

## IN THIS ISSUE

A Tribute to Noel T. Keen .....	1
Presidents Column .....	2
Calendar of Events .....	2
Comments Requested on Plant-Associated Microbe Genome Initiative .....	3
11th International Congress .....	3
Draft of White Paper .....	4-7 & 9
IS-MPMI Journal Articles .....	8-9
People .....	10
Employment .....	11
Announcements .....	11
New Members .....	12

## A Tribute to Noel T. Keen

Jan E. Leach, Kansas State University, Manhattan, KS USA

Shinji Tsuyumu, Shizuoka University, Japan



**Noel T. Keen**, a former member of the Board of Directors for IS-MPMI, passed away in his home April 18, 2002. He was serving as President of the American Phytopathological Society (APS) at the time of his death. Noel was a fellow of APS and the American Academy of Microbiology, and was elected to the National Academy of Sciences, USA in 1997. His service and leadership in our field were tremendous. Noel served on the editorial boards of *Molecular Plant-Microbe Interactions*, *Phytopathology*, *Journal of Bacteriology*, *Journal of Phytopathology*, *Annual Review of Phytopathology*, *Plant Physiology*, and *Applied and Environmental Microbiology*. In addition, he served on many Scientific Advisory Boards.

Noel was a prolific scholar who made many major contributions to the field of molecular plant-microbe interactions on very diverse systems. His studies of pathogen virulence factors spanned characterization of fungal toxins to the structural analysis of the bacterial cell wall degrading enzyme pectate lyase. He coined the term "elicitor," and then characterized a single gene involved in production of the syringolide elicitors from *Pseudomonas syringae* pv *tomato*. Because his research was at the cutting edge, Noel was a frequent invited speaker at symposia and meetings. He was the Keynote Speaker for the IS-MPMI's 5<sup>th</sup> Congress held in Seattle in 1992.

Noel developed strong and productive research relationships and friendships with many colleagues over the years, particularly those in Japan. He co-organized the 7th and 8th US-Japan Symposia on Plant-Pathogen Interactions, and participated in many more of those conferences. He served as the Distinguished Lecturer for the Japan Society for the Promotion of Science in 1998. In 2000, he helped establish the *Journal of General Plant Pathology*, a journal published in English by the Phytopathological Society of Japan, and he encouraged its development through his service as an associate editor. A tribute to Noel's warm philanthropy and dedication to quality science will appear in the coming issue of that journal.

Noel leaves behind a strong legacy in terms of the students and post-doctoral fellows he trained, and the many colleagues he mentored and collaborated with throughout his career. He was direct, efficient, and thoughtful in his approach to science and generous in interactions with his colleagues throughout the world. Noel worked hard to keep our area of science on the agenda of legislators and funding agencies, particularly over the past five years. The benefits of all of his efforts in science and policy will be with us well into the future.

Noel obtained his B.S. in botany and his M.S. in plant pathology at Iowa State University, Ames, and received his Ph.D. in plant pathology from the University of Wisconsin. He joined the faculty of the University of California, Riverside in 1968, and he remained there for his entire career. Noel is survived by his wife, Diane Ill Keen. Two Memorial Funds, the Noel T. Keen Award for Research Excellence in Molecular Plant Pathology (APS Foundation, 3340 Pilot Knob Road, St. Paul, MN 55121) and the Noel Keen Memorial Fund (UCR Foundation, University of California, Riverside, CA 92521) have been established in his honor.

## IS-MPMI REPORTER DEADLINE

**Deadline for submitting items for the next issue is October 15, 2002.**

Submission of materials as electronic files, either on disk or as e-mail attachments, will speed processing. Please submit black-and-white or color photos generated from negatives. If your image was created digitally, please submit a laser print of the image and a disk containing the electronic graphics file (.tif and .eps formats are preferred).

For more information on submitting electronic images contact Kayleen Larson at [klarson@uslink.net](mailto:klarson@uslink.net).

## Send items to:

Senior Editor: Jonathan D. Walton  
Michigan State University,  
DOE – Plant Research Lab  
East Lansing, MI 48824  
Phone: 517.353.4885  
Fax: 517.353.9168  
E-mail: [walton@msu.edu](mailto:walton@msu.edu)

## IS-MPMI's Growth Offers Opportunities



**Ben Lugtenberg, IS-MPMI President**

This year something special happened: IS-MPMI membership reached, and then surpassed, five hundred with much of the growth occurring in the past two years alone. But it's not just the sheer number of new members that's impressive; it's also the diversity of our membership across scientific disciplines and geographic lines.

Advances in biotechnology and our increasing interest in and understanding of the microbiology of plant-microbe interactions make the work of IS-MPMI members of increasing importance and interest. *MPMI* remains a major priority and recent editorial improvements promise continued success for our highly respected journal. One of our most significant activities, the International Congress on Molecular Plant-Microbe Interactions, will no doubt again draw a considerable number of our colleagues and, as in the past, result in a large number of new people joining our membership ranks.

As we grow in numbers, we also grow in opportunities. Added membership brings with it added resources and the possibility of increasing the activities of our Society and the involvement of our membership. Currently, there are several ways in which we invite members to participate in the work of our Society. We invite you to:

- Write an article for *IS-MPMI Reporter* on the work/research you are doing. Articles can be sent to editor **Jonathan Walton**, Michigan State University, walton@msu.edu
- Suggest product/service opportunities to the IS-MPMI Board for consideration.
- Consider an editorial position with *MPMI*. If you are interested in this type of an opportunity we would encourage you to contact the *MPMI* Editor-in-Chief, **Herman P. Spaink**, Leiden University, Institute of Molecular Plant Sciences, spaink@rulbim.leidenuniv.nl
- Help IS-MPMI continue to grow by recruiting new members, send your suggestions to IS-MPMI staff member Molly Cerny, mcerny@scisoc.org
- Make speaker suggestions for an upcoming meeting
- Present your research at an upcoming meeting or submit your research for publication in *MPMI*

Compared to many scientific organizations, IS-MPMI is still in its infancy. We are covering new territory in both our work and in our professional affiliations through IS-MPMI. We continue to fine-tune our identity, working to determine how best to meet the needs of our membership. Are there ways in which we might add even greater value to your membership within IS-MPMI? What information would you like to receive that we are not providing? Could IS-MPMI be playing a more active role in the work of its members, in helping members better connect? What are the next steps in our journey toward forging a scientific community grounded in cutting-edge research? I am interested in hearing your thoughts and ideas. You can reach me at:

Egbertus (Ben) Lugtenberg  
Leiden Univ.  
Inst. of Molecular Plant Sci.  
Wassenaarseweg 64  
Leiden, 2333 AL Netherlands  
Phone: 011 31 71 527 5063  
Fax: 011 31 71 527 5088  
E-mail: lugtenberg@rulbim.leidenuniv.nl

## Calendar of Events

### 13th Australian Nitrogen Fixation Conference

September 24-27, 2002,  
Adelaide, South Australia,  
Australia

Theme: Fixed nitrogen in sustainable farming systems. The program will cover a broad range of aspects of biological nitrogen fixation. For details contact: Peter Murphy, Department of Plant Science, Waite Campus, The University of Adelaide, PB 1 Glen Osmond, South Australia 5064, AUSTRALIA, Tel: +61 8 8303 7262 Fax: +61 8 8303 7109 Email: peter.murphy@adelaide.edu.au

### 3rd Asia-Pacific International Mycological Conference on Biodiversity and Biotechnology (AMC 2002)

November 4-8, 2002, Kunming, China

Contact: amc2002@china.com

### 8th International Congress of Plant Pathology (ICPP2003)

February 2-8, 2003,  
Christchurch, New Zealand  
"Solving Problems in the Real World,"

Contact: Helen Shrewsbury, Professional Development Group, PO Box 84, Lincoln University, Canterbury, New Zealand (shrewsbh@lincoln.ac.nz). Registration details and other information is available on the ICPP2003 website <http://www.lincoln.ac.nz/icpp2003/>. The Final Circular for ICPP2003 will be released in December 2001, and will be distributed to those who have completed Registration of Interest details.

### 11-th International Congress on Molecular Plant-Microbe Interactions

July 18-27 2003, St. Petersburg, Russia

Contact:  
<http://www.arriam.spb.ru/mpmi/>

## Comments Requested on Plant-Associated Microbe Genome Initiative

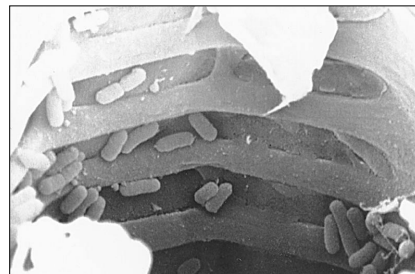
Plant-associated microbes play critical roles in agricultural and food safety and security and in the maintenance of ecosystem balance. Some of these diverse microbes, which include viruses, bacteria, oomycetes, fungi and nematodes, cause plant diseases, while others prevent diseases or enhance plant growth. Despite their importance, we know little about them on a genomic level. A concerted and coordinated genomic analysis of these microbes is essential to intervene in disease and understand the basis of biological control or symbiotic relationships.

To initiate discussions on how to achieve genome analysis of these diverse organisms, the NSF, DOE, USDA-ARS, and USDA-NRI funded a *Workshop on Genome Analysis of Plant-Associated Microbes* (Washington D.C., April 9-11, 2002).

Workshop participants were members of the international microbe-plant interaction research community and included academic, government, and industrial scientists with expertise in structural and functional analysis and bioinformatics of microbial genomes.

The product of the workshop is a draft white paper for a *Plant-Associated Microbe Genome Initiative*. The white paper has been reprinted in this issue of the *IS-MPMI Reporter* for your review, see pages 4-7. The Public Policy Board of the American Phytopathological Society (APS), who coordinated the workshop, invite the research community to review the document and send comments or suggestions to [microbegenomics@scisoc.org](mailto:microbegenomics@scisoc.org) by August 31, 2002.

For additional questions regarding this initiative, contact: **Jan E. Leach**, Kansas State University. Phone: +1.785.532.1367, Fax: +1.785.532.5692, E-mail: [jleach@ksu.edu](mailto:jleach@ksu.edu).



## 11th International Congress on Molecular Plant-Microbe Interaction

Dear colleagues,

The International Society for Molecular Plant-Microbe Interactions and the National Organizing Committee are pleased to announce that the 11-th International Congress on Molecular Plant-Microbe Interactions will take place on July 18-27 2003 at St.Petersburg, Russia.

The Scientific Program will consist of Plenary Lectures (invited), symposia Oral Presentations (invited or selected out of abstracts) and Poster Presentations.

Congress will last 6 working days, from which 2 days will be devoted to the plenary lectures (common for all participants) while 4 days devoted to the parallel symposia. In total we plan to have 6 plenary sittings and 44 symposia sittings. Each sitting will last 150 min and in the case of symposia will include 10 min Chairperson introduction, 5 fixed presentation (20 min each, including discussion) and 20 min for presentation of selected posters and/or free discussion. Each working day we shall have 3 sittings (8.00-11.00 - coffee-break - 11.30-14.00 - lunch - 15.30-18.00); in the last working day (July 26) we shall have first 2 sittings.

The Cultural Program of the Congress will include sightseeing of St. Petersburg, performance(s) and post-Congress tours.

Those who are interested to take part in the Congress are kindly recommended to monitor this Web site <http://www.arriam.spb.ru/mpmi/> that will be used for:

- Registration of participants
- Collecting the Abstracts
- Releasing all general and specific information relevant to the Congress organization.

Only the First Circular and Letters of Invitation (required for obtaining entrance visas) will be distributed by mail. All further information will be available on this web site and only after special requests it will be sent by mail.

Yours sincerely,

**Igor A. Tikhonovich**, Congress Organizer



St. Petersburg images reproduced with the permission of Mr. Peter Sobolev <http://www.enlight.ru/camera/>

## PLANT-ASSOCIATED MICROBE GENOME INITIATIVE

## Draft of White Paper

## Developed by the Plant Microbiology Research Community

June 27, 2002

Drafting Committee:

**Jan E. Leach**

Plant Pathology, Kansas  
State University,  
4024 Throckmorton,  
Manhattan, KS 66506,  
jeleach@ksu.edu

**Scott Gold**

Plant Pathology, University  
of Georgia,  
Athens, GA 30602,  
sgold@arches.uga.edu

**Sue Tolin**

Plant Molecular Biology Lab,  
Room 102, 435 Old Glade  
Road,  
Blacksburg, VA,  
stolin@vt.edu

**Kellye Eversole**

Eversole Associates,  
3208 Park View Rd,  
Chevy Chase, MD 20815,  
kellye@eversoleassociates.com

**Executive Summary**

Plant-associated microorganisms are critical to agricultural and food security and are key components in maintaining the balance of our ecosystems. Some of these diverse microbes, which include viruses, bacteria, oomycetes, fungi and nematodes, cause plant diseases, while others prevent diseases or enhance plant growth. Despite their importance, we know little about them on a genomic level. To intervene in disease and understand the basis of biological control or symbiotic relationships, a concerted and coordinated genomic analysis of these microbes is essential. Genome analysis, in this context, refers to the structural and functional analysis of the microbe DNA including the genes, the proteins encoded by those genes, as well as noncoding sequences involved in genome dynamics and function. The ultimate emphasis is on understanding genomic functions involved in plant-associations.

Members of the American Phytopathological Society (APS) developed a prioritized list of plant-associated microbes for genome analysis. With this list as a foundation for discussions, a *Workshop on Genomic Analysis of Plant-Associated Microorganisms* was held in Washington D.C. on April 9-11, 2002. The workshop was organized by the Public Policy Board of APS, and was funded by the Department of Energy (DOE), the National Science Foundation (NSF), USDA-Agricultural Research Service (USDA-ARS) and USDA-National Research Initiatives (USDA-NRI). The workshop included academic, industrial, and governmental experts from the genomics and microbial research communities and observers from the federal funding agencies. After reviewing current and near-term technologies, workshop participants proposed a comprehensive, international initiative to obtain the genomic information needed to understand these important microbes and their interactions with host plants and the environment.

Specifically, the recommendations call for a 5-year, \$500 million international public effort for genome analysis of plant-associated microbes. The goals are to (1) obtain structural sequence information for several representative groups of microbes; (2) identify and determine

function for the genes/proteins and other genomic elements involved in plant-microbe interactions; (3) develop and implement standardized bioinformatic tools and a database system that is applicable across all microbes; and (4) educate and train scientists with skills and knowledge of biological and computational sciences who will apply the information to the protection of our food sources and environment.

**Overview**

Plant-associated microbes play critical roles in agricultural and food safety and security and in the maintenance of ecosystem balance. Despite their importance, as of May, 2002, less than six percent of the microbes whose genomic sequence has been completed and made publicly available were plant-associated microbes (<http://www.tigr.org/~vinita/PPwebpage.html>, [http://www.jgi.doe.gov/JGI\\_microbial/html/index.html](http://www.jgi.doe.gov/JGI_microbial/html/index.html)). To remedy this dearth of critical information, the microbe-plant interaction community, lead by the Public Policy Board of the American Phytopathological Society (APS), initiated a planning effort to develop a strategy to undertake the structural and functional genomic analysis of viruses, bacteria, oomycetes, fungi, and nematodes that interact with plants. This white paper, which is the product of a Workshop on Genome Analysis of Plant-Associated Microbes held in Washington D.C. (April 9-11, 2002), describes the rationale and recommendations for an international public initiative for genomic analysis of these plant-associated microbes.

**Background**

Microbes can be found on or within every higher organism, including plants. Plant-associated microbes, which include viruses, bacteria, fungi, oomycetes, and nematodes, play critical roles in plant health. Some microbes cause diseases whereas others prevent diseases or enhance plant growth. Microbes also interact with each other on or within plants with the result of more or less severe disease. Within each microbe group, the diversity of species that interacts with plants is tremendous. For

example, more than 10,000 pathogenic species of fungi and viruses are estimated to cause diseases on plants, many of which are economically important. Pathogenic microbes continually erode our supply of food and fiber, causing losses to producers of over \$200 billion annually. Recent terrorist activities have heightened concern that, in the wrong hands, these agents could be used to threaten our food, environment or economic security (Schaad et al. 1999, <http://www.apsnet.org/online/feature/BioSecurity/Top.html>). The historic devastation wrought by the inadvertent introduction of exotic pathogens testifies to such potential. For example, the introduction of the chestnut blight pathogen, *Cryphonectria parasitica*, from Europe in 1904 effectively eliminated from North America the American chestnut, an important and beautiful timber tree. Similar potential damage is currently occurring with disease epidemics of forest trees including sudden oak death caused by *Phytophthora ramorum* and pitch canker of pine caused by *Fusarium circinatum*. Introductions of other pathogenic microbes have caused tremendous suffering to humans, including the famines that resulted from the *Phytophthora* late blight epidemic of potato in 1845-1846 in Ireland, and the *Cochliobolus* brown spot epidemic of rice in Bengal in 1943.

Despite their importance to our agricultural base and food security, we know little of the molecular genetics of these microbes. Our understanding of how these microbes cause disease or benefit plants is rudimentary, at best. With the recent advent of genomics, which includes the structural and functional analysis of the microbe genes and the proteins encoded by those genes, we see the opportunity to understand the nature of beneficial and pathogenic microbe-plant-associations at levels never before possible.

### **The Promise of Genome Analysis of Plant-Associated Microbes**

The knowledge of how microbes interact with plants is essential to the development of effective and environmentally-sound, chemically-based strategies for disease control. In the US, over \$600 million are spent annually on agricultural fungicides alone. Similar to what is being observed with the heavy use of antibiotics targeted to human or animal pathogens, changes in pathogen biology more and more frequently render some of these chemicals ineffective. Furthermore, increased regulatory policies are restricting the use of existing agrochemicals for pathogen control. With genome information, multiple tactics for control of pathogens could be developed. For example, the identification of more precise targets in the pathogen may allow for design of more specific and effective chemicals that are environmentally benign.

Due to powerful automated sequence technologies and advances in bioinformatics, the task of sequencing entire genomes of organisms is now routine. The sequenced genomes of a relatively few model organisms are already enabling a wide variety of new discoveries, including new genes and metabolic pathways and insights into the mechanisms of microbial pathogenesis. The continuous development of ever improving bioinformatics

tools is enhancing the discovery power of these sequences. With these exciting advances, the means to generate sequence and functional information and the tools to use that information to understand the basic biology of microorganisms that cause or prevent diseases on plants are now available.

Genome analyses will enhance our knowledge base exponentially and thereby provide tools to abrogate the problems caused by plant pathogenic microbes through genetically-based approaches and allow development of improved beneficial microbes. Historically, the molecular basis for interactions between plants and microbes was studied using a gene-by-gene approach and host resistance was a major control approach. Now, coupled with the increasing availability of plant host genomic sequences, structural and functional genomic analysis of plant-associated microbes will increase the speed of identification of genes involved in host-pathogen interactions and will allow genome-wide approaches to understanding the role of a gene or pathway in interactions with plants. Some genes will potentially be useful as sources of pathogen-derived resistance as has already been demonstrated for many viral diseases. Other genes may be involved in recognition to trigger host defense responses to the pathogen.

Comparisons of genomes of related strains or species will provide an understanding of the evolution of microbial genomes, particularly as they evolve in associations with plants. Researchers exploiting comparative genomics will be able to discern the molecular basis of how some microbes have evolved to form intimate biotrophic associations with plant cells, whereas others inhabit intercellular spaces and still others colonize only the vascular systems of their hosts. Comparisons of sequences within and between species will also provide information to develop accurate diagnostic tools. Such precision in diagnostics may be essential to track the source or origin of a pathogen (e.g., as for the anthrax strains recently released in the US, or plum pox virus recently introduced). This information may be essential for forensic purposes as well as to understand the genetic potential of the pathogen to become established or to cause an epidemic. Additionally, because of the evolutionary conservation between microbes of different genera, and because of the exchange of genetic information between some groups of microbes, genome analysis of plant-associated microbes will contribute to our understanding of how animal pathogens cause disease. For example bacterial genes involved in plant disease induction exhibit a great deal of similarity to bacterial genes involved in disease induction in animals and humans (Keen *et al.*, 2000, <http://www.pnas.org/cgi/content/full/97/16/8752>). Thus, identifying the full complement of genes involved in pathogenesis will help decipher the disease strategies of these organisms and will guide design of new control measures for use in both plants and animals.

In sum, functional, structural and comparative genome analyses will provide insights into how microbes infect and establish either disease or beneficial interac-

tions with host plants, and how they reproduce and spread in the plants and how they persist and are disseminated in the environment. This information will be critical for the development of more effective, environmentally benign control measures and for accurate diagnostic and tracking methods.

### Which plant-associated microbes should be sequenced?

Even with the costs of genome sequencing decreasing, it is clearly not feasible to sequence genomes of all plant-associated species at this time. Through a series of task forces with broad input, the APS established a prioritized list of species for genome sequencing. This list, published in a White Paper entitled "*Microbial Genomic Sequencing: Perspectives of the American Phytopathological Society*" (<http://www.apsnet.org/members/ppb/ps/top.asp>), was developed using the following criteria:

- Economic importance and relevance to U.S. and world-wide agriculture;
- Unique biological or environmental features; Broad interest to a significant community of scientists or agriculturists;
- Genetic tractability (i.e., the ease with which genetic studies, such as crosses or genome modifications, can be performed); and
- Availability of tools and other biological resources (e.g., gene libraries, genetic maps, and the genetic tractability of the host so that the system could be addressed from both sides of the host-pathogen interaction, etc.).

The intention at its publication was that the APS list, compiled in 2000-2001, would be subject to change. To encourage even wider input and a more accurate up-to-date list, the research community has been invited to revisit the list criteria and content, and make further recommendations through the chairs of each pertinent subject matter committee. These comments/recommendations will be the subject of a discussion forum at the APS meetings in July, 2002. In addition, the need for specialized lists, such as the list of organisms that are potential introduced threats to U.S. agriculture (<http://www.apsnet.org/online/feature/exotic/>), will be discussed.

### Community discussions preceding this white paper:

A workshop was held in Washington, D.C. April 9-11, 2002 to develop a strategy to expedite genome analysis of plant-associated microbes. The workshop was organized by the APS Public Policy Board, and was funded by the Department of Energy (DOE), the National Science Foundation (NSF), USDA-Agricultural Research Service (USDA-ARS) and USDA-National Research Initiative (USDA-NRI). Participants included academic, industrial, and governmental experts from the genomics and microbial research communities and observers from the federal funding agencies. The participants agreed on several key points:

- The lack of publicly available information on the

genomes of plant-associated microbes is a major impediment to research, and, as a result, to crop biosecurity;

- The APS list of microbes for sequencing is a good starting point, but requires periodic review and updating;
- Current technological and biological resources would allow for sequence analysis of a significant number of microbes from this very diverse group, given appropriate funding resources;
- The availability of genome sequence would enable and enhance the development of tools for functional and comparative genomics; and
- There is an urgent need for development and employment of flexible and broadly applicable bioinformatic tools and the establishment and continual updating of databases and genetic resource centers.

An advisory committee (Appendix C) was appointed to oversee the development of a *Plant-Associated Microbe Genome Initiative*. Discussions toward this initiative will be broadened by two means. Firstly, with the publication of this draft position paper via society newsletters and email lists, the research community will be invited to contribute ideas and feedback through email [microbegenomics@scisoc.org](mailto:microbegenomics@scisoc.org). These comments will be compiled and posted at the APS PPB website <http://www.apsnet.org/members/ppb/top.asp>. Secondly, a public open forum will be held at the Annual APS meetings in Milwaukee, WI (July 27, 2002). At this forum, the Initiative recommendations will be summarized and feedback on them will be solicited. All comments and suggestions from these various sources will be used to develop a final position paper that will be published at either societal newsletters or in an international journal (e.g., *Molecular Plant-Microbe Interactions*). This final position paper, referred to as the *Plant-Associated Microbe Genome Initiative*, will be distributed to appropriate federal research funding agencies to garner support and guide program development for promoting genome analysis of these important microbes.

### Recommendations for Genome Analysis of Plant-Associated Microbes

To remedy the paucity of genomic information available for plant-associated microbes, the workshop participants began development of the *Plant-Associated Microbe Genome Initiative* and proposed a five-year concentrated effort. The recommendations for the initiative reflect the diversity of the microbes that interact with plants and the tremendous differences in the current status of the genome analysis of those organisms. Due to the diverse group of organisms, the recommendations are meant to provide a broad outline of how an international comprehensive effort might be approached and are not meant to provide specific technical detail of how the analyses should be accomplished. To be effective, the effort must be *collaborative, well-coordinated, and international*. Industrial and public partnerships should be encouraged with the stipulation that all information must be made

rapidly available to the *public*. Finally, the effort must involve strong *education and training* programs.

Four areas are described below that should be targeted in this five-year initiative. The participants recommend a \$500 million investment to be distributed equally among these areas over the five years, except that in the first few years the proportion of resources necessarily will be greater to structural analysis than to functional analyses.

### **1. Structural analysis.**

Structural sequence information is the key to gene discovery and the first step towards learning the function of each gene. There are vast differences in the amounts of sequence information currently available for different plant-associated microbes. For example, due to their smaller genome size, many different plant viruses and a few plant bacteria have already been sequenced; whereas, no genomes of plant-associated oomycetes, fungi or nematodes have been sequenced to completion. These differences in available information, which vary widely within and between microbe groups, impact the entry level for analysis of each group. They also impact the cost of sequencing the genomes of different microbe groups.

No consensus was reached on the depth of sequence needed (i.e., draft versus complete genome sequences). One component of workshop participants suggested that to obtain useful SNP and genotype information more than one strain of an organism should be sequenced. As an example, this component recommended that the genomes of three strains of a given bacterial species should be sequenced completely followed by sequencing to 8X coverage of an additional 10-20 strains. Another component suggested that if a complete genome sequence were available from one type strain, then lower coverage draft sequence of additional strains would provide information sufficient for most purposes. Although there were other permutations of this discussion, the emerging conclusions are that the depth of sequencing will depend on the end user needs (the questions to be addressed), subject to the complexity of the microbial genome of interest and available resources.

#### **Recommendation for the Plant-Associated Microbe Genome Initiative:**

- Focus initial resources largely on sequence analysis to remedy the paucity in sequence information available for plant-associated microbes;
- Target 2,000 Mb of sequence total over all microbes over five years; and
- Determine the depth of sequence or coverage for each microbe on a case-by-case basis, based on the specific needs or questions, to be evaluated by the research community.

### **2. Functional analysis.**

Sophisticated technologies, including array-based technologies, are available for both gene expression and

proteomic analyses and will enable the dissection of the functions of genes and proteins involved in interactions of microbes with plants and the environment. Additionally, high-throughput genome-wide gene deletion and tagging methods are being developed. Although limited, there is publicly-available genome sequence information currently for a few plant-associated microbes that is sufficient to launch functional genomic studies. These microbes can serve as model systems for functional genomic efforts to identify genes/proteins and biochemical pathways that are involved in interactions with plants.

#### **Recommendation for the Plant-Associated Microbe Genome Initiative:**

- Focus initial resources on those few microbes with sufficient structural genomic and genetic resources available; and
- Invest in improvement of technologies for functional analyses.

### **3. Standardized bioinformatic tools and database system**

The underpinning for successful structural and functional genome analysis is the ability to integrate, manipulate, analyze, compare, and store all of data generated by these technologies. It was clear from the intensity of discussions surrounding the bioinformatic tools and database systems that this is an area of major deficiency and concern. It was also clear that this is a problem not only for analysis and storage of data for the genomes of plant-associated microbes, but for all databases. Participants discussed the merits of fixing the existing systems as opposed to developing new, state-of-the-art systems, or using one major database as opposed to many smaller, interconnected databases. Critical features highlighted were that these tools must be (1) flexible (e.g., usable for comparisons among different genomes, including microbes and plants), (2) scalable, (3) inter-operable, (4) easily implemented, (5) readily updateable, and (6) stably funded and maintained. Guidelines should be developed for standardization of public databases, and these should include common (1) means for electronic submission of data, (2) terminology, and (3) criteria for quality of data submitted.

#### **Recommendation for the Plant-Associated Microbe Genome Initiative:**

- Increase resources allocated to the standardization of databases and bioinformatic tools, as these are essential to the total science of genomics and the application of that science;
- Develop mechanisms for discussions, planning, and research at an international level; and
- Develop a framework to finance and manage the maintenance and continual updating of databases and information resources.

*Plant-Associated Microbe Genome Initiative continued on page 9*

**April 2002 • Volume 15, Number 4**

The Biotrophic, Non-Appressorium-Forming Grass Pathogen *Claviceps purpurea* Needs a *Fus3/Pmk1* Homologous Mitogen-Activated Protein Kinase for Colonization of Rye Ovarian Tissue. G. Mey, B. Oeser, M. H. Lebrun, and P. Tudzynski. Pages 303-312. Publication no. M-2002-0308-02R.

*Lotus japonicus* Gene *Ljsbp* Is Highly Conserved Among Plants and Animals and Encodes a Homologue to the Mammalian Selenium-Binding Proteins. E. Fliemetakis, A. Agalou, N. Kavroulakis, M. Dimou, A. Martsikovskaya, A. Slater, H. P. Spaink, A. Roussis, and P. Katinakis. Pages 313-322. Publication no. M-2002-0306-01R.

*Pseudomonas* Lipodepsipeptides and Fungal Cell Wall-Degrading Enzymes Act Synergistically in Biological Control. V. Fogliano, A. Ballio, M. Gallo, S. Woo, F. Scala, and M. Lorito. Pages 323-333. Publication no. M-2002-0221-01R.

Isolation and Identification of a Phosphate Deficiency-Induced C-Glycosylflavonoid That Stimulates Arbuscular Mycorrhiza Formation in Melon Roots. K. Akiyama, H. Matsuoka, and H. Hayashi. Pages 334-340. Publication no. M-2002-0226-01R.

Autoregulation of Root Nodule Formation: Signals of Both Symbiotic Partners Studied in a Split-Root System of *Vicia sativa* subsp. *nigra*. A. A. N. van Brussel, T. Tak, K. J. M. Boot, and J. W. Kijne. Pages 341-349. Publication no. M-2002-0304-01R.

Identification of a Family of Extensin-Like Glycoproteins in the Lumen of *Rhizobium*-Induced Infection Threads in Pea Root Nodules. E. A. Rathbun, M. J. Naldrett, and N. J. Brewin. Pages 350-359. Publication no. M-2002-0306-03R. Identification of a cDNA from the Arbuscular Mycorrhizal Fungus *Glomus intraradices* that is Expressed During Mycorrhizal Symbiosis and Up-Regulated by N Fertilization. J. M. Ruiz-Lozano, C. Collados, R. Porcel, R. Azcón, and J. M. Barea. Pages 360-367. Publication no. M-2002-0307-01R.

Analysis of *Mesorhizobium loti* Glycogen Operon: Effect of Phosphoglucosyltransferase (*pgm*) and Glycogen Synthase (*glgA*) Null Mutants on Nodulation of *Lotus tenuis*. V. C. Lepek, A. L. D'Antuono, P. E. Tomatis, J. E. Ugalde, S. Giambiagi, and R. A. Ugalde. Pages 368-375. Publication no. M-2002-0307-02R.

Expressed Sequence Tags from Roots and Nodule Primordia of *Lotus japonicus* Infected with *Mesorhizobium loti*. C. Poulsen and L. Pødenphant. Pages 376-379. Publication no. M-2002-0313-01R.

Pathogen Challenge, Salicylic Acid, and Jasmonic Acid Regulate Expression of Chitinase Gene Homologs in Pine. J. M. Davis, H. Wu, J. E. K. Cooke, J. M. Reed, K. S. Luce,



and C. H. Michler. Pages 380-387. Publication no. M-2002-0306-02R.

*Rhizobium leguminosarum* bv. *trifolii* PssP Protein Is Required for Exopolysaccharide Biosynthesis and Polymerization. A. Mazur, J. E. Król, J. Wielbo, T. Urbanik-Sypniewska, and A. Skorupska. Pages 388-397. Publication no. M-2002-0305-01R.

Virulence Genes of the Phytopathogen *Rhodococcus fascians* Show Specific Spatial and Temporal Expression Patterns During Plant Infection. K. Cornelis, T. Maes, M. Jaziri, M. Holsters, and K. Goethals. Pages 398-403. Publication no. M-2002-0308-01R.

An *Arabidopsis thaliana* Pectin Acetyltransferase Gene Is Upregulated in Nematode Feeding Sites Induced by Root-Knot and Cyst Nematodes. I. Vercauteren, J. de Almeida Engler, R. De Groot, and G. Gheysen. Pages 404-407. Publication no. M-2002-0219-02N.

**May 2002 • Volume 15, Number 5**

Novel Aspects of Symbiotic Nitrogen Fixation Uncovered by Transcript Profiling with cDNA Arrays. G. S. Colebatch, K. Kloska, B. Trevaskis, S. Freund, T. Altmann, and M. K. Udvardi. Pages 411-420. Publication no. M-2002-0320-01R.

Genomics of Phytopathogenic Fungi and the Development of Bioinformatic Resources. D. N. Soanes, W. Skinner, J. Keon, J. Hargreaves, and N. J. Talbot. Pages 421-427. M-2002-0409-01O.

Expression of Different Calmodulin Genes in Bean (*Phaseolus vulgaris* L.): Role of Nod Factor on Calmodulin Gene Regulation. A. Camas, L. Cárdenas, C. Quinto, and M. Lara. Pages 428-436. Publication no. M-2002-0311-01R.

A Novel Gene, *CBPI*, Encoding a Putative Extracellular Chitin-Binding Protein, May Play an Important Role in the Hydrophobic Surface Sensing of *Magnaporthe grisea* During Appressorium Differentiation. T. S. Kamakura, Yamaguchi, K.-I. Saitoh, T. Teraoka, and I. Yamaguchi. Pages 437-444. Publication no. M-2002-0318-01R.

Functional and Comparative Bioinformatic Analysis of Expressed Genes from Wheat Spikes Infected with *Fusarium graminearum*. W. M. Kruger, C. Pritsch, S. Chao, and G. J. Muehlbauer. Pages 445-455. M-2002-0328-01R.

Roles for Riboflavin in the *Sinorhizobium*-Alfalfa Association. G. T. Yang, V. Bhuvaneshwari, C. M. Joseph, M. D. King, and D. A. Phillips. Pages 456-462. Publication no. M-2002-0408-01R.

rpff Mutants of *Xanthomonas oryzae* pv. *oryzae* are Deficient for Virulence and Growth Under Low Iron



Conditions. S. Chatterjee, and R. V. Sonti. Pages 463-471. Publication no. M-2002-0325-01R.

hrp Genes of *Erwinia chrysanthemi* 3937 Are Important Virulence Factors. C.-H. M. Yang, Gavilanes-Ruiz, Y. Okinaka, R. Vedel, I. Berthuy, M. Boccara, J. W.-T. Chen, N. T. Perna, and N. T. Keen. Pages 472-480. Publication no. M-2002-0329-01R.

A Molecular Genetic Map and Electrophoretic Karyotype of the Plant Pathogenic Fungus *Cochliobolus sativus*. S. Zhong, B. J. Steffenson, J. P. Martinez, and L. M. Ciuffetti. Pages 481-492. Publication no. M-2002-0402-01R.

Disruption of the Alternative Oxidase Gene in *Magnaporthe grisea* and Its Impact on Host Infection. C. Avila-Adame, and W. Köller. Pages 493-500. Publication no. M-2002-0403-01R.

Auxotrophic Mutant Strains of *Rhizobium etli* Reveal New Module Development Phenotypes. S. Ferraioli, R. Taté, M. Cermola, R. Favre, M. Iaccarino, and E. J. Patriarca. Pages 501-510. Publication no. M-2002-0402-02.

#### June 2002 • Volume 15, Number 6

Enhanced Resistance to Seed-Transmitted Bacterial Diseases in Transgenic Rice Plants Overproducing and Oat Cell-Wall-Bound Thionin. T. Iwai, H. Kaku, R. Honkura, S. Nakamura, H. Ochiai, T. Sasaki, and Y. Ohashi. Pages 515-521. Publication number M-2002-0409-02R.

Nod Factor Induction of Reactive Oxygen Species Production Is Correlated with Expression of the Early Nodulin Gene *rip1* in *Medicago truncatula*. S. K. Ramu, H.-M. Peng, and D. R. Cook. Pages 522-528. Publication numbers M-2002-0501-01R.

Phylogeny and Genomic Organization of the TIR and non-TIR NBS-LRR Resistance Gene Family in *Medicago truncatula*. H. Zhu, S. B. Cannon, N. D. Young, and D. R. Cook. Pages 529-539. M-2002-0419-01R.

PPI1: A Novel Pathogen-Induced Basic Region-Leucine Zipper (bZIP) Transcription Factor from Pepper. S. J. Lee, M. Y. Lee, S. Y. Yi, S. K. Oh, S. H. Choi, N. H. Her, D.

Choi, B. W. Min, S. G. Yang, and C. H. Harn. Pages 540-548. Publication number M-2002-0429-01R.

Cloning and Characterization of an Esophageal-Gland-Specific Pectate Lyase from the Root-Knot Nematode *Meloidogyne javanica*. E. A. Doyle and K. N. Lambert. Pages 549-556. Publication number 0424-01R.

Characterization of a Novel Defense-Related *Arabidopsis* Mutant, *cir1*, Isolated by Luciferase Imaging. S. L. Murray, C. Thomson, A. Chini, N. C. Read, and G. J. Loake. Pages 557-566. Publication number M-2002-0506-01R.

Deleterious Impact of a Virulent Bacteriophage on Survival and Biocontrol Activity of *Pseudomonas fluorescens* Strain CHA0 in Natural Soil. C. Keel, Z. Ocurum, P. Michaux, M. Adrian, and D. Haas. Pages 567-576. Publication number M-2002-0408-02R.

Identification and Characterization of a Soybean Ethylene-Responsive Element-Binding Protein Gene Whose mRNA Expression Changes During Soybean Cyst Nematode Infection. M. Mazarei, D. P. Puthoff, J. K. Hart, S. R. Rodermel, and T. J. Baum. Pages 577-586. Publication number M-2002-0415-01R.

Plant Defense Genes Associated with Quantitative Resistance to Potato Late Blight in *Solanum phureja* ? Dihaploid *S. tuberosum* Hybrids. F. Trognitz, P. Manosalva, R. Gysin, D. Niño-Liu, R. Simon, M. del Rosario Herrera, B. Trognitz, M. Ghislain, and R. Nelson. Pages 587-597. Publication number M-2002-0426-01R.

The FixM Flavoprotein Modulates Inhibition by AICAR or 5' AMP of Respiratory and Nitrogen Fixation Gene Expression in *Sinorhizobium meliloti*. C. Cosseau, A. M. Garnerone, and J. Batut. Pages 598-607. Publication number M-2002-0422-01R.

*NHL25* and *NHL3*, Two *NDR1/HIN1*-Like Genes in *Arabidopsis thaliana* with Potential Role(s) in Plant Defense. A. Varet, J. Parker, P. Tornero, N. Nass, T. Nürnberger, J. L. Dangl, D. Scheel, and J. Lee. Pages 608-616. Publication number M-2002-0429-02R.

---

Plant-Associated Microbe Genome Initiative *continued from page 7*

#### 4. Train the next generation of plant microbiologists

To capitalize on the information provided from the analysis of the genomes of plant-associated microbes, a key goal of the Plant-Associated Microbe Genome Initiative must be to train new and update current plant microbiologists to ensure a research community skilled in microbe and plant biology and in computational sciences. Additionally, these scholars will need the resources to interact and collaborate in an international research arena. International collaborations are particularly important for analysis of pathogens exotic to the US.

#### Recommendation for the Plant-Associated Microbe Genome Initiative:

- Train plant microbiologists in the skills of genomics and computational sciences (e.g., this training should involve scientists at all levels of their careers to ensure an up-to-date, skilled pool of plant microbiologists); and
- Provide funding and opportunities for domestic and international research collaborations.



**Seiji Ouchi**, Kinki University, Nara, Japan, is a recipient of the prestigious Japan Agricultural Science Award for 2002. This award is presented annually by the Japan Societies for Agricultural Sciences to seven scientists. The presidents of the 45 professional societies that comprise this organization elect the awardees from the combined membership of approximately 87,000 scientists. Ouchi is

only the 28th plant pathologist to be elected during the 77-year period the award has been bestowed.

Ouchi was recognized for "Basic Studies on the Mechanisms Determining Host-Pathogen Specificity." His key contribution was the introduction of the concept of accessibility, which is defined as host cell conditioning for the establishment of pseudosymbiotic associations between the pathogen and host plants. In this context, he defined the pathogen as a biotic entity that is genetically equipped to negate or suppress the functions of specific and nonspecific resistance genes of the host plant.

During his professional career, Ouchi has held faculty positions at Kyoto University, Okayama University, and for the past 17 years, at Kinki University. While at Kinki University, he has served two years as chair of the Department of Agronomy, four years as dean of the Graduate School, including chair of the Dean's Assembly, three years as vice dean of Student Affairs, 10 years as director of the Institute for Comprehensive Agricultural Sciences, 12 years as chair of the Bio-safety Control Committee for Recombinant DNA Experiments, and most recently as a coordinator of the Technology Licensing Organization of Osaka Prefecture (representing the university) with responsibilities for policy development and technology transfer. In 2001, Ouchi retired from Kinki University after 39 years of service to his profession.

Ouchi is known worldwide for his dedicated service to plant pathology, which includes such achievements as being one of the principal organizers of the 1988 International Congress of Plant Pathology held in Kyoto and his dedication to the US/Japan Seminar Series since its inception in 1965. In recognition of his numerous significant contributions, Ouchi was elected a Fellow of the Phytopathological Society of Japan in 1986, and a Fellow of the American Phytopathological Society in 1996. He currently is an emeritus professor at Kinki University and a courtesy professor in the Department of Botany and Plant Pathology at Oregon State University. He and his wife, Naoko, will reside in Corvallis, OR, beginning June 1, 2002, for at least a year, and his plans include a balance of research and scientific writing.

#### **IS-MPMI Charter Member Donald L. Keister Retires**

**Donald Keister**, plant physiologist at the Beltsville Agricultural Research Service, USDA-ARS in Beltsville, Maryland retired this past July. He is a charter member of IS-MPMI and a member of several other societies. Keister received his M.S. and Ph.D. degrees from the Univ. of Maryland in 1959. His postdoctoral work was at The Johns Hopkins Univ. with **Anthony San Pietro**. He worked with **Bessel Kok** at the Research Institute for Advanced Studies and then moved to The Charles F. Kettering Research Laboratory where he worked on microbial photosynthesis. He is internationally recognized for his work on energy-linked reactions. Several original discoveries from this period included the mechanism of pyridine nucleotide reduction in photosynthetic bacteria and the utilization of inorganic pyrophosphate as an energy source for energy-linked reactions. In the area of nitrogen fixation, he co-discovered nitrogen fixation in free-living rhizobia.

He joined the Agricultural Research Service in Beltsville, Maryland in 1984 as research leader of the Nitrogen Fixation and Soybean Genetics Lab (currently the Soybean Genomics and Improvement Lab) and has continued to contribute to the elucidation of symbiotic plant-microbe interactions including the role of microbial cytochromes and cyclic  $\beta$ -glucans. He has contributed over 100 peer reviewed journal articles, book chapters and reviews. Recently he has served as acting associate director and director of the Plant Sciences Institute at the Beltsville Agricultural Research Center.

He is looking forward to more time for travel, sports, reading and visiting colleagues and would enjoy hearing from you at [dkeister@jhu.edu](mailto:dkeister@jhu.edu).

#### **Member Ali Azam to Complete Training in Molecular Breeding**

**Md. Ali Azam** has been working on rice breeding as a research scientist since 1980 at the Bangladesh Institute of Nuclear Agriculture, Mymensingh, Bangladesh. He received his degrees of M.S. (1975) and Ph.D. (1994) on Plant Breeding and Genetics (Biometry) under the guidance of **O.I. Joarder** at the University of Rajshai, Bangladesh. Since his joining to his institute from 1980, he has developed and released four rice varieties, one of which has become popular for its highest yield in Bangladesh. He has been a visiting scientist at Dale Bumpers National Rice Research Center, USDA-ARS, Stuttgart, for training in molecular breeding since April, 2002 under the supervision of **Yulin Jia**, the research molecular pathologist and **J. Neil Rutger**, the director and plant breeder and geneticist. This training is funded by the International Atomic Energy Agency, Austria. He will complete his training in molecular breeding in September 2002.

**Postdoctoral position using *S. meliloti* microarrays**

A postdoctoral position is available to study two sigma factors that have roles in the *S. meliloti*-legume symbiosis using microarrays and proteomics. This work is part of our ongoing interest in how *S. meliloti* cells adapt and differentiate within the nodule. A strong background in molecular biology/bacterial genetics is preferred. The position is available immediately and will be for 2 years with the possibility of renewal depending on funding. To apply, please send a CV and names of three references to: Dr. Valerie Oke, Dept. of Biological Sciences, A527A Langley Hall, University of Pittsburgh, Pittsburgh, PA, 15260, USA or [voke@pitt.edu](mailto:voke@pitt.edu). For more information about the department and lab see <http://www.pitt.edu/~biohome>.

**Ph. D. Studentships**

International Max-Planck Research School: "*The molecular basis of plant development and environmental interactions*" The Max-Planck-Institute for Plant Breeding Research together with its partner institutions the University of Cologne, the Institute of Bioorganic Chemistry (Poznan, Poland), the Institute for Plant Sciences (Gif sur Yvette, France) and the Biological Research Centre (Szeged, Hungary) invite applications for Ph.D. fellowships as part of the International Max Planck Research School (IMPRS) on "The molecular basis of plant development and environmental interactions". The constellation of participating institutions provides excellent conditions and expertise in plant genetics, structural biology/biochemistry and cell biology. The program seeks to provide an interdisciplinary education for highly motivated students. Individual projects will include: *structural and functional*

*aspects of plant enzymes and regulatory proteins, intra- and intercellular signalling, exogenous signals for cell division and differentiation, determinants of plant-microbe development, molecular genetics of plant evolution, symbiotic and pathogenic plant/microbe interactions, resistance/tolerance to abiotic stress factors.* The training includes biweekly seminars, experimental work under the supervision of two senior faculty of the research school, and practical courses on e.g. reverse genetics, gene isolation, advanced microscopy, 3-D-structural analysis of proteins, bioinformatics, and novel mass spectrometry-based protein biochemistry at the participating institutions. The program is in English and open for students from all countries. Applicants must hold a Master's degree, comparable to the German diploma, as required by the enrolling University of Cologne. The application should be in English and must include: a cover letter, a detailed CV including complete address with email, the grades of the Master's degree, and a one page thesis summary; candidates from countries with another official language should provide a proof of efficiency in English as a second language such as a certificate of TOEFL or IELTS. In addition two letters of reference should be mailed independently to the IMPRS coordinator. The fellowship application should be mailed to: IMPRS – Molecular Basis of Plant Development, Scientific Coordinator, Max-Planck-Institut für Züchtungsforschung, Carl-von-Linné Weg 10, 50829 Köln/Germany. For further information about the application and the Ph.D. program please visit [www.mpizkoeln.mpg.de](http://www.mpizkoeln.mpg.de) and follow the link to the IMPRS or contact the scientific coordinator under: [imprsc@mpizkoeln.mpg.de](mailto:imprsc@mpizkoeln.mpg.de).

**New Database On Molecular Plant Pathogen Interactions**

A new web site at <http://www.drastic.org.uk> contains information on the molecular responses of plants to infection by plant pathogens. It also is an important database of genes up- or down-regulated in response to infection, treatment with chemicals that modify resistance, and various abiotic stresses. The link to the searchable database is one of the provided quick links. The information in the database is derived from published information but uniquely brings together expression data in a searchable format. The site contains information on a wide range of plants. Information for the database is welcome in order to make it more complete and useful to everybody. Contact: **Gary D Lyon**, Scottish Crop Research Institute, Invergowrie, Dundee DD2 5DA, Scotland; Fax: +44-1382-562426; e-mail: [glyon@scri.sari.ac.uk](mailto:glyon@scri.sari.ac.uk).

**Update on Microbial Genomes - Fungi**

Jonathan Walton, Michigan State University ([walton@msu.edu](mailto:walton@msu.edu))

The National Human Genome Research Institute (NHGRI) has given a rating of 'high priority for funding' to the full

genomic sequencing of at least seven fungi. The proposal was submitted by the Whitehead Institute Center for Genome Research with input from fungal biologists. Several of the fungi are plant-associated: *Magnaporthe grisea* (pathogenic Ascomycete), *Ustilago maydis* (pathogenic Basidiomycete), *Fusarium graminearum* (synonym *Gibberella zeae*) (pathogenic mycotoxin-producing Ascomycete), *Paxillus involutus* (symbiotic ectomycorrhizal Basidiomycete), and *Aspergillus flavus* (grain-infesting mycotoxin producer). At this point the actual funding status is not known. Information including a pdf file of the Fungal Genome Initiative White Paper is available at [www.genome.gov/page.cfm?pageID=10002154](http://www.genome.gov/page.cfm?pageID=10002154).

Meanwhile, the *M. grisea* genome has been finished to 6x coverage. The work was a cooperative effort between **Ralph Dean** of North Carolina State, the International Rice Blast Genome Consortium, and the Whitehead Institute. A searchable database is available at [www.genome.wi.mit.edu/annotation/fungi/magnaporthe/](http://www.genome.wi.mit.edu/annotation/fungi/magnaporthe/). See also <http://www.riceblast.org/>.

Data from an *F. graminearum* EST project are available online at [www.cdl.umn.edu/scab/gz-consort.html](http://www.cdl.umn.edu/scab/gz-consort.html). An *F. sporotrichioides* EST project is also underway at the University of Oklahoma ([www.genome.ou.edu/fsporo.html](http://www.genome.ou.edu/fsporo.html)).

**Welcome New Members**

The following members joined IS-MPMI between March 2002 through June 2002. Please join us in welcoming them to the Society!

**Chris A. Allen**, Oklahoma State Univ,  
Stillwater, OK

**Gwyn A. Beattie**, Iowa State Univ, Ames,  
IA

**Richard M. Bostock**, Univ of California,  
Davis, CA

**Anna-Maria Botha-Oberholster**, Univ  
of Pretoria, Pretoria, REP OF SOUTH AFRICA

**Suma Chakravarthy**, Boyce Thompson  
Inst, Ithaca, NY

**Woobong Choi**, LGCI, Daejeon, SOUTH  
KOREA

**Wim D'Haese**, Univ of Georgia, Athens,  
GA

**Jolio Cezar De Mattos Cascardo**,  
UESC DCB, Ilheus, BA, BRAZIL

**Katherine J. Denby**, Univ of Cape  
Town, Rondebosch, , REP OF SOUTH AFRICA

**Timothy P. Devarenne**, Boyce  
Thompson Inst, Ithaca, NY

**Robert Fluhr**, Weizmann Inst of Science,  
Rehovot, ISRAEL

**Tatsuaki Goh**, Tokyo Univ of Science,  
Noda, Chiba, JAPAN

**Thomas Hurek**, Univ of Bremen,  
Bremen, GERMANY

**Euan K. James**, Univ of Dundee, Dundee,  
UNITED KINGDOM

**Paula E. Jameson**, Massey Univ,  
Palmenton North, NEW ZEALAND

**Jong Heon Kim**, Univ of California,  
Albany, CA

**Kris N. Lambert**, Univ of Illinois, Urbana,  
IL

**Jeffrey M. Lerner**, Worcester, MA

**Shien Lu**, Texas A&M Univ, College Station,  
TX

**Juan A. Martin Sanchez**, Univ De  
Leida, Lleida, SPAIN

**Massimo Merighi**, Ohio State Univ,  
Columbus, OH

**Javier Narvaez-Vasquez**, Washington  
State Univ, Pullman, WA

**Katarzyna Nuc**, August Cieszkowski Univ  
of Agric, Poznan, POLAND

**Yuko Ohashi**, Natl Inst of Agrobiological  
Sciences, Tsukuba, Ibaraki, JAPAN

**Patricia A. Okubara**, Washington State  
Univ, Pullman, WA

**Ramesh Raina**, Penn State Univ,  
University Park, PA

**Michael A. Savka**, Rochester Inst of  
Technology, Rochester, NY

**Naoto Shibuya**, Meiji Univ, Kawasaki,  
Kanagawa, JAPAN

**Ko Shimamoto**, Nara Inst of Sci & Tech,  
Ikoma, Nara, JAPAN

**Roberto Staneloni**, Inst De  
Investigaciones Bioquimicas, Buenos Aires,  
ARGENTINA

**Dingzhong Tang**, Indiana Univ,  
Bloomington, IN

**Z. Terefework**, Univ of Helsinki, Helsinki,  
FINLAND

**Yukio Tosa**, Kobe Univ, Kobe, Hyogo,  
JAPAN

**Archana Vasanthakumar**, Univ of  
Wisconsin, Madison, WI

**Jennifer W. Weller**, Virginia Tech,  
Blacksburg, VA

**IS-MPMI BOARD OF DIRECTORS***President*

**Egbertus (Ben) Lugtenberg**  
Leiden Univ  
Phone: 31 71 527 5063  
Fax: 31 71 527 5088  
E-mail:  
lugtenberg@rulbim.leidenuniv.nl

*President-Elect*

**Jonathan D. Walton**  
Michigan State Univ  
Phone: (517) 353-4885  
Fax: (517) 353-9168  
E-mail: walton@pilot.msu.edu

*Past President*

**Jan E. Leach**  
Kansas State Univ  
Phone: (785) 532-1367  
Fax: (785) 532-5692  
E-mail: jeleach@ksu.edu

*Secretary*

**Jeff L. Dangl**  
Univ of North Carolina  
Phone: (919) 962-5624  
Fax: (919) 962-1625-3280  
E-mail: dangl@email.unc.edu

*Treasurer*

**Carol L. Bender**  
Oklahoma State Univ  
Phone: (405) 744-9945  
Fax: (405) 744-7373  
E-mail: cbender@okstate.edu

*Director:*

**Andrew F. Bent**  
Univ of Wisconsin  
(608) 265-3034  
Fax: (608) 263-2626  
E-mail: afb@plantpath.wisc.edu

*Director*

**Dieter Haas**  
Univ de Lausanne  
Phone: 41 21 692 5631  
Fax: 41 21 692 5635  
E-mail: dieter.haas@lbn.unil.ch

*Director*

**Adam Kondorosi**  
CNRS  
Inst Des Sciences Du Vegetal  
Phone: 33 16 982 3696  
Fax: 33 16 982 3695  
E-mail: adam.kondorosi@isv.cnrs-gif.fr

*Director*

**Shigeyuki Mayama**  
Kobe Univ  
Phone: 81 78 803 5864  
Fax: 81 78 803 5865  
E-mail: mayama@kobe-u.ac.jp

*Director*

**Anne Osbourn**  
John Innes Centre  
Plant Virus Res/Sainsbury Lab  
Phone: 44 1603 452 571  
Fax: 44 1603 250 024  
E-mail: annie.osbourn@bbsrc.ac.uk

*Director*

**Herman P. Spaink**  
Leiden Univ  
Phone: 31 7 1527 5055  
Fax: 31 7 1527 5088  
E-mail: spaink@rulbim.leidenuniv.nl

*Business Executive (ex-officio)*

**Steven C. Nelson**  
IS-MPMI  
Phone: (651) 454-7250  
Fax: (651) 454-0766  
E-mail: snelson@scisoc.org

*Staff Contact (ex-officio)*

**Amy L. Hope**  
IS-MPMI  
Phone: (651) 454-7250  
Fax: (651) 454-0766  
E-mail: ahope@scisoc.org