IS-MPMI Reporter
International Society for Molecular Plant-Microbe Interactions
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IN THIS ISSUE

IS-MPMI REPORTER DEADLINE

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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 Joel Berg at jberg@scisoc.org.

Send items to:

Editor-in-Chief: Thomas Baum
Department of Plant Pathology
351 Bessey Hall
Iowa State University
Ames, IA 50011
Phone: 515.294.2398
Fax: 515.294.9420
E-mail: tbaum@iastate.edu

Work of MPMI Members Featured in Science

In a recent Special Section in *Science* (pp. 234-236; April 9, 2004), research on the molecular genetics of rhizobial symbioses was prominently featured. The article nicely summarized the tremendous progress that has been made in this area since the earlier identification of *nod* genes and nod factors. It should be particularly gratifying to members of MPMI to note that many of the genes involved in establishment of the nitrogen fixation symbiosis are also involved in the establishment of fungal mycorrhizal associations, because the MPMI Congresses are one of the few venues that bring together researchers interested in both types of symbionts. Current MPMI members who were quoted or whose work was discussed include **Sharon Long, Jens Stougaard, Martin Parniske, Peter Gresshoff,** and **Maria Harrison.** Other colleagues mentioned in the piece included: Fred Ausubel, Doug Cook, Jean Denarie, Gyorgy Kiss, Ton Bisseling, R. Varma Pemetsa, and Masayoshi Kawaguchi. Much of this work was first presented at MPMI Congresses in Amsterdam, Madison, and St. Petersburg.

MPMI Installs New Editorial Board

In January 2004, the new editorial board of MPMI began its 3-year term. **Jens Stougaard** replaces **Herman Spaink** as editor-in-chief and is joined by 11 new senior editors. To acquaint IS-MPMI members with the new board, brief biographies are presented.

Jens Stougaard was a senior editor of MPMI from 2000 to 2003 in the area of plant-bacterial symbioses. In 2003, he was elected to the board of directors of IS-MPMI and, as a function of his position as editor-in-chief of MPMI, he is also a member of the Publications Board of The American Phytopathological Society. Jens received his Ph.D. degree in 1983 from the University of Sussex, Brighton, U.K., and did postdoctoral research in the Department of Molecular Biology at the University of Aarhus, Denmark, and at the Max-Planck Institut für Züchtungsforschung, Cologne, Germany. He has been a visiting scientist in the Sainsbury Laboratory at the John Innes Centre for Plant Science Research, Norwich, U.K., and is currently a professor in the Department of Molecular Biology, University of Aarhus. His primary research is on genes regulating development of nitrogen-fixing root nodules and mycorrhiza in legumes. He is currently focusing on the mechanisms of Nod factor perception, the function of receptors involved and the downstream signal transduction cascade. The plant model system used for this research is *Lotus japonicus,* which is also used for investigating the long-range signaling integrating root nodule development into the general developmental program of the plant. Genetics, genomics, and biochemical methods are used to identify and characterize components of regulatory circuits. State-of-the-art microscopy and bioimaging are used for phenotypic description and studies at the cellular level.

Guido Bloemberg obtained his Ph.D. degree at Leiden University, Leiden, The Netherlands, in 1995, focusing on the analysis of host-specific lipochitin oligosaccharide signal molecules and the biochemical function of the host-specific nodulation gene products of *Rhizobium* spp. under the guidance of Herman Spaink and Ben Lugtenberg. He then worked as a postdoctoral fellow in the laboratories of Roberto Kolter (Harvard Medical School) and Frans de Bruijn (Michigan State University). During these periods, he began working on the visualization of rhizosphere organisms and the regu-

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Global Status of Commercialized Transgenic Crops: 2003

A Report from the International Service for the Acquisition of Agri-Biotech Applications (ISAAA)

In 2003, the global area of transgenic crops continued to grow for the seventh consecutive year at a sustained double-digit growth rate of 15% compared with 12% in 2002. The estimated global area of transgenic or genetically modified (GM) crops for 2003 was 67.7 million hectares; this includes a provisional conservative estimate of 3 million hectares of GM soybean in Brazil (the final hectarage could be significantly higher), officially approved for planting for the first time in 2003. It is noteworthy that a double-digit rate of 10% growth in GM crops was sustained in 2003, even excluding the Brazilian hectarage. The 67.7 million hectares of GM crops in 2003, equivalent to 167 million acres was grown by 7 million farmers in 18 countries, an increase from 6 million farmers in 16 countries in 2002. The increase in area between 2002 and 2003 of 15% is equivalent to 9 million hectares or 22 million acres.

During the eight-year period 1996 to 2003, global area of transgenic crops increased 40 fold, from 1.7 million hectares in 1996 to 67.7 million hectares in 2003, with an increasing proportion grown by developing countries. Almost one-third (30%) of the global transgenic crop area of 67.7 million hectares in 2003, equivalent to over 20 million hectares, was grown in developing countries where growth continued to be strong. It is noteworthy that the absolute growth in GM crop area between 2002 and 2003 was almost the same in developing countries (4.4 million hectares) and industrial countries (4.6 million hectares), with the percentage growth more than twice as high (28%) in the developing countries of the South compared with the industrial countries of the North (11%).

GM Crop Area, by Country, Crop and Trait

In 2003, six principal countries, compared with four in 2002, grew 99% of the global transgenic crop area; this reflects the broadening participation of the lead GM countries with ten countries now growing 50,000 hectares or more, of GM crops. The U.S.A. grew 42.8 million hectares (63% of global total), followed by Argentina with 13.9 million hectares (21%), Canada 4.4 million hectares (6%), Brazil 3 million hectares (4%), China 2.8 million hectares (4%) and South Africa 0.4 million hectares (1%). Of the six leading GM crop countries, China and South Africa had the highest year-on-year increase with a 33% growth rate. China increased its Bacillus thuringiensis (Bt) cotton area for the fifth consecutive year from 2.1 million hectares in 2002 to 2.8 million hectares in 2003, equivalent to 58% of the total cotton area of 4.8 million hectares in 2003. South Africa increased its combined area of GM maize, soybean and cotton to 0.4 million hectares in 2003 with particularly strong growth in white maize used for food, which has increased rapidly from 6,000 hectares in 2001 to 84,000 hectares in 2003. Canada's GM crop area grew at a significant 26% between 2002 and 2003 to reach 4.4 million hectares with increases totaling almost 1 million hectares in the three crops, canola, maize, and soybean. Despite the continuing economic constraints in Argentina, and soybean adoption rates already close to 100% in 2002, its GM crop area grew at 3% with strong growth in Bt maize. A growth rate of 10% was achieved in the U.S.A. (3.8 million hectares) reflecting strong growth in both Bt and herbicide tolerant maize, and continued growth in herbicide tolerant soybean. GM crop hectarage in Australia decreased slightly because of the continued severe drought, which is the worst in centuries, with total area planted to cotton at approximately one third of normal plantings. India increased its Bt cotton area by 100%; Spain also increased its Bt maize area by one third to reach over 6% of the national maize crop in 2003. Uruguay and Romania also reported significant growth, exceeding 50,000 hectares of GM crops for the first time, whilst countries that introduced GM crops for the first time in 2002, such as Colombia and Honduras reported modest growth.

Two countries, Brazil and the Philippines approved planting of GM crops for the first time in 2003. Brazil officially approved herbicide tolerant soybean in late September 2003, immediately before the start of the planting season. This late approval has exacerbated the difficulties in projecting provisional estimates of GM soybean hectarage in Brazil for the 2003/2004 season. At the time when this publication went to press, in late 2003, only 50% of soybeans had been planted in Brazil. A provisional conservative estimate of 3 million hectares of GM soybean has been projected for Brazil in 2003, in the knowledge that the final planted hectarage of GM soybean in Brazil in 2003 could be significantly higher. The Philippines grew approximately 20,000 hectares of Bt maize for the first time in 2003. Brazil and the Philippines joined 16 countries that already grew GM crops in 2002 for a total of 18 GM crop countries in 2003; notably, 11 are developing countries compared with seven industrial countries. Thus, the number of countries growing GM crops has increased steadily from six in 1996, to nine in 1998, to 13 in 2001, and 18 in 2003.

Globally, in 2003, growth continued in all four commercialized GM crops: GM soybean occupied 41.4 million hectares (61% of global GM area), up from 36.5 million hectares in 2002; GM maize was planted on 15.5 million hectares (23% of global GM area), up substantially from 12.4 million hectares in 2002, with the highest growth rate for all crops at 25% - this follows a 27% growth rate in GM maize in 2002; transgenic cotton was grown on 7.2 million hectares (11% of global GM area) compared with 6.8 million hectares in 2002; and GM canola occupied 3.6 million hectares (5% of global GM area), up from 3.0 million hectares in 2002.

During the eight-year period 1996 to 2003, herbicide tolerance has consistently been the dominant trait followed by

insect resistance. In 2003, herbicide tolerance, deployed in soybean, maize, canola, and cotton occupied 73% or 49.7 million hectares of the global GM 67.7 million hectares, with 12.2 million hectares (18%) planted to Bt crops. Stacked genes for herbicide tolerance and insect resistance deployed in both cotton and maize continued to grow and occupied 8% or 5.8 million hectares, up from 4.4 million hectares in 2002. The two dominant GM crop/trait combinations in 2003 were: herbicide tolerant soybean occupying 41.4 million hectares or 61% of the global total and grown in seven countries; and Bt maize, occupying 9.1 million hectares, equivalent to 13% of global transgenic area and grown in nine countries. Whereas the largest increase in Bt maize was in the U.S., growth was witnessed in all seven countries growing Bt maize. Notably, South Africa grew 84,000 hectares of Bt white maize for food in 2003, a substantial 14 fold increase from when it was first introduced in 2001. Bt/herbicide tolerant maize and cotton both increased substantially, reflecting a continuing trend for stacked genes to occupy an increasing percentage of the area planted to GM crops on a global basis.

A useful way to provide a global perspective of the adoption of GM crops is to express the global adoption rates for the four principal GM crops as a percentage of their respective global areas. In 2003, 55% of the 76 million hectares of soybean planted globally were transgenic - up from 51% in 2002. Twenty-one percent of the 34 million hectares of cotton were GM, up from 20% last year. The area planted to transgenic canola in 2003 was 16%, up from 12% in 2002. Finally, of the 140 million hectares of maize grown globally, 11% was GM in 2003 equivalent to 15.5 million hectares, up substantially from 9% or 12.4 million hectares in 2002. If the global areas (conventional and transgenic) of these four principal GM crops are aggregated, the total area is 272 million hectares of which 25%, up from 22% in 2002, was transgenic in 2003. Thus, for the first time one quarter of the aggregate area of the four crops, totaling over one quarter billion hectares is GM. The biggest increase in 2003 was a 4.9 million hectares increase in GM soybean equivalent to a 13% year-on-year growth, followed by a 3.1 million hectare increase in GM maize equivalent to a substantial 25% year-on-year growth, which follows a 27% year-on-year growth in 2002.

The Potential Contribution of GM Crops

The World Food Program recently reported that the number of people suffering from malnutrition increased by 25 million from 815 to 840 million. The most compelling case for biotechnology, and more specifically GM crops, is their capability to contribute to:

- increasing crop productivity, and thus contribute to global food, feed, and fiber security;
- conserving biodiversity, as a land-saving technology capable of higher productivity;
- more efficient use of external inputs, for a more sustainable agriculture and environment;
- increasing stability of production to lessen suffering during famines due to abiotic and biotic stresses;
- and, to the improvement of economic and social benefits and the alleviation of abject poverty in developing countries.

The experience of the first eight years, 1996 to 2003, during which a cumulative total of over 300 million hectares (approximately 750 million acres, equivalent to almost one-third of the total land area of the U.S. or China) of GM crops were planted globally in 21 countries, has met the expectations of millions of large and small farmers in both industrial and developing countries.

In 2003, coincidental with evidential confirmation that commercialized GM crops continue to deliver significant economic, environmental, and social benefits to both small and large farmers in developing and industrial countries, the global area of transgenic crops continued to grow at an annual sustained double-digit growth rate of more than 10%. The number of farmers that benefited from GM crops continued to grow and reached 7 million in 2003, up from 6 million in 2002. Notably, more than 85% of these 7 million farmers benefiting from GM crops in 2003, were resource-poor farmers planting Bt cotton, mainly in nine provinces in China and also in the Makhathini Flats in KwaZulu Natal province in South Africa.

The Global Value of GM Crops

In 2003, the global market value of GM crops is estimated to be $4.50 to $4.75 billion, having increased from $4.0 billion in 2002 when it represented 15% of the $31 billion global crop protection market and 13% of the $30 billion global commercial seed market. The market value of the global transgenic crop market is based on the sale price of transgenic seed plus any technology fees that apply. The global value of the GM crop market is projected at $5 billion or more, for 2005.

Concluding Comments and Future Prospectives

Despite the on-going debate in the European Union, there is cause for cautious optimism that the global area and the number of farmers planting GM crops will continue to grow in 2004 and beyond. Taking all factors into account, the outlook for the next five years points to continued growth in the global hectarage of GM crops to approximately 100 million hectares, with up to 10 million farmers growing GM crops in 25, or more, countries. The global number and proportion of small farmers from developing countries growing GM crops is expected to increase significantly. Established GM country markets are continuing to grow in GM area, with a more diversified portfolio of GM crop products available. New GM countries from the South, like India and Brazil, have increased their hectarage of Bt cotton and herbicide tolerant soybean respectively, and some like Uruguay have also approved new products such as GM maize, already deployed in other countries. New input trait products from industry that will contribute to sustained growth include the dual Bt gene

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IS-MPMI's diverse membership spans the globe and includes professionals who have been in their field for decades as well as those who are just starting out. To help members learn more about their colleagues, each issue of the *IS-MPMI Reporter* profiles three members chosen randomly in different career stages.

Student

Andrea Chini
University of Edinburgh, Institute of Cell & Molecular Biology
Edinburgh, Scotland

After receiving my degree in plant molecular biology from the University of Pavia, Italy, I started my Ph.D. in plant-pathogen interaction at Edinburgh University, Loake's lab, in 2000. I became a member of IS-MPMI at the beginning of my Ph.D. course and have gained several benefits from my membership.

As a student, I received particular support to participate in the IS-MPMI meeting in 2001 (Madison) and in 2003 (St. Petersburgh). In 2001, attending the international conference gave me the opportunity to discuss my project, learn new technologies, and acquire a broader scientific view.

In 2003, I presented my Ph.D. results at the St. Petersburg conference and, to my great surprise, my poster presentation received an award during the closing dinner. In addition, the MPMI journal is of fundamental importance in keeping my plant-pathogen interaction knowledge always up-to-date; hence I hope that IS-MPMI members can soon access PDF versions of all articles published in MPMI. This is my final year as a Ph.D. student, but thanks to several benefits offered by IS-MPMI, I will remain an IS-MPMI member for many years to come.

Postdoctoral/Early Career

Dennis Halterman
USDA/ARS, Iowa State University
Ames, IA, U.S.A.

My interest in the study of plant defense responses began at Cornell College in Mt. Vernon, Iowa, where I received a B.A. in biology and biochemistry in 1994. My undergraduate research project, under the supervision of Craig Tepper, involved the study of pathogenesis-related gene regulation in bean cotyledons after exposure to salicylic acid. My experiences at Cornell influenced my decision to begin a graduate career at Purdue University, where I joined the Purdue Genetics Program and studied with Greg Martin. The focus of my Ph.D. project involved the study of the tomato *Fen* gene, which confers a hypersensitive response-like phenotype after exposure to the insecticide fenthion. Specifically, my research involved the comparison of signal transduction pathways leading to the fenthion response with the bacterial resistance response mediated by a closely related gene, *Pto*.

Upon the completion of my Ph.D., I joined the lab of Roger Wise as a USDA postdoctoral fellow in the Department of Plant Pathology at Iowa State University. In his lab, I began studying the interactions between barley and the biotrophic fungal pathogen *Blumeria graminis* f. sp. *hordei* (powdery mildew). I have been successful in cloning and beginning characterization of the *Mla6*, *Mla7*, *Mla10*, and *Mla13* genes, which are responsible for race-specific resistance to powdery mildew. Recently, my research has involved the study of transcriptional and translational control of *Mla* and the unique mechanisms involved in expression of this family of resistance genes.

I have recently accepted a position within the U.S. Department of Agriculture/Agricultural Research Service Vegetable Crops Research Unit in Madison, Wisconsin. This is a joint appointment within the Department of Plant Pathology at the University of Wisconsin, so I will be working with a strong and diverse group of researchers in Russell Labs. My research project will return me to the world of the *Solanaceae* and will focus on the molecular aspects of disease resistance in potato. Initially, I plan to concentrate on the study of late blight (caused by *Phytophtora infestans*) and other diseases important to Wisconsin potato growers. I look forward to the challenges that lie ahead.

I joined IS-MPMI three years ago in May 2001. I have found that attending IS-MPMI symposia and reading about the accomplishments of other researchers in *Molecular Plant-Microbe Interactions* is a great way to stay informed of current research ideas. Through interactions with other IS-MPMI members, I have formed valuable collaborations that have assisted me throughout my career. I encourage those of you who are not IS-MPMI members to consider joining this dynamic group of people.

Distinguished member

Ann G. Matthysse
University of North Carolina
Chapel Hill, NC

I did my undergraduate work at Radcliffe in biochemical sciences, working on diphtheria with A. M. Pappenheimer, Jr. (Pap as he liked to be called). This was my initial introduction to working with bacteria and I loved it. I have continued to enjoy working with bacteria to this day. Pap was very supportive of my desire to go on to graduate work. These were the days when the first question I was asked in interviews for graduate school admission was "Why should we admit you rather than a man?" (the implication being that a man would do more and better science).

I began my graduate work at Rockefeller University in the laboratory of Ed Tatum. While there, I got married and moved with my husband back to Boston and completed my graduate work in the laboratory of John Torrey, studying the control of cell division in pea root explants. I was very impressed with the new field of molecular biology and did postdoctoral work with James Bonner, in order to gain experience in plant molecular biology. I then returned to bacteria and Harvard, where I worked with Bernie Davis and taught undergraduate microbiology. It was at this time that I began to study the interactions between bacteria, particularly *Agrobacterium*, and plants. My first job as an assistant professor was at the medical school of Indiana University in Indianapolis, teaching infectious disease. Ned Shrigley was the chair of the microbiology department at that time; he believed that all infectious disease had elements in common and hired me, although I worked on plant bacterial interactions. I moved to the Botany Department at University of North Carolina in 1975, after Ned retired from the chair position at Indiana. I have been in Chapel Hill since that time, although the department has changed from botany into biology.

My research has been focused on the initial interactions between bacteria and plants, particularly attachment of bacteria to plant surfaces. We discovered that *Agrobacterium tumefaciens* makes cellulose during the course of binding to plants. This observation has led me to study the genetics and mechanism of cellulose synthesis in bacteria. Recently, my lab has been involved in collaborative studies with William Smith of the University of California at Santa Barbara of an apparent case of gene transfer from bacteria to the tunicate, Ciona, of the gene for cellulose synthase.

IS-MPMI has provided a meeting and a journal in which the focus is on the type of studies that interest me, which is the molecular biology and genetics of the interactions between plants and microbes. From the first one I attended in Ithaca, the meetings have provided a pleasant and useful interaction with colleagues.

Plan Now to Attend the 12th International Congress on Molecular Plant-Microbe Interactions

The International Society for Molecular Plant-Microbe Interactions (IS-MPMI) and the Mexican Organizing Committee are pleased to announce that the 12th International Congress on Molecular Plant-Microbe Interactions will take place July 17-22, 2005 in Cancún, México.

The scientific program will consist of plenary lectures, plenary symposia, concurrent presentations (invited or selected from abstracts), and poster sessions.

The Congress will last for five working days. Mornings will be devoted to plenary lectures and plenary symposia, while in the afternoons, parallel symposia, and in the evenings, poster sessions will be held. In total, we plan to have 11 plenary lectures, 11 plenary symposia, 20 concurrent presentations and poster sessions. The cultural program of the Congress will include archeological sightseeing, scuba-diving and other aquatic activities, cultural performance(s), as well as pre- and post-Congress tours.

We cordially welcome you to participate in the Congress and recommend monitoring the web site that soon will be announced through the IS-MPMI.

Federico Sanchez
Congress Organizer

Ph.D. Fellowships Offered

The International Max Planck Research School (IMPRS) on "The Exploration of Ecological Interactions with Molecular and Chemical Techniques" offers five Ph.D. fellowships for graduate students in molecular biology, ecology, entomology, or chemistry. The application deadline is July 31, 2004. The Ph.D. program starts in January 2005, but earlier arrangements are possible.

The Research School in Jena will be the first graduate school worldwide where modern chemical and molecular techniques will be used to study ecological systems. For detailed information on the school, application, and admission procedures please see our homepage at www.ice.mpg.de/imprs.

Phytophthora Molecular Genetics Workshop

The NSF Research Network "*Phytophthora* Molecular Genetics" will meet in New Orleans, May 21-23, 2004. The annual workshop is preceding the 104th general meeting of the American Society of Microbiology (ASM) that is held from May 23-27, 2003 in New Orleans. If you are active in the field of molecular genetics and genomics of *Phytophthora* or related Oomycetes you are welcome to participate. For further information on program, costs and accommodation visit www.dpw.wau.nl/fyto/NSFworkshop/. For registration and submission of abstracts contact the meeting coordinators Francine Govers (Laboratory of Phytopathology, Wageningen University, Francine.Govers@wur.nl) or Paul Morris (Biological Sciences, Bowling Green State University, Ohio, pmorris@bgnet.bgsu.edu).

Wheat Leaf Rust Molecular Genetics and Genomics Postdoctoral Fellow Position

A postdoctoral fellow position at Agriculture & Agri-Food Canada, the Pacific Agri-Food Research Centre in Summerland, B.C., administered through the NSERC Visiting Fellowship in Government Laboratories Program (www.nserc.ca), is available for work on the wheat leaf rust (*Puccinia triticina*)/wheat (*Triticum aestivum*) pathosystem. We are looking for candidates who can perform independent research but work well in a larger collaborative setting and have received their Ph.D. within the last five years. The stipend is $40,800 (Canadian) per annum and is for two years, depending on performance and renewable for up to three years. Candidates must hold a degree in microbiology, biochemistry, plant pathology, or similar field and must have demonstrable experience in cDNA and genomic (preferably BAC) library construction, DNA and RNA blot, PCR, and protein techniques, as well as in the use of a wide variety of computer programs for DNA/RNA/genome analysis and manipulation, phylogeny, and database searches, preferably bioinformatics based on a Linux platform. Previous work on fungi, microarray profiling, or both would be advantageous. We have recently generated a large, 14,500 EST-containing database from this rust fungus, which is to be expanded to 30,000 reads from different life-cycle stages. A genomic library and physical contig map are needed. Collaboration with the Michael Smith Genome Sciences Centre in Vancouver, B.C. is in place. Integration with a genetic map (being constructed at the AAFC-Cereal Research Centre in Winnipeg) is envisaged. The focus will be on the isolation of several avirulence genes. However, several candidate pathogenicity and virulence genes need functional testing in an available heterologous expression system. Fungal expression profiling of the many different life-cycle stages during the infection process, using recently constructed microarrays, will be performed. Similarly, wheat and nonhost responses on barley will be assayed using microarrays. Many aspects of the program are in collaboration with other AAFC centers and USDA laboratories. For details on the program, visit http://res2.agr.ca/parc-crapac/summerland/progs/biotech/bakkeren_e.htm. Send a letter detailing how your experience would further the project, CV, and list of references to: Guus Bakkeren, Ph.D. Research Scientist, Agriculture & Agri-Food Canada, PARC, Summerland, Highway 97, BC, Canada V0H 1Z0; Phone: +1.250.494.6368; Fax: +1.250.494.0755; E-mail: BakkerenG@agr.gc.ca; Adjunct Professor, Dept. of Botany, University of British Columbia, Vancouver, B.C., Canada.

Postdoctoral Position - University of Maryland

A postdoctoral position to study host transcriptional responses to hypovirus infection using cDNA microarrays is available at the Center for Biosystems Research, at University of Maryland's Biotechnology Institute. Cytoplasmically transmitted RNA viruses of the genus *Hypovirus* cause reduced virulence (hypovirulence) in the chestnut blight fungus *Cryphonectria parasitica*. The hypovirus-*C. parasitica* system is uniquely suited to take advantage of advances in DNA microarray technology for gaining deeper insight into virus-host interactions (Eukaryotic Cell 2:1253-1265, 2003). Hypovirus infection is persistent, with stable phenotypic changes. A *C. parasitica* EST library/database consisting of over 4,200 sequences has been used to construct a spotted DNA array representing approximately 2,200 unique genes. The hypovirus-*C. parasitica* system is one of the very few examples for which both a Eukaryotic virus and its host can be genetically modified with ease. Differentially expressed genes identified in the microarray hybridizations can be disrupted, silenced, or overexpressed for follow-up functional studies. The contribution of specific viral determinants to altered host gene expression can be examined with available infectious cDNA clones of chimeric hypoviruses and deletion mutants or by transformation into uninfected *C. parasitica* for expression in the absence of virus infection. Finally, a collection of mutant *C. parasitica* strains containing deletions of genes encoding signal transduction components are available for verifying the role of specific signaling pathways in regulation of specific gene families. The combined capabilities of the hypovirus-*C. parasitica* system provide the means for utilizing DNA microarray analysis as much more than a tool for simply identifying differentially expressed genes. Applicants should send curriculum vitae to Postdoctoral Position #R3-0033, Center for Biosystems Research, University of Maryland Biotechnology Institute, Plant Sciences Building, Rm 5115C, College Park, MD 20742-4450. The University System of Maryland is an equal opportunity/affirmative action employer.

Faculty Position - Plant Molecular Virologist

The Department of Plant Pathology at Ohio State University, Ohio Agricultural Research and Development Center, Wooster, Ohio, invites applicants for a tenure-track 90% research/10% teaching position at the assistant professor level in molecular plant virology. The successful candidate will develop a research program on the molecular characterization of viral gene function and replication, the basis of virus pathogenicity and resistance, or both and will have interactions with existing interdisciplinary teams. He/she will have access to state-of-the-art laboratory, phytotron, and greenhouse facilities. Teaching responsibilities include instruction in plant virology and advising graduate students. A curriculum vitae, copies of academic transcripts and selected publications, a statement of research interests, and three letters of recommendation should be sent to: Dr. S. Kamoun, Dept. of Plant Pathology, OSU-OARDC, Wooster, OH 44691-4096. The Ohio State University is an Equal Opportunity, Affirmative Action Employer. Women, minorities, Vietnam-era veterans, disabled veterans, and individuals with disabilities are encouraged to apply. A full description of the position and related information can be found at http://plantpath.osu.edu/whatsnew.php.

Two Bioorganic/Biological Chemistry Postdoctoral Positions

A new research project to investigate secondary metabolic pathways of cruciferous biotrophic fungal pathogens requires two postdoctoral fellows. This project is part of a

research program directed at understanding and controlling plant fungal diseases. The overall program has significant technological infrastructure integrated in a challenging multidisciplinary research environment. Positions require a recent Ph.D. in bioorganic or biological chemistry or related field with a strong background in plant/fungal metabolite analysis and isolation. Extensive experience with HPLC analysis using both diode array and mass detectors to detect and quantify a broad range of metabolites is essential. Additional expertise in spectroscopic techniques necessary for chemical structure elucidation, particularly modern high field NMR spectroscopy, is highly relevant. Additionally, both positions require experience in developing biological assays to determine bioactivity (antifungal, antibacterial, phytotoxic) of secondary metabolites. Experience with microbiological techniques, protein and enzyme isolation, and plant cell culturing is considered an important asset. A strong publication record in the field should demonstrate the required qualifications. Positions are available immediately, however applications will be considered until positions are filled. Electronic applications are preferred. Candidates should send letter of application and resume and provide names, E-mail addresses, and telephone numbers of three references to the address below. Candidates whose first language is not English may be required to provide a certificate of English proficiency. Contact: Dr. M.S.C. Pedras, University of Saskatchewan, Department of Chemistry, 110 Science Place, Saskatoon, SK, S7N 5C9, CANADA; E-mail: s.pedras@usask.ca; Websites: www.usask.ca/chemistry/pedras.html; www.usask.ca/chemistry/groups/pedras.

(cry1Ac and cry1Ab) in cotton and two new traits introduced into maize in North America. The cry3Bb1 for corn rootworm control, and the cry1Fa2 gene in Bt maize, with broader control of lepidopteran pests were both introduced in the U.S. in 2003. Furthermore, five new Bt and novel gene products for maize insect resistance are expected to be launched in the next three years. Thus, the global GM maize area with insect resistance and herbicide tolerance traits, as well as the stacked traits, is likely to increase significantly in the near to mid-term. With the approval of GM soybean in Brazil for 2003/04, global GM soybean area is likely to experience renewed high growth rates in the near to mid-term.

In 2003, the three most populous countries in Asia – China, India, and Indonesia (total population 2.5 billion and a combined GDP of over $1.5 trillion), the three major economies of Latin America – Argentina, Brazil, and Mexico (population 300 million and a GDP of $1.5 trillion) and the largest economy on the continent of Africa - South Africa (population 45 million and GDP of $130 billion) are all officially growing GM crops. Their combined populations of 2.85 billion with a total GDP of over $3 trillion are recipients of the significant benefits that GM crops offer. The top 10 GM crop countries, each of which grew 50,000 hectares or more of GM crops in 2003, had a combined population of approximately 3 billion, close to half the world's population, with a combined GDP of $13 trillion, almost half of the global GDP of $30 trillion. In 2003, GM crops were grown in 18 countries with a combined population of 3.4 billion, living on six continents in the North and the South: Asia, Africa, Latin America, North America, Europe, and Oceania. Thus, despite the continuing controversy about GM crops, the hectarage and number of farmers growing GM crops have continued to grow at a double digit rate or more, every year since their introduction in 1996, with 7 million farmers benefiting from the technology in 2003.

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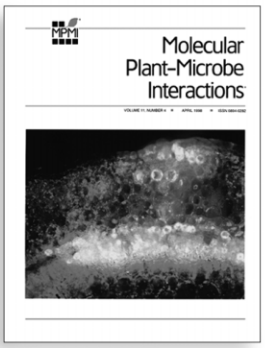

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lation of secondary metabolism in *Pseudomonas* spp. used in biocontrol. Since 2001, he has been an assistant professor in molecular microbiology at Leiden University. His research focuses on the interactions between biocontrol agents and phytopathogenic fungi, antifungal metabolite production by biocontrol strains, and bacterial biofilms, specifically the role of lipopeptide compounds in biofilm formation and degradation.

Otto Geiger received his Ph.D. degree in 1987 from the University of Hohenheim, Stuttgart, Germany. After postdoctoral work at Harvard Medical School, Boston, Massachusetts, U.S.A., with Eugene Kennedy and at Leiden University, The Netherlands, with Ben Lugtenberg and Herman Spaink, he took a position at the Technical University of Berlin, Germany. In 1999, he moved to his current position as associate professor at the Research Center for Nitrogen Fixation at the National Autonomous University of Mexico in Cuernavaca. His research focuses on the formation of bacterial membranes and other cell surface components as well as on the functions of these molecules in the interaction with eukaryotic hosts.

Godelieve Gheysen received an M.S. degree in zoology and a Ph.D. degree in plant molecular biology at Ghent University, Belgium. Her thesis work in the laboratory of Marc Van Montagu concerned the mechanism of plant transformation by *Agrobacterium tumefaciens*. In 1991, she started her own research group to study the molecular analysis of plant-nematode interactions. This research focused on i) the plant response in the compatible interaction at the molecular and cytological level, ii) characterization of the parasitism genes of nematodes, iii) unraveling the signal transduction pathway in the formation of nematode feeding sites, and iv) using this knowledge to engineer nematode resistance in plants. From 1996 to 2000, she coordinated a European project involving 12 labs that used *Arabidopsis thaliana* as a model system to study the compatible plant-nematode interaction. She is currently a professor in molecular genetics at Ghent University and teaches molecular biology and plant biotechnology.

Francine Govers is an associate professor of phytopathology in the Department of Plant Sciences of Wageningen University, The Netherlands, and a staff member at the Graduate School of Experimental Plant Sciences. She has an M.S. 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 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.

Murray Grant is a senior lecturer in plant molecular biology at the Imperial College London, Wye Campus, Wye, Ashford, Kent, U.K. He received his Ph.D. degree in 1988 from Otago University, New Zealand, investigating the regulation of glutamine synthetase following infection of *Lupinus* spp. by *Rhizobium lupini*. He continued to study the host response to *Rhizobium* infection, with particular focus on regulation of asparaginase, initially at the former Department of Scientific and Industrial Research in New Zealand and later at the Cambridge Laboratory, John Innes Centre, U.K. Moving into plant-pathogen interactions, he studied *Arabidopsis*, cloning *RPM1* in Jeff Dangl's laboratory at the Max Planck Institut in Köln, Germany. He later moved into academia and ended up at the Wye Campus in 1998. His research utilizes a combination of transcriptomic, proteomic, and real-time imaging approaches and focuses upon innate immune responses to *Pseudomonas syringae,* establishment of systemic immunity by avirulent *P syringae* isolates, and dissection of signal transduction pathways recruited following *RPM1* elicitation.

Martin Parniske has been studying the plant genetics of symbiosis at the Sainsbury Laboratory, Norwich, U.K., since 1999, focusing on the functional and evolutionary aspects of plant genes required for fungal arbuscular mycorrhiza and bacterial nitrogen-fixing root nodule symbiosis. To enable this research, the lab built a TILLING-based reverse genetics tool that allows the isolation of plants carrying point mutations in any gene of interest in the legume *Lotus japonicus*. More details about this work can be found on the lab webpage: http://www.jic.bbsrc.ac.uk/sainsbury-lab/martin-parniske/homepage.htm. In his Ph.D. studies with Dietrich Werner in Marburg, Germany, he investigated the role of legume flavonoids as symbiotic signals and defense components in the nitrogen-fixing root nodule symbiosis. He received his Ph.D. degree in 1991 and continued to work in the same lab, generating and testing the

symbiotic performance of exopolysaccharide mutants of *Bradyrhizobium japonicum*. He received a postdoctoral fellowship from the Deutsche Forschungsgemeinschaft and from 1992 to 1994 studied transcription factors involved in the regulation of plant defense genes with Klaus Hahlbrock at the Max Planck Institut für Züchtungsforschung, Cologne. From 1994 to 1998, he studied the evolution of the Cf-4/9 resistance gene clusters in tomato as an EMBO and EU postdoctoral fellow with Jonathan Jones at the Sainsbury Laboratory, Norwich.

Pam Ronald is a professor in the Department of Plant Pathology, University of California, Davis. She joined the faculty in 1992. Pam received her B.A. degree in biology from Reed College, Portland, Oregon; her M.A. degree in biology in 1984 from Stanford University, California; her M.S. degree in plant physiology in 1985 from the University of Uppsala, Uppsala, Sweden; and her Ph.D. degree in molecular and physiological plant biology in 1990 from the University of California, Berkeley. Research in her group is aimed at elucidating the signal transduction network controlling the rice defense responses after pathogen attack. Current projects in her lab include identification of the bacterial-produced signal molecule that interacts with the disease resistance gene product XA21, analysis of XA21-interacting proteins, analysis of genes expressed during the rice defense response, and characterization of the rice kinome. A more detailed overview of her research interests can be found at http://indica.ucdavis.edu/

Herman B. Scholthof is an associate professor of plant pathology and microbiology, specializing in the molecular biology of plant-virus interactions. He received B.S. and M.S. degrees from Wageningen University in The Netherlands and a Ph.D. degree from the University of Kentucky. After postdoctoral work at the University of California at Berkeley, he joined the faculty of the Department of Plant Pathology and Microbiology at Texas A&M University, College Station, in December 1994. His teaching responsibilities include graduate courses in plant virology, methods in the molecular biology of plant-microbe interactions, and a journal club on contemporary issues in biological sciences. Scholthof's research emphasizes the interactions of *Tomato bushy stunt virus* with its various hosts to understand the molecular basis for susceptibility and resistance. He has been a visiting scientist at Harvard Medical School to conduct research in protein structural biology and to use cell-permeable dyes and liposomes for studying virus entry. He most recently was a senior editor for *Phytopathology*, is currently on the editorial board of *Virology*, and has been the coordinator for molecular and cellular biology symposia for annual meetings of The American Phytopathological Society. Scholthof is a founding executive member of the Intercollegiate Faculty for Virology at Texas A&M University.

Jim Sweigard is a principal investigator in the disease-resistance group of the Crop Genetics Research Division of Pioneer, a DuPont company. His interest in fungi began as an undergraduate at Goshen College, where he worked on hyphal tip growth under Stan Grove. His graduate work at Cornell University with Hans VanEtten concerned an oomycete pathogen of peas. Additional work at Cornell involved the epidemiology of late blight of potato with Bill Fry. He joined Barbara Valent's rice blast research group at DuPont in 1986. This research focused on the mechanisms of host specificity and on the general mechanisms of pathogenicity of *Magnaporthe grisea*. More recent research has focused on the corn pathogens *Fusarium verticillioides* and *Colletotrichum graminicola*. Jim previously served as an associate editor of 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 at 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 as an 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 investigating macronutrient signaling in plants. Their work on symbiotic nitrogen fixation now focuses on the *Lotus japonicus-Mesorhizobium loti* symbiosis, and Udvardi coordinates a European functional genomics project involving nine labs that uses *L. japonicus* as a model to study mutualistic symbioses.

Frank White is a full professor in the Department of Plant Pathology at Kansas State University, Manhattan. He was appointed to this position in 1985 after both attaining his Ph.D. degree in microbiology (1981) and completing postdoctoral work at the University of Washington-Seattle. His research in Seattle involved the genetics of *Agrobacterium rhizogenes* under the direction of Eugene Nester and Milton Gordon. His undergraduate B.S. degree in molecular biology is from the University of Wisconsin-Madison. White's present studies involve the mechanisms of virulence and avirulence in *Xanthomonas* species.

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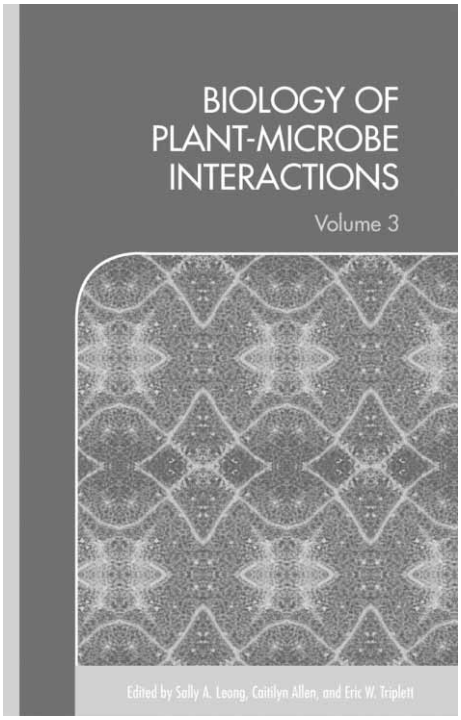

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Univ of Missouri
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Fax: +1.573.882.0588
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Univ de Lausanne
Phone: +41 21 692 5631
Fax: +41 21 692 5635
E-mail: dieter.haas@imf.unil.ch

Director
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Univ of California
Phone: +1.510.642.4174
Fax: +1.510.642.4995
E-mail: icelab@socrates.berkeley.edu

Director
Michael A. Djordjevic
Australian Natl Univ
Phone: +61 2 6249 3088
Fax: +61 2 6249 0754
E-mail: michael@rsbs.anu.edu.au

Editor-in-Chief
Dr. Jens Stougaard
University of Aarhus
Phone: +45 89425011
Fax: +45 86201222
E-mail: stougaard@mb.au.dk

Program Chair (ex-officio)
Federico Sanchez
Univ Nacional Autonoma De Mexico
Phone: +52 73 291653
Fax: +52 73 172388
E-mail: federico@ibt.unam.mx

Business Executive (ex-officio)
Steven C. Nelson
IS-MPMI
Phone: +1.651.454.7250
Fax: +1.651.454.0766
E-mail: snelson@scisoc.org

Staff Contact (ex-officio)
Amy L. Hope
IS-MPMI
Phone: +1.651.454.7250
Fax: +1.651.454.0766
E-mail: ahope@scisoc.org

MPMI EDITORS

Editor-in-Chief

Dr. Jens Stougaard
Laboratory of Gene Expression
Dept. of Molecular Biology
University of Aarhus
Gustav Wieds Vej 10
DK-8000 Aarhus C, Denmark
Phone: +45 89425011
Fax: +45 86201222
E-mail: stougaard@mb.au.dk

Senior Editors

fungus–plant interactions
Jim Sweigard
DuPont Experimental Station
P.O. Box 80402
Wilmington, DE 19880-0402, U.S.A.
Phone +1.302.695.2254
Fax: +1.302.695.4509
E-mail: jim.sweigard@cgr.dupont.com

model plant responses to pathogens
Murry Grant
Dept. of Agricultural Science
Imperial College London, Wye Campus
Wye, Ashford, TN25 5AH, U.K.
Phone: +44 2075 9428 83
Fax: +44 2075 9426 40
E-mail: m.grant@imperial.ac.uk

crop plant responses to pathogens
Pamela Ronald
228 Robbins Hall
Department of Plant Pathology
University of California, Davis
One Shields Avenue
Davis, CA 95616, U.S.A.
Phone: +1.530.752.1654
Fax: +1.530.752.5674
E-mail: pcronald@ucdavis.edu

bacterial pathogenesis
Frank White
Department of Plant Pathology
4024 Throckmorton Plant Science Center
Kansas State University
Manhattan KS 66506, U.S.A.
Phone: +1.785.532.6176
Fax: +1.785.532.5692
E-mail: fwhite@ksu.edu

plant–bacterial symbiosis
Michael Udvardi
Max Planck Institute of Molecular Plant Physiology
Am Mühlenberg 1
14476 Golm, Germany
Phone: +49 331 567 8149
Fax: +49 331 567 8250
E-mail: udvardi@mpimp-golm.mpg.de

bacterial–plant symbiosis
Otto Geiger
Centro de Investigacion sobre Fijacion de Nitrogeno, UNAM
Av. Universidad s/n, Colonia Chamilpa
Cuernavaca, Morelos, CP 62210, Mexico
Phone: +52 7773 131697
Fax: +52 7773 175581
E-mail: otto@cifn.unam.mx

virus–plant interactions
Herman B. Scholthof
Associate Professor
Department of Plant Pathology and Microbiology
Texas A&M University
2132 TAMU
College Station, TX 77843.2132, U.S.A.
Phone: +1.979.862.1495
Fax: +1.979.845.6483
E-mail: herscho@tamu.edu

molecular microbial ecology
Guido V. Bloemberg
Institute of Biology, Leiden University
Clusius Laboratory
Wassenaarseweg 64
2333 AL Leiden, The Netherlands
Phone:+31 71 5275056
Fax:+31 71 5275088
E-mail: Bloemberg@rulbim.leidenuniv.nl

nematode–plant interactions
Godelieve Gheysen
Department Molecular Biotechnology
Faculty of Agricultural and Applied Biological Sciences,
Ghent University
Coupure links 653, B 9000 Gent, Belgium
Phone: +32 9 264 5888
Fax: +32 9 264 6219
E-mail: Godelieve.Gheysen@UGent.be

mycorrhizal interactions
Martin Parniske
The Sainsbury Laboratory
Colney Lane
Norwich NR4 7UH, U.K.
Phone: +44 1603 4502 49
Fax: +44 1603 450011
E-mail: martin.parniske@bbsrc.ac.uk

oomycete–plant interactions
Francine Govers
Laboratory of Phytopathology
Wageningen University
Binnenhaven 5
6709 PD Wageningen, The Netherlands
Phone: +31 317 483 138
Fax: +31 317 483 412
E-mail: francine.govers@wur.nl

MPMI ASSOCIATE EDITORS

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Members of the International Society for Molecular Plant-Microbe Interactions

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A

Achar, Premila
Intermediate Technology Faciliator
Apt 205
No 17, Farmstead Road
Toronto, ON M2L 2X2
CANADA
Tel: (416) 441-0466
E-mail: micropna@yahoo.co.uk

Adam, Gerhard
Univ of Agricultural Sciences
Center of Applied Genetics
Muthgasse 18/05/66
Vienna, 1190
AUSTRIA
Tel: 43 1 3600 66380
Fax: 43 1 3600 66392
E-mail: adam@edv2.boku.ac.at

Akimitsu, Kazuya
Kagawa Univ
Fac of Agric - Life Sciences Dept
Miki-cho
Kagawa-ken, 761-0795
JAPAN
Tel: 81 87 891 3131
Fax: 81 87 891 3021
E-mail: kazuya@ag.kagawa-u.ac.jp

Albersheim, Peter
Univ of Georgia
315 Riverbend Road
Complex Carbohydrate Res Ctr
Athens, GA 30602-4712
Tel: (706) 542-4404
Fax: (706) 542-4412
E-mail: palbersh@ccrc.uga.edu

Allen, Caitilyn
Univ of Wisconsin
Russell Labs 885 - Plant Path Dept
1630 Linden Dr
Madison, WI 53706-1520
Tel: (608) 262-9578
Fax: (608) 263-2626
E-mail: cza@plantpath.wisc.edu

Allen, Chris
Oklahoma State Univ
Entomology and Plant Pathology Dept
127 Noble Research Center
Stillwater, OK 74078-0001
Tel: (405) 744-8268
E-mail: allenca@okstate.edu

Allen, Nina
North Carolina State Univ
Botany Dept
Box 7612
Raleigh, NC 27695-0001
Tel: (919) 515-2727
Fax: (919) 515-3436
E-mail: nina_allen@ncsu.edu

Alvarez-Morales, Ariel
Cinvestav-IPN
Plant Genetic Eng - Apdo Postal 629
Km 9.6 Lib. Norte Carret. Irapuato-Leon
Irapuato GTO, 36500
MEXICO
Tel: 52 462 623 9600
Fax: 52 462 624 5849
E-mail: aalvarez@ira.cinvestav.mx

Aneja, Punita
Agribiotics Inc
Research and Development Dept
135 Turnbull Court
Cambridge, ON N1T 1C6
CANADA
Tel: (519) 624-8975
Fax: (519) 624-8976
E-mail: punita@agribiotics.com

Antoun, Hani
Univ of California
Agronomy and Range Science Dept
C/O Prof Paul Gepts - One Shields Ave
Davis, CA 95616-8515
Tel: (530) 752-1556
E-mail: antoun@rsvs.ulaval.ca

Arce-Johnson, Patricio
P. Univ Catolica De Chile
Biologia Celular Y Molecular Dept
Alameda #340 - Lab De Bioquimica
Santiago, 114-D
CHILE
Tel: 56 2 686 2897
Fax: 56 2 222 5515
E-mail: parce@genes.bio.puc.cl

Arima, Yasuhiro
Tokyo Univ of Agric & Tech
Faculty of Agriculture
Fuchu, Tokyo, 183-8509
JAPAN
Tel: 81 42 367 5677
Fax: 81 42 367 5677
E-mail: arima@cc.tuat.ac.jp

Armstrong, Miles
Scottish Crop Research Inst
PPI Dept
Invergowrie
Dundee, Tayside, DD2 5DA
UNITED KINGDOM
Tel: 44 1382 562 731
Fax: 44 1382 562 426
E-mail: marmst@scri.sari.ac.uk

Asiegbu, Frederick
Swedish Agricultural Univ
Forest Mycology and Pathology Dept
PO Box 7026
Uppsala, 750 07
SWEDEN
Tel: 46 18 671 598
Fax: 46 18 309 245
E-mail: fred.asiegbu@mykopat.slu.se

Aufsatz, Werner
UZA-2; 2D-541 Althanstrabe 14
Vienna, 1090
AUSTRIA
Tel: 43 1 4277 29742
Fax: 43 1 4277 29749
E-mail: werner.aufsatz@gmi.oeaw.ac.at

Avila-Adame, Cruz
North Carolina State Univ
Plant Pathology Dept
2518 Gardner Hall
Raleigh, NC 27695-7616
Tel: (919) 515-6808
Fax: (919) 515-3670
E-mail: cavilaa@unity.ncsu.edu

Avni, Adi
Tel Aviv Univ
Plant Sciences Dept
Tel Aviv, 69978
ISRAEL
Tel: 972 3 640 9840
Fax: 972 3 641 0195
E-mail: lpavni@post.tau.ac.il

Axtell, Catherine
Iowa State Univ
Microbiology Dept
207 Science I
Ames, IA 50011
Tel: (515) 294-3198
Fax: (515) 294-6019
E-mail: caxtell@iastate.edu

B

Bai, Jianfa
Kansas State Univ
Plant Pathology Dept
4024 Throckmorton Hall
Manhattan, KS 66506
Tel: (785) 532-2328
Fax: (785) 532-5692
E-mail: jianfa@plantpath.ksu.edu

Bailey, Ana
Cinvestav-IPN
Apdo Postal 629
Irapuato Gto, 36500
MEXICO
Tel: 52 95 462 623 9600
Fax: 52 95 462 624 5849
E-mail: abailey@ira.cinvestav.mx

Bailey, Mark
NERC
Inst of Virology and Environ
Microbiology - Mansfield Rd
Oxford, OX1 3SR
UNITED KINGDOM
Tel: 44 186 528 1630
Fax: 44 186 528 1696
E-mail: mbailey@ceh.ac.uk

Baker, Barbara
USDA PGEC
800 Buchanan Street
Albany, CA 94710-1105
Tel: (510) 559-5912
Fax: (510) 559-5929
E-mail: bbaker@socrates.berkeley.edu

Baker, Christina
Oklahoma State Univ
Entomology and Plant Pathology Dept
127 Noble Research Center
Stillwater, OK 74078-0001
Tel: (405) 744-8268
E-mail: chickadee41780@aol.com

Bakkeren, Guus
Agric & Agri-Food Canada
Pacific Agri-Food Research Centre
Hwy 97
Summerland, BC V0H 1Z0
CANADA
Tel: (250) 494-6368
Fax: (250) 494-0755
E-mail: bakkereng@agr.gc.ca

Banta, Lois
Williams College
Biology Dept
Williamstown, MA 01267
Tel: (413) 597-4330
Fax: (413) 597-3495
E-mail: lbanta@williams.edu

Barash, Isaac
Tel Aviv Univ
Plant Sciences Dept
Tel Aviv, 69978
ISRAEL
Tel: 972 3 640 6251
Fax: 972 3 640 9380
E-mail: isaaci@post.tau.ac.il

Bauer, Wolfgang
Ohio State Univ
Hort and Crop Science Dept
2021 Coffey Road
Columbus, OH 43210-1044
Tel: (614) 292-9035
Fax: (614) 292-7162
E-mail: bauer.7@osu.edu

Baum, Thomas
Iowa State Univ
Plant Pathology Dept
351 Bessey Hall
Ames, IA 50011-1020
Tel: (515) 294-2398
Fax: (515) 294-9420
E-mail: tbaum@iastate.edu

Beachy, Roger
Donald Danforth Plant Science Ctr
975 N Warson Road
St Louis, MO 63132
Tel: (314) 587-1201
Fax: (314) 587-1964
E-mail: rnbeachy@danforthcenter.org

Beattie, Gwyn
Iowa State Univ
Microbiology Dept
207 Science I
Ames, IA 50011
Tel: (515) 294-5571
Fax: (515) 294-6019
E-mail: gbeattie@iastate.edu

Becana, Manuel
CSIC
Est Experimental De Aula Dei
Apdo 202
Zaragoza, 50080
SPAIN
Tel: 34 976 716 055
Fax: 34 976 716 145
E-mail: becana@eead.csic.es

Beffa, Roland
Bayer CropScience
14-20 Rue Pierre Baizet
Lyon, 69009
FRANCE
Tel: 33 472 852 935
Fax: 33 472 852 297
E-mail: roland.beffa@bayercropscience.com

Bender, Carol
Oklahoma State Univ
Entomology and Plant Pathology Dept
127 Noble Research Center
Stillwater, OK 74078-3033
Tel: (405) 744-9945
Fax: (405) 744-7373
E-mail: cbender@okstate.edu

Bent, Andrew
Univ of Wisconsin
Plant Pathology Dept
1630 Linden Dr
Madison, WI 53706-1598
Tel: (608) 265-3034
Fax: (608) 263-2626
E-mail: afb@plantpath.wisc.edu

Berger, David
Univ of Pretoria
Botany Dept
Agric Science Bldg, Room 6-26
Pretoria, 0002
REP OF SOUTH AFRICA
Tel: 27 12 420 4634
Fax: 27 12 362 5327
E-mail: dberger@postino.up.ac.za

Berman, Phyllis
Univ of Massachusetts
Plant and Soil Sciences Dept
211 French Hall
Amherst, MA 01003
Tel: (413) 545-2364
Fax: (413) 545-3075
E-mail: berman@pltpath.umass.edu

Bertolet, Bonnie
San Francisco State Univ
Biology Dept
1600 Holloway Ave
San Francisco, CA 94132
Tel: (415) 338-7099
E-mail: bertolet@sfsu.edu

Bhattacharyya, Madan
Iowa State Univ
Agronomy Dept
G303 Agronomy Hall
Ames, IA 50011-1010
Tel: (515) 294-2505
Fax: (515) 294-2299
E-mail: mbhattac@iastate.edu

Birch, Paul
Scottish Crop Research Inst
Plant-Pathogen Interaction Programme
Invergowrie
Dundee, DD3 0QN
UNITED KINGDOM
Tel: 44 1382 562 731
Fax: 44 1382 568 678
E-mail: pbirch@scri.sari.ac.uk

Bird, David
North Carolina State Univ
Box 7616 - Plant Pathology Dept
3415 Gardner Hall
Raleigh, NC 27695-7616
Tel: (919) 515-6813
Fax: (919) 515-9500
E-mail: david_bird@ncsu.edu

Bloemberg, Guido
Leiden University
Inst of Molecular Plant Sciences
Clusius Lab - Wassenaarseweg 64
Leiden, 2333 AL
NETHERLANDS
Tel: 31 71 527 5056
Fax: 31 71 527 5088
E-mail: bloemberg@rulbim.leidenuniv.nl

Blok, Vivian
Scottish Crop Research Inst
Mycology, Bacteriology and Nematology
Invergowrie
Dundee, DD2 5DA
UNITED KINGDOM
Tel: 44 1382 562 731
Fax: 44 1382 562 426
E-mail: vblok@scri.sari.ac.uk

Boch, Jens
Martin Luther Univ
Inst of Genetics
Weinbergweg 10
Halle (Saale), 06099
GERMANY
Tel: 49 345 552 6292
Fax: 49 345 552 7151
E-mail: boch@genetik.uni-halle.de

Bogdanove, Adam
Iowa State Univ
Plant Pathology Dept
351 Bessey Hall
Ames, IA 50011-1020
Tel: (515) 294-3421
Fax: (515) 294-9420
E-mail: ajbog@iastate.edu

Bohin, Jean-Pierre
UGSF UMR 8576 CNRS
USTL Bat C9
Villeneuve D'Ascq, 59655
FRANCE
Tel: 33 32 043 6592
Fax: 33 32 043 6555
E-mail: jean-pierre.bohin@univ-lille1.fr

Bonas, Ulla
Martin-Luther Univ
Inst of Genetics
Weinbergweg 10
Halle Salle, 06120
GERMANY
Tel: 49 345 55 26290
Fax: 49 345 55 27277
E-mail: bonas@genetik.uni-halle.de

Bonnema, Augusta
Wageningen Agricultural Univ
Dept of Plant Breeding
PO Box 386
Wageningen, 6709 PD
NETHERLANDS
Tel: 31 317 484 028
Fax: 31 317 118 3457
E-mail: gussje.bonnema@wur.nl

Boonekamp, Piet
Plant Research International
Biointeractions and Plant Health
PO Box 16 - Droevendaalsesteeg
Wageningen, 6700 AA
NETHERLANDS
Tel: 31 317 476 178
Fax: 31 317 410 113
E-mail: p.m.boonekamp@plant.wag-ur.nl

Bosco, Marco
Univ Degli Studi Di Bologna
Agro-Environmental Science and Technolog
Viale Fanin 42-44 - Alma Mater Studiorum
Bologna, 40127
ITALY
Tel: 39 51 209 6270
Fax: 39 51 209 6274
E-mail: marco.bosco@unibo.it

Bostock, Richard
Univ of California
1 Shields Ave - Plant Pathology Dept
348 Hutchinson Hall
Davis, CA 95616
Tel: (530) 752-4269
Fax: (530) 752-5674
E-mail: rmbostock@ucdavis.edu

Botha-Oberholster, Anna-Maria
Univ of Pretoria
Genetics and FABI Dept
74 Hunan Road
Pretoria, 0002
REP OF SOUTH AFRICA
Tel: 27 12 420 3945
Fax: 27 12 420 3945
E-mail: ambothao@postino.up.ac.za

Boucher, Christian
CNRS INRA
BP 27 - Biology and Molecular
Castanet Tolosan, 31326
FRANCE
Tel: 33 561 2854 16
Fax: 33 561 285 061
E-mail: boucher@toulouse.inra.fr

Bouhouche, Naima
United Arab Emirates Univ
Faculty of Science - Biology Dept
Al-Jamia St - PO Box 17551
Al-Ain,
UAE
Tel: 971 3 706 4433
Fax: 971 3 767 1291
E-mail: nbouhouche02@yahoo.com

Brown, Constance
Howard Univ
1217 45th Place SE
Washington, DC 20019
Tel: (202) 421-6225
E-mail: cbrownchdsorg@aol.com

Brown, Darby
Univ of Wisconsin
Plant Pathology Dept
1630 Linden Dr - 885 Russell Labs
Madison, WI 53706-1598
Tel: (608) 265-2060
Fax: (608) 263-2626
E-mail: dgb@plantpath.wisc.edu

Bruand, Claude
CNRS INRA
IIPM
BP 27
Castanet Tolosan, 31326
FRANCE
Tel: 33 561 285 054
Fax: 33 561 285 061
E-mail: cbruand@toulouse.inra.fr

Burdman, Saul
Hebrew Univ of Jerusalem
Plant Pathology and Microbiology Dept
Food and Environmental Quality Sciences
Rehovot, 76100
ISRAEL
Tel: 972 8 948 9369
Fax: 972 8 946 6794
E-mail: saulb@agri.huji.ac.il

Burketova, Lenka
Inst Experimental Botany CAS
Na Karlovce 1a
Prague, 16000
CZECH REPUBLIC
Tel: 420 2 2431 0108
Fax: 420 2 2431 0113
E-mail: burketova@ueb.cas.cz

Byun, Myung Ok
Natl Inst of Agricultural Biotechnology
Molecular Physiology Dept
Suwon, 441-707
KOREA
Tel: 82 31 299 1721
Fax: 82 31 299 1712
E-mail: mobyun@rda.go.kr

C

Cameron, Kimberly
Cornell Univ
Plant Pathology Dept
334 Plant Science Building
Ithaca, NY 14853-4203
Tel: (607) 255-9770
Fax: (607) 255-4471
E-mail: kdc23@cornell.edu

Cardinale, Francesca
Univ of Torino
Di Va P.R.A. - Plant Pathology Dept
Via Leonardo Da Vinci, 44
Grugliasco, TO, 10095
ITALY
Tel: 39 11 670 8875
Fax: 39 11 670 8541
E-mail: francesca.cardinale@unito.it

Carlson, Russell
Univ of Georgia
Complex Carbohydrate Research Center
220 Riverbend Road
Athens, GA 30602
Tel: (706) 542-4439
Fax: (706) 542-4412
E-mail: rcarlson@ccrc.uga.edu

Catalano, Christina
Univ of Delaware
Plant and Soil Sciences Dept
15 Innovation Way - Lab 149
Newark, DE 19711
Tel: (302) 831-3452
Fax: (302) 831-3447
E-mail: 07850@udel.edu

Cervone, Felice
Univ La Sapienza
Biology Vegetale Dept
Piazzale Aldo Moro 5
Rome, 00185
ITALY
Tel: 39 6 4991 2641
Fax: 39 6 4991 2446
E-mail: felice.cervone@uniroma1.it

Chakravarthy, Suma
Boyce Thompson Inst
Plant Research
Tower Road
Ithaca, NY 14853
Tel: (607) 254-1386
Fax: (607) 255-6695
E-mail: sc289@cornell.edu

Charkowski, Amy
Univ of Wisconsin
Plant Pathology Dept
1630 Linden Dr
Madison, WI 53706-1598
Tel: (608) 262-7911
Fax: (608) 263-2626
E-mail: amyc@plantpath.wisc.edu

Charles, Trevor
Univ of Waterloo
Biology Dept
200 University Ave West
Waterloo, ON N2L 3G1
CANADA
Tel: (519) 888-4567x5606
Fax: (519) 746-0614
E-mail: tcharles@uwaterloo.ca

Chatterjee, Arun
Univ of Missouri
Plant Pathology Dept
108 Waters Hall
Columbia, MO 65211-0001
Tel: (573) 882-2940
Fax: (573) 882-0588
E-mail: chatterjeea@missouri.edu

Chatterjee, Asita
Univ of Missouri
Plant Microbiology and Pathology Dept
108 Waters Hall
Columbia, MO 65211-6130
Tel: (573) 882-1892
Fax: (573) 882-0588
E-mail: chatterjeeas@missouri.edu

Che, Fang-Sik
Nara Inst of Science & Technology
Graduate School of Biological Sciences
8916-5 Takayama Ikoma
Nara, 630-0101
JAPAN
Tel: 81 74 372 5452
Fax: 81 74 372 5459
E-mail: fsche@bs.aist-nara.ac.jp

Chen, Chao-Ying
Natl Taiwan Univ
Plant Pathology and Microbiology Dept
Taipei,
TAIWAN REP OF CHINA
Tel: 886 2 3657735
Fax: 886 2 3657735
E-mail: cychen@ccms.ntu.edu.tw

Chen, Ruey-Shyang
Natl Chiayi Univ
Grad Inst of Biotechnology
300 University Road
Chiayi, 600
TAIWAN REP OF CHINA
Tel: 886 5 275 0396
Fax: 886 5 275 2391
E-mail: rschen@mail.ncyu.edu.tw

Chen, Zhixiang
Purdue Univ
Botany and Plant Pathology Dept
915 W State Street
West Lafayette, IN 47907
Tel: (765) 494-4657
Fax: (765) 494-5896
E-mail: zhixiang@purdue.edu

Cheng, Min-Wen
Academia Sinica
Institute of Botany
128 Yamjiouyuan Rd, Soc 2, Nankang
Taipei, 11529
TAIWAN REP OF CHINA
Tel: 886 2 2789 9590x212
Fax: 886 2 2782 7954
E-mail: b87613005@atu.edu.tw

Chet, Ilan
Hebrew Univ
Faculty of Agric
PO Box 12
Rehovet, 76100
ISRAEL
Tel: 972 8 948 1236
Fax: 972 8 946 8785
E-mail: chet@agri.huji.ac.il

Chini, Andrea
Univ of Edinburgh
Mayfield Road - Kings Building
ICMB Rutherford Bldg 106
Edinburgh, EH8 9PF
UNITED KINGDOM
Tel: 44 131 650 5339
Fax: 44 131 650 5392
E-mail: achini@ed.ac.uk

Choi, Jane
USDA ARS FDWSRU
1301 Ditto Ave
Frederick, MD 21703
Tel: (301) 619-3193
Fax: (301) 619-2880
E-mail: jchoi@fdwsr.ars.usda.gov

Churchill, Alice
Boyce Thompson Inst
Cornell Univ
Tower Road
Ithaca, NY 14853
Tel: (607) 254-1355
Fax: (607) 254-2958
E-mail: acc7@cornell.edu

Cillo, Fabrizio
CNR - Ist Di Virologia Vegetale
Protezione Piante E Microbiologia Applic
Via G. Amendola 165/A
Bari, 70126
ITALY
Tel: 39 80 544 3109
Fax: 39 80 544 2911
E-mail: f.cillo@area.ba.cnr.it

Cocking, Edward
Univ of Nottingham
Crop Nitrogen Fixation Centre
Univ Park - Life Science Dept
Nottingham, NG7 2RD
UNITED KINGDOM
Tel: 44 1159 513 056
Fax: 44 1159 513 240

Cohen, Michael
USDA ARS
Tree Fruit Research Lab
1104 N Western Ave
Wenatchee, WA 98801-1230
Tel: (509) 664-2280x205
Fax: (509) 664-2287
E-mail: vmfscohen@yahoo.com

Collmer, Alan
Cornell Univ
Plant Pathology Dept
334 Plant Science Building
Ithaca, NY 14853-4203
Tel: (607) 255-7843
Fax: (607) 255-4471
E-mail: arc2@cornell.edu

Conejero, Tomas Vicente
Univ Politecnia De Valencia
Inst De Biologia Mol Celular De Plantas
Camino De Vera S/N
Valencia, 46022
SPAIN
Tel: 34 6 387 7850
Fax: 34 6 387 7859
E-mail: vconejer@ibmcp.upv.es

Coplin, David
Ohio State Univ
Plant Pathology Dept
2021 Coffey Road
Columbus, OH 43210-1087
Tel: (614) 292-8503
Fax: (614) 292-4455
E-mail: coplin.3@osu.edu

Cravador, Alfredo
Univ De Algarve
Fern Dept
Campus De Cambelas
Faro, Algarve, 8005-139
PORTUGAL
Tel: 351 289 800 935
Fax: 351 289 814 419
E-mail: acravad@ualg.pt

Crespi, Martin
CNRS
Inst des Sciences Vegetales
1 Ave de la Terrasse
Gif Sur Yvette, 91198
FRANCE
Tel: 33 16 982 3703
Fax: 33 16 982 3695
E-mail: crespi@isv.cnrs-gif.fr

Cuero, Raul
Prairie View A&M Univ
PO Box 685
Prairie View, TX 77446-0685
Tel: (409) 857-3012
Fax: (409) 857-2325
E-mail: olimpa@aol.com

Cuppels, Diane
Agric & Agri-Food Canada
Southern Crop Prot and Food Res Ctr
1391 Sandford St
London, ON N5V 4T3
CANADA
Tel: (519) 457-1470x274
Fax: (519) 457-3997
E-mail: cuppelsd@agr.gc.ca

D

Dangl, Jeff
Univ of North Carolina
Biology Dept
Coker Hall 108 - CB 3280
Chapel Hill, NC 27599-3280
Tel: (919) 962-5624
Fax: (919) 962-1625
E-mail: dangl@email.unc.edu

Daub, Margaret
North Carolina State Univ
Botany Dept
2214 Gardner Hall - Box 7612
Raleigh, NC 27695-7612
Tel: (919) 513-3807
Fax: (919) 515-3436
E-mail: margaret_daub@ncsu.edu

Dawson, William
Univ of Florida
700 Experiment Station Road
CREC
Lake Alfred, FL 33850-2243
Tel: (863) 956-1151
Fax: (863) 956-4631
E-mail: wodtmv@gnv.ifas.ufl.edu

Dazzo, Frank
Michigan State Univ
Microbiology and Molecular Genetics
East Lansing, MI 48824
Tel: (517) 355-6463x1587
Fax: (517) 353-8953

De Vicente, Antonio
Univ of Malaga
Faculty Ciencias Microbiology
Campus Univ Teatinos
Malaga, ES-29071
SPAIN
Tel: 34 952 131 892
Fax: 34 952 132 000
E-mail: adevicente@uma.es

De Waard, Maarten
Wageningen Univ
Dept of Phytopathology
PO Box 8025
Wageningen, 6700 EE
NETHERLANDS
Tel: 31 31 748 3123
Fax: 31 31 748 3412
E-mail: maarten.dewaard@wur.nl

Deng, Wen-Ling
Cornell Univ
Plant Pathology Dept
334 Plant Science Building
Ithaca, NY 14853-5904
Tel: (607) 255-7866
Fax: (607) 255-4471
E-mail: wd15@cornell.edu

Dessaux, Yves
CNRS
Inst des Sciences Vegetales
Ave de la Terrasse
Gif Sur Yvette, 91198
FRANCE
Tel: 33 1 6982 3690
Fax: 33 1 6982 3695
E-mail: yves.dessaux@isv.cnrs-gif.fr

deWit, Pierre
Wageningen Univ
Binnenhaven 9
PO Box 8025
Wageningen, 6700 EE
NETHERLANDS
Tel: 31 31 748 3130
Fax: 31 31 748 3412
E-mail: pierre.dewit@
medew.fyto.wau.nl

D'Haeze, Wim
Univ of Georgia
Complex Carbohydrate Research Ctr
315 Riverbend Road
Athens, GA 30602
Tel: (706) 542-4418
Fax: (706) 542-4412
wim@ccrc.uga.edu

Di Pietro, Antonio
Univ De Cordoba
Genetica Dept
Avenue de S Alberto Magno
Cordoba, 14071
SPAIN
Tel: 34 9 5721 8601
Fax: 34 9 5721 8606
E-mail: ge2dipia@uco.es

Dickinson, Matthew
Univ of Nottingham
School of Biological Sciences
Plant Science Div - Univ Park
Nottingham, NG7 2RD
UNITED KINGDOM
Tel: 44 1159 513 236
Fax: 44 1159 516 334
E-mail: matthew.dickinson@nottingham.ac.uk

Dickstein, Rebecca
Univ of North Texas
Biological Sciences Dept
PO Box 305220
Denton, TX 76203-5220
Tel: (940) 565-3359
Fax: (940) 565-3821
E-mail: beccad@unt.edu

Ding, Biao
Ohio State Univ
Plant Biology and Plant Biotechnology Ct
207 Rightmire Hall - 1060 Carmack Rd
Columbus, OH 43210
Tel: (614) 247-6077
Fax: (614) 292-5379
E-mail: ding.35@osu.edu

Ding, Xinshun
Samuel Roberts Noble Foundation
PO Box 2180 - Plant Biology Div
2510 Sam Noble Pkwy
Ardmore, OK 73402
Tel: (580) 224-6600
Fax: (580) 224-6692
E-mail: xsding@noble.org

Djordjevic, Michael
Australian Natl Univ
Plant Microbe Interactions Group
PO Box 475
Canberra, ACT 2601
AUSTRALIA
Tel: 61 2 6249 3088
Fax: 61 2 6249 0754
E-mail: michael@rsbs.anu.edu.au

Dodd, Ian
Lancaster Univ
Biological Sciences Dept
Lancaster, LA1 4YU
UNITED KINGDOM
Tel: 44 1524 65201x93504
Fax: 44 1524 843 854
E-mail: i.dodd@lancaster.ac.uk

Dogimont, Catherine
INRA
Pathologie Vegetale
Domaine St Maurice BP 94
Montfavet, 84143
FRANCE
Tel: 34 4 3272 3806
Fax: 34 4 3272 2710
E-mail: catherine.dogimont@avignon.inra.fr

Doty, Sharon
Univ of Washington
College of Forest Resources
Box 352100
Seattle, WA 98195-2100
Tel: (206) 543-5774
E-mail: sldoty@u.washington.edu

Downie, J. Allan
John Innes Centre
Colney Lane
Norwich, NR4 7UH
UNITED KINGDOM
Tel: 44 1603 45 2571
Fax: 44 1603 45 6844
E-mail: downie@bbsrc.ac.uk

Driscoll, Brian
McGill Univ
MacDonald Campus - NRS Dept
21,111 Lakeshore Road
SteAnneDeBellevue, QC H9X 3V9
CANADA
Tel: (514) 398-7887
Fax: (514) 398-7990
E-mail: driscoll@nrs.mcgill.ca

Dry, Ian
CSIRO Plant Industry
Hartley Gorve - Horticulture Unit
PO Box 350
Glen Osmond, SA 5064
AUSTRALIA
Tel: 61 8 8303 8632
Fax: 61 8 8303 8601
E-mail: ian.dry@csiro.au

Dubery, Ian
RAU Univ
Biochemistry Dept
PO Box 524
Auckland Park, 2006
REP OF SOUTH AFRICA
Tel: 27 11 489 2401
Fax: 27 11 489 2401
E-mail: iad@na.rau.ac.za

Dudler, Robert
Univ of Zurich
Inst of Plant Biology
Zollikerstr 107
Zurich, 8008
SWITZERLAND
Tel: 41 1 634 8252
Fax: 41 1 634 8204
E-mail: rdudler@botinst.unizh.ch

E

Ekengren, Sophia
Boyce Thompson Inst
Tower Road
Ithaca, NY 14853
Tel: (607) 254-1386
Fax: (607) 255-6695
E-mail: ske4@cornell.edu

Ekramoddoullah, Abul
Canadian Forest Service
Pacific Forestry Centre
506 West Burnside Road
Victoria, BC V8Z 1M5
CANADA
Tel: (250) 363-0692
Fax: (250) 363-0775
E-mail: aekramoddoul@pfc.forestry.ca

Elmerich, Claudine
CNRS
Inst Des Sciences Du Vegetal
Batiment 23 - Ave De La Terrasse
Gif Sur Yvette, 91198
FRANCE
Tel: 33 1 6982 3690
Fax: 33 1 6982 3695
E-mail: claudine.elmerich@isv.cnrs-gif.fr

Emami, Kaveh
Univ of Newcastle Upon Tyne
Biological and Nutritional Sciences Dept
Newcastle Upon Tyne, NE1 7RU
UNITED KINGDOM
Tel: 44 191 222 8684
E-mail: kaveh61@hotmail.com

Emerich, David
Univ of Missouri
Biochemistry Dept
117 Schweitzer
Columbia, MO 65211-0001
Tel: (573) 882-4252
Fax: (573) 882-5635
E-mail: emerichd@missouri.edu

Emmanuelle, Lauber
CNRS INRA
Chemin De Borde Rouge
BP 27
Castanet Tolosan, 31326
FRANCE
E-mail: elauber@toulouse.inra.fr

Erokhina, Tatyana
Inst of Bioorganic Chemistry RAS
Biotechnology Dept
Miklukho-Maklaya Str 16/10
Moscow, 117 997
RUSSIA
Tel: 7 95 336 4511
Fax: 7 95 335 7103
E-mail: tne@mail.ibch.ru

Esquerre-Tugaye, Marie Therese
Univ Paul Sabatier
Pole Biotech Veg - UMR 5546 CNRS
24 Chemin De Borde Rouge
Castanet Tolosan, 31326
FRANCE
Tel: 33 5 6219 3519
Fax: 33 5 6219 3525
E-mail: esquerre@smcv.ups-tlse.fr

Expert, Dominique
CNRS
Lab De Pathologie Vegetale
16 Rue Claude Bernard
Paris, CEDEX 05, 75231
FRANCE
Tel: 33 1 4408 1706
Fax: 33 1 4408 1698
E-mail: dominique.expert@inapg.inra.fr

F

Favelukes, Gabriel
Univ Nacl de La Plata
IBBM - Fac C Exactas
Parral 46, Piso 4, Dept 10
Buenos Aires, CP, 1405
ARGENTINA
Tel: 54 114 901 0053
Fax: 54 221 226 947
E-mail: fave@mail.retina.ar

Feuillet, Catherine
Univ of Zurich
Inst of Plant Biology
Zollikerstr 107
Zurich, CH-8008
SWITZERLAND
Tel: 41 1 634 8231
Fax: 41 1 634 8204
E-mail: feuillet@botinst.unizh.ch

Finan, Turlough
McMaster Univ
LSB 539 - Biology Dept
1280 Main Street W
Hamilton, ON L8S 4L6
CANADA
Tel: (905) 525-9140
Fax: (905) 521-2955
E-mail: finan@mcmaster.ca

Flores, Margarita
Nitrogen Fixation Res Ctr
UNAM - Molecular Ecology Dept
Apdo Postal 565-A
Cuernavaca, Mor., 62170
MEXICO
Tel: 52 73 114 660
Fax: 52 73 114 660
E-mail: mflores@cifn.unam.mx

Fluhr, Robert
Weizmann Inst of Science
Plant Sciences Dept
PO Box 26
Rehovot, 76100
ISRAEL
Tel: 972 8 934 2175
Fax: 972 8 934 4181
E-mail: robert.fluhr@weizmann.ac.il

Fort, Kevin
240 El Cajon Ave
Davis, CA 95616
Tel: (530) 752-1050
E-mail: kpfort@ucdavis.edu

Foster, Carol
Iowa State Univ
Genetics Dev and Cell Biology Dept
353 Bessey Hall
Ames, IA 50011-1100
Tel: (515) 294-3509
Fax: (515) 294-1337
E-mail: cmfoster@iastate.edu

Frank, Markus
BASF Plant Science
Carl-Bosch-Strasse 38
BPS-A30
Ludwigshafen, 67056
GERMANY
Tel: 49 621 604 5142
Fax: 49 621 602 0440
E-mail: markus.frank@basf-ag.de

Franken, Philipp
Inst for Vegetable and Ornamental Plants
IGZ
Theodor-Echtermeyer-Weg 1
Grossbeeren, 14979
GERMANY
Tel: 49 3370 178 215
Fax: 49 3370 155 391
E-mail: franken@igzev.de

Frederick, Reid
USDA ARS FDWSRU
1301 Ditto Avenue
Ft Detrick, MD 21702-5023
Tel: (301) 619-7386
Fax: (301) 619-2880
E-mail: frederir@ncifcrf.gov

Freedman, Roger
Mediant Cambridge
20 Millers Yard
10/11 Mill Lane
Cambridge, CB2 1RQ
UNITED KINGDOM
Tel: 44 122 336 9936
Fax: 44 122 346 4113
E-mail: rpf@medicul.co.uk

Fritig, Bernard
IBMP CNRS
Phytopathology Dept
12 Rue du General Zimmer
Strasbourg, 67000
FRANCE
Tel: 33 388 417 210
Fax: 33 388 614 442
E-mail: bernard.fritig@ibmp-ulp.u-strasbg.fr

Fuqua, William
Indiana Univ
Jordan Hall 142 - Biology Dept
1000 E Third Street
Bloomington, IN 47405-3700
Tel: (812) 855-1861
Fax: (812) 855-6705
E-mail: cfuqua@bio.indiana.edu

G

Gabriel, Dean
Univ of Florida
Plant Pathology Dept
1453 Fifield Hall
Gainesville, FL 32611
Tel: (352) 392-7239
Fax: (352) 392-6532
E-mail: gabriel@biotech.ufl.edu

Gafni, Yedidya
ARO The Volcani Center
Plant Genetics Dept
Bet Dagan, 50250
ISRAEL
Tel: 972 3 968 3471
Fax: 972 3 968 3471
E-mail: ygafni@volcani.agri.gov.il

Gal-On, Amit
ARO The Volcani Center
Plant Virology Dept
PO Box 6
Bet Dagan, 50 250
ISRAEL
Tel: 972 3 968 3563
Fax: 972 3 968 3918
E-mail: amitg@volcani.agri.gov.il

Garcia, Preston
Univ of Connecticut
Unit 3125
91 North Eagleville Road
Storrs, CT 06269-3125
Tel: (860) 486-5923
Fax: (860) 486-4331
E-mail: preston.garcia@uconn.edu

Gassmann, Walter
Univ of Missouri
Plant Microbiology and Pathology Dept
1-87 Ag Building
Columbia, MO 65211
Tel: (573) 884-7703
Fax: (573) 882-1469
E-mail: gassmannw@missouri.edu

Gelvin, Stanton
Purdue Univ
Biological Sciences Dept
West Lafayette, IN 47907
Tel: (765) 494-4939
Fax: (765) 496-1496
E-mail: gelvin@bilbo.bio.purdue.edu

Genin, Stephane
CNRS INRA
LIPM Dept
BP 27
Castanet, Tolosan, 31326
FRANCE
Tel: 33 561 285 416
Fax: 33 561 285 061
E-mail: sgenin@touluose.inra.fr

Georgi, Laura
Clemson Univ
Genetics and Biochemistry Dept
100 Jordan Hall
Clemson, SC 29634-0324
Tel: (864) 656-3060
Fax: (864) 656-6879
E-mail: georgil@clemson.edu

Gianinazzi, Silvio
INRA CNRS
UMR INRA/Univ BBCE-IPM
BP 86510 - Centre De Dijon
Dijon, CEDEX, 21065
FRANCE
Tel: 33 38 069 3146
Fax: 33 38 069 3753
E-mail: silvio@epoisses.inra.fr

Gijzen, Mark
Agric & Agri-Food Canada
1391 Sandford Street
London, ON N5V 4T3
CANADA
Tel: (519) 457-1470x280
Fax: (519) 457-3997
E-mail: gijzenm@agr.gc.ca

Gilijamse, Eelco
Rijk Zwaan BV
Zaadteelt and Zaadhandel BV
PO Box 40
De Lier, 2678 ZG
NETHERLANDS
Tel: 31 17 453 2300
Fax: 31 17 451 8243

Goh, Tatsuaki
Tokyo Univ of Science
Applied Biological Science Dept
2641 Yamazaki
Noda, Chiba, 278-8510
JAPAN
Tel: 81 47124 1501x3414
Fax: 81 47123 9767
E-mail: j6402628@ed.noda.tus.ac.jp

Gonzalez, Esther
Univ Public De Navarra
Ciencias Del Medio Natural
Campus De Arrosadia
Pamplona, 31006
SPAIN
Tel: 34 948 168 412
Fax: 34 948 168 390
E-mail: esther.gozalez@unavarra.es

Gonzalez, Juan
Univ of Texas
Molecular and Celular Biology
FO 31 - Box 830688
Richardson, TX 75083-0688
Tel: (972) 883-2526
Fax: (972) 883-2409
E-mail: jgonzal@utdallas.edu

Goodman, Robert
Univ of Wisconsin
689 Russell Labs
1630 Linden Dr
Madison, WI 53706-1520
Tel: (608) 262-9162
Fax: (608) 262-8643
E-mail: rgoodman@wisc.edu

Gordon, Milton
Univ of Washington
Biochemistry Dept
Box 357350
E-mail: Seattle, WA 98195-7350
Tel: (206) 543-1769
Fax: (206) 685-8279
E-mail: miltong@u.washington.edu

Gottfert, Michael
T U Dresden
Inst Fur Genetik
Mommsenstrasse 13
Dresden, 01062
GERMANY
Tel: 49 351 463 4000
Fax: 49 351 463 7725
E-mail: mgoettfe@rcs.urz.tu-dresden.de

Govers, Francine
Wageningen Univ
Laboratory of Phytopathology
Binnenhaven 5
Wageningen, 6709 PD
NETHERLANDS
Tel: 31 317 483 138
Fax: 31 317 483 412
E-mail: francine.govers@wur.nl

Graham, Terrence
Ohio State Univ
201 Kottman Hall - Plant Path Dept
2021 Coffey Road
Columbus, OH 43210-1044
Tel: (614) 292-1375
Fax: (614) 292-4455
E-mail: graham.1@osu.edu

Grant, Murray
Imperial College At Wye
Agricultural Sciences Dept
High Street
Wye, Kent, TN25 5AH
UNITED KINGDOM
Tel: 44 2075 942 883
Fax: 44 2075 942 640
E-mail: m.grant@imperial.ac.uk

Grenville-Briggs, Laura
Univ of Aberdeen
Molecular and Cell Biology Dept
Inst of Medical Sciences - Foresterhill
Aberdeen, AB25 2ZD
UNITED KINGDOM
Tel: 44 1789 470 382
Fax: 44 1789 970 552
laura.grenville@abdn.ac.uk

Gresshoff, Peter
Univ of Queensland
Botany Dept
Brisbane St Lucia, QLD 4072
AUSTRALIA
Tel: 61 7 3365 7426
Fax: 61 7 3365 4771
E-mail: p.gresshoff@botany.uq.edu.au

Gross, Dennis
Texas A&M Univ
Plant Pathology and Microbiology Dept
2132 TAMU
College Station, TX 77843-2132
Tel: (979) 845-8288
Fax: (979) 845-6483
E-mail: dgross@ppserver.tamu.edu

Guerinot, Mary Lou
Dartmouth College
Biology Dept
6044 Gilman
Hanover, NH 03755
Tel: (603) 646-2527
Fax: (603) 646-1347
E-mail: guerinot@dartmouth.edu

Guinel, Frederique
Wilfrid Laurier Univ
Biology Dept
Waterloo, ON N2L 3C5
CANADA
Tel: (519) 884-0710x2230
Fax: (519) 746-0677
E-mail: fguinel@wlu.ca

H

Haas, Dieter
Univ de Lausanne
Inst De Microbiologie Fondamentale
Batiment De Biologie
Lausanne, CH-1015
SWITZERLAND
Tel: 41 21 692 5631
Fax: 41 21 692 5635
E-mail: dieter.haas@imf.unil.ch

Hackworth, Cheryl
Univ of California
MC 3102 - Plant and Microbial Biology
111 Koshland Hall
Berkeley, CA 94720
Tel: (510) 525-4523
E-mail: hackwrth@uclink.berkeley.edu

Hahn, Matthias
Univ of Kaiserslautern
PO Box 3049 - Biology Dept
Paul Ehrlich Str 22
Kaiserslautern, 67653
GERMANY
Tel: 49 631 205 2402
Fax: 49 631 205 4716
E-mail: hahn@rhrk.uni-kl.de

Halterman, Dennis
Iowa State Univ
USDA ARS - Plant Pathology Dept
405 Bessey Hall
Ames, IA 50011-1020
Tel: (515) 294-9326
E-mail: dhalterm@iastate.edu

Hammond-Kosack, Kim
IACR
Plant-Pathogen Interaction Division
Rothamsted, Harpenden
Hertfordshire, AL5 2JQ
UNITED KINGDOM
Tel: 44 1582 763 133x2240
Fax: 44 1582 715 009
E-mail: kim.hammond-kosack@bbsrc.ac.uk

Hampp, Ruediger
Univ Tubingen
Botanisches Inst
Auf Der Morgenstelle 1
Tuebingen, D-72076
GERMANY
Tel: 49 7071 297 6155
Fax: 49 7071 295 635
E-mail: ruediger.hampp@uni-tuebingen.de

Hardy, Ralph
1075 Brintons Bridge Road
West Chester, PA 19382-8111
Tel: (607) 254-1240
Fax: (716) 741-5108

Harris, Jeanne
Univ of Vermont
Botany Dept
Marsh Life Sciences
Burlington, VT 05405-0086
Tel: (802) 656-2933
Fax: (802) 656-0440
E-mail: jmharris@zoo.uvm.edu

Harrison, Maria
Boyce Thompson Inst
Plant Research
Tower Road
Ithaca, NY 14853
Tel: (607) 254-6472
Fax: (607) 254-6779
E-mail: mjh78@cornell.edu

Hata, Shingo
Kyoto Univ
Graduate School of Biostudies
Plant Physiology Lab - Sakyo-ku
Kyoto, 606-8502
JAPAN
Tel: 81 75 753 6141
Fax: 81 75 753 6470
E-mail: shing@kais.kyoto-u.ac.jp

Hataya, Tatsuji
Hokkaido Univ
Pathogen-Plant Interactions
Kita 9, Nishi 9, Kita-Ku
Sapporo, 060-8589
JAPAN
Tel: 81 11 706 2489
Fax: 81 11 706 2483
E-mail: hataya@res.agr.hokudai.ac.jp

He, Sheng Yang
Michigan State Univ
Plant Research Laboratory
206 Plant Biology Building
East Lansing, MI 48824
Tel: (517) 353-9181
Fax: (517) 353-9168
E-mail: hes@pilot.msu.edu

Heard, Jacqueline
Mendel Biotechnology Inc
21375 Cabot Blvd
Hayward, CA 94405
Tel: (510) 264-0286
Fax: (510) 264-0254
E-mail: jheard@mendelbio.com

Hernandez, Georgina
CIFN UNAM
Molecular Ecology Dept
UNAM - AP Postal 565-A
Cuernavaca, Mor., 62210
MEXICO
Tel: 52 73 139877
Fax: 52 73 116710
E-mail: gina@cifn.unam.mx

Higgins, Gillian
Univ of York
Biology Dept - Area 11
PO Box 373 - Heslington
York, Y010 5YU
UNITED KINGDOM
Tel: 44 1904 328 687
E-mail: gsh106@york.ac.uk

Hinsa, Shannon
Dartmouth Medical College
Microbiology Dept
7550 Hinman - Vail Building
Hanover, NH 03755
Tel: (603) 650-1247
E-mail: hinsa@dartmouth.edu

Hirano, Susan
28 Mondale Ct
Madison, WI 53705
Tel: (608) 262-7236
Fax: (608) 263-2626
E-mail: ssh@plantpath.wisc.edu

Hirsch, Ann
Univ of California
MCD Biology Dept
405 Hilgard Ave
Los Angeles, CA 90095-1606
Tel: (310) 206-8673
Fax: (310) 206-5413
E-mail: ahirsch@ucla.edu

Hofte, Monica
RUG Labo Phytopathology
Crop Protection Dept
Coupure Links 653
Gent, 9000
BELGIUM
Tel: 32 9 264 6017
Fax: 32 9 264 6238
E-mail: monica.hofte@rug.ac.be

Hogenhout, Saskia
Ohio State Univ
OARDC - Entomology Dept
1680 Madison Ave
Wooster, OH 44691
Tel: (330) 263-3730
Fax: (330) 263-3686
E-mail: hogenhout.1@osu.edu

Hogg, Bridget
Univ Paul Sabatier (UMR CNRS)
Chemin De Borde Rouge
SMCV
Toulouse, 31326
FRANCE
Tel: 33 562 193 536
Fax: 33 561 285 061
E-mail: hogg@smcv.ups-tlse.fr

Holsters, Marcelle
RUG Lab Molecular Genetics
K L Ledeganckstraat 35
Gent, 9000
BELGIUM
Tel: 32 9 264 5181
Fax: 32 9 264 5349
E-mail: mahol@gengenp.rug.ac.be

Hopper, Waheeta
SRM Engineering College
Biotechnology Dept
S.R.M. Nagar
Kattankulathur, 603 203
INDIA
Tel: 91 44 230 2060
Fax: 91 44 235 1504
E-mail: waheetahop@yahoo.com

Horvath, Diana
Mediant
400 E 66th Street #18A
New York, NY 10021
Tel: (212) 706-2192
Fax: (212) 706-2194
E-mail: horvatdm@yahoo.com

Huang, Guozhong
Univ of Georgia
Plant Pathology Dept
2105 Miller Plant Sciences Building
Athens, GA 30602-7274
Tel: (706) 542-1245
Fax: (706) 542-1262
E-mail: ghuang@uga.edu

Huang, Hsiou-Chen
Natl Chung Hsing Univ
Ag Biotech Labs
Taichung, 40227
TAIWAN REP OF CHINA
Tel: 886 4 285 2155
Fax: 886 4 286 1905
E-mail: hchuang@dragon.nchu.edu.tw

Huang, Xiang
BASF Corp
26 Davis Dr
Res Triangle Park, NC 27709-2910
Tel: (919) 547-2170
Fax: (919) 547-2423
E-mail: huangx@basf.com

Hulbert, Scot
Kansas State Univ
Plant Pathology Dept
Throckmorton Hall
Manhattan, KS 66506
Tel: (785) 532-1392
Fax: (785) 532-5692
E-mail: shulbrt@ksu.edu

Hurek, Thomas
Univ of Bremen
Max-Planck-Inst Marine Mikrobiology
Postfach 330440, FB2, NW2, Raum 3220
Bremen, D-28334
GERMANY
Tel: 49 421 218 4042
Fax: 49 421 218 2001x2370
E-mail: thurek@uni-bremen.de

Huss-Danell, Kerstin
Swedish Univ of Agric Sciences (SLU)
Crop Science Dept
Box 4097
Umea, 90403
SWEDEN
Tel: 46 90 786 9411
Fax: 46 90 122 195
E-mail: kerstin.huss-danell@njv.slu.se

Hutcheson, Steven
Univ of Maryland
Cell Biology and Molecular Genetics Dept
1109 Microbiology Building
College Park, MD 20742-0001
Tel: (301) 405-5498
Fax: (301) 314-9489
E-mail: sh53@umail.umd.edu

Hwang, Byung Kook
Korea Univ
Molecular Plant Pathology Laboratory
College of Life and Env Sci - Anamdong
Sungbukku, Seoul, 136-701
SOUTH KOREA
Tel: 82 2 3290 3061
Fax: 82 2 925 1970
E-mail: bkhwang@korea.ac.kr

Hwang, Cheol
Dankook Univ
Bioresource Science Dept
Anseodong San 29
Cheonan, Chungnam, 330-714
SOUTH KOREA
Tel: 82 41 550 3626
Fax: 82 41 553 1618
E-mail: sfeho@dankook.ac.kr

Hwang, Ingyu
Seoul Natl Univ
School of Agricultural Biotechnology
San 56-1, Shillim-dong, Kwanak-gu
Seoul, 151-742
KOREA
Tel: 81 2 880 4676
Fax: 81 2 873 2317
E-mail: ingyu@snu.ac.kr

Hynes, Michael
Univ of Calgary
Biology Dept
2500 Univ Drive NW
Calgary, AB T2N 1N4
CANADA
Tel: (403) 220-8473
Fax: (403) 289-9311
E-mail: hynes@ucalgary.ca

I

Iacobellis, Nicola Sante
Univ Basilicata
Biologia - Biotech Agro Forest
Via N Sauro 85
Potenza, 85100
ITALY
Tel: 39 971 205 498
Fax: 39 971 205 702
E-mail: iacobellis@unibas.it

Inagaki, Yoshishige
Okayama Univ
Fac of Agric - Genetic Engineering Lab
Tsushima-naka 1-1-1
Okayama, 700-8530
JAPAN
Tel: 81 86 251 8307
Fax: 81 86 251 8307
E-mail: yinagaki@cc.okayama-u.ac.jp

Ishimaru, Carol
Colorado State Univ
Biological Sciences and
Pest Management Department
Fort Collins, CO 80523-1177
Tel: (970) 491-7726
Fax: (970) 491-3862
E-mail: cishimar@lamar.colostate.edu

J

James, Euan
Univ of Dundee
Ctr for High Resolution Imaging/Process
MSI/WTB Complex-School of Life Sciences
Dundee, DDI 5EH
UNITED KINGDOM
Tel: 44 1382 344 741
Fax: 44 1382 345 893
E-mail: e.k.james@dundee.ac.uk

Jameson, Paula
Massey Univ
Molecular BioSciences
Private Bag 11222
Palmenton North,
NEW ZEALAND
Tel: 64 6 350 5518
Fax: 64 6 350 5688
E-mail: p.e.jameson@massey.ac.nz

Jasalavich, Claudia
469 Broad Street
Nashua, NH 03063-3410
Tel: (603) 594-1341
E-mail: cjasalavich@earthlink.net

Jenner, Carol
Warwick HRI
Wellesbourne
Warwickshire, CV35 9EF
UNITED KINGDOM
Tel: 44 24 7657 4455
Fax: 44 24 7657 4500
E-mail: carol.jenner@warwick.ac.uk

Jia, Yulin
USDA ARS
Dale Bumpers Natl Rice Res Center
2890 State Hwy 130 E-PO Box 1090
Stuttgart, AR 72160-0287
Tel: (870) 672-9300x229
Fax: (870) 673-7581
E-mail: yjia@spa.ars.usda.gov

Jones, Jonathan
John Innes Centre
Sainsbury Lab
Norwich Research Park
Colney Lane, Norwich, NR4 7UH
UNITED KINGDOM
Tel: 44 1603 450 327
Fax: 44 1603 450 011
E-mail: jonathan.jones@sainsbury-laboratory.ac.uk

Jones, Kathryn
Apartment 2L
176 Richdale Ave
Cambridge, MA 02140
Tel: (617) 253-4721
Fax: (617) 253-2643
kmjones@mit.edu

Joosten, Matthieu
Wageningen Agricultural Univ
Dept of Phytopathology
Binnenhaven 9
Wageningen, 6709 PD
NETHERLANDS
Tel: 31 317 483 411
Fax: 31 317 483 412
E-mail: matthieu.joosten@wur.nl

Jung, Christian
Univ of Kiel
Inst of Crop Science and Plant Breeding
Olshausenstrasse 40
Kiel, 24118
GERMANY
Tel: 49 431 880 7364
Fax: 49 431 880 2566
E-mail: cjung@plantbreeding.uni-kiel.de

K

Kalliopi, Papadopoulou
N.A.G.R.E.F.
Inst of Kalamata
Lakonikis 85
Kalamata, 24100
GREECE
Tel: 30 721 91984
Fax: 30 721 27133
E-mail: nagrefkal@kal.forthnet.gr

Kamakura, Takashi
Tokyo Univ of Science
Applied Biological Science Dept
2641 Yamazaki
Noda, Chiba, 278-8510
JAPAN
Tel: 81 4 7124 1501x3411
Fax: 81 4 7123 9767
E-mail: kamakura@rs.noda.tus.ac.jp

Kamoun, Sophien
Ohio State Univ
OARDC - Plant Pathology Dept
1680 Madison Ave
Wooster, OH 44691-4114
Tel: (330) 263-3847
Fax: (330) 263-3841
E-mail: kamoun.1@osu.edu

Kang, Kyu
Gyeongsang Natl Univ
Agricultural Chemistry Dept
Chinju, 660-701
SOUTH KOREA
Tel: 82 55 751 5468
Fax: 82 55 757 0178
E-mail: kykang@nongae.gsnu.ac.kr

Kauffmann, Serge
IBMP CNRS
12 rue du General Zimmer
Strasbourg, 67084
FRANCE
Tel: 33 388 417 200
Fax: 33 388 614 442
E-mail: serge.kauffmann@ibmp-ulp.u-strasbg.fr

Keel, Christoph
Univ de Lausanne
Inst De Microbiologie Fondamentale
Batiment De Biologie
Lausanne-Dorigny, CH-1015
SWITZERLAND
Tel: 41 21 692 5636
Fax: 41 21 692 5635
E-mail: christoph.keel@imf.unil.ch

Kertesz, Michael
Univ of Manchester
School of Biological Sciences
1-800 Stopford Bldg - Oxford Road
Manchester, M13 9PT
UNITED KINGDOM
Tel: 44 161 275 3895
Fax: 44 161 275 5656
E-mail: michael.kertesz@man.ac.uk

Kijne, Jan
Leiden Univ
Wassenaarseweg 64
Inst Molecular Plant Sciences
Leiden, 2333 AL
NETHERLANDS
Tel: 31 71 527 5057
Fax: 31 71 527 5088
E-mail: kijne@rulbim.leidenuniv.nl

Kim, Jihyun
Korea Res Inst of Bioscience & Biotech
Microbial Genomics Laboratory
PO Box 115
Yusong-gu, Taejeon, 305-600
SOUTH KOREA
Tel: 82 42 860 4412
Fax: 82 42 879 8595
E-mail: jfk@kribb.re.kr

Kim, Jong Heon
USDA
Plant Mycotoxini Research Unit
800 Buchanan Street
Albany, CA 94710
Tel: (510) 559-5841
Fax: (510) 559-5737
E-mail: jhkim@pw.usda.gov

Klessig, Daniel
Boyce Thompson Inst
Plant Research
Tower Road
Ithaca, NY 14853-1802
Tel: (607) 254-1300
Fax: (607) 254-6779
E-mail: dfk8@cornell.edu

Knogge, Wolfgang
Inst of Plant Biochemistry
Weinberg 3
Halle, 06120
GERMANY
Tel: 61 8 8303 6822
Fax: 61 8 8303 7109
E-mail: wolfgang.knogge@adelaide.edu.au

Kobayashi, Issei
Mie Univ
Plant Functional Genomics Division
1515 Kamihama - Life Science Res Ctr
Tsu, Mie, 514-8507
JAPAN
Tel: 81 592 31 9074
Fax: 81 592 31 9048
E-mail: issei@gene.mie-u.ac.jp

Kogel, Karl-Heinz
Justus Liebig Univ
Inst Fur Phytopath/Zoologie
Heinrich Buff Ring 26-32
Giessen, 35392
GERMANY
Tel: 49 641 993 7490
Fax: 49 641 993 7499
E-mail: karl-heinz.kogel@agrar.uni-giessen.de

Kohmoto, Keisuke
Tachikawa 5-85-7
Tottori City, 680-0061
JAPAN
Tel: 81 857 24 0799
Fax: 81 857 24 0799
E-mail: kohmoto@sage.ocn.ne.jp

Kondorosi, Adam
CNRS
Inst Des Sciences Du Vegetal
Ave de la Terrasse
Gif Sur Yvette, 91198
FRANCE
Tel: 33 16 982 3698
Fax: 33 16 982 3695
E-mail: adam.kondorosi@isv.cnrs-gif.fr

Kouchi, Hiroshi
Natl Inst of Agrobiological Sciences
2-1-2 Kannondai

Tsukuba Ibaraki, 305
JAPAN
Tel: 81 298 388377
Fax: 81 298 388347
E-mail: kouchih@nias.affrc.go.jp

Krause, Andrea
Univ of Bremen FB2
Allgemeine Mikrobiologie
Postfach 33 04 40
Bremen, 28334
GERMANY
Tel: 49 421 218 4327
Fax: 49 421 218 9058
E-mail: akrause@uni-bremen.de

Kronstad, James
Univ of British Columbia
Biotechnology Lab
237-6174 Univ Blvd
Vancouver, BC V6T 1Z3
CANADA
Tel: (604) 822-4732
Fax: (604) 822-6097
E-mail: kronstad@interchange.ubc.ca

Kuester, Helge
Univ Bielefeld
Genetics Dept
Universitaetsstrasse 25
Bielefeld, 33615
GERMANY
Tel: 49 5211 064 819
Fax: 49 5211 065 626
E-mail: helge.kuester@genetik.uni-bielefeld.de

Kunkel, Barbara
Washington Univ
Biology Dept Campus Box 1137
1 Brookings Dr
Saint Louis, MO 63130-4862
Tel: (314) 935-7284
Fax: (314) 935-4432
E-mail: kunkel@biology.wustl.edu

L

Lamb, Christopher
John Innes Centre
Norwich Research Park
Colney Lane
Norwich, NR4 7UH
UNITED KINGDOM
Tel: 44 1603 450 265
Fax: 44 1630 450 016
E-mail: chris.lamb@bbsrc.ac.uk

Lambert, Kris
Univ of Illinois
Crop Sciences Dept
1102 S Goodwin Ave
Urbana, IL 61801
Tel: (217) 265-5165
Fax: (217) 244-1230
E-mail: knlamber@uiuc.edu

Lapeyrie, Frederic
INRA
Microbiologie Forestiere
Champenoux, 54280
FRANCE
Tel: 33 8 339 4078
Fax: 33 8 339 4069
E-mail: lapeyrie@nancy.inra.fr

Lartey, Robert
USDA ARS
1500 N Central Ave
Sidney, MT 59270
Tel: (406) 433-9490
Fax: (406) 433-5038
E-mail: rlartey@sidney.ars.usda.gov

Le Gall, Olivier
INRA
Virologie Vegetale IBVM
BP 81
Villenave d'Ornon, 33883
FRANCE
Tel: 33 5 56 843 205
Fax: 33 5 56 843 221
E-mail: legall@bordeaux.inra.fr

Leach, Jan
Kansas State Univ
Plant Science Ctr - Plant Path Dept
4024 Throckmorton Hall
Manhattan, KS 66506-5502
Tel: (785) 532-1367
Fax: (785) 532-5692
E-mail: jleach@ksu.edu

Lee, Lan-Ying
Purdue Univ
Biological Sciences Dept
West Lafayette, IN 47907
Tel: (765) 494-4947
Fax: (765) 496-1496
E-mail: lylee@bilbo.bin.purdue.edu

Lefebvre, Veronique
INRA
Pathologie Vegetale
Domaine St Maurice BP 94
Montfavet, 84143
FRANCE
Tel: 34 4 3272 3806
Fax: 34 4 3272 2710
E-mail: veronique.lefebvre@avignon.inra.fr

Legocki, Andrzej
Inst of Bioorganic Chemistry
Noskowskiego 12-14
Poznan, 61-704
POLAND
Tel: 48 61 852 8919
Fax: 48 61 852 0532
E-mail: legocki@ibch.poznan.pl

Legrand, Michel
IBMP CNRS
Phytopathology Deptartment
12 Rue Du General Zimmer
Strasbourg, 67000
FRANCE
Tel: 33 388 417 280
Fax: 33 388 614 442
E-mail: michel.legrand@ibmp-ulp.u-strasbg.fr

Leister, R. Todd
Univ of California
Plant and Microbial Biology Dept
111 Koshland Hall
Berkeley, CA 94720-3110
Tel: (510) 643-7133
E-mail: leister@nature.berkeley.edu

Leon-Barrios, Milagros
Univ de La Laguna
Microbiologia Dept
Facultad de Farmacia
La Laguna, 38071
SPAIN
Tel: 34 22 318 481
Fax: 34 22 318 477
E-mail: mileonba@ull.es

Leong, Sally
USDA ARS
Plant Disease Resistance Unit
1630 Linden Dr
Madison, WI 53706-1520
Tel: (608) 262-5309
Fax: (608) 262-1541
E-mail: sal@plantpath.wisc.edu

Lerner, Jeffrey
21 Beeching Street
Worcester, MA 01602
Tel: (508) 757-7244
Fax: (413) 545-2532
E-mail: jeffreylerner@att.net

Li, Fu-Di
Huazhong Agric Univ
Inst of Agro-Microbiology
Wuhan Hubei, 430070
PEOPLES REP OF CHINA
Tel: 86 27 87280366
Fax: 86 27 87280366
E-mail: fudili@public.wh.hb.cn

Lightfoot, David
Southern Illinois Univ
Plant Soil and General Agirc Dept
Room 176
Carbondale, IL 62901-4415
Tel: (618) 453-1797
Fax: (618) 453-5886
E-mail: ga4082@siu.edu

Lin, Na-Sheng
Inst of Botany
Academia Sinica
Taipei, 115
TAIWAN REP OF CHINA
Tel: 886 2 789 9590
Fax: 886 2 782 7954
E-mail: nslin@sinica.edu.tw

Lin, Yu-Zu
Academia Sinica
Institute of Botany
128 Yamjiouyuan Rd, Soc 2, Nankang
Taipei, 11529
TAIWAN REP OF CHINA
Tel: 886 2 2789 9590x212
Fax: 886 2 2782 7954
E-mail: lin0830@gate.sinica.edu.tw

Lindow, Steven
Univ of California
Plant and Microbial Biology Dept
111 Koshland Hall
Berkeley, CA 94720-3102
Tel: (510) 642-4174
Fax: (510) 642-4995
E-mail: icelab@socrates.berkeley.edu

Lindstrom, Kristina
Univ of Helsinki
Applied Chem and Microbiology
PO Box 56 - Vilkinkaari 9
Helsinki, 00014
FINLAND
Tel: 358 970 855 282
Fax: 358 970 85322
E-mail: lindstro@millipede.helsinki.fi

Liou, Ruey-Fen
Natl Taiwan Univ
Plant Pathology and Microbiology Dept
1 Sec 4 Roosevelt Rd
Taipei, 106
TAIWAN REP OF CHINA
Tel: 886 2 3366 5208
Fax: 886 2 2362 0271
E-mail: rfliou@ntu.edu.tw

Liu, Jinyuan
Boyce Thompson Inst
Tower Road
Ithaca, NY 14853
Tel: (607) 254-6424
Fax: (607) 254-2958
E-mail: jl454@cornell.edu

Lojkowska, Ewa
Univ of Gdansk
Biotechnology Dept
24 Kladki Str
Gdansk, 80-822
POLAND
Tel: 48 58 312 241x45
Fax: 48 58 312 807
E-mail: lojkowsk@biotech.univ.gda.pl

Long, Sharon
Stanford Univ
Bio Sciences Dept
216 Gilbert Bldg - 371 Serra Mall
Stanford, CA 94305-5020
Tel: (650) 723-3232
Fax: (650) 725-8309
E-mail: srl@stanford.edu

Lorito, Matteo
Univ Degli Studi Di Napoli
Dip Arbopave, Sez Patologia Veg
Via Universita, 100
Portici (NA), 80055
ITALY
Tel: 39 81 775 5142
Fax: 39 81 775 5320
E-mail: lorito@unina.it

Lu, Shien
Texas A&M Univ
Plant Pathology and Microbiology Dept
2132 TAMU
College Station, TX 77843-2132
Tel: (979) 458-0638
Fax: (979) 845-6483
E-mail: shienlu@ppserver.tamu.edu

Lu, Shun-Wen
Cornell Univ
Plant Pathology Dept
334 Plant Science Building
Ithaca, NY 14853-5904
Tel: (607) 255-7832
Fax: (607) 255-4471
E-mail: swl2@cornell.edu

Lugtenberg, Egbertus (Ben)
Leiden Univ
Inst of Biology
Wassenaarseweg 64
Leiden, 2333 AL
NETHERLANDS
Tel: 31 71 5275 5063
Fax: 31 71 527 5088
E-mail: lugtenberg@rullbim.leidenuniv.nl

M

Manners, John
CSIRO Plant Industry
Queensland Bioscience Precinct
306 Carmody Road
St Lucia, Brisbane, QLD 4067
AUSTRALIA
Tel: 61 7 3214 2304
Fax: 61 7 3214 2920
E-mail: john.manners@csiro.au

Manulis, Shulamit
ARO The Volcani Center
Plant Pathology Dept
Bet Dagan, 50250
ISRAEL
Tel: 972 3 968 3685
Fax: 972 3 968 3686
E-mail: shulam@volcani.agri.gov.il

Marmiroli, Nelson
Univ di Parma
Environmental Science Dept
Viale Delle Science
Parma, 43100
ITALY
Tel: 39 521 905 606
Fax: 39 521 905 665
E-mail: marmirol@ipruniv.cce.unipr.it

Martin, Gregory
Boyce Thompson Inst
Tower Road
Ithaca, NY 14850
Tel: (607) 254-1208
Fax: (607) 255-6695
E-mail: gbm7@cornell.edu

Martin Sanchez, Juan
Univ De Leida
Centre R and D De Lleida
Alcalde Rovira Roure 177
Lleida, 25198
SPAIN
Tel: 34 973 702 569
Fax: 34 923 238 301

Matsuda, Yoshinori
Kinki Univ
Faculty of Agric - Plant Pathology Lab
3327-204 Nakamachi
Nara, 631-8505
JAPAN
Tel: 81 742 43 1511
Fax: 81 742 43 1155
E-mail: ymatsuda@nara.kindai.ac.jp

Matsushita, Yasuhiko
Tokyo Univ of Agric & Technology
Gene Research Center
3-5-8 Saaiwai-cho - Fuchu-Shi
Tokyo, 183-8509
JAPAN
Tel: 81 42 367 5855
Fax: 81 42 367 5855
E-mail: ymatsu@cc.tuat.ac.jp

Matthieu, Arlat
CNRS INRA
Interactions Plantes-microorganisms Lab
Chemin De Borde Rouge - BP 27
Castanet Tolosan, 31326
FRANCE
Tel: 33 561 285 055
E-mail: arlat@toulouse.inra.fr

Matthysse, Ann
Univ of North Carolina
Coker Hall CB3280
Chapel Hill, NC 27599-3280
Tel: (919) 962-6941
Fax: (919) 962-1625
E-mail: ann_matthysse@unc.edu

Mauch, Felix
Univ of Fribourg
Biology Dept
Rue Du Muser 10
Fribourg, 1700
SWITZERLAND
Tel: 41 26 300 8817
Fax: 41 26 300 9740
E-mail: felix.mauch@unifr.ch

Mauch-Mani, Brigitte
Univ De Neuchatel
Biochmie Dept
Rue Emile Argand 9 - CP2
Neuchatel, 2007
SWITZERLAND
Tel: 41 32 718 2205
Fax: 41 32 718 2201
E-mail: brigitte.mauch@unine.ch

Mavrodi, Dmitri
Washington State Univ
Plant Pathology Dept
Johnson Hall - Room 362
Pullman, WA 99163
Tel: (509) 335-3269
Fax: (509) 335-7674
E-mail: mavrodi@mail.wsu.edu

Mavrodi, Olga
Washington State Univ
Plant Pathology Dept
Johnson Hall - Room 362
Pullman, WA 99164
Tel: (509) 335-3269
Fax: (509) 335-7674
E-mail: omavrodi@mail.wsu.edu

Mayama, Shigeyuki
Kobe Univ
Faculty of Agric - Plant Pathology Dept
Nada-Ku Rokkodai-Cho
Kobe, 657-8501
JAPAN
Tel: 81 78 803 5864
Fax: 81 78 803 5865
E-mail: mayama@kobe-u.ac.jp

Mazzola, Mark
USDA ARS
Tree Fruit Research Lab
1104 N Western Ave
Wenatchee, WA 98801-1230
Tel: (509) 664-2280
Fax: (509) 664-2287
E-mail: mazzola@tfrl.ars.usda.gov

Mcdowell, John
Virginia Tech
Fralin Biotechnology Center
PO Box 0346
Blacksburg, VA 24061-0346
Tel: (540) 231-2388
Fax: (540) 231-7126
E-mail: johnmcd@vt.edu

McNellis, Timothy
Penn State Univ
Plant Pathology Dept
318 Buckhout Lab
University Park, PA 16802
Tel: (814) 863-7646
Fax: (814) 863-7217
E-mail: mcnellis@psu.edu

Meilhoc, Eliane
INSA CNRS INRA
LIPM - Chemin De Borde Rouge
BP 27
Castanet Tolosan, 31326
FRANCE
Tel: 33 561 285 046
E-mail: meilhoc@toulouse.inra.fr

Melcher, Ulrich
Oklahoma State Univ
Biochem and Molec Biology Dept
246 Noble Research Center
Stillwater, OK 74078-3035
Tel: (405) 744-6210
Fax: (405) 744-7799
E-mail: umelcher@biochem.okstate.edu

Merighi, Massimo
Ohio State Univ
Plant Pathology Dept
201 Kottman Hall - 2021 Coffey Road
Columbus, OH 43210-1087
Tel: (614) 292-1375
Fax: (614) 292-4455
E-mail: merighi.1@osu.edu

Metz, Matthew
USAID
Bureau for Economic Growth, Agric Trade
1300 Pennsylvania Ave NW
Washington, DC 20523
Tel: (202) 712-1581
Fax: (202) 216-3387
E-mail: mmetz@usaid.gov

Michelmore, Richard
Univ of California
Vegetable Crops Dept
148 Asmundson Hall
Davis, CA 95616-8746
Tel: (530) 752-1729
Fax: (530) 752-9659
E-mail: rwmichelmore@ucdavis.edu

Milbourne, Dan
TEAGASC
Crops Research Centre
Oak Park
Carlow,
IRELAND
Tel: 353 503 70200
Fax: 353 503 42423
E-mail: dmilbourne@oakpark.teagasc.ie

Moerschbacher, Bruno
Westfalische Wilhelms Univ
Inst Biochem Biotech of Plants
Hindenburgplatz 55
Muenster, 48143
GERMANY
Tel: 49 251 832 4794
Fax: 49 251 832 8371
E-mail: moersch@uni-muenster.de

Moury, Benoit
INRA
Station De Pathologie Vegetale
BP 94 - Domaine St Maurice
Montfavet Cedex, 84143
FRANCE
Tel: 33 4 3272 2843
Fax: 33 4 3272 2842
E-mail: moury@avignon.inra.fr

Muller, Peter
Philipps Univ
Biology Dept
Karl Von Frisch Strasse
Marburg, 35032
GERMANY
Tel: 49 6421 282 072
Fax: 49 6421 288 997
E-mail: muellerp@mailer.uni-marburg.de

Murphy, Peter
Univ of Adelaide
Applied and Molecular Ecology Dept
Waite Campus - PB 1
Glen Osmond, SA 5064
AUSTRALIA
Tel: 61 8 8303 7262
Fax: 61 8 8303 7109
E-mail: peter.murphy@adelaide.edu.au

Murray, Shane
Univ of Cape Town
Molecular and Cell Biology Dept
Private Bag - Rondebosch
Cape Town, 7700
REP OF SOUTH AFRICA
Tel: 27 21 650 4006
Fax: 27 21 689 7573
E-mail: smurray@science.uct.ac.za

Mysore, Kirankumar
Samuel Roberts Noble Foundation
Plant Biology Dept
2510 Sam Noble Pkwy
Ardmore, OK 73401
Tel: (580) 224-6740
Fax: (580) 224-6692
E-mail: ksmysore@noble.org

N

Naidoo, Sanushka
Univ of Pretoria
Botany Dept
Lunnon St - Agricultural Sciences Bldg
Pretoria, Gauteng, 0002
REP OF SOUTH AFRICA
Tel: 27 12 420 4239
Fax: 27 12 420 5327
E-mail: sanushka.reddy@fabi.up.ac.za

Nakahara, Kenji
Hokkaido Univ
Graduate School of Agriculture
Sapporo, 060-8589
JAPAN
E-mail: knjsn@bk.iij4u.or.jp

Namba, Shigetou
4-20-2-104 Hongo
Bunkyo-ku
Tokyo, 113-0033
JAPAN
Tel: 81 3 5800 2850
Fax: 81 3 5800 2850
E-mail: snamba@mail.ims.u-tokyo.ac.jp

Narusaka, Yoshihiro
Tokyo Gakugei Univ
4-1-1 Nukuikita-machi
Koganei-shi, Tokyo, 184-8501
JAPAN
Tel: 81 42 329 7515
Fax: 81 42 329 7515
E-mail: narusaka@u-gakugei.ac.jp

Nelson, Louise
Univ of Saskatchewan
Applied Microbiology and Food Sci Dept
51 Campus Dr - Agric Building
Saskatoon, SK S7N 5A8
CANADA
Tel: (306) 966-5027
Fax: (306) 966-8898
E-mail: louise.nelson@usask.ca

Nelson, Richard
Samuel Roberts Noble Foundation
PO Box 2180
Ardmore, OK 73402-2180
Tel: (580) 224-6600
Fax: (580) 224-6692
E-mail: rsnelson@noble.org

Nester, Eugene
Univ of Washington
Box 357242
Microbiology Department
Seattle, WA 98195-7242
Tel: (206) 616-8588
Fax: (206) 543-8297
E-mail: gnester@u.washington.edu

Nissinen, Riitta
Helsinki Univ
Dept of Applied Biology
PL 27 - Lab of Plant Pathology
Helsinki, 00014
FINLAND
Tel: 358 9 191 58373
Fax: 358 9 191 58727
E-mail: riitta.nissinen@helsinki.fi

Noel, K. Dale
Marquette Univ
Biology Dept
PO Box 1881
Milwaukee, WI 53201-1881
Tel: (414) 288-1475
Fax: (414) 288-7357
E-mail: dale.noel@marquette.edu

Norris, Joanna
Univ of Rhode Island
Biological Sciences Dept
Ranger Hall
Kingston, RI 02881
Tel: (401) 874-2623
Fax: (401) 874-5974
E-mail: jnorris@uri.edu

Nuernberger, Thorsten
Eberhard-Karls Univ Tubingen
Molecular Biology of Plants (ZMBP)
Auf Der Morgenstelle 5
Tubingen, 72076
GERMANY
Tel: 49 7071 297 6658
Fax: 49 7071 295 226
E-mail: thorsten.nuernberger@zmbp.uni-tuebingen.de

Nuss, Donald
Univ of Maryland
Ctr Agric Biotechnology Inst
5115 Plant Sciences Building
College Park, MD 20742-4450
Tel: (301) 405-0334
Fax: (301) 314-9075
E-mail: nuss@umbi.umd.edu

O

O'Donnell, Kerry
USDA ARS MWA NCAUR
1815 N University St
Peoria, IL 61604-3902
Tel: (309) 681-6383
Fax: (309) 681-6672
E-mail: kodonnell@mail.ncaur.usda.gov

Oh, Chang-sik
Cornell Univ
Plant Pathology Dept
334 Plant Science Building
Ithaca, NY 14853-4203
Tel: (607) 255-2025
Fax: (607) 255-4471
E-mail: co35@cornell.edu

Ohashi, Yuko
Natl Inst of Agrobiological Sciences
Molecular Genetics Dept
Kannondai 2-1-2
Tsukuba,Ibaraki, 305-8602
JAPAN
Tel: 81 29 838 7440
Fax: 81 29 838 7469
E-mail: yohahsi@affrc.go.jp

Ohnishi, Kouhei
Kochi Univ
Research Inst of Molecular Genetics
200 Monobe
Nankoku, Kochi, 783-8502
JAPAN
Tel: 81 88 864 5213
Fax: 81 88 864 5109
E-mail: kouheio@rimg.kochi-u.ac.jp

Oke, C. Valerie
Univ of Pittsburgh
Biological Sciences Dept
A527 Langley Hall
Pittsburgh, PA 15260
Tel: (412) 624-4635
Fax: (412) 624-4759
E-mail: voke@pitt.edu

Okon, Yaacov
Hebrew Univ of Jerusalem
Plant Pathology and Microbiology Dept
PO Box 12 - Fac of Agric - FEQS
Rehovot, 76100
ISRAEL
Tel: 972 8 948 9216
Fax: 972 8 946 6794
E-mail: okon@agri.huji.ac.il

Okubara, Patricia
Washington State Univ
USDA ARS
367 Johnson Hall
Pullman, WA 99164-6430
Tel: (509) 335-7824
Fax: (509) 335-7674
E-mail: pokubara@wsu.edu

Olivares, Jose
CSIC
Estacion Exp del Zaidin
Professor Albareda 1
Granada, 18008
SPAIN
Tel: 34 95 812 1011
Fax: 34 95 812 9600
E-mail: olivares@eez.csic.es

Oliver, Richard
Murdoch Univ
Australian Centre for
Necrotophic Fungal Pathogens
Perth, WA 6150
AUSTRALIA
Tel: 61 8 9360 7404
Fax: 61 8 9360 6303
E-mail: roliver@central.murdoch.edu.au

Osaki, Mitsura
Hokkaido Univ
Graduate School of Agriculture
Kita 9, Nishi9, Kitaku
Sapporo, Hokkaido, 060-8589
JAPAN
Tel: 81 11 706 4170
Fax: 81 11 706 4170
E-mail: mosaki@chem.agr.hokudai.ac.jp

Osbourn, Anne
John Innes Centre
Plant Virus Res/Sainsbury Lab
Colney Lane
Norwich, NR4 6UH
UNITED KINGDOM
Tel: 44 1603 452 571
Fax: 44 1603 250 024
E-mail: annie.osbourn@bbsrc.ac.uk

Osburn, Robert
Liphatech Inc
PO Box 90980
3101 W Custer Ave
Milwaukee, WI 53209-4827
Tel: (414) 462-7600
Fax: (414) 462-7186
E-mail: rmo@liphatech.com

Ouchi, Seiji
Univ of California
1 Shields Ave - Plant Pathology Dept
348 Hutchinson Hall
Davis, CA 95616
Tel: (530) 752-7043
E-mail: souchi@ucdavis.edu

Ownley, Bonnie
Univ of Tennessee
Entomology and Plant Pathology Dept
2431 Joe Johnson Dr - 205 Ellington
Knoxville, TN 37996-4500
Tel: (865) 974-0219
Fax: (865) 974-4744
E-mail: bownley@utk.edu

P

Palacios, Rafael
Nitrogen Fixation Res Ctr
UNAM
Molecular Ecology Dept
Cuernavaca, Mor., 62280
MEXICO
Tel: 52 73 114 660
Fax: 52 73 114 660
E-mail: palacios@cifn.unam.mx

Palva, Tapio
Univ of Helsinki
Genetics Div - Biosciences Dept
PO Box 56
Helsinki, 00014
FINLAND
Tel: 358 9 1915 9600
Fax: 358 9 1915 9076
E-mail: tpalva@mappi.helsinki.fi

Parniske, Martin
John Innes Centre
The Sainsbury Laboratory
Colney Lane
Norwich, NR4 7UH
UNITED KINGDOM
Tel: 44 1603 450 0249
Fax: 44 1603 450 011
E-mail: martin.parniske@bbsrc.ac.uk

Patil, Suresh
2524 Brenton Point Dr
Reston, VA 20191
Tel: (703) 391-1705
E-mail: spatil@comcast.net

Pedras, M. Soledad
Univ of Saskatchewan
Chemistry Dept
110 Science Place
Saskatoon, SK S7N 5C9
CANADA
Tel: (306) 966-4772
Fax: (306) 966-4730
E-mail: pedras@sask.usask.ca

Perez-Galdona, Ricardo
Univ de La Laguna
Facultad de Farmacia
Microbiologia Y Biol Celular
La Laguna, Tenerife, 38071
SPAIN
Tel: 34 922 318 512
Fax: 34 922 318 477
E-mail: rperezga@ull.es

Perotto, Silvia
Univ of Torino
Dept Di Biologia Vegetale
Viale Mattioli 25
Torino, 10125
ITALY
Tel: 39 11 670 5987
Fax: 39 11 670 5962
E-mail: silvia.perotto@unito.it

Piercey-Normore, Michele
Univ of Manitoba
Botany Dept
525 Buller Building
Winnipeg, MB R3T 2N2
CANADA
Tel: (204) 474-9610
Fax: (204) 474-7604
E-mail: pierceyn@cc.umanitoba.ca

Pieterse, Corne
Utrecht Univ
Section Plant Pathology
PO Box 800 84
Utrecht, 3508 TB
NETHERLANDS
Tel: 31 30 253 6887
Fax: 31 30 251 8366
E-mail: c.m.j.pieterse@bio.uu.nl

Poole, Philip
Univ of Reading
PO Box 228 - Div of Microbiiology
School of AMS - Whiteknights
Reading, RG6 2AJ
UNITED KINGDOM
Tel: 44 118 931 8895
Fax: 44 118 931 6671
E-mail: p.s.poole@reading.ac.uk

Portoni, Brian
7236 Greenhaven Dr #40
Sacramento, CA 95831-3529
Tel: (916) 428-5649
E-mail: bportoni@worldnet.att.net

Powell, Ann
Univ of California
Mann Labs
Davis, CA 95616
Tel: (530) 752-9096
Fax: (530) 752-4554
E-mail: alpowell@ucdavis.edu

Prasad, Gyaneshwar
Univ of California
Plant and Microbial Biology Dept
111 Koshland Hall
Berkeley, CA 94720
Tel: (510) 643-9307
E-mail: gyani@nature.berkeley.edu

Preston, Gail
Univ of Oxford
Plant Sciences Dept
South Parks Road
Oxford, OX1 3RB
UNITED KINGDOM
Tel: 44 1865 275 106
Fax: 44 1865 275 074
E-mail: gail.preston@
plant-sciences.ox.ac.uk

Prinsen, Els
Univ of Antwerp
Biology Dept
Universiteitsplein 1
Antwerp (Wilrijk), 2610
BELGIUM
Tel: 32 3 820 2266
Fax: 32 3 820 2271
E-mail: els.prinsen@ua.ac.be

Puhler, Alfred
Univ Bielefeld
PO Box 100131 - Genetics Dept
Fakultaet fuer Biologie
Bielefeld, 33501
GERMANY
Tel: 49 521 106 5607
Fax: 49 521 106 5626
E-mail: puehler@genetik.uni-bielefeld.de

Puthoff, David
USDA ARS - Purdue Univ
Crop Protection Pest Control Res Unit
901 W State Street - Entomology Dept
West Lafayette, IN 47907
Tel: (765) 494-0183
E-mail: david_puthoff@entm.purdue.edu

Q

Quinto, Carmen
UNAM
Institute of Biotech-Biomolec
Apdo Postal 510-3
Cuernavaca MOR, 62270
MEXICO
Tel: 52 915 622 7642
Fax: 52 917 313 6600
E-mail: quinto@ibt.unam.mx

R

Raina, Ramesh
Syracuse Univ
Biology Dept - 130 College Place
601A Biological Research Labs
Syracuse, NY 13244-0001
Tel: (315) 443-4546
Fax: (315) 443-2012
E-mail: raraina@syr.edu

Rasmussen, Jack
North Dakota State Univ
Plant Pathology Dept
Walster Hall - PO Box 5012
Fargo, ND 58105
Tel: (701) 231-1027
Fax: (701) 231-7851
E-mail: jack_rasmussen@ndsu.nodak.edu

Ravnikar, Maja
Natl Inst of Biology
Vecna pot 111
POB 141
Ljubljana, 1001
SLOVENIA
Tel: 386 14 233 388
Fax: 386 14 235 038
E-mail: maja.ravnikar@nib.si

Ribeiro, Ana
Inst Invest Cientifica Tropical
Quinta Do Marques (E.A.N.)
Centro De Invest Ferrugens Do Cafeeiro
Oeiras, 2784-505
PORTUGAL
Tel: 351 91 406 4764
Fax: 351 21 442 3023
E-mail: aribeiro32@hotmail.com

Rickauer, Martina
UMR CNRS - UPS 5546
24 Chemin De Borderouge
BP 17 Auzeville - Biotech Vegetale
Castanet - Tolosan, 31326
FRANCE
Tel: 33 562 193 518
Fax: 33 562 193 525
E-mail: rickauer@smcv.ups-tlse.fr

Rivilla, Rafael
Univ Autonoma de Madrid
Biology Dept
Facultad de Ciencia
Madrid, 28049
SPAIN
Tel: 34 1 397 8177
Fax: 34 1 397 8344
E-mail: rafael.rivilla@uam.es

Robatzek, Silke
Univ of Basel
Botanical Inst
Hebelstrasse 1
Basel, 4056
SWITZERLAND
E-mail: s.robatzek@unibas.ch

Roine, Elina
Univ of Helsinki
Dept of Applied Biology
PO Box 27
Helsinki, FIN-00014
FINLAND
Tel: 358 9 1915 8545
Fax: 358 9 1915 8727
E-mail: elina.roine@helsinki.fi

Rolfe, Barry
Australian Natl Univ
PMI Group RSBS
GPO Box 475
Canberra, ACT 2601
AUSTRALIA
Tel: 61 6 6494054
Fax: 61 6 2490754
E-mail: rolfe@rsbs-central.anu.edu.au

Romantschuk, Martin
Univ of Helsinki
Ecological and Environmental Science
Niemenkatu 73
Lahti, 15140
FINLAND
Tel: 358 3 892 20334
Fax: 358 3 892 20331
E-mail: martin.romantschuk@helsinki.fi

Ronald, Pamela
Univ of California
1 Shields Ave - Plant Pathology Dept
348 Hutchinson Hall
Davis, CA 95616
Tel: (530) 752-1557
Fax: (530) 752-5674
E-mail: pcronald@ucdavis.edu

Rose, Jocelyn
Cornell Univ
Plant Biology Dept
347 Emerson Hall
Ithaca, NY 14853-4203
Tel: (607) 255-4781
Fax: (607) 255-5407
E-mail: jr286@cornell.edu

Rose, Ray
Univ of Newcastle
Biological Sciences
School of Env and Life Sciences
Newcastle, NSW 2308
AUSTRALIA
Tel: 61 2 4921 5711
Fax: 61 2 4921 6943
E-mail: ray.rose@newcastle.edu.au

S

Saarilahti, Hannu
Univ of Helsinki
Biocenter 2 - Genetics Division
PO Box 56
Helsinki, 00014
FINLAND
Tel: 358 9 708 59107
Fax: 358 9 708 59079
E-mail: hannu.saarilahti@helsinki.fi

San Francisco, Michael
Texas Tech Univ
Biological Sciences Dept
Flint and Main
Lubbock, TX 79409
Tel: (806) 742-2706
Fax: (806) 742-2963
E-mail: michael.sanfrancisco@ttu.edu

Sanchez-Contreras, Maria
John Innes Centre
Molecular Microbiology Dept
Norwich Research Park-Colney Lane
Norwich, Norfolk, NR4 7UH
UNITED KINGDOM
Tel: 44 1603 450 377
Fax: 44 1603 450 045
E-mail: maria.sanchez-contreras@bbsrc.ac.uk

Sano, Teruo
Hirosaki Univ
Bunkyo-Chou 3
Faculty of Agric and Life Sciences
Hirosaki, 036-8561
JAPAN
Tel: 81 172 39 3817
Fax: 81 172 39 3816
E-mail: sano@cc.hirosaki-u.ac.jp

Sassi, Giovanna
Cornell Univ
Plant Pathology Dept
236 Plant Science Building
Ithaca, NY 14850
Tel: (607) 273-6021
Fax: (607) 255-4471
E-mail: gs242@cornell.edu

Sautter, Christof
Inst of Plant Science
ETH-Zurich
Universitatsstrasse 2
Zurich, 8092
SWITZERLAND
Tel: 41 1 632 5713
Fax: 41 1 632 1044
E-mail: christof.sautter@ipw.biol.ethz.ch

Saville, Barry
Univ of Toronto
Erindale Campus - Botany Dept
3359 Mississauga Road N
Mississauga, ON L5L 1C6
CANADA
Tel: (905) 569-4702
Fax: (905) 828-3792
E-mail: bsaville@utm.utoronto.ca

Savka, Michael
Rochester Inst of Technology
Biological Sciences Dept
85 Lomb Memorial Dr - A350 Gosnell
Rochester, NY 14623
Tel: (585) 475-5141
E-mail: massbi@rit.edu

Schardl, Christopher
Univ of Kentucky
Plant Pathology Dept
201F Plant Science Bldg
Lexington, KY 40546-0312
Tel: (859) 257-7445x80730
Fax: (859) 323-1961
E-mail: schardl@uky.edu

Scheel, Dierk
Inst of Plant Biochemistry
Stress and Development Biology Dept
Weinberg 3
Halle (Salle), 06120
GERMANY
Tel: 49 345 5582 1400
Fax: 49 345 5582 1409
E-mail: dscheel@ipb-halle.de

Scherrer, Beatrice
Univ of Zurich
Inst for Plant Biology
Zollikerstrasse 107
Zurich, 8008
SWITZERLAND
Tel: 41 1 634 8231
Fax: 41 1 634 8204
E-mail: bea.scherrer@botinst.unizh.ch

Scofield, Steven
Purdue Univ
USDA ARS
915 West State Street
West Lafayette, IN 47907
Tel: (765) 494-3674
Fax: (765) 494-2926
E-mail: scofield@purdue.edu

Scott, Barry
Massey Univ
Inst of Molecular BioSciences
Private Bag 11-222
Palmerstown North,
NEW ZEALAND
Tel: 64 6 350 4033
Fax: 64 6 350 5688
E-mail: d.b.scott@massey.ac.nz

Scott, Paul
Univ of Queensland
School of Agriculture and Horticulture
Gatton, QLD 4343
AUSTRALIA
E-mail: p.scott@mailbox.uq.edu.au

Sela, Marianne
De Ruiter Zonen Seeds
Research Dept
Leeuwenhoekweg 52
Bergschenhoek, 2661 CZ
NETHERLANDS
Tel: 31 10 529 2222
Fax: 31 10 520 2410
E-mail: carla.schoonus@deruiterseeds.com

Sessa, Guido
Tel Aviv Univ
Plant Sciences Dept
Ramat Aviv
Tel Aviv, 69978
ISRAEL
Tel: 972 3 640 9766
Fax: 972 3 640 9380
E-mail: guidos@post.tau.ac.il

Shah, Jyoti
Kansas State Univ
Biology Dept
303 Ackert Hall
Manhattan, KS 66506
Tel: (785) 532-6360
Fax: (785) 532-6653
E-mail: shah@ksu.edu

Shapiro, Allan
Univ of Delaware
Delaware Biotechnology Inst
15 Innovation Way
Newark, DE 19711
Tel: (302) 831-4889
Fax: (302) 831-3409
E-mail: ashapiro@udel.edu

Sheen, Jen
Massachusetts General Hospital
Molecular Biology Dept
50 Blossom Street - Wellman 9
Boston, MA 01913
Tel: (617) 726-5978
Fax: (617) 726-6893
E-mail: sheen@molbio.mgh.harvard.edu

Sherrier, D. Janine
Univ of Delaware
Delaware Biotechnology Inst
15 Innovation Way - Room 129
Newark, DE 19711
Tel: (302) 831-3550
Fax: (302) 831-0605
E-mail: sherrier@udel.edu

Sherwood, John
Montana State Univ
Plant Sciences and Plant Path Dept
Bozeman, MT 59717-3150
Tel: (406) 994-5153
Fax: (406) 994-7600
E-mail: sherwood@montana.edu

Shibuya, Naoto
Meiji Univ
Life Sciences Dept
1-1-1 Higashi-Mita, Tama-ku
Kawasaki, Kanagawa, 214-8571
JAPAN
Tel: 81 44 934 7039
Fax: 81 44 934 7039
E-mail: shibuya@isc.meiji.ac.jp

Shimamoto, Ko
Nara Inst of Sci & Tech
8916-5, Takayama
Ikoma, Nara, 630-0101
JAPAN
Tel: 81 743 72 5501
Fax: 81 743 72 5502
E-mail: simamoto@bs.aist-nara.ac.jp

Shimizu, Bun-ichi
Kyoto Univ
Inst for Chemical Research
Gokasho
Uji, 611 011
JAPAN
Tel: 81 774 38 3232
Fax: 81 774 38 3229
E-mail: bun@biofun.kuicr.kyoto-u.ac.jp

Simmonds, Jeanette
Rensselaer Polytechnic Inst
Science and Technology Studies
110 Eighth Street, Sage Bldg 5508
Troy, NY 12180
Tel: (518) 271-6084
Fax: (518) 276-2659
E-mail: simmoj@rpi.edu

Singh, Karam
CSIRO Plant Industry
Private Bag #5
Wembley, WA, 6913
AUSTRALIA
Tel: 61 8 9333 6320
Fax: 61 8 9387 8991
E-mail: karam.singh@csiro.au

Singh, Pratibha
Univ of Arkansas
RREC - USDA ARS DBNRRC
2900 Hwy 130 E - Molecular Plant Path
Stuttgart, AR 72160
Tel: (870) 672-9300x279
Fax: (870) 673-4315
E-mail: singhpratibha@hotmail.com

Slusarenko, Alan
Inst fur Biologie III
Pflanzenenphysiologie
RWTH - Worringerweg 1
Aachen, 52074
GERMANY
Tel: 49 241 802 6650
Fax: 49 241 802 2395
E-mail: slusarenko@bio3.rwth-aachen.de

Smith, R. Stewart
Nitragin Inc
3101 W Custer Ave
Milwaukee, WI 53209-4827
Tel: (414) 462-7600
Fax: (414) 462-7186
E-mail: rss@liphatech.com

Smith, Sarah
Univ of Adelaide
Soil and Water Dept
Waite Campus
Glen Osmond, SA 5064
AUSTRALIA
Tel: 61 8 8303 6704
Fax: 61 8 8303 6511
E-mail: sally.smith@adelaide.edu.au

Somerville, Shauna
Carnegie Institute of Washington
Plant Biology Dept
260 Panama St
Stanford, CA 94305-4101
Tel: (650) 325-1521x257
Fax: (650) 325-6857
E-mail: shauna@andrew2.stanford.edu

Song, Pill-Soon
Kumho Petrochemical Co Ltd
572 Sang-Am-Dong
Kumho Life and Envir Science Lab
Kwangju, 506-712
SOUTH KOREA
Tel: 82 62 970 2630
Fax: 82 62 972 5085
E-mail: pssong@ksc.kumho.co.kr

Song, Wei
Capital Normal Univ
Biology Dept
105 Xi San Huan Bei Lu
Beijing, 100037
PEOPLES REP OF CHINA
Tel: 86 10 6898 0634
Fax: 86 10 6898 1191
E-mail: songwei@mail.cnu.edu.cn

Spaink, Herman
Leiden Univ
Postbus 9606
Leiden, 2300 AB
NETHERLANDS
Tel: 31 7 1527 5055
Fax: 31 7 1527 5088
E-mail: spaink@rulbim.leidenuniv.nl

Spanu, Pietro
Imperial College of Sci Tech & Medicine
Biological Sciences Dept
Imperial College Road
London, SW7 2AZ
UNITED KINGDOM
Tel: 44 2075 945 384
Fax: 44 2075 842 056
E-mail: p.spanu@ic.ac.uk

Stacey, Gary
Univ of Missouri
Plant Microbiology and Pathology Dept
108 Waters Hall
Columbia, MO 65211-6130
Tel: (573) 884-4752
Fax: (573) 882-0588
E-mail: staceyg@missouri.edu

Stahl, Dietmar
Planta GmbH
Grimsehlstr Strasse 31
Pf 1463
Einbeck, D-37555
GERMANY
Tel: 49 556 131 1735
Fax: 49 556 131 1243
E-mail: d.stahl@kws.de

Staneloni, Roberto
Inst De Investigaciones Bioquimicas
Fundacion Campomar
Av Patricias Argentinas 435
Buenos Aires, 1405
ARGENTINA
Tel: 54 11 4863 4011
Fax: 54 11 4865 2246
E-mail: rstaneloni@leloir.org.ar

Stougaard, Jens
Univ of Aarhus
Molecular and Structural Biology
Gustav Wieds Vej 10
Aarhus, 8000 C
DENMARK
Tel: 45 8 942 5011
Fax: 45 8 620 1222
E-mail: stougaard@mb.au.dk

Strange, Richard
Univ College London
Biology Dept
Gower Street
London, WC1E 6BT
UNITED KINGDOM
Tel: 44 171 380 7777
Fax: 44 171 380 7096
E-mail: r.strange@ucl.ac.uk

Subramanian, Senthil
Donald Danforth Plant Science Ctr
Yu Lab
975 North Warson Road
St Louis, MO 63132
Tel: (314) 587-1449
Fax: (314) 587-1549
E-mail: ssubramanian@danforthcenter.org

Sweigard, Jim
DuPont Experiment Station
PO Box 80402
Willmington, DE 19880-0402
Tel: (302) 695-2254
Fax: (302) 695-4509
E-mail: jim.sweigard@cgr.dupont.com

Syono, Kunihiko
Japan Women's Univ
2-8-1, Mejirodai
Bunkyo-ku
Tokyo, 112-8681
JAPAN
Tel: 81 3 5981 3669
Fax: 81 3 5981 3658
E-mail: syono@fc.jwu.ac.jp

T

Tamada, Tetsuo
Okayama Univ
Res Inst for Bioresources
Kurashiki, 710-0046
JAPAN
Tel: 81 86 434 1229
Fax: 81 86 434 1249
E-mail: ttamada@rib.okayama-u.ac.jp

Tans-Kersten, Julie
Univ of Wisconsin
Plant Pathology Dept
1630 Linden Dr
Madison, WI 53706-1598
Tel: (608) 265-2060
Fax: (608) 263-2626
E-mail: jtk@plantpath.wisc.edu

Terefework, Z.
Univ of Helsinki
Applied Chem and Micro Dept
PO Box 56 - Biocenter 1
Helsinki, 00014
FINLAND

Thines, Eckhard
Univ Kaiserslautern
Paul Ehrlich Strase 23
Kaiserslautern, 67663
GERMANY
Tel: 49 631 205 4294
Fax: 49 631 205 2999
E-mail: thines@ibwf.uni-fk.de

Thomashow, Linda
Washington State Univ
Plant Pathology Dept
USDA ARS
Pullman, WA 99164-6430
Tel: (509) 335-0930
Fax: (509) 335-7674
E-mail: thomasho@mail.wsu.edu

Tiffany, Michael
Agdia Inc
30380 County Road 6
Elkhart, IN 46514-9514
Tel: (219) 264-2014
Fax: (219) 264-2153
E-mail: miket@agdia.com

Ton, Jurriaan
Univ of Neuchatel
Biochemistry Dept - Inst of Botanique
Rue Emile-argand 9
Neuchatel, 2007
SWITZERLAND
Tel: 41 32 718 2223
Fax: 41 32 718 2201
E-mail: jurriaan.ton@unine.ch

Torrance, Lesley
Scottish Crop Research Inst
Plant-Pathogen Interactions Programme
Invergowrie
Dundee, DD2 5BX
UNITED KINGDOM
Tel: 44 1382 562 731
Fax: 44 1382 562 426
E-mail: ltorra@scri.sari.ac.uk

Tosa, Yukio
Kobe Univ
Faculty of Agriculture
Rokko-dai 1-1
Kobe, Hyogo, 657-8501
JAPAN
Tel: 81 78 803 5866
Fax: 81 78 803 5866
E-mail: tosayuki@kobe-u.ac.jp

Toth, Ian
Scottish Crop Research Inst
PPI Dept
Invergowrie
Dundee, DD2 5DA
UNITED KINGDOM
Tel: 44 1382 562 731
Fax: 44 1382 562 426
E-mail: itoth@scri.sari.ac.uk

Triplett, Eric
Univ of Florida
Microbiology and Cell Science Dept
1052 Museum Road
Gainesville, FL 32611
Tel: (352) 392-1906
Fax: (352) 392-5922
E-mail: ewt@ufl.edu

Truve, Erkki
Inst Chemical Physics & Biophysic
Akadeemia Tee 23
Tallinn, EE 12618
ESTONIA
Tel: 372 6 398 353
Fax: 372 6 398 382
E-mail: erkki@kbfi.ee

Tsitsigiannis, Dimitrios
Univ of Wisconsin
Plant Pathology Dept
1630 Linden Dr
Madison, WI 53706-1520
Tel: (608) 265-2060
Fax: (608) 263-2626
E-mail: dimtsi@plantpath.wisc.edu

Tsuge, Takashi
Nagoya Univ
Grad School of Bioagricultural Sciences
Biodynamics Div, Furo-cho, Chikusa
Nagoya, 464-8601
JAPAN
Tel: 81 52 789 4030
Fax: 81 52 789 4030
E-mail: ttsuge@agr.nagoya-u.ac.jp

Tsuyumu, Shinji
Shizuoka Univ
Faculty of Agriculture
836 Ohya
Shizuoka, 422-8529
JAPAN
Tel: 81 54 238 4823
Fax: 81 54 237 3028
E-mail: tsuyumu@agr.shizuoka.ac.jp

Tudzynski, Paul
Westfalische Wilhelms Univ
Inst fur Botanik
Schlossgarten 3
Muenster, 48149
GERMANY
Tel: 49 251 832 4998
Fax: 49 251 832 1601
E-mail: tudzyns@uni-muenster.de

Turgeon, B. Gillian
Cornell Univ
Plant Pathology Dept
334 Plant Science Building
Ithaca, NY 14853-5904
Tel: (607) 254-7458
Fax: (607) 255-4471
E-mail: bgt1@cornell.edu

Tuzun, Sadik
Auburn Univ
Entomology and Plant Pathology Dept
209 Life Sciences Building
Auburn, AL 36849
Tel: (334) 844-1997
Fax: (334) 844-1947
E-mail: stuzun@acesag.auburn.edu

U

Uchiumi, Toshiki
Kagoshima Univ
Chemistry and Bioscience Dept
1-21-34, Korimoto
Kagoshima, 890-0065
JAPAN
Tel: 81 99 285 8164
Fax: 81 99 285 8163
E-mail: uttan@sci.kagoshima-u.ac.jp

Udvardi, Michael
Max Planck Inst
Molecular Plant Physiology Dept
AM Muhlenberg 1
Golm, 14476
GERMANY
Tel: 49 331 567 8149
Fax: 49 331 567 8250
E-mail: udvardi@mpimp-golm.mpg.de

Ugalde, Rodolfo
Univ of San Martin
Inst De Investigaciones Biotecnologicas
Av Colectora General Paz 5445
San Martin, BA 1650
ARGENTINA
Tel: 54 11 4580 7255
Fax: 54 11 4752 9639
E-mail: rugalde@iib.unsam.edu.ar

Uppalapati, Srinivasa
Oklahoma State Univ
Entomology and Plant Pathology Dept
127 Noble Research Center
Stillwater, OK 74078-0001
Tel: (405) 744-8268
Fax: (405) 744-7373
E-mail: uppalap@okstate.edu

V

Valkonen, Jari
Univ of Helsinki
Plant Path Lab - Applied Biology Dept
PO Box 27 - Latokartanonkaari 7
Helsinki, 00014
FINLAND
Tel: 358 9 191 58387
Fax: 358 9 191 58727
E-mail: jari.valkonen@helsinki.fi

Van Alfen, Neal
Univ of California
CAES Deans Office
1 Shields Ave 150 Mark Hall
Davis, CA 95616-8571
Tel: (530) 752-1605
Fax: (530) 752-9049
E-mail: nkvanalfen@ucdavis.edu

Van Brussel, Anton
Leiden Univ
Inst Molecular Plant Sciences
Clusius Lab - 64 Wassenaarseweg
Leiden, 2333 AL
NETHERLANDS
Tel: 31 71 527 5068
Fax: 31 71 527 5088
E-mail: brussel@rulbim.leidenuniv.nl

Van Den Ackerveken, Guido
Utrecht Univ
Molecular Cell Biology Dept
Padualaan 8 - PO Box 80 056
Utrecht, 3508 TB
NETHERLANDS
Tel: 31 30 253 3013
Fax: 31 30 251 3655
E-mail: g.vandenackerveken@bio.uu.nl

Van Gijsegem, Frederique
Laboratoire De Pathologie Vegetale
INRA INA-PG
16 Rue Claude Bernard
Paris, 75231
FRANCE
Tel: 33 1 4408 7259
Fax: 33 1 4408 1631
E-mail: vangijse@inapg.fr

Van Kan, Jan
Wageningen Univ
Phytopathology Dept
PO Box 8025
Wageningen, 6700 EE
NETHERLANDS
Tel: 31 317483126
Fax: 31 317483412
E-mail: jan.vankan@wur.nl

Van Loon, Leendert
Utrecht Univ
Section Phytopathology
PO Box 800 84
Utrecht, NL-3508 TB
NETHERLANDS
Tel: 31 302536700
Fax: 31 302518366
E-mail: l.c.vanloon@bio.uu.nl

Van West, Pieter
Univ of Aberdeen
Inst of Medical Science
Mol/Cell Biology - Foresterhill
Aberdeen, AB25-2ZD
UNITED KINGDOM
Tel: 44 1224 273023
Fax: 44 1224 273144
E-mail: p.vanwest@abdn.ac.uk

VanEtten, Hans
Univ of Arizona
Plant Pathology Dept
PO Box 210036 - Room 204
Tucson, AZ 85721-0036
Tel: (520) 621-9355
Fax: (520) 621-9290
E-mail: vanetten@ag.arizona.edu

Vanneste, Joel
Ruakura Research Centre
Hort Research
Private Bag 3123
Hamilton,
NEW ZEALAND
Tel: 64 7 858 4781
Fax: 64 7 858 4701
E-mail: jvanneste@hortresearch.co.nz

Vasanthakumar, Archana
Univ of Wisconsin
Plant Pathology Dept
1630 Linden Dr - Russell Labs
Madison, WI 53706-1598
Tel: (608) 263-2093
Fax: (608) 263-2626
E-mail: ava@plantpath.wisc.edu

Verchot Lubicz, Jeanmarie
Oklahoma State Univ
Plant Pathology Dept
110 Noble Research Center - Rm 127
Stillwater, OK 74078-0001
Tel: (405) 744-7895
Fax: (405) 744-6039
E-mail: verchot@okstate.edu

Verdier-Michel, Valerie
Univ De Perpignan
Lab Genome Development Des Plantes
52 Ave De Villeneuve
Perpignan, 66430
FRANCE
Tel: 33 468 661 774
Fax: 33 468 668 499
E-mail: vverdier@univ-perp.fr

Vereecke, Danny
University of Gent
Lab of Plant Genetics
K L Ledeganckstraat 35
Gent, 9000
BELGIUM
Tel: 32 9 264 5267
Fax: 32 9 264 5349
E-mail: danny.vereecke@psb.ugent.be

Vernooij, Bernard
Syngenta Biotechnology Inc
PO Box 12257
3054 Cornwallis Road
Durham, NC 27709-2257
Tel: (919) 541-8562
Fax: (919) 541-8557
E-mail: bernard.vernooij@syngenta.com

Veronese, Paola
Purdue Univ
Botany and Plant Pathology Dept
1155 Lilly Hall - 915 W State Street
West Lafayette, IN 47907-2054
Tel: (765) 494-9880
Fax: (765) 494-0363
E-mail: veronese@purdue.edu

Vinatzer, Boris
Univ of Chicago
MGCB - EBC 409
1103 East 57th Street
Chicago, IL 60637
Tel: (773) 834-1906
Fax: (773) 702-9270
E-mail: bavinatz@midway.uchicago.edu

Vleeshouwers, Vivianne
Wageningen Univ
Lab of Plant Breeding
Binnenhaven 5 - PO Box 386
Wageningen, 6709 PD
NETHERLANDS
Tel: 31 317 484 157
Fax: 31 317 483 457
E-mail: vivianne.vleeshouwers@pv.dpw.wag-ur.nl

Voegele, Ralf
Univ of Konstanz
Phytopathologie
Universit 10
Konstanz, 78457
GERMANY
Tel: 49 7531 882 356
Fax: 49 7531 883 035
E-mail: ralf.voegele@uni-konstanz.de

Vorholt, Julia
INRA
Lab Des Interactions Plantes-microrg
BP 27
Castanet Tolosan, 31326
FRANCE
Tel: 33 561 285 458
Fax: 33 561 285 061
E-mail: vorholt@toulouse.inra.fr

Vossen, Jack
Univ of Amsterdam
Plant Pathology Dept
Kruislaan 318
Amsterdam, 1090 GB
NETHERLANDS
Tel: 31 20 525 7839
Fax: 31 20 525 7934
E-mail: vossen@science.uva.nl

Walter, Christian
NZ Forest Research Institute
Sala Street
Rotorua,
NEW ZEALAND
Tel: 64 7 343 5444
Fax: 64 7 343 5453
E-mail: christian.walter@forestresearch.co.nz

W

Walton, Jonathan
Michigan State Univ
DOE - Plant Research Lab
East Lansing, MI 48824
Tel: (517) 353-4885
Fax: (517) 353-9168
E-mail: walton@msu.edu

Wang, Chunxia
Virginia Tech
Virginia Bioinformatics Inst
Washington Street (0477)
Blacksburg, VA 24061-0331
Tel: (540) 231-1958
Fax: (540) 231-1678
E-mail: cwang@vbi.vt.edu

Wanner, Leslie
USDA ARS
Rm 226, Bldg 010A, BARC-West
10300 Baltimore Ave
Beltsville, MD 20705
Tel: (301) 504-5953
Fax: (301) 504-5555
E-mail: wannerl@ba.ars.usda.gov

Wegener, Christina
Federal Centre for Breeding Research
Rudolf Schick Platz 3
Gross Lusewitz, 18190
GERMANY
Tel: 49 382 094 5211
Fax: 49 382 094 5120
E-mail: c.wegener@bafz.de

Wei, Jun-zhi
Verdia Inc
200 Penobscot Dr
Redwood City, CA 94063
Tel: (650) 980-5661
Fax: (650) 298-5812
E-mail: jun-zhi.wei@verdiainc.com

Weller, Jennifer
8549 Braxted Lane
Manassas, VA 20110-4575
Tel: (540) 231-9948
Fax: (540) 231-2606

Whalen, Maureen
San Francisco State Univ
Biology Dept
1600 Holloway Ave
San Francisco, CA 94132-1722
Tel: (415) 338-6475
Fax: (415) 338-0927
E-mail: whalen@sfsu.edu

Whisson, Stephen
Scottish Crop Research Inst
PPI Dept
Invergowrie
Dundee, DD2 5DA
UNITED KINGDOM
Tel: 44 1382 562 731
Fax: 44 1382 562 426
E-mail: swhiss@scri.sari.ac.uk

Whitham, Steven
Iowa State Univ
Plant Pathology Dept
351 Bessey Hall
Ames, IA 50011-1020
Tel: (515) 294-4952
Fax: (515) 294-9420
E-mail: swhitham@iastate.edu

Wildermuth, Mary
Univ of California
Plant and Microbial Biology
221 Koshland #3102
Berkeley, CA 94720-3102
Tel: (510) 643-4861
Fax: (510) 642-4995
E-mail: wildermuth@nature.berkeley.edu

Wilhelm, Eva
Austrian Research Center Siebersdorf
Biotechnology Dept
Seibersdorf, A-2444
SWITZERLAND
Tel: 43 50 550 3621
Fax: 43 50 550 3444
E-mail: eva.wilhelm@arcs.ac.at

Williamson, Valerie
Univ of California
Nematology Dept
One Shields Ave
Davis, CA 95616
Tel: (530) 752-3502
Fax: (530) 752-5809
E-mail: vmwilliamson@ucdavis.edu

Winston, Eugenia
USDA ARS DB NRRC
2890 Hwy 130 East
PO Box 1090
Stuttgart, AR 72160
Tel: (870) 672-9300x238
Fax: (870) 673-7581
E-mail: jenes1s@yahoo.com

Wise, Roger
Iowa State Univ
USDA ARS - Plant Pathology Dept
411 Bessey Hall
Ames, IA 50011-1020
Tel: (515) 294-9756
Fax: (515) 294-9420
E-mail: rpwise@iastate.edu

Wobbe, Kristin
Worcester Polytechnic Inst
Chemistry and Biochemistry Dept
100 Institute Road
Worcester, MA 01609-2247
Tel: (508) 831-5375
Fax: (508) 831-5933
E-mail: kwobbe@wpi.edu

Wright, Sandra
Goteborg Univ
Cellular and Molecular Biology Dept
Box 462
Goteborg, 405 30
SWEDEN
Tel: 46 31 773 3801
Fax: 46 31 773 3895
E-mail: sandra.wright@molbio.gu.se

Wu, Changjian
Univ of Delaware
Delaware Biotechnology Inst
Newark, DE 19711
Tel: (302) 831-6168
Fax: (302) 831-6170
E-mail: cwu@udel.edu

Wu, Sheng-Cheng
Univ of Georgia
220 Riverbend Road
Complex Carbohydrate Res Ctr
Athens, GA 30602-4712
Tel: (706) 542-4446
Fax: (706) 542-4412
E-mail: wusc@ccrc.uga.edu

X

Xue, Chaoyang
Purdue Univ
Botany and Plant Pathology Dept
1155 Lilly Hall
West Lafayette, IN 47907-1155
Tel: (765) 496-7496
Fax: (765) 494-5896
E-mail: xuec@purdue.edu

Y

Yalpani, Nasser
Pioneer Hi-Bred Intl
7250 NW 62nd Ave
PO Box 552
Johnston, IA 50131-0552
Tel: (515) 270-4391
Fax: (515) 253-2149
E-mail: nasser.yalpani@pioneer.com

Yamakawa, Takeo
Kyushu Univ
Agricultural Chemistry Dept
Hakozaki, Higashi-Ku
Fukuoka, 812-8581
JAPAN
Tel: 81 92 642 2847
Fax: 81 92 642 2864
E-mail: yamakawa@agr.kyushu-u.ac.jp

Yamamoto, Mikihiro
Okayama Univ
Faculty of Agric
1-1-1 Tsushima-naka
Okayama, 700-8530
JAPAN
Tel: 81 86 251 8301
Fax: 81 86 251 8301
E-mail: myama@cc.okayama-u.ac.jp

Yasmin, Ruksana
Kings College London
Life Sciences Dept - 150 Stamford St
Franklin-Wilkins Bldg
London, SE1 8WA
UNITED KINGDOM
Tel: 44 7789 011528
E-mail: ruksanayasmin@hotmail.com

Yoshioka, Hirofumi
Nagoya Univ
Grad School of Bioagricultural Sciences
Furo-cho, Chikusa
Nagoya, Aichi, 464-8601
JAPAN
Tel: 81 52 789 4283
Fax: 81 52 789 5525
E-mail: hyoshiok@agr.nagoya-u.ac.jp

Z

Zhang, Yan
Samuel Roberts Noble Foundation
Forage Biotechnology Group
2510 Sam Noble Pkwy
Ardmore, OK 73401
Tel: (580) 224-6841
Fax: (580) 224-6802
E-mail: yzhang@noble.org

Zhao, Bingyu
Kansas State Univ
Plant Science Ctr - Plant Path Dept
4024 Throckmorton Hall
Manhattan, KS 66506-5502
Tel: (785) 532-2328
Fax: (785) 532-5692
E-mail: bzhao@ksu.edu

Zhou, Jian-Min
Kansas State Univ
Plant Pathology Dept
4024 Throckmorton Hall
Manhattan, KS 66506-5502
Tel: (785) 532-2415
Fax: (785) 532-5692
E-mail: jzhou@plantpath.ksu.edu

Zhou, Lecong
VPI & State Univ
Virginia Bioinformatics Inst
Blacksburg, VA 24061-0447
Tel: (540) 231-5664
Fax: (540) 231-2606
E-mail: lzhou@vbi.vt.edu