

**MOLECULAR PHYLOGENY OF *FUSARIUM* INFERRED FROM PARTIAL RNA POLYMERASE II GENE SEQUENCES.**

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Currently there are no robust phylogenetic hypotheses for *Fusarium* based on large-scale sampling across the breadth of this important group of mycotoxigenic phytopathogens. Nucleotide variation within the second largest RNA polymerase subunit (*RPB2*) protein-coding gene, however, has clearly demonstrated the utility of partial sequences from this gene for resolving evolutionary relationships among clades of medically important fusaria (O'Donnell *et al.*, *J. Clin. Microbiol.* **45**: 2235-2248, 2007). Two attractive features of this gene for phylogeny reconstruction within *Fusarium* include: 1) strong support for relationships among many clades was obtained for the first time, and 2) the region sequenced (1.8 kb) can be easily aligned across the genus, thereby establishing positional homology. A comprehensive *RPB2* dataset is being constructed to assess the contribution of this gene for resolving phylogenetic relationships within *Fusarium*. As strongly supported, monophyletic species complexes (i.e., clades) are identified, genealogical concordance of multilocus DNA sequence data is being used to identify phylogenetically distinct species. This data will be incorporated into the next version of the web-accessible *Fusarium*-ID database.

**THE STATUS OF DNA BARCODING FOR *FUSARIUM*.**

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DNA barcoding is the use of DNA sequences from standardized genes to identify species in all kingdoms of life. The mitochondrial gene, Cytochrome oxidase 1 (*Cox1*) is being used to barcode many animal groups, and preliminary experiments are underway with fungi. We developed and tested primers for amplification and sequencing of the barcode region of *Cox1* of *Fusarium* and other genera of *Hypocreales*. The primers successfully amplified and sequenced nine genera and 19 species of *Fusarium* in preliminary tests. Multiple copies of *Cox1* occurred in several strains of *Fusarium*. In some, copies of the same length were detected by heterozygous bases in otherwise clean sequences; this may indicate multiple transcribed copies. Other strains included copies with one, two or three introns. One intron insertion site included at least two non-homologous intron sequences. Five different *Cox1* amplicons were recovered from strains of *F. graminearum*; their sequences did not cluster together in phylogenetic analyses. Using reverse transcriptase PCR, we are now attempting to determine which *Cox1* copy is expressed. The overall divergence among the *Cox1* sequences obtained is low, with many species sharing identical sequences, so developing a precise *Cox1*-based barcoding system for *Fusarium* may not be feasible. We will discuss the informal proposal to employ the internal transcribed spacer (ITS) as the fungal barcode. The requirement for a standardized barcoding gene across as much of the *Eumycota* as possible provides a challenge to those wishing to barcode *Fusarium*.

***FUSARIUM* COMPARATIVE GENOMICS REVEALS GENOME DYNAMICS AND ITS IMPACTS ON PATHOGENESIS.**

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Collectively, *Fusaria* are the most important plant pathogens, causing disease in nearly every agriculturally important plant. To employ the power of comparative genomics in understanding pathogenesis of this group of organisms, three closely related species *F. graminearum*, *F. verticillioides* and *F. oxysporum*, have been sequenced and analyzed. The sequence relatedness among these carefully selected genomes allows an unprecedented ability to determine orthologs, and to identify species-specific features. Over 90% of the *F. verticillioides* genome can be unambiguously aligned to the syntenic regions in *F. oxysporum* with an average 90% sequence identity. Specifically, all the eleven chromosomes in *F. verticillioides* have corresponding chromosomes in *F. oxysporum* and *F. graminearum*. In contrast, four of the *F. oxysporum* chromosomes, accounting for over 15 Mb, lack significant orthologous sequence in the other two genomes. These *F. oxysporum*-specific chromosomes are enriched for genes that encode secreted proteins including the known virulence factors such as *SIX* (Secreted in Xylem) proteins and plant cell wall degrading enzymes. Over representation of various transposable elements are also observed in these chromosomes. Karyotype variation among field isolates of *F. oxysporum* and the preliminary analysis of the EST sequences from *F. oxysporum* f. sp. *vasinfectum* reveals the chromosomal polymorphism among different strains. The prevalence of the chromosomal polymorphism among *F. oxysporum* species complex, which has wide host range, may indicate the association of genetic plasticity provided by these species-specific chromosomes and the ability of the organism to adapt to diverse ecological niches. Examining sequence content and evolutionary mechanisms underlying the acquisition and diversification of such genetic material will open the door to understand the development of pathogenesis and host specificity.

**GLOBAL GENE EXPRESSION DURING PLANT INFECTION AND TOXIN BIOSYNTHESIS IN *FUSARIUM GRAMINEARUM*.**

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To understand trichothecene accumulation and the infection cycle of the head blight pathogen *Fusarium graminearum sensu stricto*, fungal gene expression profiles were monitored during plant infection using the *F. graminearum* Affymetrix GeneChip. Strains containing mutations in genes for three transcription factors were found to control trichothecene accumulation *in planta* and pathogenicity. Expression profiles were compared between wildtype and these mutants during infection of wheat. Mutants deleted for the *StuA* gene were greatly decreased in sporulation and produced no perithecia in culture. Unlike  $\Delta$ *StuA* mutants in *F. oxysporum*, *F. graminearum*  $\Delta$ *StuA* mutants were greatly re-



duced in pathogenicity. Reduced pathogenicity may be due to decreased trichothecene levels *in planta*, which in the mutant were <1% the levels of wildtype. Levels of transcripts corresponding to *TRI5*, but not other genes involved in trichothecene biosynthesis, were extremely diminished in the *ΔstuA* mutant. Thus both sporulation and trichothecene synthesis may be regulated under the control of *StuA*. Mutants deleted for the transcription factors *TRI6* and *TRI10* also were diminished for both trichothecene accumulation and pathogenicity to wheat. Largely overlapping sets of approximately 200 genes were altered in expression  $\geq$  two-fold in either *Δtri6* or *Δtri10* strains. In addition to genes responsible for trichothecene biosynthesis, genes involved in primary metabolism and transport also were significantly regulated by *TRI6* and *TRI10*. A model for global regulation and cross pathway control of sporulation, mycotoxin biosynthesis and pathogenicity will be presented.

**DIFFERENT SECRETED LIPASES ARE VIRULENCE FACTORS OF *FUSARIUM GRAMINEARUM*.** N.N. Long, M. Fehrmann, S. Salomon and W. Schäfer. *University of Hamburg, Biocenter Klein Flottbek, Molecular Phytopathology and Genetics, Ohnhorststr. 18, D22609 Hamburg, Germany. E-mail: schaefer@botanik.uni-hamburg.de*

The cereal-*Fusarium* pathosystem is characterized by non-race and non-host specific relationships. The outcome of infection varies between total destruction of the host and minor damage. Virulence of *F. graminearum* is most probably the consequence of a specific collection of several, additively acting virulence factors. However, only mycotoxins of the trichothecene-class were known to be secreted virulence factors towards wheat. We have shown recently that a secreted fungal lipase is a new virulence factor, in addition to the already known secreted trichothecenes. We identified 17 putatively secreted lipase genes in the genome of *F. graminearum*. We are currently cloning and further characterizing these genes. So far we can say, that three of them act as virulence factors, whereas other secreted lipases are not involved in fungal virulence. One of the tested lipases seems to uphold vital functions in the fungal cell, as we were unable to disrupt the gene. We demonstrate the infection behaviour of the different lipase-mutants on wheat and analyse transcriptional activity of the different lipase genes in wild type and knock out mutants during wheat head infection.

**GOING FOR THE VEGGIES AND THE MEAT: EXPLORING THE GENETIC BASES OF TRANS-KINGDOM PATHOGENICITY IN *FUSARIUM OXYSPORUM*.** A. Di Pietro<sup>1</sup> and J. Guarro<sup>2</sup>. <sup>1</sup>Departamento de Genética, Universidad de Córdoba, 14071 Córdoba, Spain. <sup>2</sup>Unitat de Microbiologia, Facultat de Medicina y Ciències de la Salut, Universitat Rovira y Virgili, 43201 Reus, Spain. E-mail: ge2dipia@uco.es

Plant pathogenic fungi produce devastating losses in global agriculture, whereas opportunistic human pathogens cause life-threatening infections in immunocompromised patients. To which extent infection mechanisms are conserved between plant and human pathogens remains an open question. A number of *Fusarium* species such as *F. solani* and *F. oxysporum* have been reported as pathogens of plants and humans. To study the genetic basis for this remarkably broad host range, we have established a multihost infection model based on a single strain of the vascular wilt pathogen *F. oxysporum* f. sp. *lycopersici*, able to cause disease both on tomato plants and immunodepressed mice (Ortoneda et

al., *Infec. Immun.* **72**: 1760-1766, 2004). Mutants generated in this strain can be directly tested for the effect on virulence on plant and mammalian hosts. Using both forward and reverse genetics, we have identified a number of virulence determinants including signalling components, transcription factors, cell wall biogenesis enzymes and secreted proteins. The results obtained so far support the view that fungal infection of plant and mammalian hosts requires distinct sets of pathogenicity genes and thus may have different evolutionary origins. Our long-term goal is to understand the unique genetic setup that enables *F. oxysporum* to adapt to and cause disease on a range of hosts across different eukaryotic kingdoms.

**USE OF PROTECTIVE STRAINS OF *FUSARIUM OXYSPORUM* TO CONTROL FUSARIUM WILTS.** C. Alabouvette, C. Olivain and C. Steinberg. *UMR Microbiologie du Sol et de l'Environnement, INRA, Université de Bourgogne, 21065 Dijon Cedex, France. E-mail: ala@dijon.inra.fr*

Soil-borne strains of *Fusarium oxysporum* are involved in the mechanisms of soil suppressiveness to Fusarium wilts, and many attempts have been made to use non pathogenic strains of *F. oxysporum* to control Fusarium diseases. The modes of action of the protective strains are diverse; they include direct antagonism, such as competition for nutrients or for root colonisation and indirect antagonism through induced resistance of the plant. The use of newer tools has enabled a reconsideration of these modes of action. The use of marked strains contributed to minimize the importance of competition for infection sites and the use of cell cultures permitted to make progress in the understanding of the interactions between the plant and either pathogenic or protective strains of *F. oxysporum*. Even though the mechanisms of biocontrol of *F. oxysporum* are far from being understood, several processes of mass production have been developed to enable field application of the biocontrol strains. These strains possess a great ecological fitness and establish in soil with different physico-chemical properties. Their introduction into the soil does not durably modify the structure of the soil-borne communities of fungi and bacteria, indicating that their use does not present any risk to the environment.

***FUSARIUM* IDENTIFICATION DATABASES, PRESENT AND FUTURE.** D.M. Geiser<sup>1</sup>, S. Kang<sup>1</sup> and K. O'Donnell<sup>2</sup>. <sup>1</sup>Department of Plant Pathology, The Pennsylvania State University, State College, Pennsylvania, USA. <sup>2</sup>NCAUR-ARS-USDA, Peoria, IL, USA. E-mail: dgeiser@psu.edu

DNA-sequence based identification of fungi is now in wide practice. For a community molecular identification tool to be effective, it must be based on an appropriately informative locus or set of loci, technology that is broadly available, and most importantly, connected to a definitive database. A first rudimentary attempt at creating such a database was FUSARIUM-ID (Geiser et al., *Eur. J. Plant Pathol.* **110**: 473-479, 2004). This database consists of a web-accessible BLAST server of partial translation elongation factor-1-alpha sequences. A key feature for this or any effective identification database is that all sequences be connected to vouchered, publicly available cultures. Shortcomings of the first version database include an incomplete representation of *Fusarium* species, a lack of accession data about isolates in the database, and an inability to download sequences. Here we outline features of a new *Fusarium* database, which includes substantial improvements with regard to these shortcomings, as well as new features. The database, which is based on the Phytophtho-

raDB (<http://www.phytophthoradb.org>), will include identification tools for multiple loci attached to far more isolates. In addition, users will have access to isolate information, and be able to generate alignments, phylogenetic trees and virtual RFLP gels. New tools will allow users to link data from a query isolate to the released *Fusarium* genomes, and geographic information systems (GIS) functions.

**THE EXO-METABOLOME IN *FUSARIUM*.** U. Thrane. *Technical University of Denmark, Center for Microbial Biotechnology, Department of Systems Biology, Søtofts Plads 221, 2800 Kgs. Lyngby, Denmark. E-mail: ut@bio.dtu.dk*

*Fusarium* species are efficient producers of biologically active metabolites including mycotoxins, e.g. the trichothecenes, zearalenones, fumonisins, moniliformin, and beauvericins and other cyclic peptides. These metabolites and all other metabolites produced by *Fusarium* species intended for interaction with the environment are called the exo-metabolome (earlier known as the secondary metabolites). The metabolite production is highly influenced by the growth conditions and this information is of high value to feed and food safety as *Fusarium* and its mycotoxins are unwanted in agricultural crops. The available information on *Fusarium* mycotoxins is overwhelming. A search for scientific peer-reviewed papers using the keywords “*Fusarium* AND mycotoxin” retrieve > 250 hits published in 2007! This accounts for over 20 papers per month or nearly one scientific paper every day at work. In addition, not all journals are covered by these search engines and books, congress proceedings and technical reports are certainly not! Unfortunately the quality of the information is varying and in this context both the identification of mycotoxin and the producing organisms are the weak points. Updated information on the species-specific profiles of metabolites will be presented and discussed with a focus on future exploitation of the biotechnological use of *Fusarium* as a microbial cell factory together with the increasing information on the genetics behind metabolite production. To ensure that microbial products from *Fusarium* are toxin free a future integration of *Fusarium* phenetics and *Fusarium* genomics are foreseen as deeper knowledge on regulation of mycotoxin genes is crucial.

**MOLECULAR DETECTION AND DIAGNOSTICS OF *FUSARIUM* SPP. ISOLATED FROM COTTON.** K.A. Abd-El salam<sup>1,2</sup>, A. Asran-Amal<sup>1</sup>, J.R. Guo<sup>3</sup> and J.A. Verreet<sup>3</sup>. <sup>1</sup>Agricultural Research Center, Plant Pathology Research Institute 9, Gamaa St., Giza, Egypt. <sup>2</sup>King Saud University, Faculty of Science, Botany and Microbiology Department, P.O. Box 2455, 1145 Riyadh, Saudi Arabia. <sup>3</sup>Institute of Phytopathology, Christian Albrechts University of Kiel, Hermann Rodewald St. 9, 24118, Kiel, Germany. E-mail: abdel salamka@gmail.com

*Fusarium* is one of the most heterogeneous fungal genera and taxonomy of species within this genus is very intricate. Because species may differ in minor morphological features, identification can be a difficult task for those not familiar with these fungi. Consequently, there is a need for tools that can provide accurate diagnostics and reproducible identification of *Fusarium* species. Formerly, a PCR assay based on a pair of oligonucleotide primers targeting the 16S and 23S rRNA genes was used to detect *Fusarium oxysporum* f. sp. *vasinfectum* (Fov), a fungus causing *Fusarium* wilt of cotton in infected cotton seedlings. Additionally, we developed an improved real-time PCR assay for the identification of *F. solani* isolates recovered from cotton. A search in *F. gramin-*

*earum* genome database was conducted for sequences containing microsatellite repeats. The raw data sets for each of fungal genomes are accessible at <http://www.mmrl.med.usyd.edu.au/ssr.html>. The aim of this search was to explore repetitive sequences that were expected to have a very high degree of polymorphism. Twenty microsatellites were selected and primers were designed. Two microsatellite primers, distinctive and reproducible sets of amplification products were observed for all *Fusarium* species tested. Twelve *Fusarium* species could be readily distinguished by their PCR fingerprint patterns.

**DIAGNOSTIC TOOLS TO CHARACTERIZE TOXIGENIC *FUSARIUM* SPECIES.** T.A.J. van der Lee<sup>1</sup>, X. Xu<sup>2</sup>, C. Huang<sup>3</sup>, L. Yang<sup>4</sup>, D.Z. Yu<sup>4</sup>, Z. Zhang<sup>5</sup>, H. Zhang<sup>5</sup>, J. Feng<sup>5</sup> and C. Waalwijk<sup>1</sup>. <sup>1</sup>Plant Research International, Droevendaalsesteeg 1, 6708 PB Wageningen, The Netherlands. <sup>2</sup>Institute for Plant Protection, LAAS, Shenyang, PR China. <sup>3</sup>Institute of Agricultural Resources and Regional Planning, CAAS Beijing, PR China. <sup>4</sup>Institute for Plant Protection, HAAS, Wuhan, PR China. <sup>5</sup>Institute for Plant Protection, CAAS, Beijing, PR China. E-mail: Theo.vanderlee@wur.nl

Wheat, maize, and barley are among the world's most important food and feed crops, yet quantity and quality of the production is threatened by *Fusarium* head blight (FHB) caused by a complex of *Fusarium* species. The *Fusarium* genus is represented by a large number of evolutionary related but epidemiological and toxicologically diverse organisms that cause similar symptoms on their hosts. Some *Fusarium* species can be distinguished morphologically but molecular research has shown that isolates with similar morphology represent different species. Molecular methods are therefore required to identify the different species. Preferably these methods should be reliable, fast and inexpensive thereby allowing the screening of large number of samples. Previously we generated TaqMan real-time PCR methods for *F. culmorum*, *F. avenaceum*, *F. poae*, members of the *F. graminearum* clade and fumonisin producers. These TaqMan PCRs have been applied to study the incidence and infection levels of *Fusarium* in wheat and maize samples. In addition we developed an inexpensive diagnostic PCR based on SNP identified between species using a duplex PCR strategy. We applied this diagnostic PCR and characterized over 2500 single spore isolates collected from maize, wheat and barley. Currently we are adapting the various diagnostic PCRs for the BioTrove open array PCR platform to perform both quantitative and qualitative analysis.

**INTEGRATED STRATEGIES FOR SUPPRESSING *FUSARIUM* DISEASES OF ORNAMENTALS.** W.H. Elmer. *Department of Plant Pathology and Ecology, The Connecticut Agricultural Experiment Station, New Haven, CT 06504, USA. E-mail: Wade.Elmer@po.state.ct.us*

The most successful strategy for the suppression of *Fusarium* diseases has been host resistance. Although success has been achieved for some vegetable crops, little attention has been paid to ornamentals. Thus, multifaceted approaches need to be developed and tailored to each host-*Fusarium* system. Three strategies were studied: sanitation, fungicides (chemical and biological), and induced resistance. Sanitation was the most cost-effective strategy. We found that the incidence of pathogenic isolates of *Fusarium oxysporum* on seeds of China aster and coreopsis was between 5 and 7%. Simple seed disinfestations alone dropped disease incidence to less than 1%. Despite these measures, orna-

mental crops need preventative treatments. The fungicides azoxystrobin, fludioxonil, and triflumizole provided the most protection when compared to benzimidazoles. In addition, specific combinations of fludioxonil and commercially available biological fungicides suppressed *Fusarium* wilt on cyclamen more than any one treatment alone. However, these combinations were ineffective in suppressing *Fusarium* corm rot of gladiolus. On the contrary, products such as acibenzolar-s-methyl, which activate the systemic acquired resistance pathway in plants, were effective in providing season-long protection of gladiolus from *Fusarium* corm rot but had marginal effects on *Fusarium* wilt of cyclamen. Other conflicting examples using nonpathogenic *F. oxysporum* strains to suppress disease were observed as well. On gladiolus, nonpathogenic *F. oxysporum* were equal to chemical fungicides in suppressing *Fusarium* corm rot, but when these strains were applied to cyclamen, they did not suppress *Fusarium* wilt. Until *Fusarium* resistance can be identified, specific multifaceted approaches must be developed for each crop.

**FUSARIUM WILT OF CHICKPEA: PROGRESS AND PROSPECTS FOR DISEASE MANGEMENT.** R.M. Jiménez-Díaz<sup>1,3</sup>, M.M. Jiménez-Gasco<sup>2</sup>, B.B. Landa<sup>3</sup>, P. Castillo<sup>3</sup> and J.A. Navas-Cortés<sup>3</sup>. <sup>1</sup>Departamento de Agronomía, Universidad de Córdoba, Edificio C4 "Celestino Mutis", Campus Rabanales, Carretera de Madrid Km 396, Córdoba, Spain. <sup>2</sup>Department of Plant Pathology, The Pennsylvania State University, University Park, PA 16802, USA. <sup>3</sup>Departamento de Protección de Cultivos, Instituto de Agricultura Sostenible, Consejo Superior de Investigaciones Científicas, Apartado 4084, 14080 Córdoba, Spain. E-mail: agljdir@uco.es

*Fusarium* wilt of chickpea is caused by soilborne, monophyletic *Fusarium oxysporum* (Schlechtend.:Fr.) f. sp. *ciceris* (Padwick) Matuo & K. Sato (*Foc*). Resistant cultivars are the most practical disease management strategy, which efficiency may be influenced by ecological and pathogenicity features in *Foc* populations. Eight *Foc* races (0, 1B/C, 1A, 2, 3, 4, 5, and 6) have been identified, each forming a monophyletic lineage. Cultivar-specific pathogenicity in *Foc* races was acquired in a simple stepwise pattern with few parallel gains or losses. *Foc* races cause a yellowing (races 0 and 1B/C) or wilting syndrome and differ in the inoculum density needed for severe disease in a chickpea genotype. Virulence increases from race 0 through races 1B/C, 1A, and 5, in this sequence, and shows a differential interaction with temperature. Cultivars with resistance to *Foc* races have been developed. Resistance to races 1A, 2, 3, 4 and 5 is monogenic or oligogenic and recessive. Individual genes for oligogenic resistance confer late wilting but two late-wilting genes are required for complete resistance. Slow wilting was also identified which confers reduced disease progress and final disease. Complete resistance in some cultivars against specific *Foc* races can be overridden by 3-4 °C temperature increase or infection by the root-knot nematode *Meloidogyne artiellia*. Late-wilting/slow-wilting cultivars can be combined with early sowings in winter for *Fusarium* wilt management. Efficiency in the combined use of late-wilting chickpeas and choice of sowing date for disease management can be reinforced if integrated with seed and soil treatment with biological control strains such as *Bacillus subtilis*, *Pseudomonas fluorescens* and non-pathogenic *F. oxysporum*.

**THE MISSING LINK IN FUSARIUM HEAD BLIGHT-CROWN ROT CONTINUUM OF WHEAT.** S. Chakraborty, J.B. Scott, K. Abeywickrama, F. Obanor and C. Liu. CSIRO Plant Industry, Queensland Bioscience Precinct, 306 Carmody Road, Brisbane,

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The same *Fusarium* species can infect spike tissue to cause head blight (FHB) and/or stem base to cause crown rot (CR). A key factor underlying the global prominence of FHB is the concern for mycotoxin contamination and its impact to human and animal health. Both diseases are found in most cereal growing regions of the world. With warm and wet weather at flowering favouring FHB it is far more widespread and severe in many countries, while CR, favored by dry weather is more severe in Australia. Of the 17 *Fusarium* species that can cause either disease, the dominant two, *F. graminearum* and *F. pseudograminearum* can be equally aggressive for both diseases. Both have a necrotrophic phase allowing survival between cropping seasons with similar saprophytic fitness and host range. The level of genotypic and phenotypic diversity and population differentiation are similar for both species; neither is strictly clonal or panmictic. Despite these similarities links in their epidemiology are not well studied. It is believed that stem base infection in CR does not lead to FHB and FHB infection does not cause CR but systemic spread is not well-understood. The colonisation of stubble remains the missing link in the FHB-CR continuum. Whether the FHB pathogen travels from spike to the base of plants between flowering and harvest or sub-clinical infection of stem base or saprophytic colonisation of the stubble leads to the production of primary inoculum on stubbles have not been studied. Improved understanding of the FHB-CR continuum will benefit disease management.

**FUSARIUM HEAD BLIGHT: A DISEASE COMPLEX.** P. Nicholson. John Innes Centre, Norwich Research Park, Colney, Norwich NR4 7UH, UK. E-mail: paul.nicholson@bbsrc.ac.uk

*Fusarium* head blight (FHB) of wheat and barley is caused by several fungal species that cause similar symptoms. Although members of the *Fusarium graminearum* clade are the major pathogens worldwide, other *Fusarium* species are of significance in many countries. In maritime regions *F. culmorum* is often associated with FHB while *Fusarium avenaceum* and *F. poae* routinely predominate in Northern Europe. In addition to the true *Fusarium* species, *Microdochium nivale* and *M. majus* are particularly prevalent where cooler, wetter conditions prevail. The relative contribution of each of the above species in causing disease will depend upon a range of variables, possibly the most important of which is environment. The *Fusarium* species that cause FHB produce a range of mycotoxins, in particular trichothecenes that frequently contaminate blighted grain. Several chemotypes exist within *F. graminearum* and *F. culmorum*. Deoxynivalenol (DON) is the predominant mycotoxin produced by some isolates while others produce mainly nivalenol (NIV). Two genes, *Tri7* and *Tri13*, have been found to be non-functional in all isolates examined to date that are unable to make NIV. Although DON has been shown to be a virulence factor towards wheat, it is not clear how host or environmental factors influence the production of DON. Furthermore, it is not known what selective pressures are operating to maintain both NIV and DON producers in populations. Studies involving different *Fusarium* species and mixtures of *Fusarium* and *Microdochium* species are being undertaken to understand how these fungi interact and to identify the factors that determine which species is dominant in a particular situation. In addition, the potential role of different cereal hosts in selection for the DON and NIV chemotypes is also being investigated. Molecular diagnostics are being used extensively in this work and it is anticipated that these tools will shed light on the consequences of fungal/host/environment interactions for disease development and mycotoxin accumulation.