LETTER TO THE EDITOR

X INTERNATIONAL *FUSARIUM* WORKSHOP AND INTERNATIONAL *FUSARIUM* GENOMICS WORKSHOP 2008

The X International *Fusarium* Workshop took place in Alghero, Italy, from August 30 through September 2, 2008, in conjunction with the *Fusarium* Genomics Workshop 2008. As local organisers, we had both the honour and the pleasure of welcoming an international group of over 230 colleagues to a lively conference that included topic areas ranging from genomics and systematics to diagnostics and disease management.

The two keynote speakers were Professor Lester W. Burgess (University of Sidney, Australia) and Dr. Marie-Josée Daboussi (Université Paris-Sud Orsay, France).

Professor Burgess gave an overview of the present status of the mycogeography and ecology of Fusaria, with a special emphasis on the *Fusarium* species recovered from Australia, a large island continent ideally suited for such studies. Ecological investigations have contributed to understand how climate affects the distribution of species in grassland soils, and showed that some important pathogens can be isolated as endophytes from tropical grasses remote from cropping areas.

Dr. Daboussi’s keynote address targeted *Fusarium* transposable elements, particularly those found in *F. oxysporum*. An exhaustive analysis of their representation, diversification, and chromosomal distribution based on recently available genome sequence provides evidence that this species has been subjected to invasion and proliferation of active transposable elements, providing a major challenge to our vision of the *Fusarium* genome.

At the end of her talk, Dr. Daboussi announced to our International Society that she would retire at the end of 2008. As scientists and *Fusarium* community members, we expressed our concern about the loss of research on transposable elements in plant pathogenic fungi in general and particularly in *Fusarium* species. Dr. Daboussi’s laboratory has been the center of research activity on fungal transposable elements and genome plasticity for the past two decades. Most of what we know on fungal transposons is the direct result of studies made in her laboratory or by researchers who have passed through her laboratory as students, post-docs or visiting scientists. It is a pity that after Dr. Daboussi’s retirement her research group will be dispersed among different projects, with dramatically negative consequences and a waste of skills, energies and knowledge that ground more than 20 years of collective experience.

Organised by the *Fusarium* Committee of the International Society of Plant Pathology, the *Fusarium* workshops are held every 5 years in conjunction with the International Congress of Plant Pathology. The next workshop is being planned for the 2013 Beijing Meeting by the newly elected *Fusarium* Committee Chair Ulf Thrane and Vice-Chair David Geiser.

We wish to thank all session leaders who kindly agreed to summarise the main achievements presented by the *Fusarium* community during the Workshop.

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**SYSTEMATICS AND PHYLOGENETICS**

(Session leaders: K. O’Donnell, K. Seifert)

The first session of the Workshop, after the keynote addresses, concerned Systematics and Phylogenetics, topics that are central to applied and experimental studies of *Fusarium*. Indeed, ideas introduced by the keynote address of Lester Burgess developed into themes as the session continued. The recent discovery of a plethora of undescribed species was discussed by several speakers and presented in multiple posters. The morphological legacy of Wollenweber was acknowledged several times and the complex interplay between traditional morphological taxonomies and the emerging phylogenetic classifications and molecular identification systems was a recurring topic. Data sets derived from independent technology platforms, including microscopy, DNA sequencing, GC-MS and other mycoxin profiling methods, as well as the sampling and bioinformatics dimensions inherent in population biology and genomics research, are now all part of modern systematics. Cooperation and collaboration between different laboratories is now essential for promoting urgently needed progress in taxonomy and systematics.

The session opened with an invited presentation on DNA barcoding by Keith Seifert (Canada). DNA barcoding is the development of comprehensive DNA sequence databases for identifying species in all kingdoms of life. The marker genes are standardized by the Consortium for the Barcode of Life to function across the broadest possible taxonomic groups. The sequences must be supported by authoritative identification of organisms, deposit of voucher specimens or cultures in public collections, meta-data on the vouchers in on-line accessible databases, and the deposit of sequence traces in on-line archives. Seifert’s studies revealed that the standard barcoding gene used for animals, mitochondrial Cytochrome C Oxidase I (COX1, often referred to as CO1), is unsuitable for identification of *Fusarium* because of the lack of resolution, frequent occurrence of introns, and the presence of divergent alleles derived from duplicated genes (paralogs) in many strains. The proposed DNA barcode marker for fungi, the nuclear ribosomal internal transcribed spacers (ITS), provides some resolution for species in *Fusarium*, but has considerably less resolution than the now widely used translation elongation factor 1α gene (TEF, see below). Thus, the development of a sanctioned barcoding database for *Fusarium* may have to await the acceptance of alternative markers for fungi or for Ascomycetes in general.

The utility of partial RNA polymerase (RPB2) gene sequences for phylogenetics and identification of *Fusarium* species was discussed in the invited presentation by Kerry O’Donnell (USA). This gene was used extensively in the Assembling the Fungal Tree of Life (AFTOL) project (see *Mycologia* 98: 829-1103, 2006), which laid the groundwork to allow amplification and sequencing of the RPB2 gene as two contiguous fragments from virtually all Fusaria, using 5′f2x7cr and 7cfx1ar as PCR and sequencing primers. Attractive features of this gene for phylogeny reconstruction within *Fusarium* include: (i) its existence as a single copy in the genome, eliminating complications caused by paralogy; (ii) ease of alignment across the genus because of the absence of indels, maximizing positional homology; (iii) the sequenced region is protein coding, and translation facilitates recognition and correction of sequence data; (iv) a phylogeny concordant with those obtained from other loci, but with strong support for relationships among many clades obtained for the first time; (v) sufficient variation to be informative at or near the phylogenetic species level. RPB2 and similar phylogenetically informative genes yet to be discovered, will play a key role in developing a robust phylogenetic framework for studying the evolution of fusarial toxins and other biologically relevant characters. However, because the RPB2 data failed to recover strongly supported nodes near the base of the phylogeny, including the branching order of the *Fusarium aquaeductuum* species complex and *Cylindrocarpon* spp., it remains an open question as to whether *Fusarium* represents a monophyletic group. A comprehensive RPB2 dataset will be incorporated into the next version of the web-accessible *Fusarium*-ID database presently based only on TEF (Geiser et al., *European Journal of Plant Pathology* 110: 473-479, 2004) to facilitate isolate identification via the internet (http://Fusarium.cbio.psu.edu/).

The shorter contributed papers focused on the three particular clades within *Fusarium*. The intensive international attention paid to the Gibberella fujikuroi complex (GFC) continued with a paper by Jimenez-Gasco et al. (USA) on a multigene phylogenetic study of 500 strains from the Penn State *Fusarium* collection, which revealed the existence of several previously unknown species nested within the African clade of the GFC, a few of which were shown to produce fumonisins. An additional new species from the African clade was discussed by Elmer and Marra (USA), based on strains isolated from the coastal salt marsh grass *Spartina alterniflora*. Van Hove et al. (Belgium) isolated a new species from banana that is closely related to *F. verticillioides*, but which is unable to produce fumonisins. An additional new study from the African clade was presented by Seifert et al. (South Africa), documenting the existence of several previously unknown species from the coastal salt marsh grass *Spartina alterniflora*. Van Hove et al. (Belgium) isolated a new species from banana that is closely related to *F. verticillioides*, but which is unable to produce fumonisins. The poster session also included several studies of other members of the GFC, including *F. cinctatum* on pines (Berbegal et al., Spain), *F. guttiforme* on pineapple (Lima et al., Brazil), *F. thapsinum* on Sorghum (Petrovic et al., Australia) and novel species lineages on *Syzygium cordatum* (Kvas et al., South Africa) and sugar beet (Rivera et al., USA).

The *Fusarium oxysporum* complex (FOC) is another group of important plant pathogenic species that receives international attention. Fourie et al. (South Africa) presented a multifaceted study including multi-
gene phylogenies, microsatellite characterization, and vegetative compatibility tests of the important banana wilt pathogen *F. oxysporum* f. sp. *cubense*. They were unable to induce mating between strains with compatible mating type genes. The f. sp. *cubense* was shown to be polyphyletic, derived in at least two distinct clades. Alves-Santos *et al.* (Spain) presented preliminary results on the pathogenicity, sporulation capacity, and molecular variation of the tobacco pathogen *F. oxysporum* f. sp. *batatatis*, with their data suggesting the hypothesis that strains assigned to this f. sp. may be heterogeneous. Additional data on the FOC was presented in the poster session, with studies of the f. sp. on tomato (Inami *et al*., Japan) and cotton (Laurence *et al*., Australia), and a presentation of a two-locus DNA sequence database for typing pathogenic and saprobic *F. oxysporum* strains (O’Donnell *et al*., USA).

The basal clades of *Fusarium*, which have received little taxonomic attention over the past twenty years, were the focus of two presentations. An overview was presented by Gräfenhan *et al.* (Canada) on *Cosmospora*, one of the lesser-known, but very diverse, teleomorph genera associated with *Fusarium*. Multi-gene phylogenies suggested this genus to be polyphyletic, but species with *Fusarium* anamorphs may be confined to one clade. Unfortunately, the literature on anamorph-teleomorph connections in this complex is filled with errors. Schroers *et al.* (Slovenia) presented a taxonomic revision of the *F. dimerum* complex. Previously considered a single species, the study showed the existence of twelve phylogenetically distinct species, each with characteristic macroconidia when examined using carnation leaf agar. Several species included strains isolated from humans.

All of these papers emphasized the need for collaborative, multidisciplinary approaches to taxonomy, and contributed to our understanding of the rapidly expanding species diversity across all the major clades of *Fusarium*. Several presentations in the sessions on ‘Ecology and Biogeography’ and ‘Diagnostics’ sessions were also relevant to the Systematics and Phylogeny session, and the reader is referred to those summaries for additional information.

K. O’Donnell and K. Seifert

**GENOMICS**

(Session leaders: H.C. Kistler, L.-J. Ma)

The session on *Fusarium* Genomics began the first full day of the X International *Fusarium* Workshop and was one of the highlights. Ordinarily organized as a satellite meeting of the Fungal Genetics Conference at Asilomar or of the European Conference on Fungal Genetics, the 2008 *Fusarium* Genomics Workshop met with the ISPP *Fusarium* Workshop and was focused on research springing from the four publicly accessible genomic sequences and whole genome microarrays developed within the past few years. Despite the short presentation time, each speaker was able to deliver a complete and interesting story in the selected field.

The section was led by the co-chair H.C. Kistler who presented “Global gene expression during plant infection and toxin biosynthesis in *Fusarium graminearum*”. The global regulation and cross pathway control of sporulation, mycotoxin biosynthesis and pathogenicity was illustrated by monitoring gene expression profiles during plant infection using the *F. graminearum* Affymetrix GeneChip. Strains containing mutations in genes for transcription factors tri6 and tri10, were found to control trichothecene accumulation in planta and pathogenicity. Largely overlapping sets of approximately 200 genes were altered in expression in either tri6 or tri10 strains. In addition to genes responsible for trichothecene biosynthesis, genes involved in primary metabolism and transport also were significantly regulated by tri6 and tri10.

Co-chair L.-J. Ma presented “*Fusarium* comparative genomics reveals genome dynamics and its impacts on pathogenesis” based on comparison of three *Fusarium* genomes generated at the Broad Institute. The most interesting result from the comparative studies was the discovery of significant amount of *F. oxysporum* lineage-specific (Fol LS) genomic regions, accounting for more than one quarter of the *F. oxysporum* genome, including 4 of the 15 *F. oxysporum* chromosomes. These Fol LS regions are enriched in secreted proteins, transcription factors, and genes involved in signalling transduction. The secreted proteins encoded in the Fol LS regions include known virulence factors such as JIX (Secreted In Xylem) proteins, necrosis and ethylene-inducing proteins, peroxidases, and plant/fungal cell wall degrading enzymes. The potential impacts of the Fol LS on the wide host range of *F. oxysporum* and the development of pathogenicity were discussed.

M. Pasquali presented “Gene expression profiling and functional analysis of spore germination in *Fusarium graminearum*”, a full genome study on conidial and ascospore germination using *F. graminearum* Affymetrix GeneChips and on the comparison of gene expression during germination and drought stress for both spore types. The authors discovered that the majority of the genes that are annotated with known function have a common expression pattern in both conidia and ascospores. Genes involved in primary metabolism and energy production are expressed similarly in conidia and ascospores, indicating shared fundamental biological processes during germination of these different spore types. Interestingly the greatest differences in gene expression between conidia and ascospores were found upon desiccation. Desiccated ascospores con-
tained over 6000 expressed genes, a surprisingly high number (similar to the other germination stages) compared to the less than 3000 genes expressed in desiccated conidia under identical conditions. Gene expression changes were found to reflect differences in the biological behaviour of the spore types: desiccated ascospores are more viable and pathogenic on wheat than conidia after drought stress. Moreover expression profiles of ascospore and conidial germination showed some unique patterns of genes. A transcription factor was observed to be constitutively expressed in all stages, but in ascospores, transcript levels were at least 2 fold more than in conidia. Site-specific mutagenesis showed that this gene had a crucial role in both conidiation and perithecial development as well as in other cellular activities.

In the talk “Comprehensive phosphoproteomics approach to identify regulatory mechanisms of deoxynivalenol synthesis in Fusarium graminearum”, C. Rampitsch discussed the potential role for protein phosphorylation in initiating DON synthesis by probing the phosphoproteome of F. graminearum after the onset of DON synthesis using multidimensional separation and analysis (GeLCMS). The authors identified 53 unique phosphopeptides in 33 samples from F. graminearum grown on nitrogen-poor media at three time points and confirmed that the peptides were from proteins involved in the regulation of protein synthesis, general metabolic enzymes, biosynthetic enzymes and proteins of unknown function. Many contained consensus kinase sequences.

A high-throughput, transposon mutagenesis strategy for the functional analyses of genes in F. graminearum was discussed through the presentation of “Tagging pathogenicity genes in Fusarium graminearum using the transposon system mimp/impala” by T. van der Lee. This study revealed that mimp1 is reinserted close to or within genes in over half of the mutants. A collection of over 300 mutants derived from F. graminearum isolate Fg820 was screened for growth on a wide set of media, for pathogenicity on wheat and for perithecial development. One mutant displayed altered growth characteristics, 10 mutants showed altered virulence phenotypes and 11 were impaired in perithecial development. In one of these mutants (Fg820-6-11-r112) mimp1 reinserted into an ORF encoding a transcription factor. The wild-type phenotype could be restored by complementation with a non-disrupted copy of the gene, proving that the observed mutant phenotype is caused by the mimp1 insertion. The author's results indicate that mimp1 is a powerful mutator that can be exploited for high-throughput analysis of F. graminearum and potentially other ascomycete fungi.

A. Chakrabarti presented the study entitled “Identifying the secretome of Fusarium oxysporum f. sp. vasinfectum (Fov)” with the objective to discover proteins involved in virulence of Fov, the causal pathogen of vascular wilt disease in cotton. Full length cDNA libraries were prepared from Fov-infected cotton root and stem tissues showing visible external symptoms of the disease. The libraries were screened for the presence of Fov-specific genes expressed during infection. Differentially expressed cDNAs were subjected to bioinformatic as well as molecular analysis to confirm their fungal origin. Subsequent analysis of the differentially expressed full length cDNAs was used to predict secretory proteins that constitute the infection stage ‘secretome’ of Fov and that may act as effector proteins important in virulence and determining host range.

The last oral presentation of the section “Analysis of the newly sequenced Fusarium genomes using PHI-base and ONDEX” given by K. Hammond-Kosack described the repertoire of genes of these genomes using the Pathogen-Host Interactions Database (http://www.phi-base.org/), which contains information on experimentally verified pathogenicity and virulence genes for multiple species, combined with the data integration system called ONDEX. This analysis revealed pathogenicity genes and gene families which have either expanded or have been lost from each species as well as the extent of sequence relationships among genes.

The poster presentations of the Genomics section were focused in two main areas: functional studies of genes and methodology development. Several posters dealt with functional analysis by way of expression profiling. The study “The transcription factor FgStuA influences sporulation development, pigmentation, pathogenicity and trichothecene production in Fusarium graminearum” demonstrated the involvement of FgStuA in several different processes. Microarray analysis, conducted under conditions at which the wild-type produced asexual spores and the mutant produced no spores, showed that genes encoding several groups of cell-wall related proteins, such as chitinases, glycanases and GPls, were mostly down-regulated in the mutant, and that 17 continuous genes, including the known aurofusarin genes, were virtually completely turned off in the mutant. Also eight continuous genes, including genes encoding a putative PKS-NPS hybrid, were found to be down-regulated in the mutant during conditions that favored spore production. The poster “Expression of defence-related genes in four banana cultivars infected with Fusarium oxysporum f. sp. cubense” presented gene expression profiles in the highly susceptible Cavendish cv. Williams, the tolerant hybrid FHIA 17 and the resistant cvs Rose and Calcutta IV, using cDNA-AFLP analysis. The authors identified genes that may be involved in the Fusarium wilt defence response including genes associated with cell wall strengthening such as S-adenosylmethionine synthase (SAMs) and Isoflavone reductase, as well as transcription factors such as a putative WRKY6 and bZIP proteins. Quantitative real-time RT-PCR confirmed the expression patterns of selected genes. “Func-
tions of the sex pheromones of *Gibberella zeae* investigated whether predicted pheromones retain a role in sexual reproduction of the homothallic fungus *F. graminearum* (*G. zeae*). Genes for predicted pheromone (*Ppg*) and pheromone receptor (*Pre*) genes were identified. Gene *Ppg1*, a homolog of the *Saccharomyces* α-factor pheromone precursor gene, was expressed in germinating conidia and mature ascospires. Expression of *Ppg2*, a further homolog of the α-factor pheromone precursor gene, was not detected in any cells. *Pre2* was expressed in all cells, but *Pre1* was expressed weakly and only in mature ascospires. Deletion mutations Δ*Ppg1* or Δ*Pre2* reduced fertility in self-fertilization tests. Δ*Ppg1* reduced male fertility and Δ*Pre2* reduce female fertility in outcrossing tests. In contrast, Δ*ppg2* and Δ*pre1* had no discernable effects on sexual function. Δ*Ppg1/Δppg2* and Δ*Pre1/ΔPre2* double mutants had the same phenotype as the Δ*Ppg1* or Δ*Pre2* single mutants. Thus, one of the putative pheromone/receptor pairs (*Ppg1*/*Pre2*) enhances, but is not essential for selling and outcrossing in *G. zeae*, whereas no functional role was found for the other pair (*Ppg2*/*Pre1*).

Among the posters dealing with development of new methodologies for *Fusarium* species, the authors of “Highly efficient single step construction of vectors for targeted genome modifications in filamentous fungi by USER friendly cloning” developed a system that allows for single step construction of vectors for targeted gene modification, thereby reducing construction time, screening and verification work. The vector system is dependent on the Uracil-Specific Excision Reagent cloning technology (USER Friendly™), which in its commercial version offers efficient directional cloning of a single PCR amplicon. USER Friendly cloning was used for the simultaneous directional fusion of two PCR amplicons with two vector fragments, at an efficiency of 85%, thus allowing a single step construction of replacement vectors, independently of restriction enzymes used during cloning. The poster “The use of SSR markers to predict Fusarium head blight resistance in chosen spring barley genotypes” presented the results of testing the genetic diversity of parental genotypes of spring barley with declared resistance or susceptibility to FHB using a set of 60 microsatellites. Four alleles at three loci of microsatellite markers were specifically amplified only in the group of the genotypes with declared susceptibility (Bmag0353 and Bmag0382) or declared resistance to FHB (Bmag0382 and EBmac0806). The presence of markers predicting resistance to FHB was confirmed in DH lines with maternal genotypes PEC210 and Zao Zhou. The SSR marker EBmac0806 was localized on the linkage map of chromosome 6H, where QTLs for resistance to FHB and for low DON accumulation were identified. SSR marker Bmag0382 was localized on chromosome 1H where a QTL for low DON accumulation in kernels was identified.

“An update of the genetic map of *Gibberella zeae*” aligned the third assembly of *Fusarium graminearum* genomic sequence of strain PH-1 using seven structural genes and 108 sequenced AFLP markers based on a cross between Kansas strain Z-3639 (*F. graminearum*) and Japanese strain R-5470 (*F. asiaticum*). Despite the inferred history of genetic isolation, the chromosomes were capable of recombination along their entire length, even within the inversions. This genetic map will be used in conjunction with the physical sequence to study recombination frequency as well as phenotypes, such as fertility and fitness, and genetic features, such as centromeres, that have unknown molecular signatures in the genome.

The authors of the poster “Nonhomologous end joining and DNA replication participate in DNA integration during transformation of *Fusarium graminearum*” reported that 1-3 copies of input DNA were first joined end-to-end to produce either linear or circular structures, probably mediated by the nonhomologous end-joining (NHEJ) system. The end joins typically had 1-5 nucleotides in common and were near or within the original cleavage site of the plasmid. For ectopic integrations, linear DNAs were joined to two ends of genomic DNA with the same join characteristics. Integration at the target site involved replication around circularized input DNA, beginning and ending within the flanking homologous DNA, and resulting in the integration of multiple copies of the entire structure. Resulting integrations deleted or duplicated the target site, or left a single copy at either end of the integrated multimer.

L.-J. Ma and H.C. Kistler

**PATHOGENICITY AND DISEASE EPIDEMIOLOGY**

(Session leaders: P. Nicholson, S. Chakraborty)

The session on pathogenicity and disease epidemiology was very well attended despite being the last in a series of exciting and informative sessions and the inviting picturesque surroundings of Alghero. There was one 20 min presentation on ‘The missing link in Fusarium Head Blight and Crown Rot continuum’ as my co-chair P. Nicholson was not able to attend. This talk raised unanswered questions on stubble colonisation that serves as the source of primary inoculum to both Crown Rot and Head Blight diseases of cereals. Following a summary of the similar aetiology, epidemiology and pathogen biology for Crown Rot and Head Blight the presentation by Chakraborty et al. highlighted the lack of knowledge on pathogen movement within plant tissue. In case of Head Blight, there is a relatively small window of opportunity for infection to occur at anthesis under favourable weather conditions of high humidity...
and temperature. With the crop maturing soon afterwards, much of the inoculum from the infected spikelets is removed at harvest. The shrivelled and light-weight infected spikelets, blown out by the harvester while screening, may fall on stubble, where Fusarium can persist as a saprophyte. However, the extent or significance of this route for stubble colonisation has not been clearly demonstrated from field studies. Alternatively or concurrently, the fungus may grow down the stem to colonise the crown tissue or it can directly infect the stem base/crown during the crop growing season, but these have not been demonstrated from field studies. Pinpointing the route to stubble colonisation is essential to understand the relative importance of the two Fusarium diseases of wheat in the production and survival of inoculum that is relevant to both diseases. If infection of crown/stem base during the crop season proves to be a major contributor to stubble-borne infection of crown/stem base during the crop season, the importance of Crown Rot will need to be reassessed in areas where Head Blight is the dominant disease.

The importance of Fusarium Crown Rot of wheat was evident from four other abstracts. Ozdemir et al. discussed the pathogenicity of F. culmorum isolates from Turkey for the selection of aggressive isolates for germplasm screening. In a second abstract, Erginbas et al. described the use of a seedling bioassay to screen germplasm. From a comparison of three different screening methods, the authors selected a seedling dip method to be used for rapid screening of germplasm. All methods gave a significant variety x isolate interaction, indicating the presence of differential aggressiveness that could mean using more than one isolate in screening for resistance. A study of F. culmorum, F. avenaceum, F. pseudograminearum and Microdochium nivale from Tunisia by Kammoun et al. showed no difference in Crown Rot aggressiveness of isolates originating either from spike or crown tissue. This study is similar to earlier studies using F. pseudograminearum isolates from Australia and there seems to be no specialisation in Fusarium species for crown or spike infection. A second abstract from this group by Chakali et al. dealt with the impact of water stress on crown and foot rot in wheat. The findings that Crown Rot severity increased with increasing water stress is congruent with observations that, in areas where both Head Blight and Crown Rot are prevalent, a dry finish to the wheat growing season leads to severe Crown Rot, while a wet finish leads to severe Head Blight.

Several abstracts have dealt with changing in pathogen species and/or genotypes causing Head Blight, studied using field surveys and various diagnostic tools. These changes have led to increase in the level or type of mycotoxin contamination and low levels of T-2 toxin are now consistently observed in wheat grains in some regions. In surveys of oat and barley crops in Finland, Parikka et al. found F. lansethiae as the most common pathogen producing both T-2 and HT-2 toxins, more on oats than on barley. A presentation from Canada by Fernando et al. showed that in Manitoba the 15ADON chemotype of F. graminearum is increasingly being replaced by more potent isolates that have a 3ADON chemotype. Several other abstracts dealt with mycotoxin from field surveys and its production under different conditions. Grain moisture content, temperature, mixture of different Fusarium species, prevailing weather in the field and insect pests were among the factors studied for their effect on mycotoxin production by Fusaria in culture or in grains. Two abstracts dealt with the interaction between insect pest and Fusaria. Munkvold et al. reported that infestation of corn by western bean cutworm in the USA increased Fusarium ear rot symptoms and fumonisin levels by as much as 9.5 times. The second abstract by Bagga from India reported increased F. nivale lesion size following infestation by wheat aphids. The poorly understood role of insect pests in the expression of Head Blight symptom and mycotoxin levels deserves further investigation.

Other studies dealt with disease and pathogen surveys to further enrich knowledge on the distribution of Fusarium pathogens. In one study by Davis and Burgess, the pathogen population was surveyed and characterised following a Head Blight epidemic in Australia. High levels of F. pseudograminearum were found from wheat spikes in fields where wheat was rotated with other susceptible cereals, whereas the frequency of F. graminearum was not affected by cropping sequence. The authors attributed this to the long distance dispersal of G. zeae ascospores. Surveys from China by Li et al. report that nearly 80% of isolates from Head Blight areas are F. asiaticum of 3ADON, 15ADON and NIV chemotype, and about 19% of the isolates belong to F. graminearum of the 15ADON chemotype. A survey of wheat grains in Serbia by Krmaja et al. reporting very high levels of F. graminearum (63%) and F. sporotrichioides (>20%) has also raised concerns of grain mycotoxin.

A number of contributions dealt with Fusarium diseases of other crops including mango in Israel (Gamliel-Atinsky et al.), lentil in Italy (Haegi et al.), coffee in East and Central Africa (Hindorf), the succulent Hoodia gordoni from South Africa (Lamprecht et al.), chickpea in Mexico (Lopez-Lopez et al.), sugarcane in Africa (McFarlane and Rutherford), rice grain spotting in Cameroon and Nigeria (Ngala and Adeniji), chickpea and pigeonpea in India (Pande et al.), vanilla in Indonesia (Pinaria et al.), carnation in Colombia (Quinche et al.), sugar beet in the Netherlands (Schneider et al.) and cotton and snow pea in Australia (Yousiph et al.). These reports highlight the versatility and the broad host range of Fusarium species that makes them such successful pathogens.
Two studies have dealt with *Fusarium* species as human pathogens causing skin, eye and nail infections. In a study by Sanna *et al.*, of the 68 cases of subcutaneous and deep mycoses during 2006-2007, *Fusarium* represented the second most frequent genus isolated (15/68) after *Alternaria*. All the species isolated, *F. verticillioides*, *F. solani* and *F. oxysporum* are known plant pathogens. In addition to these, *F. solani* is often linked to the occurrence and severity of respiratory allergies such as bronchial asthma, rhinitis, allergic fungal sinusitis, etc. These abstracts serve as a timely reminder to *Fusarium* researchers and technicians of the potential health hazard to humans from Fusaria.

With excellent keynote presentations, reviews and overviews the workshop offered a timely update on all aspects of *Fusarium* research in a compact program. The organisers deserve congratulations for the selection of excellent invited speakers, a well-organised schedule of scientific sessions and social events and the excellent food and entertainment.

S. Chakraborty

**ECOLOGY AND BIOGEOGRAPHY**
(Session leaders: D.M. Geiser, B. Summerell)

*Fusarium* ecology and biogeography has come along way, with striking advances in our ability to analyze large numbers of isolates, in characterizing *Fusarium* populations and communities, and attention given to new habitats and regions of the world. Palermo and colleagues characterized Fusaria from waters derived from Spanish sea beds and fluvial channels, finding a variety of *Fusarium* species to be widespread. Liew *et al.* analyzed species of pathogenic Fusaria from wild and cultivated ecosystems in Australia, and found little genetic differentiation between them, with isolates from wild sources showing some degree of pathogenicity on cultivated hosts. Gagkaeva and Gavrilova isolated Fusaria from small grain cereals across agricultural areas in Russia, uncovering some distinct geographic patterns and an apparent increase in the geographic range of *F. graminearum*. Karlovsky and colleagues described the results of a three-year experiment looking at the effects of organic versus conventional cultivation methods on the accumulation of mycotoxins in corn. Of course, large amounts of data present bioinformatics problems, as ideally the results from such a variety of studies would be accessible together for comparison. We have a long way to go before we get to that point, but perhaps a small step forward is represented in the ongoing improvements to the FUSARIUM-ID DNA sequence identification database described by Geiser *et al.* (European Journal of Plant Pathology 110: 473-479, 2004). Perhaps the *Fusarium* research community can create a comprehensive database to coordinate diverse data from *Fusarium* ecological and biogeographic studies with other efforts in the realms of plant pathology, genomics and systematics.

D.M. Geiser

**BIOLOGICAL CONTROL**
(Session leaders: C. Alabouvette, A. Garibaldi)

The session Biological Control was relatively poor in comparison to other sessions or to the workshops previously organized on the theme of “Biological control of Fusarium diseases”. Indeed, in addition to the invited lecture there were only six oral presentations and three posters.

The invited lecture (Alabouvette *et al.*) presented a synthesis of the studies dealing with the use of non pathogenic strains of *F. oxysporum* to control Fusarium wilts. After having compared the infection processes of the tomato root by pathogenic and protective strains, the most recent research in this field, aims at identifying fungal genes involved in the protective capacity of the non pathogenic strains. One poster (L’Haridon *et al.*) illustrated this aspect, reporting an approach based on the use of Rapid Subtraction Hybridisation technique to identify genes differentially expressed during the interaction between tomato cells and either a protective *F. oxysporum* f. sp. *melonis* or its non protective mutant. Two other posters were related to the use of protective strains of *F. oxysporum*, and described the use of: (i) molecular tools to monitor the biocontrol agent in soil and assess its environmental impact (Edel-Hermann *et al.*), and (ii) transformed strains expressing GFP or DsRed2 to visualize the interactions of the protective and pathogenic strain at the root surface (Olivain *et al.*).

One presentation from Morocco (My.H. Sedra) dealt with “bayoud”, the Fusarium wilt of date palm. Antagonistic microorganisms isolated from suppressive soils, secreted secondary metabolites that reduced pathogen growth. Different formulations of the antagonists were compared. Their ability to control Fusarium wilts of crops other than date palm makes them interesting potential biological control agents.

To gain a deeper understanding on the biochemical and molecular mechanisms underlying bacterial antagonism of soil-borne fungi, strains of *Bacillus* and *Pseudomonas*, isolated from suppressive soils, were confronted with genetically characterized mutants of *F. oxysporum* f. sp. *lycopersici*. Scanning electron microscopy was used to characterize the interactions between bacterial cells and tomato roots. Results illustrated the complexity of the tritrophic interactions between biocontrol bacteria, the pathogen and the host plant (Vitullo *et al.*).

The last presentation on biocontrol of Fusarium wilts
reported the results of a study comparing the beneficial effects of several composts of agricultural and urban wastes. For the two most suppressive composts, the reduction of disease caused by *F. oxysporum* f. sp. *lycopersici* was attributed to both general and specific suppressiveness mechanisms. Specific suppression was mostly related to the activity of a strain of *Trichoderma asperellum* which is able to reduce disease incidence when added to conducive peat or perlite (Trillas et al.).

One presentation addressed the use of plant extracts to control *F. graminearum* in wheat and to reduce the mycotoxin content. Antifungal plant preparations were tested *in vitro* and *in vivo* against *F. graminearum*. The most active preparations from *Rheum palmatum* and *Frangula alnus* were tested in the field for two years. Reduction of disease incidence was as good as that of the best chemical pesticide. Moreover, plant extracts reduced the content of nivalenol and zearalenone in the grains to the same extent as chemicals. These results showed that antifungal plant preparations are as effective as chemicals to control head blight and decrease the toxin content (Forrer et al.).

V. Vujanovic isolated and characterized biotrophic mycoparasites for the biological control of pathogenic *Fusarium* spp. Seventeen indigenous fungal strains associated with *Fusarium* pathogens were isolated and used to study their phylogenetic relationships. Six new biotrophic mycoparasites belonging to Sordariales and Pleosporales were characterized. They were confronted with several species of pathogenic *Fusarium* and can be regarded as potential biocontrol agents.

Finally, there was an original presentation, by Campanile et al., showing how a non pathogenic strain of *F. tricinctum* may control the oak canker induced by *Dipodius corticola*. The main objective of the study was to identify the secondary metabolites produced by *F. tricinctum* and to determine their role in the antagonistic effect against *D. corticola*.

Considering the world importance of *Fusarium* head blight and of the mycotoxin contamination of grains, we would have expected many more presentations dealing with biological control of this disease. What are the reasons for such a lack of research in this specific field? We hope to get more presentations during the next International *Fusarium* workshop.

C. Alabouvette

**DISEASE MANAGEMENT**

(Session leaders: R. Jiménez, W. Elmer)

The disease management session was held in the afternoon of September 1, 2008. Although the session suffered the absence of Co-moderator R. Jiménez, we managed to have a well-attended session with eight oral presentations and 13 posters, addressing management of *Fusarium* diseases of chickpeas, maize, oats, ornamentals (annual and woody), pea, pigeonpea, potato, and wheat. The session began with a keynote lecture by Elmer on management strategies to suppress *Fusarium* diseases on ornamentals. This presentation highlighted the three components of the disease triangle, i.e. host susceptibility, the presence of a virulent pathogen, and a conducive environment. The talk reiterated a basic principle in *Fusarium* disease management, that the most successful and cost-effective strategy for disease control is host resistance. When that option is not available, sanitation and/or eradication with judicious use of fungicides provide the next best chance for management. Lastly, manipulations of the environment via fertilization, crop rotation, and/or tillage were presented as methods to reduce disease incidence and severity but, typically, these methods were less effective than practices that increase host resistance. Most host/disease systems require a multifaceted approach combining all these strategies. The following summary attempts to demonstrate how each strategy was employed by the contributors.

**Disease management through host resistance.**

Screening available germplasm. The majority of oral talks and poster presentations were aimed at identifying and incorporating sources of resistance to *Fusarium* into commercially acceptable germplasm. Two presentations discussed a program to screen for resistance to *Fusarium* head blight (FHB) and crown rot caused by *F. graminearum*, *F. avenaceum*, and *F. culmorum*. A team of Turkish scientists, (Nicol et al.) collaborating with the International Maize and Wheat Improvement Center (CIMMYT), screened over 8000 wheat lines in the greenhouse and field, identifying 19 sources of resistance, many of which had equivalent or better resistance than the two resistant parents (2-49 and Sunco). This germplasm is currently being incorporated into advanced high-yielding backgrounds along with some standard and popular Turkish cultivars. Additional work from these researchers and other colleagues (Nicol et al.) reported that 121 spring and winter wheat lines were screened in the field for resistance to crown rot (*F. culmorum*) in Turkey, and in Mexico and Austria for resistance to FHB (*F. graminearum* and *F. culmorum*). The preliminary data are promising and showed that 15% of the lines had resistance to both FHB in Mexico and Austria and crown rot in Turkey. One-third of these lines were of Chinese origin.

In the Czech Republic, Slezažkova et al. surveyed transgenic Bt-maize and nontransgenic maize germplasm for the spectrum of toxigenic species of *Fusarium*. The most frequent species encountered were *F. subglutinans, F. verticillioides, F. proliferatum, F. sporotrichioides, and F. graminearum*. A lower incidence of these species was found in Bt-maize.
A research team in India (Pande et al.) associated with the International Crops Research Institute for the Semi-Arid Tropics, searched for host resistance to *F. oxysporum* f. sp. *ciceris* in 17,000 lines of chickpea and 12,000 lines of pigeonpea. Candidates were further selected and evaluated at locations in Asia and Africa where disease pressure is high. Several breeding lines were shown to have stable and durable resistance to Fusarium wilt of chickpea and pigeonpea. Many wilt-resistant varieties have since been adopted by farmers. These screening programs provide the extremely important function of identifying resistance germplasm.

**Breeding for resistance.** Two papers examined the inheritance of resistance to FHB in wheat from specific crosses. In New Zealand, 141 doubled haploid lines produced from a cross between a highly susceptible (18% ears infected) and a moderately resistant cultivar (1% ears infected) produced several lines that were as resistant to FHB as the resistant parent (Cromey et al.). There was a close relationship between the percentage of infected grains and mycotoxin concentrations. Breeding trials in Italy had the same objective (Ferrazzano and Demontis). A Chinese cultivar resistant to FHB (PSB Ning 7840) was crossed with the Durum elite cultivars. Selected progeny had lower levels of infection, higher weights, and lower deoxynivalenol (DON) content than the susceptible parent. Given that disease management with host resistance remains the most attractive strategy, it is encouraging to see these studies and learn of their findings. Developing high yield crop with resistance to *Fusarium* requires long term commitments in time, labour, and funding. However, it is equally disappointing to realize that there is a large number of crops in which little or no resistance has been identified.

**Disease management through reducing inoculum.**

**Effect of fungicides.** The fact that most *Fusarium* inoculum is ubiquitous makes sanitation a difficult strategy to implement. However, there were many reports that discussed experiments to directly reduce the inoculum with applications of fungicides. The use of fungicide treatments to reduce FHB and the crown rot disease of wheat were explored in Finland, Italy, and Kenya. Colleagues in Finland (Elen et al.) conducted field trials with azoxystrobin + propiconazole (Amistar Duo) and prothioconazole (Proline) on wheat to monitor mycotoxin concentrations of zearalenone, DON, 3-AcDON, enniatin B, and enniatin B1. Real-time PCR was used to measure DNA levels of Fusaria in the grain. No significant statistical effects were observed due to variation, but DON levels and the amount of DNA of *F. graminearum* were reduced by 70% in fungicide-treated plots. In oats, prothioconazole-treated plants did not differ in mycotoxin content or DNA of *F. langsethiae/sporotrichoides*.

Two Italian papers reported the efficacy of fungicide treatments to suppress FHB of wheat and the resulting DON levels in the grain. When the fungicide, prothioconazole, was applied at the beginning of wheat anthesis, significant reductions were achieved in both FHB disease severity (up to 70%) and DON content (up to 90%) in the grain as compared to the inoculated control (Pascale et al.). Yields were higher in plots treated with fungicides. Another Italian study found that when DMI fungicides were applied individually or combined at anthesis stage (GS 60-61), there was significantly less incidence and severity of FHB than in the untreated control (Pancandi et al.). The fungicides and the combinations that performed best were bromuconazole, cyproconazole combined with prochloraz, epoxiconazole combined with prochloraz, metconazol, and prochloraz combined with tebuconazole. Bromuconazole, prochloraz, and tebuconazole significantly reduced the percentage of *F. graminearum*- and *F. culmorum*-infected kernels by an average of 63% and reduced DON content by 66%, when compared with the untreated control.

In Kenya, surveys by Muthomi et al. found that FHB incidence was 7% and disease severity was 24%, while Fusarium contamination of the ears was 35% and of the grain was 53%. While co-inoculation with *Trichoderma* spp. reduced FHB severity, it increased DON content. However, tebuconazole and copper oxychloride both reduced FHB severity by 49% and 32%, respectively, and reduced DON content by 93%.

On maize, there was one Italian report by De Curtis et al. on using fungicides to reduce the inoculum of species that belong to the *Gibberella fujikuroi* complex and the fumonisins B1, B2, and B3. Although disease incidence and fumonisin contamination were quite severe, field trials showed that some fungicides resulted in significant reductions of Fusarium ear rot and fumonisin contamination. These presentations underscored the valuable role that fungicides have and will continue to have in providing suppression of disease and mycotoxin levels. However, since most of the reported products provided only partial control, new chemistries are still urgently needed. In addition, given the probability that fungicide resistance in Fusaria may be high, multiple chemistries combined with alternative methods of disease management must be developed.

**Role of over-wintering inoculum.** Another method to reduce inoculum is to understand its source, so that methods can be devised to limit its increase. Over-wintering inoculum of *F. verticillioides* on maize in the USA was shown by Kendra and Busman to be affected by the previous soybean crop. Although *F. verticillioides* did not affect soybean growth, the interaction did affect inoculum levels for the following maize crop. The use of “Round-up Ready” soybean cultivars may require that more attention be devoted to their possible role as symptomless carriers of *Fusarium* spp.

Canadian colleagues (Fernandez et al.) discovered a
similar phenomenon. They determined that when pea was regularly treated with glyphosate for weed control, there was more F.avenaceum damage on it and, in turn, there was more FHB and root rot on the cereal crops grown in rotation. The use of glyphosate on leguminous crops may need to be revaluated for its direct effect on increasing over-wintering inoculum.

Canadian researchers, Peters and Seifert, also studied the role of Fusarium inoculum on potato seed pieces in Northeastern Canada. They surveyed Fusarium species associated with potato seed and tuber rot and identified F. sambucinum, F.coeruleum, and F.avenaceum as the predominant species. The amount of rot in potato seed did not correlate with the severity of rot in storage which highlighted the role of wounds made during harvest. Furthermore, the Fusarium species that predominated in any particular seed-lot was often the major pathogen of concern in subsequent storage confirming the importance of seedborne inoculum for initiation of postharvest disease. These presentations reveal how understanding the source of inoculum and the factors that directly influence its ability to over-winter lead to strategies for reducing inoculum.

Disease management through manipulating the environment. There are multiple ways for the environment to influence the development of Fusarium disease, but a general understanding of how these factors can be manipulated to suppress disease and reduce mycotoxins is still unclear. Yet, our knowledge was advanced from studies on Fusarium diseases of cereal crops in Finland, South Africa, and the UK.

The role of tillage (autumn plowing and direct drilling) on Fusarium infection and mycotoxin contents of different oat cultivars was investigated with field trials in Finland by Parikka et al. The succession of species found on oats was that F. langsethiae and F. poae were prevalent early in the season, then were displaced by F. culmorum and F. graminearum. F. poae was most abundant in autumn-plowed plots and direct drilling increased the infection by F.avenaceum and reduced that by F.culmorum. Direct drilling of oats decreased DON and NIV contents in the grain, but increased HT2 and T2. DON was highest in cv. Roope, whereas HT2 and T2 toxins were highest in cv. Belinda.

The effect of changing rotation crops combined with soil treatments was examined in South Africa by Lamprech et al. to suppress Fusarium diseases on maize. Disease incidence was lowest in roots of plants subjected to anhydrous ammonia, methyl bromide, rotations with canola, crambe, or with maize followed by fallow, soybean followed by fallow, and wheat combined with tillage.

In the UK, a survey of trichothecenes in cereal grains showed that wheat had a high incidence of DON, oats were high in HT2 and T2, and barley was low in all trichothecenes (Edwards). Using these data, models were developed, which correlated the mycotoxin content with agronomic and climatic characteristics for each crop. The model for DON in wheat found that the site, climate, previous crop cultivation, variety, and fungicide use are all associated with DON levels. However, there was no difference in mycotoxins levels between organic and conventionally-grown wheat. In oats, the model revealed only minor correlation between HT2 and T2 content, the site or the year. On the other hand, there was a strong correlation with cultural practices: organic samples had significantly lower HT2 and T2 content than conventional samples. These presentations on grains lead to one frustrating conclusion, i.e. manipulations of environment that favour the suppression of one pathogenic species and its associated mycotoxins on one crop may not necessarily favour other pathogenic Fusaria and their toxins. The fractionation of the data makes it very difficult to generalize the role that cultural management has on Fusarium diseases.

The effect of monoculture may also influence the genetic structure of the pathogen. Spanish researchers (Landa et al.) discovered that new races of F.oxysporum f. sp. ciceris appeared in a chickpea field that had originally been infested with just one race. It was hypothesized that chickpea monoculture may have induced changes in the virulence and/or pathogenicity structure of the pathogen and/or F.oxysporum populations that initially inhabited the soil.

Efforts to reduce stress from other pests can also have profound effects on disease severity. One Italian paper by Blandino et al. showed that reducing stress on maize from the European corn borer suppressed disease by reducing infection sites caused by feeding. The severity of European corn borer, F. verticillioides infestation, and fumonisin concentration were all highly correlated. Insecticide treatments that were applied early against the 2nd larval generation resulted in significantly lower Fusarium infection and fumonisin contamination than treatments applied after the adult flight peak.

All the aforementioned papers on environment manipulation highlight not only what we have learned, but the large knowledge gaps in understanding how these methods can be integrated so as to control effectively Fusarium diseases. The general finding was that until we discover the underlying environmental factors that govern these pathogen/host/toxin systems, manipulations of the environment as a disease management strategy will remain specific to each disease situation.

The overriding message from the session was that each disease requires multifaceted management strategies. The objectives of identifying resistance genes, developing new chemistries and application methods, and understanding how to better manipulate the environment to reduce inoculum and suppress disease, remains a daunting task for all. However, the stimulating exchange of ideas and concepts will hopefully fuel ongo-
ing and future investigations. More importantly, the session sparked several new potential collaborations that may increase the number of weapons in our arsenal to fight Fusarium diseases.

W. Elmer

**MOLECULAR DETECTION AND DIAGNOSTICS**

(Session leaders: K. Abd-Elsalam, T. van der Lee)

The session on molecular detection and diagnostics was very well attended. The session encompassed a 20 min introduction and ten short communications. The speakers provided an informative overview of the large diversity of the methods applied in the struggle to understand the diversity of Fusarium pathogens and to monitor their presence and the toxin they produce. The keynote speech by T. van der Lee reviewed the different methods applied to understand the Fusarium populations causing Fusarium Head Blight (FHB) on wheat, barley and maize in China. *Fusarium* is a major constraint in the production of wheat and barley along the Yangtze River and a serious problem for maize production in the North-Eastern part of China, where over 50% of the maize kernels are infected. More than 2500 single spore isolates collected from maize, wheat and barley between 2002 and 2005 were characterized. Based on the pioneering work by K. O’Donnell, diagnostic primers for the different members of the *Fusarium graminearum* clade species were designed exploiting discriminating SNPs in the EF-1α gene by using a competition PCR assay. For isolates that could not be identified in this way, the EF-1α gene was sequenced and BLASTed using the web tool developed by D. Geiser et al. For several hundred isolates the results of the competition PCR assay were confirmed by Ward et al. using the Luminex technology. In addition, the application of the VNTR markers by Suga et al. was used to study the genetic diversity in China. Combined analyses indicate that the different species of the *F. graminearum* clade live sympatric and the distinction of the different species was crucial to uncover a recent sweep in *Fusarium* isolates with a positive selection for *F. asiaticum* isolates producing DON. The presentation stressed the need for large scale sampling in monitoring and the use of robust markers. New methods for high throughput SNP detection can be adopted to screen both diagnostic and neutral markers.

G. Brodal et al. showed that TaqMan and chemotype analysis are ready for large scale field analysis. They developed qPCRs for *F. poae* and *F. sporotrichioides*, collecting in 2006 and 2007 approximately 300 samples of naturally infected grains of oats and spring wheat from farms in the main cereal growing areas. T2 toxin was not found in wheat samples, but high levels were observed in oats.

C. Fanelli et al. developed a non-invasive method to image fungal infections in maize. Four toxigenic fungal species were imaged: *Aspergillus parasiticus, A. flavus, A. niger* and *F. graminearum*. The results obtained indicate that spectral imaging can discriminate different fungal strains, each producing their unique spectral fingerprint. A desktop spectral scanner equipped with an imaging based spectrometer ImSpector- Specim V10, working in the visible-near infrared spectral range (400–1000 nm) was used in the experiments. These authors also presented recent advances to detect infection based on this non-invasive spectral imaging. In the future this technique could be applied to discriminate infected from non-infected maize kernels.

L.H. Pfennig and co-workers used sequences of EF-1α gene to design species-specific primers for PCR detection of the causal agents in plant tissue. Three clusters of isolates were observed in AFLP analysis, one being specific for Brazilian isolates. EF-1α sequences allowed the development of specific primers for this Brazilian clade.

A. Minnaar-Ontong performed AFLP analysis using three different primer pairs on 860 isolates that were morphologically identified as *Fusarium* spp. Analyses detected genetic variation among and within *Fusarium* species isolated from wheat in South Africa. Although AFLP can only provide dominant and anonymous markers, the high resolution of this marker technology can still provide clear evidence for population substructures.

L. Niessen used Loop-mediated isothermal AMPlification (LAMP) of DNA as a simple, cost effective, and rapid novel method for the specific detection of genomic DNA by using a set of eight nested primers that bind specifically to different regions of a target gene in combination with a thermophilic DNA polymerase from *Bacillus stearothermophilus*. They showed that LAMP is effective and fast in detecting and quantifying *F. graminearum*, by targeting the *goaA* gene that encodes galactose oxidase. The detection limit was found to be less than 100 fg per reaction.

E. Nitschke and M. Varrelmann identified 12 species of *Fusarium* on sugar beet based on EF-1α sequences. This interspecific divergence could be translated into a PCR-RFLP assay using only two independent restriction digests for the differentiation of 17 out of 18 species. The developed EF-1α based PCR-RFLP assay was able to identify and differentiate a sugar beet-derived broad spectrum of *Fusarium* species including pathogenic species relevant for cereals in crop rotations, as well as saprophytic species. The authors showed that the EF-1α sequence provides a good source for species identification. Their approach of PCR in combination with restriction digest can provide a cheap alternative to sequencing.

S. Pande et al. combined AFLP analyses with viru-
brane assays on chickpea. The authors were able to
discriminate virulent and avirulent strains of *F. oxysporum*
*f. sp. ciceris* providing evidence of the high discrimina-
tory power of AFLP analysis for the molecular charac-
terization of this pathogen.

A. Moretti confirmed that only few genes in Ascomy-
cota seem to be free from introns and, among them,
ND6, ND2 and ND4 genes could really be the best bar-
code candidates. As discussed in other sessions identify-
ing a good candidate for barcoding in fungi is not easy.
Mitochondral genes such as the cytochrome oxidase
gene *CO1*, that were selected for other organisms, such
as insects, may not be good candidates. Attempts to find
more robust genes in the fungal mitochondrial genome
have so far not resolved this issue.

Several posters in the session dealt with the develop-
ment of new diagnostic tools such as additional TaqMan
assays and diagnostic SCAR primers and the application
of these diagnostic markers for field studies. These re-
ports emphasize the large diversity in the genus *Fusari-
um*. Moreover, the need for monitoring requires the
continuous development and improvement of diagnos-
tic tools at reduced cost. Hopefully in this new genomic
era with improved insights in phylogeny and the emer-
gence of new equipment, we can meet future demands
and get a better understanding of *Fusarium* populations
in the field. This session and workshop surely will con-
tribute to this task.

T. van der Lee

**HOST-FUNGAL INTERACTIONS**

(Session leaders: A. di Pietro, W. Schäfer)

This session covered a wide array of topics: plant de-
defence reactions, fungal physiology and its relation to
pathogenicity, as well as specific fungal pathogenicity
factors. The diversity was further documented by the
different *Fusarium* species, namely *F. oxysporum*, *F. cul-
morum*, and *F. graminearum*.

Specific fungal pathogenicity factors active in differ-
ent host kingdoms were described for *F. oxysporum*. A
single strain of *F. oxysporum* *f. sp. lycopersici* is able to in-
fect both tomato plants and immunocompromised mice.
A. Di Pietro and co-workers showed that different sets
of pathogenicity genes are required by this fungal strain
to successfully colonize either plant or mammalian hosts,
pointing to distinct evolutionary origins. M. Rep and co-
workers applied a large scale insertional mutagenesis ap-
proach by transforming *F. oxysporum* *f. sp. lycopersici*
with *Agrobacterium tumefaciens*, leading to random inte-
gration of the transforming T-DNA into the fungal
genome. Using this insertional mutagenesis approach
they identified 20 non-pathogenic mutants and 86 mu-
tants reduced in virulence. This so called unbiased ap-
proach paves the way to the identification of new path-
ways and components relevant for fungal pathogenicity.

*F. graminearum* infects wheat heads in moderate cli-
mate, whereas in dry areas, like parts of Australia, it is a
seedling pathogen causing crown rot disease. J.M. Man-
ners and co-workers reported about their ongoing char-
acterization of fungal and plant genes transcribed dur-
ing crown rot disease of wheat. The groups of H. Giese
from Denmark and W. Schäfer from Germany reported
about fungal pathways and components instrumental
for pathogenicity of *F. graminearum* on wheat and
maize. H. Giese and co-workers demonstrated that au-
tophagy, the ability of the fungus to recycle its own
components for nutritional use, is necessary for success-
ful infection. W. Schäfer reported that a network of dif-
ferent secreted lipases are instrumental for the ability
to colonize both wheat and maize plants, most likely by
suppressing a specific plant defence reaction.

Plant defence against *F. graminearum* was improved
by generating transgenic wheat plants. R. D’Ovidio and
co-workers generated wheat plants overexpressing a
polygalacturonase-inhibiting protein (PGIP) from bean.
In addition, they also expressed an enzyme which modi-
fies deoxynivalenol, a fungal toxin known to be essential
for colonization of wheat heads. Both approaches indi-
vidually or in combination, lead to increased resistance
against *F. graminearum*. This demonstrates that the fun-
gal toxin is indeed a virulence factor and suggests that
fungal polygalacturonases are also involved in virulence
of *F. graminearum* on wheat.

Fungal pectolytic enzymes were detected by the
group of G. Chilosi and co-workers in the apoplastic
fluid during *F. culmorum* infection of wheat, together
with an increase of secreted ammonia and extracellular
pH. The shift in pH coincided with increased pecti-
olytic activity and a decrease of plant peroxidase activ-
ity, suggesting that modulation of the plant apoplastic
pH by the fungal pathogen could favour fungal viru-
ulence factors while repressing plant defence reactions.

A. di Pietro and W. Schäfer

**MYCOTOXINS AND METABOLISM**

(Session leaders: N. Magan, U. Thrane)

This session was very well attended with more than
30 papers presented orally or as posters. The potential
of *Fusarium* species to produce a series of biological ac-
tive metabolites including mycotoxins, e.g. the tri-
chothecenes, zearalenones, fumonisins, moniliformin,
and beauvericins and other cyclic peptides was outlined
as well as updated information on the species specific
profiles of metabolites. The future of *Fusarium* as a mi-
crobial cell factory was also presented highlighting that
microbial products from *Fusarium* should be toxin-free,
which requires a future integration of *Fusarium* phenetics and *Fusarium* genomics to gain a deeper knowledge on regulation of mycotoxin genes. This issue was addressed during the session, as a gene cluster coding for the pigment of perithecia was presented and, by use of gene targeting tools, it was shown to possibly regulate the biosynthesis of polyketides to the production of novel metabolites. The effect of temperature and humidity on mycotoxin production was also addressed in details by evaluation of the gene expression levels under different conditions in two different species, and it was concluded that a succession of species during grain development may not reduce the risk for mycotoxins.

To illustrate the challenges with *Fusarium* mycotoxins in agriculture, data from South Africa were presented, highlighting that there is a lot to be done in the future to reduce the toxin contamination. It was also shown that Italian rice may contain high levels of mycotoxins originating from the rice pathogen, *F. fujikuroi*. Co-products from bio-ethanol production may also contain high amounts of mycotoxins, which should be taken into consideration before feeding animals.

During the oral session and the following poster session there was a lively discussion illustrating that *Fusarium* mycotoxins are very important in many scientific areas such as gene regulation, natural products chemistry, agriculture and of course human and animal health on a global scale.

N. Magan and U. Thrane
XV NATIONAL MEETING
OF THE ITALIAN SOCIETY FOR PLANT PATHOLOGY (SIPaV)

Locorondo (Bari), September 28th - October 1st, 2009