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Review

2003 Asilomar meeting report

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In March of 2003, nearly 800 biologists came from all over the world to the Asilomar Conference Grounds in Pacific Grove, California to attend the XXII Fungal Genetics Conference, organized by the Genetics Society of America. The Fungal Genetics Conferences were initiated by the *Neurospora* community over 40 years ago, when the focus was primarily on classical genetics. It now encompasses work on a tremendously diverse array of fungi, many of which have attracted attention because of their ecological or economic importance. *Neurospora crassa* was long a work-horse for classical geneticists, not least because it is amenable to ordered tetrad analysis and so is ideal for studies of Mendelian inheritance. Since then, quantum leaps in science have taken the fungal community through molecular genetics and fungal transformation and into the genomics and post-genomics era. It is fitting that one of the highlights of the XXII Fungal Genetics Conference was the formal unveiling of the full sequence of the *N. crassa* genome in a talk given by Bruce Birren from the Whitehead Institute, Cambridge, MA. Many exciting findings are emerging as a result of the availability of the complete genome sequence of this fungus (Galagan et al., 2003. Nature 422, 859–868), and it is clear that many more revelations are likely to emerge as an increasing amount of activity is focused on exploiting the output of the genome sequencing.

In all of this, it is important to remember that classical genetics still has a lot to offer for modern-day fungal biology. This was elegantly demonstrated by Bob Metzenberg's talk, "Listening to Silenced Genes," which was a magnificent exposition of the role that observation, logic and pure genetics can still play in our genomics-dominated age. Metzenberg and colleagues showed that *N. crassa* genes that are unpaired during meiosis are silenced by a novel mechanism in which single stranded RNA is implicated. Candidates for other components of this pathway (known as meiotic silencing by unpaired DNA, or MSUD) have been identified based on sequence relatedness to other known RNA silencing components, initially by surveying the *N. crassa* genome sequence. Integrated approaches that combine the many tools that are available to fungal biologists (such as biochemistry, cytology, classical genetics, molecular biology, genome mining, and other genomics-related activities) will be key in accelerating our understanding of filamentous fungi.

The diversity of interesting biological problems and the availability of new cell biological and molecular tools with which to tackle them generated an exciting and enthusiastic background for this ambitious conference. Each day began with a Plenary Symposium dealing in turn with Fungal Cell Biology, Fungal–Host Interactions, Signaling and Silencing, and Genomes and Evolution. Concurrent sessions of shorter platform talks and poster sessions were held in the afternoons and evenings. The magnificent beach at Asilomar and the congenial atmosphere were instrumental in making this meeting enjoyable. The following brief descriptions of the Symposia and of selected platform sessions were provided by the session chairs and have been lightly edited by Ron Morris (Robert Wood Johnson Medical School) and Anne Osbourn (Sainsbury Laboratory), the meeting organizers. Abstracts from the meeting are available online at the Fungal Genetics Stock Center (www.fgsc.net).

Symposium on fungal cell biology. The meeting opened with a remarkable symposium chaired by **Stephen A. Osmani** (Ohio State University, USA). Most of the talks in this symposium took advantage of the fact that the hyphae of filamentous fungi are polar and highly elongated, and so are perfect for studying asymmetrical processes. **Gero Steinberg** (Max-Planck-Institute for Terrestrial Microbiology, Marburg, Germany) showed that microtubules undergo striking changes in

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their polarity during production of germ tubes from *Ustilago maydis* (corn smut) spores. He also presented data to suggest that vesicles switch from dynein-mediated to kinesin-mediated transport during this process. **Mike Plamann** (University of Missouri, USA), as part of a genetic and biochemical analysis of nuclear migration through the mycelial cytoplasm in *Neurospora crassa*, showed that mutations in *ro15* (the human ortholog of this gene, *Lis1*, is required for brain development) inactivate the dynein motor without affecting binding of the dynein/dynactin complex to microtubules and membranous cargo. **Michelle Momany** (University of Georgia, USA) presented evidence for a novel morphogenesis checkpoint that couples branch emergence to mitosis in *Aspergillus nidulans*, showing that the *AspD* septin is involved. **Reinhard Fischer** (Max-Planck-Institute for Terrestrial Microbiology, Marburg, Germany) demonstrated that the spindle-pole associated protein, *ApsB*, is involved in determining nuclear positioning along the mycelium in the multinucleate, coenocytic fungus *A. nidulans*. Simultaneous in vivo analysis of nuclear migration, *ApsB*, and microtubules revealed a "cable-car" mechanism for nuclear migration with nuclei gliding along microtubule tracts. Steve Osmani, who showed that the NIMA kinase of *A. nidulans* promotes a dramatic restructuring of the nuclear pore complex at mitosis, gave the only talk that did not depend on fungal asymmetry. Many fungi differ from animal cells by having a "closed" mitosis, i.e., at mitosis the nuclear envelope does not disassemble. **Osmani's** novel result suggests that the apparently closed fungal mitosis may in fact be open to allow nuclear entry of cytoplasmic proteins via gating of the nuclear pore complex.

A related series of short talks on **the fungal cytoskeleton** chaired by **Xin Xiang** (Uniformed Services University of the Health Sciences, USA) and **Robby Roberson** (Arizona State University, USA) stressed the value of combining light and electron microscopy with genetics to understand cytoplasmic organization during hyphal growth and development. **Roberson** emphasized the use of rapid cryofixation, freeze substitution, serial section reconstruction, and electron tomography. Several talks provided unique new data about microtubules. **Xin Xiang** showed that KINA, an *A. nidulans* kinesin, is required for the microtubule-plus end localization of dynein and dynactin. **Berl Oakley** (Ohio State University, USA) showed γ-tubulin plays an important role in the coordination of late mitotic events (disjunction, anaphase A, anaphase B, chromosomal decondensation) and suggested that this protein has a microtubule-independent mitotic checkpoint function. **Bo Liu** (University of California, Davis, USA) showed that the septation-signaling molecule AnMOB1 requires microtubules for its localization at the septation site and the spindle pole body. Other talks described new findings about the roles of actin and myosin in hyphal tip growth and septation. **Gero Steinberg** showed that a class V myosin in *Ustilago maydis* that localizes to the growing tip of germinating spores and hyphae is crucial for mating tube formation and hyphal growth. He also presented data suggesting that Myo5 is involved in delivery of chitin synthase to growing hyphal ends. **Greg May** (University of Texas, USA) discussed the affinity purification of proteins that interact with MYOA, the myosin I of *A. nidulans*, including the actin-related proteins ARP2/3 and others that play a critical role in establishing and maintaining polar hyphal growth. **Erfei Bi** (University of Pennsylvania, USA) presented data showing that *Saccharomyces cerevisiae* Msb3p and Msb4p link actin organization to exocytosis in conjunction with Cdc42p and Bni1p (formin) and also function as GAPs for the Rab GTPase Sec4p to regulate exocytosis. **Salomon Bartnicki-Garcia** (University of California, Riverside, USA) used time-lapse microscopy to study hyphal growth and demonstrated that mitotic events do not interfere with the apical growth of fungal hyphae.

Symposium on fungal–host interactions. This symposum was chaired by **Christopher L. Schardl** (University of Kentucky, USA). The talks covered a wide range of interactions between fungi and plant or animal hosts, ranging from mutualism to pathogenesis. **Chris Schardl** led off with a description of mutualistic endophytes (*Neotyphodium* species) that are seed-transmitted in grasses, and discussed their relationships to plant pathogens (Epichloë species) that share many biological and life history features. Phylogenetic analysis indicated that the mutualists were descended from the pathogens by a series of evolutionary steps involving colonization of new hosts, loss of sexuality, and somatic interspecific hybridization. The next two presentations concerned the classical plant pathogens, *M. grisea* (rice blast) and *Ustilago maydis* (corn smut). **Marc-Henri LeBrun** (CNRS-Bayer Crop Science, Lyon, France) described a B-zip transcription factor in *M. grisea* that is specifically expressed during infection, and so may be involved in the regulation of pathogenesis-related processes. He also reported on a novel avirulence gene *ACE1* that is predicted to encode a combined polyketide synthase/non-ribosomal peptide synthase. The evidence from his group indicates that ACE1-mediated avirulence is likely to be mediated by a low molecular weight metabolite rather than by the ACE1 protein itself. **Regina Kahmann** (Max-Planck-Institute for Terrestrial Microbiology, Marburg, Germany) addressed signal transduction in *U. maydis*, a basidiomycete fungus that has a complex tetrapolar mating system (two loci, two or more alleles each) and requires mating to initiate host colonization and pathogenesis. She reported the discovery of a MAP kinase (KPP6) that is crucial for pathogenesis but not for sexual development. Furthermore, microarray analysis identified 283 genes upregulated by sex pheromones, and several such genes have iron uptake

functions. **Aaron Mitchell** (Columbia University, USA) described a novel marker system for insertional mutagenesis of genes in the human pathogen *Candida albicans*, which is a diploid. This procedure allows selection of transformants that have undergone disruption of both alleles of a locus and has been used to identify genes that are likely to be required for pathogenicity, including genes for pH responses. Finally, **Axel Brakhage** (University of Hannover, Germany) presented a study of melanin biosynthesis genes in *Aspergillus fumigatus*, an important opportunistic human pathogen. Spores of this fungus enter human monocytes by phagocytosis. Of particular interest was his evidence that the polyketide synthase gene, *pksP*, is crucial for suppressing host resistance. In particular, the gene was required to inhibit fusion of lysozomes with the phagosomes, a process that would otherwise kill the invading fungus.

Other related short talks were presented in the session on **Medical Mycology**, which was co-chaired by **David Denning** (University of Manchester, UK) and **Joseph Heitman** (Duke University, USA). Several talks in this session were concerned with the use of molecular approaches to investigate pathogenesis in *A. fumigatus*. Studies on the cAMP pathway were presented by **Burghard Liebmann** (University of Hannover, Germany), while **Sven Krappmann** (Georg-August Univsersity, Germany) described the role of a cross-pathway control activator. The work of **Alex Andrianopoulos** (University of Melbourne, Australia) which indicated clear parallels between transcriptional regulation in the dimorphic human pathogen *Penicillium marneffei* and *A. nidulans*. This session also featured a talk from **Joe Heitman** on molecular determinants of virulence in the pathogenic basidiomycete, *Cryptococcus neoformans*. **Barb Steen** from **Jim Kronstad's** lab (University of British Columbia, Camnada) described the use of SAGE analysis to investigate patterns of pathogenesis-related gene expression.

Short talks on **Parasitic Interactions among Nematodes, Insects, and Fungi** were co-chaired by **Anders Tunlid** (University of Lund, Sweden) and **Raymond St. Leger** (University of Maryland, USA). Technical issues such as using transcriptome- and proteome-based approaches to identify genes that are crucial for the infection process were addressed. Studies with pathogens of diverse hosts have converged on the area of signaling pathways, since signal transduction is central to infection-related development and information about these processes can be exploited for strain improvement of biocontrol agents against pest species.

Symposium on signalling and silencing. Some highly novel and interesting results were presented in this symposium, which was chaired by **Louise Glass** (University of California, Berkeley, USA). **Louise Glass** presented a talk entitled "Fatal attraction: Vegetative incompatibility in *Neurospora*," in which she described the results of a screen for suppressors of vegetative incompatibility. This talk also contained memorable movies of hyphal and cytoplasmic fusion between compatible strains and the absence of these processes in genetically incompatible strains. **Peter Phillipsen** (University of Basel, Switzerland) shed new light on the establishment, maintenance and maturation of hyphal tip growth in the yeast-related filamentous ascomycete *Ashybya gossypii* by using GFP fused to various proteins involved in these processes. **Guiseppe Macino** (University La Sapienza, Rome, Italy) described recent findings on the light response of *N. crassa* and showed that PKC regulates the stability of WC-1 in response to light. **Bob Metzenberg** (University of California, Los Angeles, USA) presented his talk on meiotic silencing by unpaired DNA in *N. crassa.* **Nick Talbot** (University of Exeter, UK) described his recent findings in the area of appressorium-mediated plant infection by the rice blast fungus *M. grisea*, and reported on a novel metallothionin that is required for pathogenesis.

Related to this symposium were a series of short talk sessions. The first of these was an exciting session of on **Photobiology and Clocks**, co-chaired by **Jennifer Loros** (Dartmouth Medical School, Hanover, USA) and **Martha Merrow** (University of Munich, Germany). The preeminent plant physiologist **Winslow Briggs** (Stanford University, USA) opened the session with a guest lecture on phototropins, LOV domain-containing blue light photoreceptors in plants. The workshop then focused on recent fast-paced progress in dissecting mechanisms of light sensitivity in the fungi. Two LOV domain containing blue light photoreceptors in *Neurospora*, White-Collar-1 (WC-1, also a transcriptional activator) and Vivid (VVD), have been identified and biochemically confirmed within the past year. Genetic & genomic screens for light regulatory proteins in *Coprinus* and *Trichoderma* are turning up novel orthologs of the WC-1 photoreceptor and in *Neurospora* are indicating the presence of additional light receptors beyond WC-1 as well as previously unidentified circadian phenotypes that allow rhythmicity in constant light. Specific serines in the PEST domain of the *Neurospora* clock component FRQ were shown to directly effect the production of the WC-1 protein.

C.Raper (University of Vermont, USA) and **R. Debuchy** (University Paris-Sud, France) co-organized a fascinating session dealing with **Mating and Sexual Development**. Mating in heterothallic, cross-fertile, fungi requires partners with complimentary, transcriptionally regulating, mating-type (MAT) genes. Homothallic species contain MAT genes that permit selfing. Evidence of a functional relationship between the MAT genes of homothallic vs. heterothallic species of the plant pathogen *Cochliobolus* was shown by an exchange of these genes that resulted in a corresponding switch in mode of reproduction (**Shun-Wen Lu**, University of California,

Davis, USA). There is some evidence from population genetics that pathogenic *Fusarium oxysporum*, thought to be asexual, may reproduce sexually but there is no support for recent mating (**Keith Klein**, Minnesota State University, USA). Fungal mating is initiated by peptide pheromones and their cognate G protein-binding receptors. Homobasidiomycetes have many mating types and multiple pheromone and receptor genes. Small amino acid differences in either pheromone or receptor can significantly alter the spectrum of coupling to activate a pathway of nuclear migration leading to fertilization (**Meritxell Riquelme**, Oxford University, UK; **Susanne Gola**, Friedrich-Schiller University, Jena, Germany). *Schizophyllum commune* has two linked loci encoding pheromones and receptors. Surprisingly, in a few instances pheromones from one locus can activate receptors from the other locus. The low fitness of the resulting strains may explain why these combinations are not found in natural populations (**Thomas Fowler**, University of Vermont, USA).

Symposium on genomes and evolution. **Gillian Turgeon** (Cornell University, USA) chaired the **Genomes and Evolution**. The session consisted of five talks, two on plant pathogens (*Cochliobolus heterostrophus*, *M. grisea*), one on the saprobe *N. crassa*, one on the plant pathogenic oomycete, *Phytophthora infestans*, and one on the systemic dimorphic animal pathogen, *H. capsulatum.* All these genomes, except that of *P. infestans* (for which a large EST collection exists), have recently been sequenced. **Gillian Turgeon** contrasted plant attack strategies of *C. heterostrophus* with those of *M. grisea* and emphasized the power of comparative phylogenomics in determining gene function. **Bruce Birren** highlighted discoveries issuing from analysis of the *N. crassa* genome, including expected features (e.g., the prediction that RIP, which inactivates duplicated sequences, would arrest evolution occurring by gene duplication), and surprises (e.g., the previously unreported presence of genes for secondary metabolism, and the presence of phytochrome-like histidine kinases for red light photobiology). **Ralph Dean** (North Carolina State University, USA) reported on the current status of the *M. grisea* genome project and comparative analyses with genomes of other fungi, especially *N. crassa*. **Sophien Kamoun** (Ohio State University, USA) described mining the *P. infestans* EST collection for genes up-regulated during infection, encoding extracellular proteins, and undergoing diversifying selection, followed by screening candidates using a variety of functional assays to identify *P. infestans* effector genes that trigger cellular and molecular responses in plant cells. **Anita Sil** (University of California, San Francisco) highlighted the use of functional genomics to identify *H. capsulatum* phase-specific genes. Genomic shotgun microarrays have been used to identify genes and regulatory circuits that are implicated in *Histoplasma* cell fate.

A session of short talks on the **Evolution of Gene Clusters**, co-chaired by **Heather Wilkinson** (Texas A&M University, USA) and **Jonathan Walton** (Michigan State University, USA), provided a brilliant codicil to the Symposium on Genes and Evolution. Unlike bacteria, where clustering of genes into operons is common, clustering in eukaryotes is rare. Nonetheless, there are now more than twenty examples of gene clusters in filamentous fungi. All of the known clusters encode enzymes for secondary metabolite pathways or for utilization of rare substrates. At this session novel gene clusters as well as their putative evolutionary history were discussed. **Walton** presented an overview of gene clusters in fungi and the theory that clustering promotes survival of the component genes by facilitating their transfer by horizontal movement between microorganisms. Several talks, by **Wilkinson, Barry Scott** (Massey University, New Zealand), and **Daniel Panaccione** (West Virginia University, USA), discussed secondary metabolite clusters in endophytic fungi. In these fungi, secondary metabolites such as indole diterpenes, lolines, and ergot alkaloids provide enhanced fitness to the grass hosts through increased resistance to insect and mammalian herbivores. The roles of these alkaloids in other established host fitness enhancements (e.g., drought tolerance, disease resistance, improved competitive ability) remain unknown. Identification of the pathway genes now makes it possible to use targeted mutation to test the multifarious roles of secondary metabolites in endophyte symbioses. For the cluster implicated in loline biosynthesis (**Wilkinson**) primary metabolism paralogs for at least two of the secondary metabolism genes are closely linked elsewhere in the genome, thus supporting a hypothesis that the cluster was seeded by a duplication event within the genome of a progenitor to the loline producing endophytes. **Heidi Bohnert** (CNRS-Bayer Crop Science, Lyon, France) provided more detail on the novel *M. grisea* gene, *ACE1*, which was introduced by Marc-Henri LeBrun in the Fungal–Host Interactions Symposium session. *ACE1* encodes a predicted fusion between a polyketide synthase (PKS) and a non-ribosomal peptide synthetase (NRPS) and is a specific avirulence gene for the *Pi33* resistance gene of rice. Furthermore, it appears to be part of a gene cluster, the other members of which are probably involved in the synthesis, regulation, and secretion of a host-selective secondary metabolite. **Esteban Temporini** (Arizona State University, USA) spoke about the PEP gene cluster of *Nectria haematococca* that contributes to virulence of this fungus on pea. The genes of this cluster, which are on an unstable 'dispensable' chromosome, are also present in other fungal species, and the predicted phylogeny of the PEP genes does not correspond to the accepted phylogenetic relatedness of the fungi. The cause of this 'phylogenetic incongruence,' which has been reported for other gene clusters as well, was

proposed to involve horizontal transfer. **Scott Kroken** (Diversa, San Diego, USA) presented his analysis of PKS and NRPS genes in the completed genomes of several fungi. Surprisingly, many of these genes are restricted in distribution; even two species in the same genus had relatively few PKS and NRPS genes in common. Apparently, genes for secondary metabolism undergo rapid evolutionary gain and/or loss.

A second evolution-related short talk session on **secondary metabolites and mycotoxins** was co-chaired by **Motoichiro Kodama** (Tottori University, Japan) and **Bettina Tudzynski** (University of Munster, Germany). **Bettina Tudzynski** described evolutionary aspects of secondary metabolites and gene clusters in *Gibberella funikuroi*. **JinWoo Bok** from Nancy Keller's laboratory (University of Wisconsin, USA) described an extremely interesting global regulatory gene that affects the secondary metabolism of penicillin, toxin, and pigment production in *Aspergillus* that encodes a DNA methyltransferase. Several speakers, **Robert Proctor** (NCUAR-USDA, USA) and **Scott Baker** discussed fumonisin and polyketide production in genes and gene clusters from a variety of fungi including *Fusarium oxysporum*, *Gibberella moniliformis*, and *Cochliobolus heterostrophus.* Several other talks by **Motoichior Kodama, Daren Brown** (NCUAR-USDA, USA), **Donald Gardiner** (Melbourne University, Australia) and **Carolyn Young** (Institute of Molecular BioSciences, Palmerston North, New Zealand) also discussed biosynthetic gene clusters in various pathogens and endophytes.

Michael J. Hynes (University of Melbourne, Australia) and **Dan Ebbole** (Texas A&M University, USA) co-chaired a session on the **regulation of primary metabolism** with short talks on various aspects of the control of gene expression with respect to metabolism. The problems of distinguishing between primary and secondary metabolism were pointed out by **Bettina Tudzynski** (University of Muenster, Germany) who showed that in *Gibberella* the catabolic nitrogen regulatory gene *areA* is involved in regulating the gibberellin biosynthetic pathway. Fungi can grow on a diverse array of carbon sources and the synthesis of many catabolic enzymes is under investigation (e.g., **M. Penttila**, VTT Biotechnology, Finland) including at a genome wide level (**Rolf Prade**, Oklahoma State University, USA). However, the nature of signaling of carbon status is not well understood and **Margaret Katz** (University of New England, USA) presented an interesting analysis of a gene encoding a hexokinase-like protein that is involved in determining the response of extracellular protease production to carbon starvation.

Talks on **stress responses in fungi**, organized by **Paul Tudzynski** (University of Muenster) and **Jesús Aguirre** (UNAM, Mexico), reflected an increasing interest in and novel roles for reactive oxygen species (ROS) infungal physiology and development. Subjects ranged from ROS MAPK sensing and NADPH oxidase-mediated production (**J. Aguirre**), to ROS responses in conidiation (**W. Hansberg**, Inst. Univ. Nacional, Mexico), copper homeostasis, senescence (**H. Osiewacks**, J.W.Goether University, Frankfurt, Germany), and pathogenicity, e.g., different strategies of biotrophic vs. necrotrophic plant–pathogen interactions (**P. Tudzynski, Z. Zhang**, Oxford University, UK) and impact on sclerotia development (**C. Chen**, University of Nebraska. USA).Other stress forms were dealt with by **J. Henson** (Montana State University, USA), who dealt with thermotolerance conferred by endophytic fungi, and **K. Abe** (Tohoku University, Japan), who spoke about the role of a histidine kinasein osmostress response.

A session of short talks on the **targeting and secretion of proteins** was co-chaired by **Merja Penttilä and David Archer**. The efficient targeting and secretion of proteins underpins the success of many fungal species as primary degraders or as pathogens. The ability of some fungal species to secrete copious amounts of enzymes in culture has led to their industrial exploitation as cell factories for production of native and heterologous enzymes. The availability of genome sequence information and gene arrays has provided a new opportunity to investigate the protein secretion process and, especially, the stress responses established (initiated in the endoplasmic reticulum—ER) when heterologous proteins are expressed. **Andrew Sims** (University of Manchester, UK) described the construction and use of *A. nidulans* gene arrays and demonstrated that the arrays were effective at identifying genes that are transcriptionally up regulated under ER stress conditions. **Mari Valkonen** (VTT Biotechnology, Finland) showed that the constitutive up-regulation of the unfolded protein response (UPR), which is a stress response initiated by unfolded proteins within the lumen of the endoplasmic reticulum, in *Aspergillus niger* improved the secreted yield of a heterologous laccase several-fold. *A. niger* was also shown to be a promising cell factory for the production of full-length antibodies and antibody fragments and *A. niger* may provide a commercially competitive production system (**Mick Ward**, Genencor International, Palo Alto, USA). For some clinical applications of heterologously expressed proteins it is necessary that the glycosylation is of the human type. Therefore **Roland Contreras** (University of Gent, Belgium) has made progress in humanizing the high mannose type of glycans found in fungal glycoproteins. In many processes and often in nature, fungi secrete enzymes whilst attached to surfaces. **Rob te Biesebeke** (TNO Nutrition, Utrecht, Netherlands) has demonstrated that a wide range of genes are specifically induced under Solid Substrate Fermentation conditions and his approaches provide a platform to understand the regulatory systems. The expression and secretion of starch-degrading enzymes by *A. niger* is subject to several levels of regulation including the *AmyR* regulator.

Ronald de Vries (University of Utrecht, Netherlands) showed that *AmyR* has wider regulatory functions than the amylase-encoding genes. **Cristina Filippi** (Texas A&M University, USA) described a genome-wide approach for predicting proteins secreted by *Magnaporthe grisea* as part of a program to identify the role of secreted proteins in its pathogenicity towards plants.

There were also short talk sessions dealing with s**pores, sporulation, and hyphal morphogenesis, fungal–plant interactions, fungal population genetics, fungal genomics, signal transduction, membrane transporters, DNA repair/genome dynamics**, and for the first time a session on **teaching fungal genomics**.

Hans Van Etten (University of Arizona, USA) delivered the banquet lecture on **"A Sick View of Fungi,"** his amusing and informative personal view of the history of the fungal plant pathology. In his talk Hans emphasized how the molecular methods for fungi that had been initially developed with the "model" organisms *N. crassa* and *A. nidulans* have enabled substantial progress to be made in the field of molecular phytopathology.

The Fungal Genetics Conferences have undoubtedly played a key role in facilitating the exchange of the new methods and ideas that have led to these advances.

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