

Department of Plant Pathology

**The Biennial
Nusbaum Conference**

*Linking Genomic Advances
to the Understanding and Management
of Plant Disease:
Research Priorities for the Coming Decade*

**An Introduction to the
Invited Speakers**

(In Order of Appearance)

Douglas R. Cook

University of California - Davis; Department of Plant Pathology. Professor and Faculty Director of the College of Agricultural and Environmental Sciences Genomics Facility

Ph.D. University of Wisconsin-Madison (1990-Plant Pathology)

B.S. Santa Clara University (1982-Biological Sciences)

Dr. Cook's research involves the biology and mechanisms of symbiotic nitrogen fixation in legumes and the development of genomic platforms in plant species, particularly legumes and grapes. His laboratory works with the legume species *Medicago truncatula* and its symbiotic partner *Sinorhizobium meliloti*, and the grape species *Vitis vinifera* and its bacterial pathogen *Xylella fastidiosa*.

The first area of interest involves structural and comparative genomics of legumes. Dr. Cook's lab is using the annual legume, *Medicago truncatula*, as a model for genome structure throughout the Papilionoid legumes. His projects include determining the genomic architecture of resistance gene homologs, developing a sequence-based genetic map of *Medicago truncatula*, and examining a conserved genome structure across the Papilionoideae by means of comparative mapping and phylogenetic methods. He currently has a NSF funded project that aims to develop a complete physical map for this species. The physical map is serving as the basis of an international effort to segment the gene space of *Medicago truncatula*.

Dr. Cook is also involved in the genetic and molecular characterization of plant genes that regulate associations with symbiotic and pathogenic microorganisms. His laboratory is currently examining the genetic characterization and map-based cloning of plant genes that regulate infection by symbionts and/or pathogens, as well as, the mechanistic overlaps between genetic programs for plant development and interactions with the symbionts and pathogens. In particular, they have cloned plant genes that function to transduce exogenous bacterial signals and endogenous hormonal cues.

Finally, Dr. Cook's lab is involved with characterizing transcriptional pathways in *Vitis vinifera* (grape) that are either correlated with infection by the bacterial pathogen *Xylella fastidiosa*, or influenced by viticultural practices. The projects in this area include EST sequencing, bioinformatics and microarray expression analysis.

Representative Publications:

1. Riely, B.K., Ané, J.M., Penmetsa, R.V., and Cook, D.R. (2004) Genetic and genomic analysis in model legume systems bring Nod factor signaling to center stage. *Current Opinion in Plant Biology* (in press).
2. Choi, H.K., Kim, D., Uhm, T., Limpens, E., Lim, H., Kalo, P., Penmetsa, R.V., Seres, A., Kulikova, O., Bisseling, T., Kiss, G.B., and Cook, D.R. (2004). A Sequence-based Genetic Map of *Medicago truncatula* and comparison of marker co-linearity with *Medicago sativa*. *Genetics* Vol. 166: 1463-1502.
3. Jean-Michel Ané, György B. Kiss, Brendan K. Riely, R. Varma Penmetsa, Giles E. D. Oldroyd, Céline Ayax, Julien Lévy, Frédéric Debellé, Jong-Min Baek, Peter Kalo, Charles Rosenberg, Bruce A. Roe, Sharon R. Long, Jean Dénarié, and Douglas R. Cook (2004). *Medicago truncatula* DMI1 required for bacterial and fungal symbioses in legumes. *Science*, 303:1364-1367.

Georgiana May

University of Minnesota; Department of Ecology, Evolution, and Behavior. Associate Professor.

Ph.D. University of California - Berkeley, 1987

Dr. May's lab studies the genetic and molecular basis of plants' evolutionary interactions with other organisms, with an emphasis on fungi. Her research interests are the evolution of host/microbe interactions, molecular evolution and genome organization of plant resistance to pathogens, as well as fungal population genetics. Some of her projects include the evolutionary interactions between corn and smut fungus, evolution of resistance genes, and the role of genome rearrangement in pathogenesis. In her work, Dr. May's lab uses both field and laboratory techniques such as experiments in systematics, genetics, and molecular biology. Additionally, Dr. May and her students are actively involved with Community Genetics, an interdisciplinary research group. The goal of this group is to investigate the role of genetic variation in influencing species interactions and determining community structure. In addition, she was awarded research money from the University of California, Berkeley, for "Development of Tools for Potato Functional Genomics" and she is part of a group awarded a five-year National Science Foundation award for "Biocomplexity - Evolution and Ecology of Perturbed Interactions: Modeling Disequilibria in Time and Space".

Representative Publications:

1. Natvig, D.O., and May, G. 1998. Invited Review: Fungal evolution and speciation. *J. Genetics* 75:441-452
2. May, G., Shaw, F., Badrane, H. and Vekemans, X. 1999. The signature of balancing selection: fungal mating genes. *Proc. Natl. Acad. Sci.* 96: 9172-9177
3. May, G. and Munkasci, A. 2000. Recombination, rearrangement and selection, common themes in the evolution of self recognition genes. submitted to *Heredity*

Michael Milgroom

Cornell University; Department of Plant Pathology. Professor.

Ph. D. Cornell University, 1987

M.S. University of Michigan, 1982

B.A. University of Vermont, 1978

Dr. Milgroom's research program is directed towards understanding the population biology and evolution of plant pathogens, and bridging the fields of population biology and plant disease epidemiology. His specific research interests fall into three areas:

- Population biology of fungal viruses and their transmission in fungal populations
- Evolution of fungal mating systems
- Evolution of virulence

The majority of Dr. Milgroom's research has been on the chestnut blight fungus, *Cryphonectria parasitica*, and biological control with hypovirulence, caused by double-stranded RNA hypoviruses. Studies on the dynamics of virus transmission in fungal populations has required a comprehensive knowledge of the genetics of vegetative incompatibility and the population biology and mating system of the fungus, as well as the population genetics of hypoviruses. Recently, Dr. Milgroom's program has begun research on the evolution of virulence in plant viruses.

Representative Publications:

1. Carbone, I., Liu, Y.-C., Hillman, B.I., and Milgroom, M.G. 2004. Recombination and migration of *Cryphonectria hypovirus 1* as inferred from gene genealogies and the coalescent. *Genetics* (in press)
2. Jiménez-Gasco, M.M., Milgroom, M.G., and Jiménez-Díaz, R.M. 2004. Stepwise evolution of races in a plant pathogenic fungus inferred from fingerprinting with repetitive DNA sequences. *Phytopathology* 94:228-235.
3. McGuire, I.C., Marra, R.E., and Milgroom, M.G. 2004. Mating-type heterokaryosis and selfing in *Cryphonectria parasitica*. *Fung. Genet. Biol.* 41:521-533.

Christopher L. Schardl

University of Kentucky; Department of Plant Pathology. Professor. Harry E. Wheeler Chair in Plant Mycology. Director of the University of Kentucky Advanced Genetic Technologies Center.

Ph.D. University of California – Davis, 1983.

B.S. Cornell University, 1978

Dr. Schardl is involved in many research projects funded by the NSF, USDA and United States Aid and International Development including:

- Molecular biology and biosynthesis of lolines by grass endophytes. MCB/IBN-0213217, C.L. Schardl, R.B. Grossman and L.P. Bush
- A multidisciplinary test of mutualistic benefits fungal endophytes provide their host plants. NSF DBI-0330840, T.L. Bultman et alii (Hope College, Holland, MI)
- Toxin biosynthesis genes in ergopeptine-producing fungi. USDA National Research Initiative (NRI) 2001-35319-10930, D.G. Panaccione and C.L. Schardl
- Deletion of ergot alkaloid production genes in a tall fescue endophyte. USDA-Agricultural Research Service Specific Cooperative Agreement, C.L. Schardl and T.D. Phillips
- Pierce's disease of grapes caused by *Xylella fastidiosa*: a survey for the pathogen, identification of reservoir hosts, and identification of insect vectors in Kentucky vineyards. Subcontract 42405-6995 for USDA-CSREES Eastern Grape Consortium, J.R. Hartman et alii
- Extraction and identification of antimycotic compounds from *Acremonium implicatum* infected *Brachiaria* grasses. Collaboration with Centro Internacional de Agricultura Tropical, Colombia. 200308081413, S. Kelemu and C.L. Schardl

Representative Publications:

1. Schardl, C.L., Leuchtman, A., and Spiering, M.J. 2004. Symbioses of grasses with seedborne fungal endophytes. *Annual Review of Plant Biology* 55: 315–340.
2. Schardl, C.L., and Craven, K.D. 2003. Interspecific hybridization in plant-associated fungi and oomycetes: a review. *Molecular Ecology* 12: 2861–2873.
3. Schardl, C.L. 2001. *Epichloë festucae* and related mutualistic symbionts of grasses. *Fungal Genetics & Biology* 33: 69-82.

Howard Judelson

University of California, Riverside; Department of Plant Pathology. Associate Professor.

Ph.D. University of Wisconsin – Madison, 1985.

B.S. Cornell University, 1980.

Dr. Judelson's research focuses on the characterization of the genetics, developmental biology, and pathology of oomycete fungi, particularly those within the genus *Phytophthora* and with special emphasis on *Phytophthora infestans*, which causes the late blight diseases of tomato and potato.

His program employs multidisciplinary techniques and incorporates the tools of molecular and classical genetics, biochemistry, genomics, and bioinformatics. Specific research projects involve asexual sporulation and germination, promoter analysis in transcriptional networks, mating and sexual sporulation, plant pathogenesis, fungicide resistance, the role of retroelements in genome evolution, development of advanced genetic transformation procedures, and the genomics of *P. infestans*. In the long term, his work will lead to a greater understanding of the oomycetes and strategies for their control.

Representative Publications:

1. Judelson, H.S., and Roberts, S. (2002) Novel protein kinase induced during sporangial cleavage in the oomycete *Phytophthora infestans*. *Eukaryotic Cell* 1, 687-695.
2. Judelson, H.S., and Tooley, P.W. (2000) Enhanced polymerase chain reaction methods for detecting and quantifying *Phytophthora infestans* in plants. *Phytopathology*. 90, 1112-1119.
3. Judelson, H.S., and Yang, G. (1998) Recombination pathways in *Phytophthora infestans*: polyploidy resulting from aberrant sexual development and zoospore-mediated heterokaryosis. *Mycological Reports* 102, 1245-1253.

Dr. Bart Fraaije

Rothamsted Research, Harpenden, UK; Plant Pathogen Interactions (PPI) Division. Project Leader of the Fungicide Resistance Group.

Ph.D. Wageningen University

Dr. Fraaije's current research involves the diagnostics of fungal cereal pathogens and evolution of fungicide resistance. The main pathogens he is working on are *Mycosphaerella graminicola* in wheat, *Rhynchosporium secalis* in barley and powdery mildews (*Blumeria graminis*) in both wheat and barley.

Representative Publications:

1. Ward E., Foster S.J., Fraaije B.A., McCartney, H.A. 2004. Plant pathogen diagnostics: immunological and nucleic acid-based approaches. *Annals of Applied Biology* 145(1):1-16.
2. Fraaije B.A., Lucas J.A., Clark W.S., Burnett F.J. 2003. QoI resistance development in populations of cereal pathogens in the UK. *Proceedings of the BCPC International Congress 2003*. 2, 689-694.
3. Fraaije, B.A.; Burnett, F.J.; Clark, W.S.; Motteram, J.; Lucas, J.A. (2003). Resistance development to QoI inhibitors in populations of *Mycosphaerella graminicola* in the UK. *Reinhardtsbrunn Conference* (in press).
4. McCartney H.A., Foster S.J., Fraaije B.A., Ward E. 2003. Molecular diagnostics for fungal plant pathogens. *Pest Management Science* 59(2):129-142.
5. Rohel E.A., Laurent P., Fraaije B.A., Caelier N. and Hollomon D.W. 2002. Quantitative PCR monitoring of the effect of azoxystrobin treatments on *Mycosphaerella graminicola* epidemics in the field. *Pest Management Science* 58(3):248-254.
6. Fraaije B.A., Butters J.A., Coelho J.M., Jones D.R., Hollomon, D.W. 2002. Following the dynamics of strobilurin resistance in *Blumeria graminis* f. sp. *tritici* using quantitative allele-specific real-time PCR measurements with the fluorescent dye SYBR Green I. *Plant Pathology* 51(1):45-54.

James R. Alfano

University of Nebraska at Lincoln; The Plant Science Initiative and the Department of Plant Pathology, Associate Professor

Ph.D. Washington State University, 1993

B.S. San Diego State University, 1986

Research interests in the Alfano laboratory are focused on understanding how bacterial pathogens cause disease in plants and how their strategies differ from the strategies employed by bacterial pathogens of animals. The primary focus is on understanding a specialized protein secretion apparatus, called the type III secretion system, present in gram-negative bacterial pathogens of plants and animals. Type III systems secrete multiple virulence proteins, some of which are transferred directly into eukaryotic cells in a contact-dependent manner. Acquisition of a type III secretion system appears to be a key adaptation that allowed many gram-negative bacteria to become pathogens – mutants with a disabled type III system are essentially nonpathogenic.

The Alfano research group studies the type III secretion system present in the bacterial plant pathogen, *Pseudomonas syringae*. *P. syringae* is a leaf spotting pathogen whose various strains display host specificity. Different strains are only capable of causing disease in certain plants. The lab studies the interactions of *P. syringae* with such crop plants as tobacco, soybeans, and tomato, as well as the interactions of *P. syringae* with the genetically amenable plant *Arabidopsis*. Studying the interaction of *P. syringae* and *Arabidopsis* is particularly attractive because it allows a relatively easy identification of key molecular attributes of both the pathogen and the host with the long-term goal of understanding the intimacies involved in bacterial parasitism.

Representative Publications:

1. Petnicki-Ocwieja, T., K. van Dijk, and J.R. Alfano. The hrpK operon of *Pseudomonas syringae* pv. tomato DC3000 encodes two proteins secreted by the type III (Hrp) protein secretion system: HopB1 and HrpK, a putative type III translocator. 2005. *J. Bacteriol.* 187: 649-663.
2. Espinosa, A., and J.R. Alfano. 2004. Disabling surveillance: Bacterial type III secretion system effectors that suppress innate immunity. *Cell. Microbiol.* 6: 1027-1040.
3. Alfano, J.R., and A. Collmer. 2004. Type III secretion system effector proteins: Double agents in bacterial disease and plant defense. *Annu. Rev. Phytopathol.* 42:385-414.

Rytas J Vilgalys

Duke University; Department Biology. Professor and Director of Mycology Lab.

Ph.D. Virginia Polytechnic Institute and State University, 1985

Dr. Vilgalys' research program uses the techniques of molecular biology as well as more conventional approaches (culturing, mating studies, etc.) to answer questions about the natural history of fungi. Current research is focused on three areas:

- Fungal diversity, including systematics and evolution of early basal lineages in Fungi
- Genetics of speciation, including evolution of incompatibility systems that control mating in mushrooms, or otherwise contribute to origin of species.
- Population biology of fungi, estimation of breeding systems and measurement of gene flow in fungal populations.
Fungi currently under investigation include the oyster mushroom (*Pleurotus ostreatus*) as well as several species of medically important fungi (*Candida albicans* and *Cryptococcus neoformans*)

Phylogeny: The major research effort in our laboratory for the last 10 years is still aimed at understanding molecular evolution of ribosomal RNA genes in fungi, and their use for estimating evolutionary relationships of the higher *Basidiomycotina*. We are presently surveying rDNA sequence variation from various families of the Agaricales (mushrooms) and related fungi.

Population Biology: Unique features of fungal life history have profound relevance for their population biology. We have been investigating the significance of mating systems and life history for determining genetic structure using molecular markers, both in wild mushroom species (*Pleurotus ostreatus* and *Schizophyllum commune*) as well as in several human pathogenic fungi (*Candida albicans* and *Cryptococcus neoformans*), in collaboration with Dr. Thomas G. Mitchell of the Duke University Medical Center). A variety of approaches and markers are being employed to address questions ranging from how far do spores disperse, to how much clonality vs recombination occurs in natural populations.

Representative Publications:

1. S Diezmann, CJ Cox, G Schenck, R Vilgalys, TG Mitchell, *Phylogeny and evolution of medical species of Candida and related taxa: a multigenic analysis.*, J Clin Microbiol, United States, vol. 42 no. 12 (December, 2004), pp. 5624-35 [abs].
2. R Yahr, R Vilgalys, PT Depriest, *Strong fungal specificity and selectivity for algal symbionts in Florida scrub Cladonia lichens.*, Mol Ecol, England, vol. 13 no. 11 (November, 2004), pp. 3367-78 [abs].
3. TY James, SR Liou, R Vilgalys, *The genetic structure and diversity of the A and B mating-type genes from the tropical oyster mushroom, Pleurotus djamor.*, Fungal Genet Biol, United States, vol. 41 no. 8 (August, 2004), pp. 813-25 [abs].

Ignazio Carbone

North Carolina State University; Department of Plant Pathology. Assistant Professor.

Ph.D. University of Toronto, 2000

M.Sc. University of Toronto, 1994

B.Sc. University of Toronto, 1992

Dr. Carbone's primary research interest is fungal evolution. His interdisciplinary research is involved in evolution of fungal secondary metabolism, evolutionary population genetics, development of integrative evolutionary software tools, bioinformatics, phylogeography, and systematics (especially fungi). An important aspect is to develop new methodologies and tools to examine the influence of mutation, recombination, gene flow, selection and demography on the evolution of fungal genomes, populations and species

His laboratory is examining the evolution of fungal secondary metabolism in sterigmatocystin (ST), O-methylsterigmatocystin (OMST) and aflatoxin (AF) biosynthetic pathways in *Aspergillus*. The genes are clustered and the compounds are synthesized by numerous ascomycetes, but the biological and evolutionary significance in fungi is unknown. Through macro- and micro-evolutionary analyses he is trying to understand the conservation of these metabolites in *Aspergillus* species and how diversity is generated and maintained within species over time.

Dr. Carbone has also developed new methodologies and tools for integrating genetic and phenotypic data within an evolutionary framework and has recently released a workbench tool that manages a series of population genetic programs. This workbench provides a framework for integrating summary statistic and population genetic models to enhance inferences of population processes. Currently, his laboratory is developing tutorials for the workbench for teaching and training.

Representative Publications:

1. Price, E. W. and I. Carbone. 2004. SNAP: Workbench management tool for evolutionary population genetic analysis. Bioinformatics, Advance Access published on September 7, 2004; doi: 10.1093/bioinformatics/bti003)
2. Carbone, I., Y. Liu, B. I. Hillman and M. G. Milgroom. 2004. Recombination and migration of *Cryphonectria hypovirus 1* as inferred from gene genealogies and the coalescent. Genetics 166, 1611-1629
3. Carbone, I. and L. M. Kohn. 2001b. Multilocus nested haplotype networks extended with DNA fingerprints show common origin and fine-scale, ongoing genetic divergence in a wild microbial metapopulation. Molecular Ecology 10: 2409-2422.