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nomes of Plant Associated Microbes, Part II: Fungi and mycetes

Jonathan D. Walton
Department of Energy Plant Research Lab
Michigan State University
E. Lansing, MI 48824
email: walton@msu.edu

In the last issue of the *Reporter* I gave a brief synopsis of the major genome projects on plant-associated bacteria, both symbionts and pathogens. In this issue I cover plant-associated fungi, including Oomycetes.

The most significant feature of the fungi compared to bacteria is, of course, their larger genomes. Whereas bacterial genomes fall in the 2-6 MB range, those of fungi range from 8 Mb (*Ashyba*) to 40 Mb (a typical Ascomycete) on up to 240 Mb (the Oomycete *Phytophthora infestans*). This is the the main reason that at this point there are no *known* completed genomes. (Among filamentous fungi in general, *Neurospora crassa* will be the first; see www.genome.wi.mit.edu/annotation/fungi/neurospora/). I emphasize “known” because another difference between the genomes covered in the last issue and most of the projects covered here is that whereas most of the bacterial projects are publicly financed and therefore their results are being made rapidly available to all researchers without restrictions, many fungal projects are being privately financed by for-profit entities. Most of the companies who have paid for genomic sequencing realize that they cannot capture all of its value by their own in-house efforts and therefore welcome collaborations. Such collaborative access, however, is typically restricted to academic researchers, mediated through the agency of a company employee (who may not have sufficient time or interest to devote to the task), limited to searching on a gene-by-gene basis, and subject to the willingness of researchers (and their University administrations) to comply with whatever intellectual property rights policies the company imposes.

There are apparently a number of private genome efforts in both fungi and bacteria that have not been announced. I have avoided mentioning any projects that exist only by rumor; all of the private efforts listed here are those that have been publicly acknowledged to exist.

Due both to their larger genomes and to the relative lack of public funding, to date much of the “genomics” emphasis on plant-associated filamentous fungi and Oomycetes has not been on direct genomic sequencing but rather on efforts such as EST sequencing, construction of BAC libraries, generation of mapping markers, and population surveys of variability. Many of these projects

have been “pilot-scale,” designed to prove feasibility to granting agencies for funds to support more serious large-scale EST and genomic sequencing. In some cases the efforts have borne fruit, but many have not yet done so.

A report by Sophien Kamoun and Saskia Hogenhout (Ohio State University) on the recent Agricultural Microbes Genome 2 Conference held in San Diego in January, 2001, will be published in the March issue of *Plant Cell*. It covers both prokaryotic and eukaryotic microbes associated with plants.

1. *Phytophthora*. This genus of Oomycetes contains major pathogens of hundreds of crops including potato, tomato, cocoa, and soybean. Species are diploid with rather large genomes (estimated to be 62 Mb for *P. sojae*, 240 Mb for *P. infestans*, and 60-120 Mb for other species). Some EST sequences (<5000) are currently available in the public databases. The U.S. Department of Agriculture has recently funded a project, headed by Brett Tyler at UC Davis and including Howard Judelson, Ralph Dean, and Callum Bell, to sequence >50,000 ESTs from *P. infestans* and *P. sojae*. A description of the project was presented at the Agricultural Microbes Genome 2 conference in January, 2001; see http://www.intl-pag.org/amg/2/abstracts/W05_09.html. An international consortium of researchers called the Phytophthora Genome Initiative (PGI) has been established; information including sequence access is being coordinated through the National Center for Genome Resources (NCGR) (website: www.ncgr.org/pgi). Members of the PGI have to date constructed BAC libraries, cDNA libraries from various lifecycle and infection stages, and ~100 kb of genomic sequence. Syngenta (formerly Novartis) is also sequencing ~35,000 ESTs from *P. infestans*. The data from this project will not be immediately publicly available, but the goal is to integrate the results into the NCGR database by the end of 2002. See the article by Kamoun and Hogenhout cited above for more details.

2. *Magnaporthe grisea*. This Ascomycete is a major pathogen of rice. An international consortium dedicated to the eventual sequencing of the entire genome has been established (http://www.cals.ncsu.edu:8050/fungal_genomics/int_rice.html). Ralph Dean (NC State) and Dan Ebbole (Texas A&M) were recently funded by the USDA to sequence a 4.2-Mb chromosome of *M. grisea* and to sequence 35,000 ESTs. All data will be released to the major databases immediately. For details see http://www.intl-pag.org/amg/2/abstracts/W05_02.html. Intensive work on *M. grisea* at Paradigm Genetics, Inc. (Research Triangle Park, North Carolina) is focusing on a combination of genomic sequencing and high throughput gene knockouts (http://www.fgsc.net/asilo99/posterabs5.htm).

3. *Ashbya gossypi*. This Ascomycete attacks cotton and also citrus and tomato. It is transmitted by insect vestors. *A. gossypi* is distinctive in having a small genome (~8.8 Mb) and efficient homologous integration of transforming DNA. Sequencing of the genome has been almost completed through a collaboration of Syngenta (Novartis) at Research Triangle Park, North Carolina, and the University of Basel. Collaborators include Tom Gaffney, Peter Philippsen, and Fred Dietrich (http://www.fgsc.net/asilo99/posterabs1.htm). The sequence will eventually be published; in the meantime, academic labs can request defined *A. gossypi* sequences of interest via a material transfer agreement through one of the two involved institutions.

4. *Fusarium*. This large genus of ascomycetous fungi includes many important plant pathogens. *F. graminearum* (*Gibberella zeae*) is currently causing outbreaks of head scab (head blight) in wheat and other cereals and is of particular concern due to its production of grain-contaminating mycotoxins. A

public project to construct a BAC library and to sequence upwards of 16,000 ESTs has been funded and started; for more details see the article by F. Trail in the July, 2000, IS-MPMI Reporter. The genome is being sequenced by the Torrey Mesa Research Institute (TMRI), formerly Novartis Agricultual Discovery Institute (NADII), San Diego, California. Access to the data as well as from other plant pathogenic fungi being sequenced at TMRI (see below) will be possible via collaborative agreements. Information will be posted on the TMRI web site (http://www.nadii.com/) or contact Gillian Turgeon at gillian.turgeon@syngenta.com.

5. *Ustilago maydis* is a heterobasidiomycete that causes hypertrophy on maize. Its genome of ~20 Mb has been sequenced to 85% coverage under the direction of Regine Kahmann (University of Munich and University of Marburg) with funding from Bayer. Bayer currently has no intentions to make the data public but are willing to establish cooperations with individuals who intend to study certain genes and who have signed secrecy agreements. Exelixis, Inc. has announced that it has also sequenced 97% of the coding region of *U. maydis*, but no information on public access is given (http://www.exelixis.com/webpage_templates/press_release.php3?page_name=961681455).

6. *Cochliobolus heterostrophus* is the ascomycete pathogen that caused the 1970 Southern corn leaf blight epidemic. Its genome of ~35 MB is being sequenced by TMRI (Syngenta) in San Diego. Microarrays are also being designed. See above for contact information.

7. *Leptosphaeria maculans* is a filamentous ascomycete that causes blackleg disese of oilseed rape. An 180-kb genomic region that contains at least one avr gene is being sequenced by Genoscope in France. Funding has come from the EU-FAIR-IMASCORE project, coordinated by M.H. Balesdent (INRA). Collaborators include T. Rouxel (INRA), L. Cattolico and F. Artiguenave (CNS), and T. Rouxel (INRA). The BAC sequences will be freely available within 6 months of completion. See http://www.genoscope.cns.fr/externe/English/Projets/Projet_DM/DM.html. An Australian group under the direction of Barbara Howlett has sequenced some ESTs and genomic sequence from *L. maculans* (www.botany.umelb.edu.au/blackleg.htm).

8. *Mycosphaerella graminicola* (*Septoria tritici*) causes leaf blotch of wheat, a serious disease in Europe. Its genome is being studied by a Dutch consortium that includes Plant Research International (Dr. G.H.J. Kema), Syngenta, and the University of Wageningen (http://www.greenomics.nl/index_profile.html and http://www.plant.wageningen-ur.nl/news/). At the moment the data are not public but “later parts may be public.”

9. *Botrytis cinerea* is a non-specialized filamentous ascomycete that attacks hundreds of crops. Genomic sequencing efforts are ongoing at TMRI (Syngenta; see under *Fusarium* above for contact information). Genoscope, France, is doing BAC-end sequencing of *B. cinerea*. See: http://www.genoscope.cns.fr/externe/English/Projets/Projet_DI/DI.html.

10. *Blumeria* (*Erysiphe*) *graminis* is an obligate ascomycete pathogen of barley, causing the disease known as powdery mildew. Related species attack many other plants. Approximately 5000 ESTs have been sequenced by a project coordinated by Richard Oliver (Carlsberg Laboratories, Copenhagen; current address Murdoch University, Perth, Australia) and are publicly available at www.crc.dk/phys/blumeria.

11. *Trichoderma* spp. The genus contains several mycoparasitic species that offer potential for biocontrol of pathogenic fungi. Genomics research is being used as one avenue to a better understanding of the molecular mechanisms of parasitism. A consortium to produce >7000 unique EST sequences from *Trichoderma* grown under a variety of conditions (in association with fungal hosts and with plants, and on different media) is headed by New BioTechnic, S.A., a Spanish biotech company, along with researchers at the University of Salamanca, the University of Seville, Cornell University, Texas A&M University, the University of Naples, and the Technical University of Vienna. "The results will be evaluated for commercial applications and protected in specific cases. After this process, they will become available to the academic community." Contact Matteo Lorito, University of Naples (lorito@unina.it) for further information.

12. Mycorrhizal fungi. ESTs (~1200) have been sequenced from *Glomus intradices* by groups at the Noble Foundation (Ardmore, Oklahoma) and New Mexico State University, and are scheduled to be submitted to GenBank in the near future.

I apologize for any omissions. Comments, corrections, and updates are cordially welcome for inclusion in a future issue of the Reporter. Many thanks to all those who contributed the information on which this article is based.

The Scholarly Communication Crisis

Jan E. Leach
Professor of Plant Pathology and President of IS-MPMI
Kansas State University
Manhattan 66506-5502
e-mail: jeleach@ksu.edu

How many times in the past few years have you been asked to "prioritize" journals or scholarly publications for your institutional library with the knowledge that subscriptions to low priority journals would not be renewed by the library? And how many times have the libraries refused your request to add a new journal or publication because they have no funds to add new journals? While I cannot speak to the situation in other countries, the situation in the USA is abysmal.

Even with additional funds committed to our libraries, they still cannot keep up with the sharply increasing costs of scholarly journals. The Association of Research Libraries (ARL) reports that while their member libraries spent 2.7 times more money for serials in 1998-99 compared to 1985-86, they purchased 6% fewer titles (Kyrillidou, 2000a). If the same trends hold, our libraries will purchase 16% fewer serials in 2020 than in 1986.

What is happening? Since 1986, the average journal price has more than tripled. Why the huge increases in the prices of journals? Because publishing scholarly journals has become extraordinarily profitable. While there are real costs to publishing, i.e., copy editing, printing, and distribution costs, the costs of publishing scholarly journals are low compared to magazines because (1) we, the authors, using resources from our institutions and granting agencies, perform the research and contribute the papers to the journals for free or even pay a fee to have them published, and (2) we, the reviewers and editors, review submissions for free. Since our career advancement is dependent on our publishing in widely read journals, we bite the bullet and pay the cost.

Not-for-profit societies that publish journals, such as IS-MPMI, usually charge lower prices for their journals. For example, the institutional subscription prices for Molecular Plant-Microbe Interactions, which is published jointly by IS-MPMI and the American Phytopathological Society, are $410 per year for print only and $550 per year for online and print. Plant Cell, which is published by the American Society of Plant Physiologists, and the Journal of Bacteriology, which is published by the American Society for Microbiology, are $1690 (print and online) and $688 (print only) per year, respectively. The institutional rates for Plant Journal and Molecular Microbiology, both published by Blackwell Science, Ltd, a for-profit-publisher, are $2019 and $2,645 (print and online), respectively.

Even our own not-for-profit societies have recognized the value of publishing scholarly journals. Provost David Shulenburger of the University of Kansas reports that the costs of journals published by not-for-profit publishers (such as our scientific society publishers) have increased by 34.16% between 1994 and 1998 (Shulenburger, 1998). Although this is lower than the 56.63% increase for the 'for-profit' published journals over the same period, he reminds us that "it is dramatically higher-three times higher-than the 10.58% increase in the U.S. Consumer Price Index for this same period." It is interesting that "most journal publishers report operating profit margins of nearly 40% of revenue, roughly double the profit margins in the rest of educational publishing" (Kirkpatrick, 2000).

Will electronic publishing save the day? Electronic publishing offers many advantages. It gives us speedier access to articles, reduced costs for some parts of publishing, e.g., color images, and access to marvelous search engines. In fact, increasing numbers of libraries are spending more and more of their budgets on electronic publications (Kyrillidou, 2000b). But, there also are problems. Preservation and access to electronic resources are unresolved issues: will electronically stored materials be accessible in ten or fifteen years as paper journals are now? Perhaps more disturbing, electronic access may be severely restricted by license agreements, that is, once you lease the information, you may not be able to share it.

Clearly, the high costs and restrictive licenses imposed by many publishers of our journals are not going to be resolved by continued journal cancellations in our libraries. Recognizing this, groups of stakeholders in the scholarly publishing process have worked to build a set of principles to guide improvement of the ailing publishing system (http://www.arl.org/scomm/tempe.html) and have proposed alternative means to publish (http://www.createchange.org/home.html). Some of these are:

- Obligatory submission of all scholarly publications to NEAR, the National Electronic Article Repository, a centralized repository that is completely publicly accessible. Under a proposal suggested by David Shulenburger, journals would retain copyrights to their (your) articles only for a certain period of time, say 90 days, after which they would have to be available at NEAR. Publishers would thereby give up some of the value that their efforts add to scholarly research, but this seems reasonable since the value of articles also derives from the significant and largely unpaid efforts of authors, editors, and reviewers. It is unknown if such a policy would, in fact, result in any journals decreasing their subscription rates. This would quite likely not be the case for fast-moving fields, which arguably includes plant-microbe interactions, in

which 90 days is an inordinately long time to wait to see the latest results. It seems unlikely that readers of journals in hot areas would allow their libraries to cancel such subscriptions.
- An alternative offered by Charles Phelps (Provost, U. Rochester) complements Shulenburger's proposal. This model proposes separating the functions currently performed by the system of journal publication (quality certification, editorial improvement, distribution, indexing, and archiving), that is, breaking the link between the peer review process and the publication process. One way to do this would be by paying scholarly societies to conduct peer evaluation of manuscripts, and leaving functions such as publication and dissemination to other entities, for example, discipline-based or university-based computer servers.
- SPARC, the Scholarly Publishing and Academic Resources Coalition, fosters competition by providing member-generated incentive funding to competitive online journals as a means of introducing more balanced market forces into the publication industry (http://www.arl.org/sparc/home/index.asp?page=0).

Many scholars have urged the creation of electronic means for scholars to communicate directly with colleagues without the intervention of publishers. For example, the Open Archives initiative proposes to provide the means for such an exchange (http://www.openarchives.org/).

PubMed Central, created by the National Institutes of Health, allows publishers and other independent organizations to deposit articles and reports in the life sciences into a central online system that is freely available to the public (http://www.nih.gov/about/director/pubmedcentral/pubmedcentral.htm).

What can you, the authors, reviewers and editors, do to regain control of the scholarly communication system that was originally created to benefit our students, colleagues, and ourselves? I would urge you to:

- submit papers to quality journals that have reasonable pricing practices (for example, MPMI).
- examine the pricing, copyright, and licensing agreements of any commercially published journal you contribute to as an author, reviewer, or editor.
- consider using your influence by refusing to review for unreasonably expensive journals or to serve on their editorial boards.
- modify any contract you sign with a commercial publisher to ensure your right to use your work as you see fit, including posting it to a public archive.
- consider, if you are an editor of a too-costly journal, moving your journal to a non-profit publisher or resigning and allying yourself with a more reasonably priced competitive publication, in accordance with any applicable contractual provisions.

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MPMI 10th International Congress

On behalf of the organizing committee and International Society of Molecular Plant-Microbe Interactions, I invite you to participate in the upcoming 10th International Congress on Molecular Plant-Microbe Interactions. This Congress is the premier venue for communication of new biology related to the molecular study of plant-microbe interactions. The main Congress will take place from July 10-14, 2001 at the Memorial Union of the University of Wisconsin, Madison U.S.A. A satellite meeting on Medicago will be held from July 7-9, 2001 immediately before the Congress. Douglas Cook is organizing this latter event. A workshop on new and innovative methods being used to teach molecular plant-microbe interactions will be held on July 10, 2001. Caitilyn Allen is hosting this event. A preliminary copy of the program of the Congress is available at the web site (http://www.plantpath.wisc.edu/mpmi/). We have invited 56 world-class speakers and all have agreed to participate. Thirteen additional speakers will be chosen based on information provided in the abstracts. We hope that this will be the largest MPMI meeting to be held to date. Attendance of this Congress has increased steadily since its inception some 20 years ago. Our facilities at the University of Wisconsin can accommodate 1300 participants. To encourage attendance by students we have reduced the student registration fee and are making available university residence halls for housing at a reasonable cost.

We look forward to seeing you at the Congress!
Sally Ann Leong

MPMI Announces New Editorial Board Members

In January, 2001, the new editorial board of MPMI began its 3-year term. **Herman Spaink** replaces **Jan Leach** as editor-in-chief and is joined by 10 new senior editors. To acquaint IS-MPMI members with the new board members, brief biographies are presented.

Herman Spaink was a senior editor of MPMI from 1997 to 2000 in the area of microbe-plant symbioses. In 1999, he was elected to the board of directors of IS-MPMI. As a function of his position as editor in chief of MPMI, he is also a member of the publication board of The American Phytopathological Society. Since January 1998, he has been a full professor in molecular cell biology at Leiden University, Leiden, the Netherlands. His research currently focuses on the mechanism of signal transduction of Nod factors and chitin oligosaccharides. The plant model system now used for this research is *Lotus japonicus*. He is also studying the link with chitin oligosaccharide signaling in zebrafish embryogenesis. His expertise is mainly in the biochemical aspects of biology. More recently, he became involved in the establishment of a state-of-the-art microscopy center at Leiden University, which focuses on modern fluorescence analyses techniques such as two-photon microscopy, correlation

spectroscopy, and (in collaboration with the Leiden biophysics department) single molecule dynamics. A more detailed overview of his research interests can be found at his homepage: http://rulbim.leidenuniv.nl/~spaink/.

Christian Boucher started his professional career as a researcher in plant pathology in Versailles. Directeur de Recherches at INRA and former Director of the Laboratory of Molecular Biology of Plant Microbe-Interactions (CNRS-INRA) in Castanet Tolosan (1994-1998), he devotes his research to molecular analysis of pathogenicity determinants of *Ralstonia solanacearum*. He spent one sabbatical year (1975) in Madison, WI, with **Luis Sequeira** and one (1989) in Berkeley, CA, with **Brian Staskawicz**.

Jane Glazebrook is a senior staff scientist for Novartis Agricultural Discovery Institute, Inc. in San Diego, CA. Jane received a B.Sc. degree in Biochemistry from Case Western Reserve University in 1985. Her graduate work with **Graham Walker** concerning nodulation by *Sinorhizobium meliloti* led to a doctoral degree in Biology from the Massachusetts Institute of Technology in 1991. From 1991 to 1995, she was a post-doctoral fellow in **Fred Ausubel's** laboratory, where she began her work on genetic dissection of plant defense responses using *Arabidopsis thaliana*. For much of this time, she was supported by an NSF Plant Sciences Postdoctoral Fellowship. From 1995 to 1998, she was an assistant professor at the Center for Agricultural Biotechnology of the University of Maryland. Jane joined the Novartis Agricultural Discovery Institute, Inc. in 1998. Research in her group is aimed at elucidating the signal transduction network controlling activation of plant defense responses after pathogen attack, and at understanding the contribution of specific defense mechanisms to resistance to particular pathogens. She previously served as an Associate Editor of *MPMI*.

Francine Govers is an associate professor in phytopathology at the Department of Plant Sciences of Wageningen University, the Netherlands, and staff member at the Graduate School Experimental Plant Sciences. She received an M.Sc. degree in plant pathology and a Ph.D. degree in plant molecular biology. Her thesis work in the laboratory of **Ton Bisseling** involved studies on nodulin gene expression in developing pea root nodules. She joined the Laboratory of Phytopathology in 1990. Her research interest is in the biology and pathology of the oomycete *Phytophthora infestans,* the causal agent of potato late blight. Her research group focuses on (i) characterizing pathogenicity factors and elicitors of defense responses, (ii) unraveling signal transduction pathways underlying pathogenicity, (iii) developing a molecular toolbox, (iv) mapping the *P. infestans* genome, and (v) genomics and functional genomics of *Phytophthora*. Results from these areas of research are directed toward designing rational control strategies for late blight and other diseases caused by oomycete pathogens. She teaches introductory plant pathology and advanced plant-microbe interaction courses to undergraduates and more specialized, thematic courses to graduate students.

Dieter Haas obtained his Ph.D. degree in his native country, Switzerland, after studies at the Swiss Federal Institute of Technology (ETH) in Zürich, with emphasis on microbiology and biochemistry. From 1974 to 1978, he was a postdoctoral fellow at Monash University (Melbourne, Australia), University of Kansas Medical Center (USA), and Institut Pasteur (Paris, France). In 1978, he returned to ETH to lead a group studying the metabolic versatility of pseudomonads. In a collaboration with **Geneviève Défago** (ETH), he became interested in the mechanisms of biological control exerted by fluorescent pseudomonads. Since 1993, he has been the director of the Laboratoire de Biologie Microbienne at the University of Lausanne, where he teaches general

microbiology. His current research focuses on the regulation of secondary metabolism in pseudomonads, especially on the genetic mechanisms that are pertinent to biological control or virulence of these bacteria.

Maria J. Harrison received her Ph.D. degree in biochemistry and applied molecular biology in 1988 from the University of Manchester, Institute of Science and Technology. From 1988 to 1990, she was a postdoctoral fellow in **Richard Dixon's** lab in the Plant Biology Division at The Samuel Roberts Noble Foundation, where she worked on transcription factors responsible for the regulation of a pathogen-inducible chalcone synthase gene in *Phaseolus vulgaris.* In the latter part of 1990, she became a group leader and subsequently initiated research using a model legume, *Medicago truncatula,* for molecular and genetic investigations of the arbuscular mycorrhizal (AM) symbiosis. She is currently an associate scientist in the Plant Biology Division at The Noble Foundation and also holds adjunct positions in the Biology Department at Texas A&M University and in the Biochemistry Department at Oklahoma State University. Her research interests include mechanisms underlying development and functioning of the AM symbiosis and phosphate perception, signaling, and transport in plants. She is a member of the editorial boards of *Mycorrhiza* and *New Phytologist* and served previously as an associate editor and senior editor (Mycorrhizal Associations) for *MPMI*.

Jim Kronstad earned his Ph.D. degree at the University of Washington in Seattle. His thesis work involved the isolation and characterization of genes encoding the crystal protein toxins from *Bacillus thuringiensis*. He then worked on cell-type specific gene expression and the pheromone response in *Saccharomyces cerevisiae* as a postdoctoral scientist at ZymoGenetics, Inc., in Seattle. This work led to an interest in mating-type regulation in fungal pathogens of plants, and he moved to the University of Wisconsin to begin research on *Ustilago maydis*. He joined the faculty at the University of British Columbia in 1989 and is currently a professor in a multidisciplinary research department called the Biotechnology Laboratory. His research program now focuses on the role of mating functions in the pathogenesis of *Ustilago* species and on cAMP signaling in *U. maydis* and *Cryptococcus neoformans.*

James Schoelz received a B.A. degree in biology-chemistry at Point Loma College in 1980 and a Ph.D. degree in plant pathology at the University of Kentucky in 1986. After completing his Ph.D. under the direction of **Robert Shepherd**, he worked as a postdoctoral associate at Cornell University with **Milton Zaitlin** from 1986 to 1987. Schoelz joined the faculty at the University of Missouri at Columbia in 1987 and is currently an associate professor in the Department of Plant Microbiology and Pathology. His primary research interests there have concerned host-virus interactions that condition host resistance and biotechnology risk assessment of viral transgenes. He teaches an undergraduate course, Theory and Concepts of Plant Pathology, and portions of the graduate course, Genetics of the Plant-Microorganism Interaction. Schoelz served as an associate editor for *MPMI* from 1999 to 2001 and also has served on the editorial board of *Virology* since 1992.

Jens Stougaard received his Ph.D. degree in 1983 from the University of Sussex, Brighton, U.K. From 1983 to 1989 he did postdoctoral research in the Department of Molecular Biology at the University of Aarhus, Aarhus, Denmark. In 1984, he received an OECD fellowship from the Max-Planck Institut für Züchtungsforschung, Cologne, Germany, and in 1990 an EMBO fellowship from The Sainsbury Laboratory at the John Innes Centre for Plant Science Research, Norwich, U.K. He is currently a full professor in the Department of Molecular and Structural Biology, University of Aarhus. He is a member of the

International Society for Plant Molecular Biology, The American Phytopathological Society, and IS-MPMI.

Michael Udvardi received his Ph.D. degree in 1989 from the Australian National University (ANU) where he studied symbiotic nitrogen fixation. After postdoctoral work at Washington State University in the United States and then the CSIRO Division of Plant Industry in Australia, he took a faculty position back at the ANU in 1994. From 1994 to 1998, he worked on both symbiotic nitrogen fixation and the acquisition of inorganic mineral nitrogen (nitrate and ammonium) in plants. In 1998, he moved to his current position of associate professor at the Max Planck Institute of Molecular Plant Physiology in Germany, where his group continues to work on nitrogen acquisition in plants. As an extension of this work, they are also studying nitrogen and redox regulation of gene expression in plants. Their work on symbiotic nitrogen fixation now focuses on the *Lotus japonicus-Mesorhizobium loti* symbiosis, and he coordinates a European functional genomics project involving nine labs that uses *Lotus japonicus* as a model to study mutualistic symbioses.

Valerie Moroz Williamson received a B.A. degree in biology in 1971 from Northeastern University, Boston, MA, and a Ph.D. degree in biochemistry in 1978 from the University of California, Davis. From 1978 to 1981 she was a postdoctoral fellow in the Department of Biochemistry at the University of Washington, Seattle, and from 1981 to 1987 she was a research scientist and lab leader, Molecular Biology Group, ARCO Plant Cell Research Institute, Dublin, CA. She is now a professor in the Department of Nematology, University of California, Davis. She has served as both an associate editor and senior editor of *MPMI* and was a co-organizer in 1996 of the Keystone Symposium, Molecular Helminthology: An Integrated Approach. In 1995, she was a member of USDA-CGRO Entomology Competitive Grant Review Panel and in 1993 served on the NATO Advanced Research Workshop on Molecular Plant Nematology Organizing Committee. She is a member of the American Association for the Advancement of Science, The American Phytopathological Society, and the Society of Nematologists.

People

Theses Completed at the Graduate School Experimental Plant Sciences in 2000.

A.C. Andrade
ABC transporters and multidrug resistance in *Aspergillus nidulans*. Prof.dr. P.J.G.M. de Wit, (promotor); dr. M.A. de Waard (co-promotor), WU, Wageningen, 19 September 2000, 157 pp.

The aim of this thesis was to characterise molecular mechanisms of drug resistance in *Aspergillus nidulans*, with special emphasis on drug-efflux proteins of the ABC-transporter superfamily. We have identified seven of these genes (*atrA-G*). Expression studies in a wild-type isolate demonstrated that the basal level of expression for most *atr* genes is low and can be strongly enhanced by treatment with unrelated toxicants. Time course experiments indicated that within 5 min after treatment with toxicants enhanced transcript levels of some *atr* genes can be observed. Mutants in which *atrB* and *atrD* have been disrupted, display increased sensitivity to a number of unrelated toxicants. Mutants overexpressing *atrB* display decreased sensitivity to toxicants. These results indicate that AtrBp and AtrDp from *A. nidulans* are multidrug transporters with different substrate specifities. In conclusion, data presented in this thesis demonstrated that some of the identified ABC transporters from *A.*

nidulans function in protection against natural toxicants and xenobiotics.

P.J.A. Bertens
Molecular characterisation of the cowpea mosaic virus movement protein. Prof.dr. A. van Kammen (promotor); dr. J.E. Wellink (co-promotor), WU, Wageningen, 31 October 2000, 143 pp.

Plants infected with cowpea mosaic virus (CPMV) contain typical tubular structures filled with virus particles in modified plasmodesmata. These tubules mainly consist out of virus-specific movement protein (MP) and are involved in cell-to-cell spread of CPMV. Mutational analysis of the MP has revealed that the N-terminal and central regions of the MP are involved in tubule formation and that the C-terminal domain probably has a role in the interaction with virus particles. The C-terminal border of the tubule-forming domain was mapped between amino acids 292 and 298. Results with a tripartite virus encoding wild-type MP and MP lacking amino acids 314-331 indicate that all C-termini are necessary for efficient incorporation of virus particles. In epidermal cells MP fused to the green fluorescent protein (MP:GFP) mainly accumulated in fluorescent spots in the cell wall, which presumably are short tubular structures in modified plasmodesmata. Co-inoculation experiments with mutant MP:GFP and wild-type MP identified several regions in the MP involved in targeting to the cell membrane in protoplasts and cell wall/plasmodesmata in plants and a small region in the C-terminus of the tubule-forming domain of the MP essential for tubule initiation and elongation.

A. ten Have
The *Botrytis cinerea* endopolygalacturonase gene family. Prof.dr. P.J.G.M. de Wit (promotor); dr. J.A.L. van Kan (co-promotor), WU, Wageningen, 22 May 2000, 119 pp.

The thesis describes the analysis of the role of endopolygalacturonases (endoPG), a class of cell wall degrading enzymes, in virulence of the plant pathogenic fungus *Botrytis cinerea*. A family of 6 endoPG genes from *B. cinerea* was cloned and character- rized. The genes display a different expression pattern in vitro under various growth conditions. On four distinct host plant tissues, the genes display a differential temporal and/or spatial expression pattern. One of the endoPG genes, denominated *Bcpg1*, was mutated hygene replacement. The virulence of the BcPG1-deficient mutant was reduced by approximately 25% on four distinct host tissues. This was determined by using a synchronised disease assay specially developed for quantifying relative virulence levels.

S. Mlotshwa
The helper component-proteinase of cowpea aphid-borne mosaic virus. Prof.dr. A. van Kammen (promotor); dr. J.E. Wellink, dr. I. Sithole-Niang (co-promotors), WU, Wageningen, 8 December 2000, 111 pp.

Sequencing of overlapping RT-PCR clones of cowpea aphid-borne mosaic (CABMV) resulted in 9,465 nucleotides of the genomic sequence of the virus. Sequence alignments confirmed the original classification of CABMV as a distinct virus species of the BCMV subgroup of legume infecting potyviruses. Further analyses focussed on gaining insights into the functions of the HC-Pro protein. The HC-Pro gene was expressed in *E. coli* and an antiserum specific to the HC-Pro protein was obtained. Using this antiserum, the HC-Pro protein was found localised in the cytoplasm. The expression of the HC-Pro protein as part of the cowpea mosaic virus (CPMV) genome revealed its striking ability to enhance the virulence of CPMV, which appears consistent with the established

role of HC-Pro in promoting virus infections by suppressing host defence responses. Upon infection of transgenic *N. benthamiana* plants transformed with HC-Pro sequences with the parental CABMV and heterologous viruses, a symptom enhancing effect was observed, confirming the role of HC-Pro as a pathogenicity factor and modulator of host defence responses. It was also shown that transgene-induced silencing of HC-Pro resulting in complete resistance to CABMV is possible in *N. benthamiana* despite the ability of HC-Pro to suppress post transcriptional gene silencing.

S.S. Snoeijers
Regulation of the avirulence gene *Avr9* of the fungal tomato pathogen *Cladosporium* fulvum. Prof.dr. P.J.G.M. de Wit (promotor); dr. T. Goosen, dr. M.H.A.J. Joosten (co-promotors), WU, Wageningen, 10 October 2000, 120 pp.

Cladosporium fulvum is a biotrophic fungal pathogen of tomato. The interaction between this fungus and tomato complies with the gene-for-gene system. Many resistance genes in tomato and their matching avirulence genes in *C. fulvum* have been cloned. Interaction between the products of the gene pairs leads to a hypersensitive response in tomato and resistance. The research presented in this thesis focuses on the regulation of the avirulence gene *Avr9*. The expression of *Avr9* is only induced in *C. fulvum* after it has passed the stomatal pore, which is the natural opening used by the fungus to penetrate tomato leaves. In addition, in vitro the expression of *Avr9* can be induced under nitrogen-limiting growth conditions. Indeed, in the promoter of *Avr9* (TA)GATA sequences are present to which GATA-type transcription factors bind. These factors are usually involved in global regulation of nitrogen metabolism. Of the twelve (TA)GATA sequences present in the promotor of *Avr9* only two invertedly-oriented sequences appeared to be required for inducibility of the *Avr9* promotor. The transcription factor *Nrf1* (for nitrogen response factor 1) is also required for *Avr9* inducibility in vitro During growth in planta, an additional transciption factor seems to be active, as transgenic strains of *C. fulvum* lacking *Nrf1* are still avirulent on *Cf-9* plants. This observation indicates that, although very strongly reduced, sufficient amounts of AVR9 elicitor are still produced by *Nrf1*-minus strains.

N.N. van der Wel
Interaction between the Alfalfa Mosaic Virus Movement Protein and plasmodesmata. Prof.dr. R.W. Goldbach (promotor); dr. J.W.M. van Lent (co-promotor), WU, Wageningen, 20 September 2000, 119 pp.

This thesis research was part of an ALW programme aiming to unravel the role of the plant's plasmodesmata in virus transport and in cell-cell communication. Using protoplasts as a test system, it was shown that alfalfa mosaic virus (AMV) was able to form virus-containing tubular structures on infected plant cells, indicating that in planta the virus employs a mechanism of tubule-guided movement of mature virus particles. This was further confirmed by analysis of mutants with specific mutations in the coat (CP) and movement protein (MP) and defective in systemic spread, which were tested for their (in)capability to induce virus-filled tubules. The results with these mutants indicated that the inability to produce virion-filled tubules on protoplasts coincides with a transport-deficient phenotype. In plant tissues, at the front of infection, modified plasmodesmata were found containing both the AMV CP and MP and having a significantly wider diameter than those in non-infected as well as fully infected tissues. Also the number of plasmodesmata had increased nearly two-fold at the infection front. This implies that structural modification of plasmodesmata occurs, but only transiently and restricted to the front of infection. Cryo-sectioning of such plasmodesmata showed the presence of rows of virus

particles within the interior of the plasmodesmal pore suggesting that only short tubules are formed. A two-hybrid analysis was performed, using the AMV-MP as bait, to identify host proteins that were specifically targeted by this viral MP during the infection process. Analysis of an AMV MP-binding plant protein (AD3) of which the expression could be verified in plant tissue revealed that AD3 is specifically found in membrane fractions of both leaf and root tissues and immuno-gold EM demonstrated its localisation at the plasma membrane. This protein may have a potential function in support of the intercellular movement of viruses.

P. van West
Molecular tools to unravel the role of genes from *Phytophthora infestans*. Prof.dr. P.J.G.M. de Wit (promotor); dr. F.P.M. Govers (co-promotor), WU, Wageningen, 14 January 2000, 150 pp.

The oomycete *Phytophthora infestans* is the causal agent of potato late blight, a serious threat for potato crops world wide. This thesis describes the characterisation of four *P. infestans* genes with presumed functions in pathogenicity and virulence, and the development of tools to study expression and function of two of these. The four genes are the in planta-induced genes *ipiB* and *ipiO*, the elicitin gene *inf1*, and the stress-induced gene *ric1*. We used the ß-glucuronidase reporter gene for expression analysis of *ipiO*. GUS staining was specifically found in hyphal tips at the edge of expanding lesions where the pathogen is invading healthy leaf tissue. The IPI-O protein seems to be localised at the interface between the invading hyphae and the plant cells and this suggests a role for IPI-O in pathogenicity. By homology-dependent gene silencing expression of *inf1* was abolished. With the engineered INF1-deficient *P. infestans* strains is was demonstrated that resistance of *Nicotiana benthamiana* to *P. infestans* is mediated by the elicitor protein INF1. Detailed analysis of the mechanism of *inf1* gene silencing indicated the involvement of a diffusible silencing factor that is able to establish gene silencing in non-transgenic nuclei. This novel silencing phenomenon was named internuclear gene silencing.

L.J.G. van Enckevort
Identification of potato genes involved in *Phytophthora infestans* resistance by transposon mutagenesis. Prof.dr. E. Jacobsen (promotor); dr. A. Pereira (co-promotor),
WU, Wageningen, 4 December 2000, 144 pp.

Potato genes acting in the R1 type HR resistance reaction upon infection with *Phytophthora infestans* were identified using a transposon tagging strategy in diploidised potato. Somatic and germinal Ac and Ds transposition was characterised both phenoty pically and molecularly. Protoplast isolation and cell specific selection for Ds excision enabled the direct selection of somatic excision events, resulting in the regeneration of a potato transposon tagged population with predominantly new independent Ds mutations. Inoculation with *P. infestans* race 0 and quantification of the HR resistance response identified four putative transposon tagged mutants that showed a distinct altered R1 resistance response. Sequence analysis on the Ds insertions in one mutant identified significant homology to receptor kinase-like proteins. In total, 11 different *Solanum tuberosum* protein kinase (StPK) homologs were isolated and the transposon mutated StPKs were designated *rpr1* and *rpr2*, genes required for *P. infestans* R1 resistance.

J.P.W. Haanstra
Characterization of resistance genes to *Cladosporium fulvum* on the short arm

of chromosome 1 of tomato. Prof.dr. P. Stam (promotor); dr. W.H. Lindhout (co-promotor), WU, Wageningen, 4 January 2000, 119 pp.

A number of *Cf* genes, conferring resistance to *Cladosporium fulvum* in tomato, with novel specificities were identified and mapped to the short arm of tomato chromosome 1. To this end an integrated high density AFLP/RFLP linkage map was constructed using different *L. esculentum* x *L. penelli* F2 mapping populations. Resistant *Lycopersicon* accessions were used to indentify a novel gene, *Cf-ECP5*, whhose product recognizes the extracellular protein ECP5 of *C. fulvum*. *Cf-ECP5* mapped four centimorgans proximal to the *Hcr9* locus 'Milky Way' and was designated 'Aurora.' By hypersensitive reaction upon specific recognition of protein ECP2, five accessions were shown to harbour the gene *Cf-ECP2*. This gene was also accurately mapped; it was shown to be a member of a previously unidentified *Hcr9* locus, now designated the 'Orion' gene cluster. The study demonstrates that functional *Cf* genes can be located on several distinct *Hcr9* clusters on the short arm of tomato chromosome 1 and that these *Hcr9* loci are highly polymorphic.

M.C. Verberne
Introducing the microbial salicylic acid pathway into plants. Influence on plant gene expression and pathogen resistance. Prof.dr. J.F. Bol, prof.dr. R. Verpoorte (promotors), IMP-LU, Leiden, 19 October 2000, 145 pp.

After the recognition of invading pathogens, plants activate the biosynthesis of salicylic acid (SA), resulting in a 500-fold increase in the level of this plant hormone. Subsequently, SA mediates the expression of numerous plant defense genes. Available evidence indicates that plants synthesize SA along the phenylpropanoid pathway, which involves the conversion of chorismic acid into phenylalanine followed by five enzymatic steps that are poorly characterized. A number of bacteria are able to convert chorismic acid into SA in two enzymatic steps by making use of the enzymes isochorismate synthase and isochorismate-pyruvate lyase. Bacterial genes encoding these two enzymes were put under the control of the CaMV 35S promoter and introduced in the tobacco genome. When the bacterial enzymes were targeted to the plant chloroplasts, the transgenic plants accumulated SA at levels exceeding the levels in control plants by 500 to 1000 fold. The transgenic plants constitutively expressed a number of defense genes and showed an increased resistance to infection with Tobacco Mosaic Virus and the fungus *Oidium lycopersicon* (powdery mildew). Overexpression of SA did not interfere with the ethylene-mediated expression of wound-responsive plant genes.

S.J. Zheng
Towards onions and shallots (*Allium cepa* L.) resistant to beet armyworm (*Spodoptera exigua* Hübner) by transgenesis and conventional breeding. Prof.dr. E. Jacobsen (promotor); dr. C. Kik, dr. F.A. Krens (co-promotors), WU, Wageningen, 20 November 2000, 146 pp.

This thesis describes the development of onions and shallots (*Allium cepa* L.) resistant to beet armyworm (*Spodoptera exigua*) via genetic transformation and via molecular marker-assisted breeding. Because no high level of resistance was found *in A. cepa* and its wild relatives, a marker-assisted breeding approach was abandoned and emphasis was laid on the development of a transformation system. A reliable and efficient *Agrobacterium*-mediated transformation system both for onion and shallot was developed with two different strains EHA105(pCAMBIA1301) and LBA4404(pTOK233). This transformation system can be used year-round. Transgenic plants from a total of 11 independent callus lines were molecularly characterized by means of

standard PCR, genomic DNA blot hybridization, and FISH (fluorescence in situ hybridization). An adapator-ligation PCR (AL-PCR) followed by sequencing of the genomic DNA flanking the T-DNA borders was developed. The AL-PCR patterns obtained were specific and reproducible. The results showed how T-DNA integration took place and also gave insight into the number of T-DNA copies present. After cloning and sequencing the AL-PCR products, the junctions between plant genomic DNA and the T-DNA insert were analysed in detail. We concluded that, in the case of the introduction of resistance to beet armyworm into onion and shallot, genetic transformation is the most promising method.

T.F.C. Chin-A-Woeng
Molecular basis of biocontrol of tomato foot and root rot by *Pseudomonas chlororaphis* strain PCL1391. Prof.dr. E.J.J. Lugtenberg (promotor); dr. G.V. Bloemberg (co-promotor), IMP-LU, Leiden, 7 June 2000, 167 pp.

Using scanning electron microscopy it was shown that the *Pseudomonas* rhizosphere isolate *P. fluorescens* WCS365, a good root-colonising biocontrol strain, proliferates rapidly on tomato seeds and colonises tomato roots in microcolonies. The molecular basis of the biocontrol action of the tomato rhizosphere isolate *P. chlororaphis* PCL1391 was elucidated. The AFF responsible for biocontrol was structurally identified as phenazine-l-carboxamide (PCN). The complete PCN biosynthetic operon (*phz*) including a novel biosynthetic gene (*phzH*) was identified. In addition, genes regulating PCN production, namely the quorum sensing genes *phzI* and *phzR*, a global regulator GacS, and the repressor LexA were identified. Finally, the construction of colonisation mutants showed that colonisation is another essential factor for biocontrol activity of this strain.

R.P.L. Bell
Total synthesis of lactarane and marasmane sesquiterpenes. Prof.dr. Æ. de Groot (promotor); dr. J.B.P.A. Wijnberg (co-promotor), WU, Wageningen, 30 October 2000, 119 pp.

Lactarane and marasmane sesquiterpenes are found in nature as metabolites from mushrooms of the genera *Lactarius* and *Russula*. Many of these compounds posess interesting biological activities and they are assumed to take part in the mushroom's chemical defence mechanism. The total synthesis of these natural products was undertaken based on the base-induced rearrangement of perhydronaphthalene-1,4-diol monosulfonate esters, which was developed in our laboratory. This approach, in combination with new methodology for the annulation of furan rings, led to the synthesis of the lactarane furanether B. As a second objective the synthesis of marasmanes was undertaken via a completely new tandem rearrangement-cyclopropanation reaction. An interesting study of this reaction sequence led to the optimal structural requirements, which allowed a high yield one step key transformation, in which all characteristic structural elements of the marasmane skeleton were constructed. This new methodology was demonstrated with the total synthesis of optically pure (+)-isovelleral.

A.T. Groot
Sexual behaviour of the green capsid bug. Prof.dr. M. Dicke (promotor); dr. J.H. Visser (co-promotor), WU, Wageningen, 15 September 2000, 156 pp.

The green capsid bug (*Lygocoris pabulinus* (L.), Heteroptera; Miridae) is an unpredictable pest in fruit orchards in Northwestern Europe. The sexual behaviour of this bug was studied in detail, in order to identify its sex

pheromone. Males are more sensitive to pheromone-like compounds and females more sensitive to plant compounds. At long range, males were attracted to virgin and mated females, with and without plants. At close range, males were attracted to female-specific, low volatile compounds present on female legs. These compounds are also deposited on the substrate on which females walk. At long and close range, males vibrate with their abdomen when they perceive signals from females. For pest management, another pheromone of *L. pabulinus*, i.e. the alarm pheromone, may be exploited to prevent bug damage in fruit orchards.

O.E. Krips
Plant effects on biological control of spider mites in the ornamental crop gerbera.

Plant characteristics affect both herbivorous arthropods and their carnivorous enemies. Plant breeding programs usually ignore that plant characteristics influence biological control agents. However, partially resistant crops rely on biological control in addition to the resistance. Gerbera is an important ornamental crop and spider mites are one of the key pests. Gerbera cultivars vary largely in resistance to spider mites which allows for resistance breeding. However, there is no absolute resistance and so biological control with carnivorous mites is essential for environmentally benign gerbera production. Biological control agents are attracted to spider-mite induced gerbera volatiles. The predators are seriously hampered by gerbera trichomes. Both volatile induction and trichome density vary between gerbera cultivars. This should initiate a tritrophic approach in gerbera breeding.

T.M. Meulemans
The total synthesis of insect antifeedant (-)-dihydroclerodin starting from R-(-)-carvone. Prof.dr. Æ. de Groot (promotor); dr. B.J.M. Jansen (co-promotor), WU, Wageningen, 10 May 2000, 111pp.

Diterpenoids possessing the clerodane skeleton are widely distributed in nature. Of the clerodanes that were tested for biological activity, many were found to possess interesting properties, which vary from antifeedant to antiviral, antitumor, antibiotic, antipeptic ulcer, and piscicidal activity. Noone has yet succeeded in the total synthesis of highly oxidized clerodanes with a chiral center at the difficult C-11 position. Much effort was put into tackling this problem, but it has proven to be difficult to develop strategies in which either a hexahydrofuro [2,3-b]furan fragment could be attached to a completed decalin part or in which the decalin part could be finished with an already attached hexahydrofuro[2,3-b]furan moiety. We now have solved this problem by completion of the total synthesis of the natural enantiomer of dihydroclerodin and lupulin C, starting from R-(-)-carvone. In our strategy the hexahydrofuro[2,3-b]furan moiety was introduced in an early stage of the synthesis. The correct configuration at C-11 was established by application of a remarkably diastereoselective Mukaiyama reaction. The desired configuration at C-10 was obtained by catalytic reduction of an intermediate enone. After annulation of the second ring, the structural features at C-4, C-5, and C-6 were introduced. The successful completion of the synthesis included a Chugaev elimination to give the exocyclic double bond that is present in lupulin C. Oxidation of this double bond with m-CPBA afforded dihydroclerodin. For the completion of this synthesis new synthetic methodology was developed for the preparation of C2,C3 functionalised chiral cyclohexanones starting from R-(-)-carvone. These compounds were converted into the corresponding cyano ketones, which were submitted to Robinson annulation reactions with methyl vinyl ketone. The scope and limitations of these annulations were investigated as well. A series of highly

functionalised chiral decalones were obtained which can be used as starting compounds in total syntheses of enantiomerically pure clerodanes.

For more information on the EPS see: http://www.wau.nl/eps/epshome.html and http://www.wau.nl/phd-courses/.

Plant-Microbe Interactions Heat up Down Under
Perth, Western Australia is becoming quite a centre for *Medicago truncatula* research and is attracting some new recruits from the Northern Hemisphere. Research at the CSIRO, Floreat Park (**Carol Andersson**, **Owain Edwards** and **Karam Singh**) on aphid resistance and soil pathogens in *Medicago* will soon be boosted by the arrival of **John Klinger** who has been doing some of the pioneering molecular studies on aphid/plant interactions at the University of Arizona, Tucson. **Simon Ellwood**, who was a key member of the team that cloned the *Arabidopsis* mildew resistance gene *RPW8* (Science (2001) 291:118) has recently joined Richard Oliver's new unit at Murdoch University called the Australian Centre for Necrotrophic Fungal Pathogens. Simon will be working on the genetic analysis of resistance to foliar necrotrophic pathogens of *Medicago*. These projects are in addition to projects on *Medicago* bioinformatics (**Matt Bellgard**, **Geoff Dwyer** and **Mike Jones**, based in the WA State Agricultural Biotechnology Centre, Murdoch University), *Rhizobium* (**John Howieson**, in the Centre for Rhizobium Studies, Murdoch), and pathology (**Martin Barbetti** at Agriculture Western Australia) ongoing in the region.

Dr. Seiji Ouchi to Retire
IS-MPMI member Dr. S. Ouchi will retire from the professorship and chair of plant pathology at Kinki University, Japan, as of March, 2001.
Dr. Ouchi received his Ph.D. degree from Kyoto University. In 1963, he joined the faculty of Agriculture at Kyoto University and from 1970 to 1985 was an associate professor of plant pathology in Okayama University. Since 1985, he has been professor and chair at Kinki University, where he has also served as director of the Institute of Comprehensive Agricultural Sciences (since 1991) and as assistant dean of Student Affairs (from 1991 to 1994). Throughout his distinguished career, Dr. Ouchi and coworkers worked on the induction mechanisms of susceptibility in the interaction between the pathogenic fungus *Mycosphaerella* and pea. One of his current research efforts focuses on the development of methodologies for introducing foreign genes into single cells of host and pathogen. Dr. Ouchi has published over 150 scientific papers and has served for more than a decade on the editorial boards of *Physiological and Molecular Plant Pathology* and the *Annals of the Phytopathological Society of Japan*. He has chaired sessions at more than 25 international symposia and conferences, and was the co-organizer of the 5th International Congress of Plant Pathology in Kyoto in 1988, the US-Japan Cooperative Science Seminar in Hawaii in 1990, and the 1st Asian Conference on Plant Pathology in Beijing in 2000. In addition to IS-MPMI, Dr. Ouchi is a member of the American Phytopathological Society and the Phytopathological Society of Japan, for which he served as President in 1997. His colleagues in the IS-MPMI wish him a joyful and rewarding retirement.

Safemaize Project
The European Union (INCO-DEV) has funded a new programme entitled **GENETIC IMPROVEMENT OF MAIZE TO ENHANCE FOOD SAFETY BY INTRODUCING RESISTANCE TO *FUSARIUM MONILIFORME*** (known as the "SAFEMAIZE" project). The program will run from January, 2001, to December, 2003. The objectives are to develop improved maize genotypes with increased resistance to *Fusarium moniliforme*. Approaches include screening genotypes for resistance; evaluation of the syngergistic effects of four plant anti-fungal

defense genes; the use of directed evolution by DNA shuffling to produce new anti-fungal genes; and the generation and testing of transgenic maize lines. Collaborators include scientists from South Africa (Professor **David Berger**, University of Pretoria, Dr. **Santie de Villiers**, ARC-Roodeplaat Vegetable and Ornamental Plant Institute, and Dr. **Maureen Louw**, CSIR-Bio/Chemtek); Zambia (**Irene Nawa**, University of Zambia); Italy (Professor **Felice Cervone**, Universita di Roma "La Sapienza"); and the Netherlands (Dr. **Olga Scholten**, Plant Research International).

New IS-MPMI Reporter Editorial Board member
The Reporter is pleased to announce that Professor **David Berger** has joined the Editorial Board. Dr. Berger is Associate Professor of Botany at the University of Pretoria, South Africa. He can be contacted at: dberger@postino.up.ac.za.

Employment

Postdoctoral Research Position
Samuel Roberts Noble Foundation.
Available immediately

A postdoctoral position is available to join a group investigating aspects of the arbuscular mycorrhizal symbiosis and mechanisms of phosphate acquisition by plants [Selected publications from the lab include: Ann. Rev. Plant Phys. and Plant Mol. Biol., **50**: 361-389 (1999), Plant Journal, **6**: 531-542 (2000), Mol. Plant-Microbe Interactions 11: 14-22 (1998), Plant Journal, 9 (4) 491-505 (1996); Nature, 378: 626-629 (1995); Plant Journal, 6: 9-20 (1994).]

Projects available include gene expression profiling using cDNA arrays and the analysis of T-DNA tagged mutants of *M. truncatula*. The project is supported by the Noble Foundation and the position is available for initially for two years with the possibility of renewal for an additional year. Applicants should have a strong background plant molecular biology and genetics. To apply, send a letter outlining research interests, a CV and names of 3 references to: Dr Maria J. Harrison, Plant Biology Division, Samuel Roberts Noble Foundation, 2510 Sam Noble Parkway, Ardmore, OK 73401; phone 580-223-5810, fax 580-221-7380, e-mail mjharrison@noble.org.

Professorship and Chair
Racheff Chair of Excellence in Plant Molecular Genetics
Department of Ornamental Horticulture and Landscape Design
The University of Tennessee
Knoxville, Tennessee

The Department of Ornamental Horticulture and Landscape Design in the College of Agricultural Sciences and Natural Resources (CASNR) and the Tennessee Agricultural Experiment Station (TAES) seeks outstanding applicants to fill a 12-month, tenure-track Professorship and Racheff Chair of Excellence in Plant Molecular Genetics. The Chair is expected to maintain an internationally recognized and extramurally funded research program and will be expected to participate in the graduate program in CASNR by advising doctoral students and teaching a doctoral-level course in plant genetics. The Chair's research laboratory will be located in a 120,000 sq. ft. plant biotechnology building currently under construction. The Chair will have opportunities to collaborate with other CASNR scientists, as well as scientists in the College of Arts and Sciences at The University of Tennessee and those at the Oak Ridge National Laboratory. A start-up package is available, as well as recurring funds

for graduate students and postdoctoral research scientists.

Nominations should be sent to Dr. C. A. Speer, Dean, CASNR/TAES, 2621 Morgan Circle, 126 Morgan Hall, The University of Tennessee, Knoxville, TN 37996-4500. Telephone 865/974-6756; Fax 865/974-9329; e-mail caspeer@utk.edu.

Applications consisting of a letter of application, professional mission statement including teaching and research philosophies, curriculum vitae, and names, addresses (postal and e-mail) and telephone numbers of five references should be sent to Dean Speer. The review of applications will begin on April 2, 2001, and continue until a suitable candidate has been identified.

UT is an EEO/AA/Title VI/Title IX/Section 504/ADA/ADEA institution in the provision of its education and employment programs and services. Women and minorities are encouraged to apply

Postdoctoral Position Available
Molecular genetics of *Mycosphaerella fijiensis.*

A Postdoctoral Associate is sought to study *Mycosphaerella fijiensis*, the fungus that causes black Sigatoka disease of bananas and plantains. The successful applicant will join a project aimed at identifying and characterizing genes important in virulence, pathogenicity, and mating of the fungus. The work will require experience with molecular biology techniques, including Southern/northern analyses, PCR amplification, library construction, and DNA sequence analyses. This is an excellent opportunity to gain experience in fungal molecular biology and genetics, while working on a devastating worldwide pathogen of bananas and plantains.

Funding is available for 2-3 yr, beginning as early as January 2001. Applicants must have a Ph.D. in a relevant discipline and skills in molecular biology. A command of written and spoken English is required, as well as excellent interpersonal and organizational skills, and willingness to work as a team player. Experience with filamentous fungi is preferred but not required; scientists with training in other systems (e.g., plants) are welcome to apply.

Contact information for applications and questions is listed below. To apply, please send cover letter, curriculum vitae and the names of three references, including postal and email addresses and telephone numbers. Please label email attachments with your last name. Boyce Thompson Institute for Plant Research is an equal opportunity employer.

Dr. Alice C. L. Churchill, Boyce Thompson Institute for Plant Research,Tower Road, Cornell University, Ithaca, New York 14853-1801 USA. E-mail: acc7@cornell.edu, Fax: 607-254-2958.

Postdoctoral Position in Fungal Molecular Genetics
A postdoctoral position is available immediately in the laboratory of **Jonathan Walton**, DOE-Plant Research Lab and Department of Botany and Plant Pathology, to work on histone deacetylases (HDAC) in maize, *Arabidopsis*, and the maize pathogen *Cochliobolus carbonum*. HDAC is the site of action of HC-toxin, a critical virulence determinant for *C. carbonum* (Brosch et al., Plant Cell [1995] **7**:1941). We have characterized three HDAC genes in *C. carbonum* and one of them regulates cell-wall-degrading enzyme expression and plant virulence. Current research questions include (1) how does *C. carbonum* protects itself against HC-toxin? (2) how do HDACs control fungal virulence? (3)

why does HDAC inhibition in maize cause disease compatibility? Depending on interests of the successful applicant and the state of the program at the time of starting, the research will involve some combination of enzyme characterization and purification, fungal and plant gene cloning and gene disruption, microarrays, and natural products analysis. Funding is for one year with possibility of renewal for up to three years. Contact: DOE-PRL, MSU, E. Lansing MI 48824; telephone 517-353-4885; email: walton@msu.edu. MSU is an affirmative-action equal-opportunity employer.

Postdoctoral Research Opportunity to study "Metabolites involved in fungus-bacterium interactions in the rhizosphere"

TEAMS:
UMR INRA (Institut National de la Recherche Agronomique)/Université "Interactions Arbres-Microorganismes", Nancy, France.

UMR INRA/ENSAR "Biologie des Organismes et des Populations appliquée à la Protection des Plantes", Rennes, France

PROJECT LEADERS:

Alain Sarniguet (INRA Rennes) tel: 33 2 23 48 51 94, fax: 33 2 23 48 51 80, e-mail: sarnigue@rennes.inra.fr

Pascale Frey-Klett (INRA Nancy) tel: 33 3 83 39 41 49, fax: 33 3 83 39 40 69, e-mail: klett@nancy.inra.fr
http://mycor.nancy.inra.fr

Project:
To identify the factors that explain relationships among the microbial communities in the rhizosphere, focusing on fungus-bacterium associations on the roots. The goal is to better understand the role of beneficial rhizobacteria through synergism with ectomycorrhizal symbiosis and through antibiosis against phytopathogenic fungi. The study will be mainly focused on the role of carbohydrates as discriminant compounds for the structure of microbial communities. The research steps will be in parallel: (1)) *in vitro* et ***in situ*** assessment of carbohydrates in fungi and bacteria, and their involvement in direct and indirect plant growth promotion, (2) the creation of bacterial mutants (*Pseudomonas*) impaired in the metabolism and/or the storage of carbohydrates and analysis of the consequences of these mutations on root colonisation, antagonism and synergism functions.

References:
Frey P., Frey-Klett P., Garbaye J., Berge O. et Heulin T. 1997. Metabolic and genotypic fingerprinting of fluorescent pseudomonads associated with the Douglas fir-*Laccaria bicolor* mycorrhizosphere. Appl. Environ. Microbiol. 63:1852-1860.

Sarniguet A., Le Rouzic J., Fleury D. et Gloux K. 1997 Relationships between antibiotic production, biocontrol efficiency and osmoadaptation in *Pseudomonas fluorescens* Pf-5. Pseudomonas '97, VI International Congress on *Pseudomonas* : molecular biology and biotechnology, Madrid , Sept. 4-8, 1997.

Qualifications:
The candidate must have a PhD in bacterial genetics and physiology, some experience in bacteria-eukaryote (plant or animal) relationships preferred; good

knowledge of molecular biology techniques (trangenesis, reporter genes, RT-PCR). Additional skills in biochemistry and in separation and identification techniques (HPLC, NMR) will be appreciated.

Duration:

Two years from the second trimester of 2001. The molecular biology work will be done in Rennes (west part of France) and the biochemistry work in Nancy (east part of France).

Meeting/Events

2001

IS-MPMI Meeting
July 10-15, 2001, Madison, Wisconsin USA. Contact: The Congress and its program can be accessed at the Congress Website http://www.plantpath.wisc.edu/mpmi/ or by contacting Sally Leong at sal@plantpath.wisc.edu. The 2003 meeting will be in St. Petersburg, Russia.

Environmental Signalling: Arabidopsis as a model.
August 27-29, 2001, Utrecht University, The Netherlands. Contact: Corné Pieterse, Section Phytopathology, Utrecht University, E-mail: C.M.J.Pieterse@bio.uu.nl. The program and registration form can be accessed at website www.bio.uu.nl/EPS-summerschool. Deadlines: 15 April 2001 for reservation student housing, 1 June 2001 for registration and abstract submission.

The 14th John Innes Symposium.
September 5-8, 2001. The topic is “Chromosome Dynamics and Expression.” Further information can be obtained through the symposium website: http://www.jic.bbsrc.ac.uk/events/symposium

Biology of Type IV Secretion Processes: Euroconference on the Medical and Ecological Implications.
September 7-12, 2001. Castelvecchio Pascoli, Italy. Type IV secretion machineries mediate direct cell-to-cell transfer or secretion of virulence factors from Gram-negative pathogens to modulate their hosts’ defense response. This strategy is used by many important human and animal pathogens. Type IV secretion machineries also mediate the spread of plasmids carrying antibiotic resistance genes and genetic transformation of plants by Agrobacterium. Talks and posters will presesnt recent work on basic aspects such as DNA processing, transfer of virulence factors, host response and ecological implications. Chariman: Christian Baron (University Munich), Vice-Chairman: David O’Callaghan (INSERM, Nimes, France). The conference is open to researchers world-wide, whether from industry or academia. Participation will be limited to 100. The Conference Fee covers registration and full board and lodging. Grants will be available, in particular for nationals from EU or Associated States under 35. Deadline for applications: 30 April, 2001. For information, contact the Head of the EURESCO Unit: Dr. J. Hendekovic, European Science Foundation, 1 quai Lezay-Marnesia, 67080 Strasbourg Cedex, France, telephone +33 388 76 71 35; fax 33 388 36 69 87; email euresco@esf.org. Website: http://www.esf.org/euresco.

EMBO Practical Course on the New Plant Model System Medicago
November 19 - December 1, 2001. Institut des Sciences Végétales CNRS, Gif-sur-Yvette, France.Organizers: Adam Kondorosi (Gif-sur-Yvette) and Jean

Dénarié (Toulouse). The aim of the course is to provide participants with a basic training in handling *M. truncatula*, a model leguminous plant, and its use in the context of both molecular and cellular biological studies, as well as for genetic and genomic approaches. Practical work will include regeneration and transformation methods, genetic and physical mapping, transcriptome analysis, bioinformatics, optical and confocal microscopy.

Instructors and lecturers: David Barker (Toulouse), Anke Becker Bielefeld), Ton Bisseling (Wageningen), Spencer Brown (Gif-sur-Yvette), Douglas Cook (Davis), Martin Crespi (Gif-sur-Yvette), Fréderic Debellé (Toulouse), Dorus Gadela (Wageningen), Pascal Gamas (Toulouse), Jérôme Gouzy (Toulouse), Maria Harrison (Oklahoma, Ardmore), Thierry Huguet (Toulouse), Etienne Journet (Toulouse), Daniel Kahn (Toulouse), Attila Kereszt (Szeged), György Kiss (Szeged), Eva Kondorosi (Gif-sur-Yvette), 0lga Kulikova (Wageningen), Peter Mergaert (Gif-sur-Yvette), Andreas Perlick (Bielefeld), Pascal Ratet (Gif-sur-Yvette),Charles Rosenberg (Toulouse), Pierre Rouzé (Gent), Beatrice Satiat-Jeunemaître (Gif-sur-Yvette), Hanh Trinh (Gif-sur-Yvette), Kathryn VandenBosch (Minn. St. Paul). Applications: Deadline for application is September 1, 2001. The number of participants is limited to 16. For applicants from academic laboratories lodging and meals during the course will be paid by the EMBO course budget. The application, consisting of a short CV including a list of publications, a short synopsis of current research, and a short letter of recommendation from the supervisor or group leader should be sent to: Dr. Adam Kondorosi, Institut des Sciences Végétales CNRS, 1 Avenue de la Terrasse, F-91198 Gif-sur-Yvette, France. Phone: 33 1 69 82 36 96, Fax: 33 1 69 82 36 95

E-mail: Adam.Kondorosi@isv.cnrs-gif.fr. More information about the course and application can be found on the web at: http://www.isv.cnrs-gif.fr/embo.

Welcome New Members

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Oklahoma State Univ
Plant & Soil Sciences Department
Stillwater, OK

Adam J. Bogdanove
Iowa State Univ
Plant Pathology Department
Ames, IA

Hai-Ping Cheng
Lehman College/City Univ of New York
Biology Department
Bronx, NY

Marcus C. Chibucos
1520 Rosewood Dr
Bowling Green, OH

Xinshun Ding
Samuel Roberts Noble Foundation
Plant Biology Division
Ardmore, OK

Thomas Dodd

Kyoto Univ
Inst for Chemical Research
JAPAN

George Tsiamis
Imperial College At Wye
Biological Sciences Department
Wye, Kent, UNITED KINGDOM

Michael Udvardi
Max Planck Institute of Molecular Plant Physiology Golm, GERMANY

Renier Van Der Hoorn
Wageningen Agric Univ
Wageningen, NETHERLANDS

Irma Vijn
Wageningen Agric Univ
Wageningen, NETHERLANDS

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