uni-jena.de; http://www.uni-jena.de/biologie/mikrobio/) also, besides other projects, works on mycorrhizal interactions. The experimental system is an arbuscular mycorrhizal fungus, *Glomus intraradices* and its host plant clover. The aim is to perform expression studies on key genes that control the cell cycle in the fungus and the host. The group is also involved in analyzing at the molecular level the host relationships between the mucoralean fungus *Parasitella parasitica* and its numerous fungal hosts. The parasite is a fusion biotroph. Infection is accompanied by the formation of a limited cytoplasmic continuum between the partners. During this process genes are stably transferred from the parasite to the hosts.

### University of Rostock

The Institute of Phytomedicine (head: Andreas von Tiedemann, e-mail: avt@agrarfak.uni-rostock.de; http://www.agr.uni-rostock.de/phyto/version_gb/research.htm) works on a number of different plant pathogens and their control. The group is developing and testing biological plant protection systems for control of fungal pathogens, and biological control of root knot nematodes. Another focus is on oxidative stress by pathogens and environmental influence and the impact of atmospheric trace gases on fungal plant diseases. Some of the current projects focus on the role of active oxygen radicals in pathogenicity of *Botrytis cinerea,* genetic characterisation of *Verticillium dahliae* populations, and the use of *Coniothyrium minitans* for control of *Sclerotinia sclerotiorum* in infested agricultural soils.

As you can see, there is a lot happening and I must say that for me personally these are exciting and challenging times. I apologize for being incomplete and would like to thank my colleagues in Halle and Jena for their help.

**Ulla Bonas**
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Halle, Germany
August 30, 1999

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## A COLUMN FROM THE PRESIDENT

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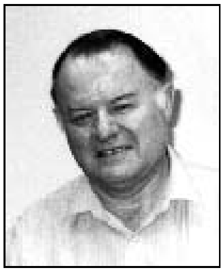
### Shifting Times



I would first like to thank Pierre de Wit and all his helpful colleagues for the excellent MPMI Congress Meeting in Amsterdam in July this year. Not only was it an exciting science meeting but a very memorable one as well. The momentum in the various sections of the field has not been lost during our three year break from the 1996 get together. This is one of the most pleasing aspects to all involved in the organization of the IS-MPMI.

I would like to wish Jan Leach the very best as the incoming President and to thank the various members of the Board and the folks, Kayleen and Steve at headquarters for their help over the years.

We have, however, another challenge that is now starting to gather momentum - the increased anxiety of the general public to the sale and use of genetically modified plant products. At the end of June the environment ministers of the European Union met in Luxembourg with the aim of examining the rules for approving new Genetically Modified Organisms (GMOs). This was largely in response to the growing public concern about the safety of gene technology especially as applied to food.

The EU's Commission has proposed changes to the process by which new GMOs will be authorized in the future. All ongoing applications are currently blocked until a new approval process is in place which might take up to 18 months. France and Greece, supported by Italy, Denmark and Luxembourg, have led calls for a moratorium on their use. The environmental pressure group, Greenpeace, welcomed the moratorium stating "GMOs are an environmental threat and an unjustified experiment with food" and it hoped that a temporary halt to approvals might lead to a future complete ban.

In July, Greenpeace became more militant in UK by sending its "eco-warriors" in on dawn raids to trash GMO field crop trials. The press and the TV reporting, generally in Britain, during this period was very negative to the use of GMOs. In early August, the pharmaceutical company AstraZeneca, which has a very substantial commitment to GM food, was "reconsidering" its "options" in this area of agribusiness. The "feed-back signal" from Europe to the USA has now been successful in that the Department of Agriculture and various farmers are reconsidering their commitment to GMOs in the future.

What has this got to do with our IS-MPMI? Well, I suspect that a substantial amount of recent molecular genetic research in areas of Plant-Microbe Interactions has been based on the notion that one day GMO plants, containing spin-offs from this research, would be used in 21st century agriculture. So what has happened? There has been a growth of an anti-science movement, fear of multi-national corporate control of food production, arrogance by the multi-nationals in their public relations, and a miscalculation by the corporations and the science community of the public response to GMO technologies when applied to food products as opposed to healthcare and medicine for which there has been greater public support to date. There are a whole series of overlapping issues and various political agendas running in parallel here and the public responses often do not discriminate between them but just react with a blanket condemnation. The two opposite views have been summarized well in the recent New Scientist, 14th August, pages 46-47.

If we do not listen perceptively and carefully to the public demands and become an active and informed part of the debate, we in the PMI fields of research might be looking at 5-10 years or more inhibition of GMO development. Therefore, I ask all participating scientists in PMI research to take every opportunity to explain to the general public why they are doing their research, evaluating the positives and the negatives, and to seek to have support for well thought-out risk assessment experiments. Remember the question that Professor John Beringer poses to the reader (*New Scientist,* 14th August, page 47): "Why did they burn witches in the Middle Ages? Easy. It was easier to kill them than to find out if they really caused harm!"

Barry Rolfe

Barry Rolfe

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## Editor's Note

### Editor's Note

It has been a pleasure to serve for the last five years as the editor of the IS-MPMI Reporter. This issue has been especially exciting to edit as it is filled with contributions that were generated by our members. The research in this field is truly moving to an impressive level of technical sophistication and knowledge and the subjects of study continue to expand. When I first joined this field in 1976, the two major systems of study were *Rhizobium* and *Agrobacterium* and there was little emphasis on the host. New techniques were just being developed for gene transfer and molecular genetic manipulation of these organisms.

It has been truly exciting to see how this field has grown and matured and the cadre of bright scientists which has been attracted to the study of molecular plant-microbe interactions from around the world. Let us hope that our membership will continue to expand and that the Reporter continues to serve as a mechanism for communication of the exciting research opportunities that exist in the field the MPMI.

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# *Lotus Japonicus:*
# Functional Genomics Update

## Introduction

The study of nodulation and nitrogen fixation provides insight into plant developmental processes as well as mechanisms of plant-microbe interactions. Fueled by the success of *Arabidopsis,* model legumes have facilitated a concentrated and cooperative research approach into this exciting area of plant science. While model legumes are not suited for all types of investigation, they excel in the analysis of nodulation biology and mycorrhizal associations, both processes being absent in *Arabidopsis* (Kolchinsky et al., 1996).

Functional genomics combines structural analyses of the genome with expression studies. Indeed, classical structure: function paradigms are being addressed. Because of bioinformatics and new multiplexing technologies such as high throughput sequencing, microarrays, virtual mapping, and multi-locus DNA profiling, multiple genes can be analyzed concurrently, permitting investigation of gene systems, rather than single genes.

For legumes, two species, namely *Lotus japonicus* and *Medicago truncatula,* have developed as tools of genomics. Although some duplication of effort, division of already limited funding sources, and friendly competition are expected, one sees advantages: the possibility to compare legume genome structure and function to develop paradigms and data sets useful for other legumes such as soybean, chickpea, bean, and pea, which are plagued by either larger genomes, low transformation frequencies, or both. Additionally, commonalties and differences produced by the different nodulation patterns (determinate vs. indeterminate nodule type) can be addressed.

## *Lotus japonicus:* biology and genetics.

These features have been extensively reviewed (Handberg and Stougaard, 1992; Jiang and Gresshoff, 1997). The plant is the diploid (n=6) relative of *L. corniculatus* (birdsfoot trefoil), a forage legume. Chromosomes are heteromorphic. The genome size is given as "two and a half times" that of *Arabidopsis.* Since this value has changed over the last decade, but with its sequencing being nearly completed (J. Byrum, World Soybean Research Conference, Chicago, Aug. 1999), one should assume a *L. japonicus* genome size of about 300-350 Mb. Genotype Gifu was arbitrarily chosen as the reference genotype.

*Mesorhizobium loti* strain NZP2235 nodulates *L. japonicus* efficiently, but has a limited genetic database. It is of additional value to Lotus research that the broad host range bacterium, NGR234, also nodulates and fixes nitrogen with *L. japonicus* (Hussain et al., 1999) and provides information, including bacterial mutants, a completely sequenced and transcriptionally mapped 534 kb symbiotic plasmid and structural knowledge of lipo-oligosaccharide nodulation factors and surface molecules involved in plant-microbe interactions.

To facilitate mapping of genes, several useful populations were produced. The Aarhus lab created an interspecific cross between *L. japonicus* cv. Gifu and *L. falciflora.* Molecular polymorphisms based mainly on AFLPs and EST were mapped. Our group made a F2 population from a cross between *L. japonicus* ecotypes Gifu and Funakura (Q. Jiang, pers. comm.). Molecular markers were mainly based on DAF markers and supplemented with morphological markers. The F2 population was advanced to an F6 of recombinant inbred lines

(RILs) to facilitate fixation of markers as homozygotes. An additional F2 population of a cross between Funakura and Gifu carrying the *har-1* (hypernodulation and altered root phenotype) mutation is available.

The F2 map at present contains about 60 markers, and spans 500 cM in 11 linkage groups. Linkage groups are defined by dominant DAF markers from either parent as well as some co-dominant markers obtained by using soybean SSR primers. Group joining using codominant markers is urgently required. EST polymorphisms were detected in the Funakura/Gifu cross and are being mapped on the RIL map. RILs are available for international sharing (see Limani et al., 1999). The *har1* gene was mapped between two DAF markers, but at distances of about 5-7 cM, not close enough for positional cloning. An allelic mutation, *sym16,* was also mapped closer to two AFLP markers on the interspecific map (J. Stougaard, pers. comm.). Map-based cloning of the *har1* (sym16) locus is in progress.

### BAC library of Lotus japonicus.

Pillai et al. (1996) described the first isolation of BACs and YACs of *L. japonicus.* Clones were small on average and their number was limited. A library of Gifu was constructed in vector V41, which is transformable into *Lotus* (A. Men, unpublished data). The average insert size is about 95 kb. With 25,000 clones being arrayed in 384 well format as well as on Nylon membranes, this represents a 6-7 fold genome coverage. Pools and filters are available upon request and for a small handling charge. The V41 library was derived from nuclei of dark treated plants and has low organelle DNA content. Clones homologous for *Lotus* ESTs were isolated. A second library was constructed by Skot et al. (pers. comm.) with Gifu but using vector pBACBelo11 (F factor-based). Insert size is about 75 kb, with about 30,000 clones available. Having multiple libraries increases the chance for successful gene detection.

### Expressed sequence tags (ESTs).

Considerable effort was placed into this aspect of functional genomics. Szczyglowski et al. (1998) described the isolation of about 100 nodule-related ESTs. Further characterization of some of these was published. Major efforts exist in Japan (Dr. Tabata at the Kisawa Institute, Chiba) and Germany (M. Udvardi, MPI Golm, pers. comm.) to isolate and sequence ESTs from *L. japonicus.* For example, the Golm group has isolated 1000 *Lotus* nodule ESTs, sequenced them, and deposited the information in a public database. Funds for sequencing another 10,000 ESTs are available from the German group. The Aarhus group has sequenced 640 ESTs and will deposit these. The Japanese group aims to release all 40,000 ESTs, although it is unclear at this moment, how far the program has progressed. cDNA libraries for nodules, symbiosome membrane proteins, roots and shoots are available.

### Mutants.

To couple structure with function, genetic analysis of mutants is essential. A large number of symbiotic mutants affecting mycorrhizal as well as *Rhizobium* associations exist in *L. japonicus* (Szczyglowski et al., 1997; Schauser et al., 1998; Wegel et al., 1998). Mutagenesis was carried out by EMS, fast neutrons, T-DNA as well as Ac/Ds insertions. Fast neutron-induced mutants isolated in our laboratory include non-nodulators as well as non-fixers (A. Hussain, pers. comm.). Such mutants provide the advantage that if large regions of the genome are deleted, gene addition of recessive alleles will lead to gene expression. Molecular comparison of deletion mutant vs. wild type can reveal quickly linked molecular markers. Mutant and parent can be used as near-isogenic material differing only in the deleted region containing the gene of interest. For example, in *Glycine soja* our group used fast neutrons (provided by Dr. Helmut Brunner, IAEA, Vienna) to make a supernodulation mutant (*fn37*), that lacks about 100 kb of DNA covered by a BAC contig. Clearly the supernodulation gene is located on that region as defined by the physical loss of endclone markers, ESTs, and RFLPs (A. Men and A. Hussain, pers. comm.; Gresshoff et al., 2000).

The most exciting advance in *L. japonicus* is the recent application of insertional mutagenesis and subsequent gene isolation (Schauser et al., 1999). T-DNA insertion allowed the isolation of a non-nodulation mutant (*nin1*). Characterization of the flanking DNA revealed a transcriptional factor gene, which shares homology to a gene involved in gametogenesis in the green alga *Chlamydomonas reinhardtii.* Interestingly, but perhaps insignificantly, both nodulation and gametogenesis are regulated by external nitrogen supply. This is the first time that the gene causative for a symbiotic phenotype has been isolated. Up to now we were restricted to a collection of symbiotic mutants for which the causative gene was unknown, or a collection of well-characterized nodulin clones, for which a phenotype, and thus causal involvement, was not demonstrated.

Mutants altered in both nodulation and mycorrhizal association were isolated and characterized (Wegel et al., 1998). This interaction between symbiotic processes on a genetic level supports agronomic and biological studies suggesting the same.

### Promoter trapping for gene discovery.

*Lotus japonicus* is efficiently transformed by *Agrobacterium tumefaciens* as well as *A. rhizogenes* (Handberg and Stougaard, 1992; Stiller et al., 1997; Oger et al., 1996; Limani et al., 1999). Transgenic plants are fertile and nodulate. This ability has been used to study promoter activities of symbiotic genes [e.g., *enod40* (an early nodulin gene of unknown function), *nod26* (a symbiosome membrane protein gene (M. Udvardi, pers. comm.) or lbc3 (leghemoglobin)] fused to the beta-glucuronidase (gus) gene]. Over-expression and anti-sense studies with genes of symbiotic interest such as the root-specific glutamine synthetase (Limani et al., 1999), uricase, auxin-response elements, the putative lectin-like, the dominant ethylene insensitivity receptor ETR-1 (D. Lohar, pers. comm.), and PEP-carboxylase (D. Lohar with K. Schuller, Adelaide) are being conducted.

One of the unique applications of high transformation frequency of *L. japonicus* comes through promoter-trapping as well as activation tagging (J. Webb, pers. comm.; M. Chirazzu, pers. comm., H. Schlaman, pers. comm.1999). The former approach uses a promoter-less reporter gene such as gus, delivered through an insertional vector such as T-DNA. The second approach uses a strong promoter cassette to activate genes. One dreams of a spontaneously nodulating plant, defining new genes in the receptor or the connected signal transduction pathway.

The promoter trapping technique allows: (i) evaluation of the expression pattern of a gene combining biology with genetics; (ii) detection of a gene that is expressed in multiple organs such as roots and nodules, which would otherwise not be difficult to access by molecular tests such as subtractive hybridization or differential display (Appel et al., 1999); (iii) isolation of flanking DNA assuming that a single insertion line was isolated or segregated; and (iv) isolation of a mutant phenotype in a homozygous segregant assuming that the trapped gene is not redundant on either genetic (i.e., duplication), biochemical (i.e., alternative pathways), or physiological (i.e., the activity is a response) levels. Promoter trapping has been successful (Martirani et al., 1999). About 2.2% of *A. tumefaciens* transformed lines (using strain LBA4404 carrying a pDBIN19GUS) showed expression in either early root or nodule development (D. Lohar and J. Stiller, pers. comm.). Trapping frequencies were 5-fold higher using *A. rhizogenes* transformation of roots (Martirani et al., 1999). However, the significance of this difference requires further investigation. It may reflect preferential insertion into tissue-active genes, or an artifact of the selection system. For example, we discovered that *Agrobacterium* strains carrying the promoter-less gus construct were able to express glucuronidase activity, presumably from promoter read-through. Insertion of the gus-intron gene prevented this residual, but problematic activity. Great care needs to be taken before interpreting blue tissue and positive PCR bands as evidence for transformation!

Schlaman et al. (1999) constructed a new trapping vector in which the gus gene is interrupted with a plant intron, the gfp gene is fused to the gus gene, and several termination, and intron splice sites have been introduced in the upstream region. Using this vector they detect about 10% nodule related trapping.

We have isolated and propagated a high number of tagged lines with varying expression patterns. Different parts of the root, or nodule are concomitantly expressing the reporter gene, showing that common genes are used in "developmental symphonies." To illustrate, a few lines will be described.

Line *FATA MORGANA* expresses gus in the nodule interior, even at an early stage before emergence from the cortex. Mature nodule are intensively blue suggesting a strong promoter. Some activity, seen as a faint "mirage" in the uninoculated plant roots exists in the pericycle. Flanking DNA suggests that the *FATA MORGANA* gene is similar to the leghemoglobin multigene family of legumes. While it is rewarding to prove that a known nodule gene can be trapped, it is even more significant that the gene has residual expression in the pericycle, and that this expression is not affected by inoculation. The phylogenetic and ontogenetic significance of such expression pattern is immense as it may provide a clue of where symbiosis genes originated.

Line *TIMPA* is similar but expresses only in the nodule. Expression is intense even 4 days after inoculation. The primary transgenic of *TIMPA,* as well as *FATA MORGANA,* has three gus inserts of which only one is active as judged by segregation analysis. A general conclusion in this area is that insertions are independent and tend to segregate from each other.

Line *CHEETAH* is again similar to the previous two as it expresses in nodule primordia and nodules. However, expression in the nodule subsides 11 days after inoculation with *Rhizobium,* first being restricted to the nodule vascular trace, then the nodule base, then disappearing totally by 14 days after inoculation. *CHEETAH* expression in nodule primordia can be detected 24 hours after inoculation. In parallel *CHEETAH* also expresses in root meristems (both apical and lateral), where expression is persistent. Expression is also found in the base of the lateral root suggesting an activity separate from cell division activity, perhaps involving metabolite transfer. *CHEETAH* is expressed within one day of germination of the seed in the radicle's meristem. Its overall pattern is similar to the *aux1* gene in legumes as determined by in *situ* hybridizations.

*CHEETAH* also has three independent gus insertions and single insert lines showed that a 4.7 kb *Eco*RI fragment is required for activity. Flanking upstream and downstream DNA was isolated which in turn hybridized to the 4.7 kb fragment. The two flanking regions are contiguous on an *Arabidopsis* BAC clone, suggesting that the genomic "supermarket" of the crucifer can serve for further functional genomic analysis of nodulation and lateral root initiation and growth. Detailed analysis of this and other promoters is in progress.

A key question remains unanswered. What happens when *CHEETAH* is knocked out? Preliminary data suggest that most (17/18) T2 lines with gus expression are heterozygous, indicating perhaps strong selection against the homozygote (D. Lohar and J. Stiller, unpubl. data). Even stronger distortions of segregation for gus expression also occurred in *FATA MORGANA* as well as *TIMPA,* suggesting that yet unexplained mechanisms controlling gene expression in transgenic lines occur.

## Future outlook.

*Lotus japonicus* has demonstrated its utility for investigating genetic and biochemical processes underlying legume development and symbioses. Important tools are being developed which allow the investigation of gene systems. We can foresee the development of expression microarrays and proteomics, as well as a more complete analysis of mutant genes. Trapping and activation strategies will lead to an understanding of how genes work together in different organs. Their phylogeny will aid in extension of knowledge from model legumes to crop legumes through microsynteny.

Gene discovery is an important, yet publicly overlooked component of biotechnology. Knowledge of genes will allow our directed improvement of plants through metabolic engineering (altering oils, secondary products, phytoestrogens, etc.) as well as the engineering of plant architecture. Legumes offer a new perspective in metabolic engineering as well as pharmacological engineering because of their abundance of novel biochemical pathways such as novel hydroxylations. The combination of functional genomics, structural genomics, bioinformatics, and gene transfer technologies promises to provide crop plants with properties designed to meet the challenges of the new millennium.

We can see that a lot has been done, but more is needed. We need to establish a functional electronic network beyond the present website (http://www.psu.missouri.edu/lnl/lotusjaponicus/lj.htm).

The map needs to be more complete, and deposits of tissue-specific cDNA libraries need to be made and micro-arrayed. More transgenic lines expressing reporter genes behind tissue or process-specific promoters are required. ESTs need to be placed on the map, and regional contigs need to be generated. The application of chromosome painting to align genetic and physical maps is valuable, as is the development of a proteomics database. More tagged genes need to be isolated and understood. Studies of gene interaction is a major goal. The extent of synteny to other legumes and indeed to other plants needs to be determined.

The experimental advantages of *Lotus japonicus* and the strong sense of international and national cooperativity and sharing, as well as published results and related insights, will naturally draw researchers to this organism. The next few years will indeed be exciting for the nodulation community as we start to understand the processes relating to nodule induction and function, as well as its relation to other symbioses.

Thanks go to the members of my laboratory work and other colleagues for sharing unpublished results. Apologies to those whose work I either failed to mention or misrepresented; either occurred without intent. NSF and The Eppley Foundation are thanked for support.

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**Agricultural Microbes Genome I Conference**
**January 13-14, 2000, San Diego, CA**
In order to address the growing area of agricultural microbial genome research, the first annual Agricultural Microbes Genome meeting will be held in San Diego, CA, January 13-14, 2000. This meeting will consist of a poster session and three lecture sessions in the areas of: sequencing; technology and bioinformatics; and functional genomics/applications. This program will be held at the Town & Country Hotel immediately following the Plant & Animal Genome VIII meeting. Information on the meeting (including on-line registration forms and abstract instructions) is available on the web at http://www.ag-microbial.org/

**Signals and Signal Perception in Biotic Interactions in Plants (C3)**
**February 22 - February 27, 2000, Taos, New Mexico**
Organizers: Richard A. Dixon and Maria J. Harrison
**Early Registration: December 20, 1999**
Sponsored by Monsanto Company and The Samuel Roberts Noble Foundation, Inc., Contact: Paul Lugauer, Keystone Symposia, Drawer 1630, 221 Summit Place, Unit 272, Silverthorne, CO 80498, Telephone 970-262-1230 ext. 111, Fax: 970-262-1525 FAX, E-mail: keystone@symposia.com
Website: http://www.symposia.com/home.html

**28th Rice Technical Working Group Meeting**
**February 27-March 1, 2000**
Beau Rivage 875 Beach Blvd., Biloxi, MS 39530
Meeting website: http://www.msstate.edu/dept/drec

**5th European Conference on Fungal Genetics**
**March 25-29, 2000, Arachon, France**
Contact Beatrice Turcq: ecfg5.arachon@ibcg.u-bordeaux2.fr

**2nd International Biometals Symposium "Biometals 2000"**
**April 24-29, 2000, University of Tubingen, Tubingen, Germany**
Meeting website: http://www.uni-tuebingen.de/biometals2000

**Plant Signalling 2000**
**May 18-20, 2000, Pennsylvania State University, University Park, PA**
Meeting website: http://www.lsc.psu.edu/phys/annualsym.html

**The Canadian Phytopathological Society and the Pacific Division of the American Phytopathological Society joint meeting.**
**June 18-21, 2000, Victoria, British Columbia, Canada**
Contact: Conference Management, Division of Continuing Studies, University of Victoria, PO Box 3030, Victoria, B.C.
V8W 3N6 or visit the meeting website at: http://www.uvcs.uvic.ca/conf/cps_aps/

**6th International Congress of Plant Molecular Biology**
**June 18-24, 2000, Quebec, Canada**
Meeting website: http://www.ispmb-2000.org

**Molecular Biology of Model Legumes**
**June 24-28, 2000, John Innes Centre, Norwich, U.K.**

The meeting will cover recent advances in the Molecular Biology of Model and Crop legumes with special emphasis on *Lotus japonicus*. The scientific program includes: Development of molecular and genetic resources; functional genomics; genetics and comparative mapping; map-based cloning programmes; root nodule development; genes involved in: Arbuscular mycorrhiza, root nodule symbiosis, leaf/flower/seed development, nitrogen/carbon metabolism. To receive a first circular, send an e-mail message "circular" to legume@uea.ac.uk

**IV European Nitrogen Fixation Conference**
**September 16-20, 2000, Sevilla, Spain**
Contact: Profs. A.J. Palomares and J. Olivares Dept. Microbiologia, Facultad de Farmacia, Universidad de Sevilla, 41071 Sevilla, Spain, Fax: +34 954556924, E-mail: 4thenfc@cica.es
Website: www.eez.csic.es/~4thenfc/

**4th International Rice Genetics Symposium**
**October 22-27, 2000, IRRI, Los Banos, The Philippines**
Contact Dr. G. S. Khush at email: g.khush@cgiar.org

**International Symposium on Durable Disease Resistance: Key to Sustainable Agriculture**
**November 28 - December 1, 2000**
Contact: Dr. J.E. Parlevliet, Plant Breeding, Wageningen UR, PO Box 386, NL 6700 AJ Wageningen, The Netherlands
Fax: +31 317 483457, E-mail: jan.parlevliet@users.pv.wau.nl
Website: http://www.spg.wau.nl/pv/symposium.htm

**Third International Conference on Mycorrhizas**
**July 8-13, 2001, Adelaide, South Australia**
Contact: icom3@camtech.net.au
Website: http://www.waite.adelaide.edu.au/soil_water/3icom.html

**IS-MPMI Meeting**
**July 10-15, 2001, Madison, Wisconsin USA**
The 2003 meeting will be in St. Petersburg, Russia

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## EMPLOYMENT OPPORTUNITIES

### Postdoctoral Position in Molecular Plant Pathology

A postdoctoral position is available immediately for 3 years at the Ohio State University-OARDC Wooster campus to study nonhost resistance of *Nicotiana* to the oomycete plant pathogen *Phytophthora infestans*. The research will focus on the use of molecular genetic approaches to identify and dissect components of nonhost resistance in the plant and the pathogen (*Plant Cell,* 1998, 10:1413-1425; *Mol. Plant-Microbe Interact.,* 1997, 10:13-20; 10:1028-1030; *Trends in Plant Sciences,* 1999, 4:196-200). Background in molecular genetics or molecular biology and experience with genomic and cDNA library construction is required. Applicants should submit a cover letter describing experience, a cv, a list of publications, and the names of three references to Sophien Kamoun, Dept. of Plant Pathology, The Ohio State University-OARDC, 1680 Madison Ave., Wooster, OH 44691; kamoun.1@osu.edu; http://www.ag.ohio-state.edu/~plantdoc/faculty/sk.html.

### Postdoctoral Research Fellowship

A postdoctoral position is available to improve pathogen detection in an in vitro-virus elimination program. We have established a large in vitro collection of single and mixed infections in *Malus, Prunus* and *Pyrus* and have ample experience with in vitro elimination of viruses. The successful candidate will be involved in the application of newly developed diagnostic tools on the level of ELISA, tissue printing, PCR and nucleic acid hybridisation. The successful candidate should have a thesis related to the topics mentioned above and ample practical experience in phytopathology, preferably in virology of fruit trees and/or grapevines. Some knowledge in plant tissue culture would be beneficial. The candidate MUST be available for a personal interview. Please send a curriculum vitae, list of publications, 2 letters of reference to: Ao.Prof. Dr. Margit Laimer da Câmara Machado, Institute of Applied Microbiology, University of Agricultural Sciences, Nußdorfer Laende 11, 1190 Wien. AUSTRIA Tel. 43-1-36006-6560 FAX 43-1-3697615 e.mail: m.laimer@iam.boku.ac.at

### Postdoctoral Research Fellowships

Two postdoctoral positions are available to investigate the fate of transgenic fruit trees carrying marker genes and different sequences derived from viral genomes. Work will have to be carried out in vitro, in the greenhouse, in a screenhouse and finally in the field under natural conditions. We have transformed a large number of *Prunus* and *Vitis* cultivars and rootstocks and have gained experience with in vitro and in vivo challenge infection experiments with Plum Pox Virus. The successful candidates will be involved in construction of new transformation vectors including tissue-specific and pathogen-inducible promoters, characterization of currently naturally occurring isolates and challenge infection experiments. Successful candidates must have extensive experience in plant genetics, plant molecular biology, and phytopathology, preferably in virology of fruit trees and/or grapevines. The candidates MUST be available for a personal interview. Please send a curriculum vitae, list of publications, 2 letters of reference to: Ao.Prof. Dr. Margit Laimer da Câmara Machado, Institute of Applied Microbiology, University of Agricultural Sciences, Nußdorfer Laende 11, 1190 Wien. AUSTRIA Tel. 43-1-36006-6560 FAX 43-1-3697615 e.mail: m.laimer@iam.boku.ac.at

### Research Assistant/Technician

The successful candidate will be involved in a project to investigate the fate of transgenic fruit trees carrying marker genes and different sequences derived from viral genomes. Work will have to be carried out in vitro, in the greenhouse, in a screenhouse and finally in the field under natural conditions. We have transformed a large number of *Prunus* and *Vitis* cultivars and rootstocks and have gained experience with in vitro and in vivo challenge infection experiments with Plum Pox Virus. The successful candidates will be involved in construction of new transformation vectors including tissue-specific and pathogen-inducible promoters, transformation experiments using *Agrobacterium tumefaciens,* characterization of currently naturally occurring isolates and challenge infection experiments. Some knowledge in plant tissue culture would be beneficial. The candidates MUST be available for a personal interview. Please send a curriculum vitae, list of publications, 2 letters of reference to: Ao.Prof. Dr. Margit Laimer da Câmara Machado, Institute of Applied Microbiology, University of Agricultural Sciences, Nußdorfer Laende 11, 1190 Wien. AUSTRIA Tel. 43-1-36006-6560 FAX 43-1-3697615 e.mail: m.laimer@iam.boku.ac.at

### Postdoctoral Research Fellowship

A 2 years postdoctoral position in Cytology is currently available in the Plant Biotechnology Unit at the IAM to investigate various aspects of a fruit tree breeding programme, especially the

fate of transgenic fruit trees carrying marker genes and different sequences derived from viral genomes. An efficient method of chromosome preparation, staining and in situ hybridization techniques for karyotyping of the major fruit tree cultivars should be established. Localization of genome-specific as well as introduced sequences should be achieved by FISH and other techniques. The successful candidate will be involved in the application of newly developed diagnostic tools on the level of ELISA, tissue printing, PCR and nucleic acid hybridisation. The successful candidate should have a strong cytogenetic background and be familiar with CLSM. Some knowledge in plant tissue culture would be beneficial. The candidate MUST be available for a personal interview. Please send a curriculum vitae, list of publications, 2 letters of reference to: Ao.Prof. Dr. Margit Laimer da Câmara Machado, Institute of Applied Microbiology, University of Agricultural Sciences, Nußdorfer Laende 11, 1190 Wien, AUSTRIA. Tel. 43-1-36006-6560
FAX 43-1-3697615 e.mail: m.laimer@iam.boku.ac.at

**Postdoctoral Position in Plant-Potyvirus Interaction**

A posdoctoral position is available to work on the genetics of resistance to potyvirus in pepper and tomato. The candidate will be in charge of a program we have already initiated : (i) fine mapping of a recessive potyvirus resistance gene in pepper using AFLP technology and (ii) study of synteny between pepper and tomato for potyvirus resistance genes. The ultimate achievement of this project (funded by INRA and GENOPLANTE) is to isolate a multiallelic recessive potyvirus resistance locus in pepper and to search for homologs in tomato. The position is located at the Genetics and Breeding of Fruit and Vegetable station of INRA (French National Institute for Agronomical Research, http://www.avignon.inra.fr/sapm/sapmO.html) near the city of Avignon (South of France). The pepper and tomato groups involve 7 research scientists. All the laboratories and greenhouse facilities necessary for the project are available. Applicants should have a PhD and demonstrated research experience in plant molecular biology and plant genetics, including genetic analysis and mapping. English language is required, some familiarity with French would be useful.

The position is available immediately for one year renewable. It is not open to a French candidate. Salary ranges 10-14 000 FF per month depending on experience. To apply or to receive more information, please contact Dr. Carole Caranta, INRA, Genetics and Breeding of Fruits and Vegetables, Dom. St Maurice, BP94, 84 143 Montfavet cedex, France. Phone : 33 (0)4 90 31 63 03, Fax : 33 (0)4 90 31 63 98, E-mail: carole.caranta@avignon.inra.fr (in case of absence, palloix@avignon.inra.fr) or directly send a CV, including a list of publications, along with the name and addresses of three possible references.

**Bioinformatics Scientist**

Looking for Bioinformatics Scientist to work in a lab that is discovering and developing novel mechanism-based drugs for the treatment of dysfunctions associated with memory and learning. Candidate should have knowledge of advanced data mining techniques (e.g. HMMs, PSI- BLAST, Smith-Waterman), gene family classification, EST database searching. This person will review genomic aspects to identify DNA sequences on the sub region of the brain, look at unknown functions of newly identified genes and look at new pharmaceutical targets. The candidate will also be proficient in at least one of the following programming languages: Perl, C, or Java. The candidate should possess M.S. or Ph.D. degree in a biological science, or related field with experience in bioinformatics. Our client is an emerging pharmaceutical company with research facilities in New Jersey and can provide excellent benefits. A high impact, high profile position with excellent opportunity for advancement. Geographic Location of Position: US-New Jersey. If interested, please contact: Sam Saint, DMC, Fax: 609-584-9575 Voice: 609-584-8733 Ext. 218, Email: 915608@candseek.com

**Two Ph.D. Positions**

Two Ph.D. positions are currently open in Molecular Microbial Ecology, involving research on the impact of PGPR inoculation on plant microbial populations and on the ecological significance of the bacterial parasite *Bdellovibrio.* Educational background in molecular biology necessary. For more information, contact Edouard Jurkevitch, Ph.D., Departement of Plant Protection and Microbiology, Faculty of Agricultural, Food and Environmental Quality Sciences, Hebrew University of Jerusalem, P.O. Box 12, 76100, Rehovot, Israel. Tel: 972-8-9481167, Fax: 972-8-9466794, E-mail: jurkevi@agri.huji.ac.il

**Two Postdoctoral Positions**

Two postdoctoral positions are available at LBMRPM, (http://www.toulouse.inra.fr/lbmrpm/eng/lbmrpm.htm) a CNRS-INRA institution in Toulouse, France, to work on the genomics of the plant-interacting bacteria, *Ralstonia solanacearum* and *Sinorhizobium meliloti.* This laboratory hosts 12 teams involved in the genetics and molecular biology of plant-microbe interactions (both on the microbe and plant partners) and has a recognized experience in bioinformatics. Both postdoctoral projects concern the analysis of genomic sequence data which are being produced by Genoscope (Evry, France) for R. *solanacearum* and by an international consortium for *S. meliloti* (http://sequence.toulouse.inra.fr/meliloti.html).
Projects will include the following tasks:

- expert sequence annotation

- integrated genome analysis (identification of genes of interest, genome organisation etc)

- development of functional approaches including transcriptome analysis.

The *Ralstonia* project will be developed in Chris BOUCHER's team that includes 9 people with substantial experience in the molecular genetic analysis of pathogenicity determinants. The *S. meliloti* project will be run in Jacques BATUT's group that includes 7 people involved in analyzing the nitrogen-fixing symbiosis between *S. meliloti* and its *Medicago* host-plants. Positions are open only to NON-FRENCH Citizens for up to two years. Salary, paid by Institut National de la Recherche Agronomique, will be ca 8000FF (1300Euros), net income. Candidates should have a strong background in molecular genetics. Solid knowledge of microbial physiology and/or prior experience in global genomic approaches will be appreciated. Interested applicants should send a CV, a letter stating his/her research interests and contact information for two references to C. BOUCHER, LBMRPM CNRS-INRA BP27, 31326 CASTANET-TOLOSAN CEDEX , France Tel: (33) 5 61 28 50 45, Fax: (33) 5 61 28 50 61 E-mail: boucher@toulouse.inra.fr or J. BATUT, LBMRPM. CNRS-INRA BP 27, 31326 CASTANET-TOLOSAN CEDEX, France Tel: (33) 05 61 28 50 54, Fax: (33) 05 61 28 50 61 E-mail: jbatut@toulouse.inra.fr
Visit Toulouse at http://www.mairie-toulouse.fr/accueilU.htm

**Postdoctoral Research Associate**

Applications are being accepted for an postdoctoral research associate position (pending funding approval) at the Pacific Forestry Centre Natural Resources Canada, Canadian Forest Service. The successful candidate should have demonstrated experience in molecular biology. Skills in recombinant DNA and familiarity with proteomic, yeast two hybrid systems, transgenic plant experience including the *Agrobacterium transformation* system, and in microarray-based screening of plant genetic material are required. Familiarity with techniques relating to protein/DNA interactions, RNA splicing and turnover, and/or protein purification are desirable. The applicant should possess writing, analytical and forward-thinking skills. The applicant is expected to interact and collaborate with the existing molecular biologist and protein biochemist in the laboratory. Send current curriculum vitae, list of publications, and names and addresses of three references to Dr. Abul K M Ekramoddoullah, Senior Research Scientist, Forest Biotechnology Network, Canadian Forest Service, Pacific Forestry Centre, 506 West Burnside Rd, Victoria, BC, V8Z 1M5, Canada, Tel: 250-363-0692 Fax: 250-363-0775 E-mail: aekramoddoul@pfc.forestry.ca, Website: http://www.pfc.cfs.nrcan.ca Electronic applications may be e-mailed.

**Delaware Biotechnology Institute/DuPont Corporation Joint Initiative in Ph.D. Training**

## in
Plant Biology and Biotechnology

As part of the graduate program in Plant Biology at the University of Delaware, the Delaware Biotechnology Institute offers a unique Ph.D. training in Plant Molecular Biology and related skills including biotechnology in collaboration with DuPont. Incoming students do one rotation at the university, followed by one rotation in a DuPont lab. Students can choose to complete their Ph.D. thesis at either institution. All students will have the opportunity to see how science is approached in both industry and academia. Coursework will be chosen from offerings at the University of Delaware so as to be individually tailored to student needs. Admission is open to students of all nationalities. Further information, a list of the participating University of Delaware faculty and DuPont participating scientists, and application are available on-line (http://www.udel.edu/plants/index.html). Or contact: Allan D. Shapiro, Assistant Professor, Department of Plant and Soil Sciences, 149 Townsend Hall University of Delaware, Newark, DE 19717-1303, Tel: 302-831-4889, Fax: 302-831-0605, Website: http://udel.edu/~ashapiro/

## Postdoctoral Research Associate Positions

Two postdoctoral fellow positions are available immediately to study the molecular basis of satellite RNA associated with bamboo mosaic virus. Topics includes the structure and function, satellite-based vector development and the interactions between the virus, satellite and hosts. Candidates with Ph.D. degree and experience in molecular biology are encouraged to apply. Salary ranges from US$25,000 - 31,000 per year depending on experience. Interested persons are encouraged to send curriculum vitae, copies of transcripts and three reference letters to: Dr. Na-Sheng Lin, Institute of Botany, Academia Sinica, Taipei, Taiwan 115, R. O. C. or FAX: 886-2-782-7954 or e-mail: nslin@ccvax.sinica.tw.edu

## Postdoctoral Position in Molecular Genetics/Molecular Cell Biology/Molecular Phytopathology

A postdoctoral position is available immediately for a molecular geneticist or molecular cell biologist to study *Phytophthora infestans,* the oomycete pathogen that causes late blight disease of potato and tomato. *P. infestans* is one of the world's most important plant pathogens, with an enormous economic impact.

The project is aimed at improving and optimizing DNA transformation and targeted mutagenesis in *P. infestans.* PEG mediated DNA transformation of *P. infestans* protoplasts is an established technique. However, as the transformation efficiency is relatively low, there is need for improvement. To this end transformation vectors modified with various DNA elements and strong oomycete promoters will be constructed and tested. Also the feasibility of *Agrobacterium*-mediated DNA transformation of *P. infestans* will be analysed. Recently we showed for the first time that targeted mutagenesis in *P. infestans* can be accomplished by homology dependent gene silenicing (van West *et al.* Molecular Cell 1999, 3, 339-348). As a target gene we used *inf1,* a gene encoding a protein elicitor of the hypersensitive response in tobacco. To optimize targeted mutagenesis we want to know whether homology dependent gene silencing is applicable to inactivate other genes in *P. infestans* and what the minimal requirements are to accomplish gene silencing.

The project will be performed within the framework of a *Phytophthora* Research Consortium composed of European and North-American research groups and funded by industry. The consortium research involves the generation of a *P. infestans* EST catalogue and gene expression profiling using DNA microarrays. The industrial partner will provide the genomics facilities whereas the university-based research groups will focus on the biology and functional genomics. Funding for the two positions is available for up to three years.

Applicants must be highly motivated and well trained, and must have a PhD in a relevant discipline. We prefer a candidate with experience in molecular cloning and/or transformation of filamentous fungi or plants. To apply send a curriculum vitae and names of three references to:

Dr. Francine Govers, Laboratory of Phytopathology, Wageningen Agricultural University, Binnenhaven 9, 6709 PD Wageningen, The Netherlands. For information Dr. Francine Govers, phone +31 317 483 138 E-mail francine.govers@ medew.fyto.wau.nl

### New MPMI Editor

A new Senior Editor position to cover the area of Mycorrhizal-Plant Interactions has been added to the MPMI Editorial Board. The Editorial Board is pleased to announce that Dr. Maria Harrison of the Samuel Roberts Noble Foundation, who has served as an Associate Editor for MPMI in the past, has accepted this 3 year position. Authors submitting manuscripts dealing with Mycorrhizal-Plant Interactions should submit their manuscripts (with original figures) to Dr. M. J. Harrison, Plant Biology Division, Samuel Roberts Noble Foundation, P.O. Box 2180, Ardmore, OK 73402. Two copies of the manuscript should be sent to the MPMI Editorial Office, 3340 Pilot Knob Road, St. Paul, MN 55121-2097.

If you have an employment or position wanted announcement you would like to see included in the next issue of the IS-MPMI Reporter to be published May/June send it to: Kayleen Larson, IS-MPMI Reporter, 3340 Pilot Knob Road, St. Paul, MN 55121 USA. Phone: +1.651.454.7250, FAX: +1.651.454.0766, e-mail: klarson@uslink.net.

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## People

This new section of the *Reporter* is devoted to keeping track of our members. We invite submissions listing your new address and responsibilities at a new post. Students: we want to publish the degree you obtained, discipline of degree, graduation date, home institution, and your thesis abstract. In addition, we solicit job advertisements and job requests at all levels. Send your information to Kayleen Larson at IS-MPMI headquarters, e-mail: klarson@uslink.net. Please feel free to include a photo of yourself and we will print it along with your information.

### Lamb appointed new director of the John Innes Center

The John Innes Centre (JIC) has announced the appointment of Professor Christopher Lamb as Director. Professor Lamb took up his appointment on October 1st. The John Innes Centre is Europe's premier research Centre in plant and microbial science with a worldwide reputation for scientific excellence.

"I welcome the challenge and opportunity to lead the JIC into the new century" said Professor Lamb. "JIC, together with its partners on the Norwich Research Park, is one of the most exciting life science research facilities in the world. I am delighted to be taking up this appointment at a time when the Centre is embarking on yet another phase of growth and development."

Professor Lamb is a world-renowned research scientist with particular interest in understanding the mechanisms by which plants resist disease and pest attack. He completed both his undergraduate and graduate degrees at the University of Cambridge before taking up a

Research Fellowship at the University of Oxford. He subsequently moved to the USA where he has spent much of his career, holding senior positions at the Salk Institute, La Jolla California, and the University of California, San Diego. At Salk he founded and directed an innovative plant biology department and guided the development of internationally recognized programs in plant metabolism, growth and development as well as disease resistance. Immediately prior to his appointment at the JIC Professor Lamb was, for a short period, Regius Professor of Plant Science at the University of Edinburgh.

### Gresshoff takes new position at the University of Queensland

Professor Peter M. Gresshoff has left the University of Tennessee and is now head of the Department of Botany at the University of Queensland (P.Gresshoff@botany.uq.edu.au). He continues to investigate the plant's genetic control of nodulation in legumes with specific attention to the functional genomic analysis of the supernodulation (*nts1*) region of soybean, combining the use of a BAC contig, ESTs and endclones, and fast neutron as well as chemically induced mutants to understand the genetic basis of systemic nodule and lateral root development. He and his fellow researchers are also using the high efficiency transformation system of the model legume *Lotus japonicus* to tag nodule and root-expressed genes using a promoter-less gus construct. They have initiated map-based cloning of symbiotic genes using molecular markers, and a transformation-ready BAC library.

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## IS-MPMI BOARD NEWS

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### IS-MPMI Board News

Congratulations to newly-elected members of the IS-MPMI Board: Carol Bender (USA), Jeff Dangl (USA), Shigeyuki Mayama (Japan) Anne Osbourn (Great Britain), and Herman Spaink (The Netherlands). The new officers for 1999-2001 are: Jan Leach, President; Ben Lugtenberg, President Elect; Carol Bender, Treasurer; Alan Collmer, Secretary. Other continuing members on the board include Pierre deWit, Noel Keen, Barry Rolfe (ex-president). Sally Leong, organizer of the next IS-MPMI meeting, was also appointed to the board. Thanks to members rotating off the board: Ulla Bonas, Eugene Nester, and Linda Thomashow. The next IS-MPMI meeting will be held in Madison, WI (USA), July 10-15, 2001. Announcements for this meeting will be forthcoming. An invitation from Professor Igor Tikhonovic to hold the 2003 ISMPMI Meeting in St. Petersburg, Russia was discussed and accepted. The facilities in St. Petersburg include a hall for more than 1000 people with many nearby hotels. St. Petersburg is the cultural capital of Russia, and 2003 will be the 300th anniversary of the city.

### IS-MPMI Board of Directors

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