Saturday 31 March

Keynote lecture

From Genotype to Phenotype ---An Inconvenient Truth

Gerald R. Fink
Whitehead Institute/MIT Nine Cambridge Center Cambridge, MA 02467

Genome wide comparisons of transcriptional circuits among different fungal species have shown that these regulatory networks are extremely variable. This network plasticity has been most thoroughly documented in the comparison of mating type regulation between the evolutionarily distant species *Candida abicans* and *S. cerevisiae*. Although the group of genes controlling mating and the transcriptional regulators are similar, the circuit that regulates the mating genes uses an activator in Candida and a repressor in Saccharomyces. As this change in circuitry between species involves many mutational changes that are unlikely to have occurred simultaneously, the conversion of one circuit to another raises the question: How much network variation exists within a single species?

To address this question we compared the deletion phenotypes of two closely related strains of *Saccharomyces cerevisiae*, the reference strain S288c and a closely related strain, Σ1278b, by individually deleting every gene in Σ1278b. Despite their overall sequence similarity, these strains show dramatic differences in phenotype even among those genes considered "essential." This difference in essentiality is polygenic, often depending on more than 5 genes. A second comparison of the two strains for the genes that affect adhesion/filamentation again revealed unexpected differences. Adhesion in Sigma is controlled by the filamentation MAPK pathway (fMAPK), which activates the transcription of a downstream structural gene *FLO11*.

However, in Sigma the fMAPK pathway is not required to activate *FLO11* for adhesion/filamentation despite the fact that the MAPK pathway is still present and active in mating. In S288c the requirement for the fMAPK pathway is bypassed by many different polymorphisms that lead to fMAPK independence. We identified one of these suppressors of the fMAPK pathway SUP1(S288c), a transcription factor, capable of bypassing the fMAPK pathway in both S288c and Sigma. The Sigma allele, SUP1(Sigma) cannot bypass the fMAPK pathway either in S288c or Sigma. Thus, both for essential genes and morphological traits there are fundamental differences in gene control. Our studies show that even within a species there is substantial variation in the networks that control gene expression. These polymorphisms are the obvious grist for speciation.

Monday 2 April

Keynote lecture

***Ustilago maydis*: an experimental organism for 21st century biology**

William Holloman
Cornell University Medical College

The fundamental principles of cell growth, division, differentiation, communication, and development have come from discoveries made in an odd collection of organisms including flies, worms, and fungi. Given that advances in DNA sequencing technologies and gene transfer methods makes exploration of genetic questions possible in almost any organism, a question for students to ponder is why do only a handful of organisms serve as model systems? The answer is that the choice of species as systems for experimentation has often been driven by need and desire for improving agriculture and industry, expedience and amenity for laboratory study, and more often than not, simply the vagaries of the day. Organisms that emerged in the last century as choice models did so because their entire biology was explorable, interesting mutants were obtained, enabling methodologies were developed, and devoted scientific groups coalesced. The same criteria still apply now in the twenty-first century.

Ustilago maydis, a biotrophic fungal plant pathogen that is the causative agent of smut disease of maize, has emerged at the beginning of the twenty-first century, as an outstanding model system for genetic analysis. It has proven to be valuable for understanding genetic mechanisms involved in numerous cellular pathways including parasite virulence and host defense during pathogenesis, homologous recombination, cytoskeleton architecture, intracellular trafficking and movement of macromolecules, secondary metabolite production, evolution of sex determining loci, cell cycle regulation, dikaryosis, and so on. The story of its development as organism for experimentation in genetics is remarkable in that it has came to light as model system more lately, but originating, nonetheless, from the currents of intellectual and scientific fervor from which *Drosophila melanogaster* and *Neurospora crassa* emerged.

Saturday 31 March

Plenary session 1: Plant and Human Pathogens

PL1.1
How arbuscular mycorrhizal fungi and plants recognize each other?
Guillaume Becard
LRSV, UMR 5546 Toulouse University 3/CNRS, 31326, Castanet-Tolosan, France

Before physical contact between the partners of the arbuscular mycorrhizal symbiosis each partner, the plant and the fungus, secretes diffusible molecules that can trigger in the opposite partner rapid metabolic responses, new gene expression and developmental modifications. Trace molecules such as strigolactones present in root exudates serve as plant host recognition signals for AM fungi.

They induce spore germination and/or hyphal branching at extremely low concentrations by rapidly stimulating the fungus mitochondrial activity. Interestingly strigolactones are also germination stimulant of the obligate parasitic weeds *Orobanche* and *Striga* and they have recently been proposed as a new class of hormones controlling various developmental stages in plants.

Symmetrically, based on genetic, molecular, biochemical and physiological evidence, AM fungi were also expected to produce important early signals perceived by their plant host. The so called Myc factors were expected to trigger the plant mycorrhization programme via the common SYM pathway (CSP), like the Nod factors produced by rhizobia trigger nodulation of legumes. Molecules that respond to the definition of Myc factors have recently been identified. They are simple lipochitooligosaccharides (LCOs) that can stimulate, at extremely low concentration, mycorrhization and lateral root formation of non legumes (dicots and monocots). In *Medicago truncatula*, activity on root development is dependent on DMI1, DMI2, DMI3 and NSP2, four proteins involved in the CSP.

The fact that LCOs, involved in a very ancient plant biotic interaction, are also important signals in “modern” interactions with rhizobia, raises the question of their possible occurrence in other plant biotic interactions, including in other plant- fungus interactions.

PL1.2
Dissecting phospholipid signalling in *Phytophthora infestans*
Francine Govers
Laboratory of Phytopathology, Wageningen University, Wageningen, The Netherlands

Phytophthora, which literally means plant destroyer, is a genus in the Stramenopile lineage in the class oomycetes with over a hundred species. Well known is *Phytophthora infestans,* the causal agent of potato late blight. Its ~ 240 Mb genome is the largest and most complex in the Stramenopile lineage. Comparative genome analysis revealed features illuminating its success as a pathogen, such as rapid turnover and massive expansion of families encoding secreted proteins and peculiar gene innovations resulting in proteins with oomycete-specific domain combinations. One outstanding class of novel proteins comprises GPCR-PIPKs. The 12 members all have a N-terminal 7-transmembrane domain typical for G-protein coupled receptors (GPCRs) combined with a phosphatidylinositol phosphate kinase (PIPK) domain at the C-terminus. Their differential expression and localization suggest distinct roles in various cellular processes. Another typical class represents secreted proteins with hallmarks of phospholipase D (PLD). We demonstrated PLD activity in medium of mycelium cultures and are currently investigating how these secreted PLDs effect plant cells. Other well-known proteins in the *Phytophthora* secretome are the RXLR effectors that act inside host cells where they function as virulence factors, mostly by suppressing host defence. In certain interactions they act as avirulence factors that are recognized by corresponding resistance proteins thereby triggering host defence. For the RXLR effector IPI-O, we identified a putative host target and demonstrated that this lectin receptor kinase is a *Phytophthora* resistance component in Arabidopsis.

PL1.3

Metabolic adaptation and virulence factor expression in *Cryptococcus neoformans*

J. Kronstad, G. Hu, M. Caza, B. Cadieux, S. Saikia, R. Attarian, W.H. Jung

The Michael Smith Laboratories, University of British Columbia, Vancouver, B.C., Canada, Department of Biotechnology, Chung-Ang University, 72-1 Nae-ri, Daedeok-Myeon, Anseong-Si, Gyeonggi-Do, 456-756, Republic of Korea

The pathogenic basidiomycete fungi *Cryptococcus neoformans* and *Cryptococcus gattii* cause life-threatening meningoencephalitis in immunocompromised and immunocompetent people. We are employing genetic and genomics approaches to identify the factors in the *Cryptococcus* species that contribute to metabolic adaptation and virulence factor expression in the host environment. The emerging view is that these processes are tightly integrated to support colonization and proliferation. One area of investigation focuses on elucidating the mechanisms of iron acquisition during mammalian infection by *C. neoformans.* We previously found that the reductive, high-affinity uptake system encoded by the *CFT1* (iron permease) and *CFO1* (ferroxidase) genes is required for iron use from transferrin, for full virulence and for dissemination to the CNS. The fact that the mutants still caused some disease in mice suggested that other iron sources were important during infection. Heme is a likely candidate because of its abundance in mammals and because *C. neoformans* grows particularly well on heme as the sole iron source. We found that the extracellular mannoprotein Cig1 is important for iron utilization from heme. In addition, transcriptional profiling and an insertional mutagenesis screen via Agrobacterium-mediated transformation identified a number of additional functions involved in heme utilization. One of these functions is endocytosis and mutants with defects in this process are debilitated for growth on heme.

Saturday 31 March

Plenary session 2: Epigenetics and RNA Biology

PL2.1

Centromeres of filamentous fungi

Kristina Smith, Pallavi Phatale, Lanelle Connolly, Sarah Ferrer, Alec Peters, Jonathan Galazka Michael Freitag

Department of Biochemistry and Biophysics, Center for Genome Research and Biocomputing, Oregon State University, Corvallis, OR, USA

Centromeric DNA, the centromere-specific histone H3 variant (CenH3), and centromeric DNA binding proteins form the foundation for attachment of kinetochore protein complex assembly. Correct assembly and proper maintenance of these large and cell cycle-regulated complexes is essential for attachment of spindle microtubules, which transport chromosomes into daughter nuclei during nuclear division. Over the past decade little information has emerged on centromere and kinetochore organization in filamentous fungi, even though these protein complexes are essential, and to date, only centromeres of *Neurospora crassa* have been studied in any detail. This was enabled by early groundbreaking studies on the underlying centromeric DNA structure [1, 2] and the availability of an arsenal of genetic, biochemical and cytological tools to study centromere proteins and centromere DNA composition. We analyzed the genomes of *Neurospora*, *Fusarium* and *Mycosphaerella* species for the presence of satellite or other near-repetitive sequences, confirming earlier studies that predicted centromeric DNA to be composed of active or silent transposable elements. To learn more about centromere assembly and maintenance, we subjected *Neurospora crassa* and *Fusarium graminearum* to ChIP-sequencing with tagged CenH3 and antibodies against histone modifications thought to be required for centromere function [3]. Our findings suggest that centromere maintenance in Neurospora is qualitatively different from that in fission yeast, where expression of small RNA and subsequent heterochromatin formation is required for the assembly but not maintenance of centromeres. To better understand centromere assembly we are dissecting protein interactions between different centromere foundation proteins, namely CenH3, CEN-B, CEN-C and CEN-T, by genetic and biochemical means.

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PL2.2

Diverse Small RNA Biogenesis Pathways in *Neurospora*

Yi Liu

Department of Physiology, The University of Texas Southwestern Medical Center, 5323 Harry Hines Blvd., Dallas, TX 75390, USA

A variety of small RNAs, including miRNAs and Piwi-interacting RNAs (piRNAs), associate with Argonaute family proteins to regulate gene expression in diverse cellular processes. In *Neurospora crassa*, we identified several types of Argonaute-associated small RNAs. The analyses of these sRNAs uncovered the existence of diverse sRNA production mechanisms. qiRNAs are a type of Argonaute QDE-2 associated sRNAs that are induced after DNA damage. qiRNAs originate from the highly repetitive rDNA locus and their biogenesis the RDRP QDE-1, the recQ DNA helicase QDE-3 and the Dicers. Our genetic and biochemical results suggest that, after DNA damage, QDE-1 is recruited to ssDNA by RPA and QDE-3. QDE-1 first acts as a DNA-dependent RNA polymerase to produce ssRNA and then as an RDRP to converts the ssRNA into dsRNA, a process that is strongly by RPA. miRNA-like small RNAs (milRNAs) and Dicer-independent sRNAs (disiRNAs) are two additional types of QDE-2 associated sRNAs. Despite their similarities to miRNAs in higher eukaryotes, there are at least four different pathways for milRNA production, including Dicer-dependent and Dicer-independent pathways. On the other hand, although disiRNAs may originate from dsRNA, they are generated independent of all known RNAi components. The mechanistic diversity observed for sRNA biogenesis in *Neurospora* shed lights on the diversity, evolutional origins, and biogenesis of eukaryotic small RNAs.

PL2.3

Post-Transcriptional Operons in the Rice Blast Fungus

Ane Sesma

Centre for Plant Biotechnology and Genomics - UPM/INIA Universidad Politécnica de Madrid (UPM), Autopista M-40 (Km 38)28223-Pozuelo de Alarcón (Madrid, SPAIN)

Transcriptional (*de novo* transcription) and post-transcriptional mechanisms (mRNA stability/degradation, export/localisation, translation, silencing...) coordinate the expression of related genes that drive a biological process, i.e. invasive growth during host colonisation. RNA-binding proteins orchestrate the expression of these gene networks at post-transcriptional level. They normally form RNA-protein complexes and regulate the translation of functionally related subpopulations of mRNAs. Very little is known about the post-transcriptional mechanisms that control fungal infection of plants and animals.

Formation of pre-mRNA 3' ends occurs in two steps: cleavage of the pre-mRNA (at a ***canonical*** polyA site) followed by synthesis of the adenosine tail. Isoforms of mRNAs with different exons or 3' untranslated region (UTR) lengths are generated by ***alternative*** polyadenylation (APA), a mechanism that regulates the presence of cis elements in the mRNA. Proteins involved in APA include the Cleavage Factor I complex (CFI_m) in metazoans and Hrp1 in yeast.

A virulence-deficient mutant in *Magnaporthe oryzae* led us to the identification of RBP35, a novel RNA-binding protein component of *M. oryzae* polyadenylation machinery that is missing in yeasts, plants or metazoans. RBP35 interacts *in vivo* with the orthologue of the metazoan cleavage factor I 25kDa (CFI_m25), indicating that RBP35 is the functional equivalent of CFI_m68 in filamentous fungi. Intriguingly, *M. oryzae* genome contains a clear orthologue of Hrp1, suggesting that combined mechanisms regulate the 3' end processing of *M. oryzae* pre-mRNAs. In *M. oryzae*, RBP35 is not essential for fungal viability but acts as a gene-specific polyadenylation factor regulating alternative 3' UTR processing of infection-related mRNAs.

Sunday 1 April

Plenary session 3: Secondary Metabolism

PL3.1

Secondary metabolism in Fusarium fujikuroi – the role of nitrogen availability and histone modifications

Bettina Tudzynski, Philipp Wiemann, Caroline Michielse, Lena Studt, Eva-Maria Niehaus, Sabine Albermann, Dominik Wagner

Westfälische Wilhelms-University Münster, Intitute of Biology and Biotechnology of Plants, Hindenburgplatz 55, 48143 Münster, Germany

The species *F. fujikuroi* was first *discovered* more than 100 years ago as the causative agent of the "Bakanae" (foolish seedling) disease of rice leading to hyperelongation of etiolated seedlings due to the secretion of gibberellins (GAs) by the fungus. Today, GAs are biotechnologically produced worldwide as plant growth regulators in large scale. Beside GAs, the fungus produces a broad range of other secondary metabolites such as bikaverin, fusarubin, fusarins, and fusaric acid. This spectrum of secondary metabolites and the distinct response of biosynthetic genes to nitrogen quantity and quality encouraged us to sequence the genome of *F. fujikuroi*, the first member of the Asian clade of the *Gibberella fujikuroi* species complex. The genome sequence enabled us not only to identify all genes coding for key-enzymes of secondary metabolites (PKS, NRPS, terpene cyclases), but also to link these genes and entire gene clusters to natural products. Furthermore, the discovery that the biosynthesis of many secondary metabolites in *F. fujikuroi* depends on nitrogen in different ways intensified our attempts to shed light on the nitrogen regulation network and the cross-link to secondary metabolism. We have applied microarray- and ChIP-seq analyses under different nitrogen conditions (no nitrogen, glutamine, nitrate) to study in detail, how secondary metabolite gene clusters are regulated by nitrogen, and which histone modifications are characteristic for active/silenced expression. These genome-wide analyses of gene clusters and their nitrogen-dependent regulation deepened our understanding on the biological role of secondary metabolites in the fungus' life style and the potential link with growth, differentiation and virulence.

PL3.2

LaeA-directed natural product discoveries

Nancy Keller, Saori Amaike, JinWoo Bok, Yiming Chiang, Ry Forseth, Dirk Hoffmeister, Fang Yun Lim, Berl Oakley, Daniel Schenk, Frank Schroeder, Ali Soukup, Clay Wang, Wenbing Yin

Medical Microbiology and Immunology-The University of Wisconsin

Several years ago the methyltransferase LaeA was identified in a mutagenesis screen for genes important in secondary metabolite (also termed natural products) synthesis in the model ascomycete *Aspergillus nidulans*. Since its discovery, LaeA has been characterized as a conserved member of the fungal specific nuclear Velvet Complex required for orchestration of fungal secondary metabolism with morphological and physiological competence in many Ascomycete genera. The power of LaeA led the discovery of a number of fungal natural products and their associated biosynthetic pathways to understand hows and whys of fungal natural product formation. This has proven unrivaled by any other single fungal protein as demonstrated by pertinent examples of our newest understanding of LaeA directed fungal biology in *Aspergillus* species.

PL3.3

Secondary metabolites of *Leptosphaeria maculans*, the causal agent of blackleg of canola

Barbara Howlett
School of Botany, the University of Melbourne, Vic 3010 Australia

Like many filamentous fungi, *Leptosphaeria maculans*, the blackleg pathogen of canola, secretes a diverse range of secondary metabolites. Such metabolites are synthesized by gene clusters that include key genes such as non-ribosomal peptide synthases (NRPSs) or polyketide synthases (PKSs). The *L. maculans* genome has 13 NRPSs and 12 NRPS and we are identifying the end products of several of these genes. An NRPS designated as *sirP* is involved in biosynthesis of sirodesmin, which is the major secreted metabolite. Sirodesmin is toxic due to its disulphide bridge, which can inactivate proteins via reaction with thiol groups, or via generation of reactive oxygen species by redox cycling. Sirodesmin is produced during infection of canola by *L.maculans* and contributes to virulence during colonization of the stem. A candidate NRPS involved in the biosynthesis of the depsipeptide, phomalide, which causes necrosis on Indian mustard, has also been identified. The most abundantly secreted polyketide is phomenoic acid, which like sirodesmin, has antifungal activity. Domain modelling and comparative genomics with closely related fungi has been used to predict a candidate PKS for phomenoic acid biosynthesis. Silencing of this gene resulted in significantly reduced levels of phomenoic acid in culture, indicating that this PKS is responsible for phomenoic acid production. It is likely that the toxicity of these secondary metabolites allow *L. maculans* to outcompete other micro-organisms including fungi *in planta* and also during its saprophytic growth phase on canola stubble in the soil.

Sunday 1 April

Plenary session 4: Synthetic and Systems Biology

PL4.1

Mathematical modeling of yeast stress response and cell cycle regulation

Edda Klipp
Humboldt-Universität zu Berlin, Theoretical Biophysics

Cells have to grow and to divide. This is a well-organized, highly regulated process. Since cells also have to react to changes in the environment, cell cycle must be both robust against and sensitive to changes. The ability to perceive and respond to information from their environment is one of the most ubiquitous properties of cellular organisms. It is crucial for a cell to react appropriately to changes or signals in its environment. This becomes apparent in many situations such as the search for nutrients, the detection of potentially harmful external conditions and in cell-cell communication as it is required for any multi-cellular organism. Even though there is a huge selection of perceivable signals the underlying mechanisms are surprisingly alike, which suggests that they are highly conserved in the course of evolution.

Here, we apply different modeling techniques to understand cell cycle progression and cell cycle regulation in changing environments, with specific focus on mechanisms and experimental data for the model organism *Saccharomyces cerevisiae*. Specifically, new aspects in cell cycle regulation and the interaction of stress-activated signaling pathways with cell cycle progression will be discussed. The results indicate that yeast cells have developed different mechanisms for coping with external stress during different periods of their life time.

PL4.2

***Aspergillus* spp.: ironing out iron problems**

Hubertus Haas

Division of Molecular Biology/Biocenter, Innsbruck Medical University, Fritz-Pregl-Str. 3, A–6020 Innsbruck/Austria

Iron is an essential but in excess toxic nutrient. Therefore, fungi evolved fine-tuned mechanisms for uptake and storage of iron, such as the production of siderophores (low-molecular mass iron-specific chelators). In *Aspergillus fumigatus,* iron starvation causes extensive transcriptional remodeling involving two central transcription factors, which are interconnected in a negative transcriptional feed-back loop: the GATA-factor SreA and the bZip-factor HapX. During iron sufficiency SreA represses iron uptake, including reductive iron assimilation and siderophore-mediated iron uptake, to avoid toxic effects. During iron starvation HapX represses iron-consuming pathways, including heme biosynthesis and respiration, to spare iron and activates synthesis of ribotoxin AspF1 and siderophores, the latter partly by ensuring supply of the precursor ornithine. In agreement with the expression pattern and mode of action, detrimental effects of inactivation of SreA and HapX are confined to growth during iron sufficiency and iron starvation, respectively. Deficiency in HapX, but not SreA, attenuates virulence of *A. fumigatus* in a murine model of aspergillosis, which underlines the crucial role of adaptation to iron limitation in virulence. Consistently, production of both extra- and intracellular siderophores is crucial for virulence of *A. fumigatus*. Recently, the sterol-regulatory element-binding protein SrbA was found to be essential for adaptation to iron starvation, thereby linking regulation of iron metabolism, ergosterol biosynthesis, azole drug resistance and hypoxia adaptation.

The studies were supported by Austrian ScienceFoundation Grants FWF P-21643-B11 and I-282-B09.

PL4.3

Systems Biology of Industrially Important Filamentous Fungi

Jens Nielsen

Department of Chemical and Biological Engineering, Chalmers University of Technology, Gothenburg, Sweden

Aspergilli are used extensively in the fermentation industry for the production of a range of different industrial enzymes, organic acids and high-value secondary metabolites. In connection with further development of bioprocesses for the production of fuels and chemicals these fungi are interesting versatile cell factories as they tolerates low pH, can utilize a wide range of carbon sources and has relatively high conversion rates. Furthermore, their metabolism extends to cover many different secondary metabolites. Due to these factors the metabolism of *Aspergilli* is quite complex and involves a very large number of enzyme catalyzed reactions, probably among the microorganisms containing the largest number of metabolic capabilities. With the availability of the genome sequence for several different *Aspergilli* it has become possible to query the metabolic capabilities of these microorganisms at the genome-level. Using a bottom-up approach using genomic information together with information from databases, research papers and books, we have reconstructed the metabolic networks of *A. nidulans*, *A. niger*, *A. oryzae* and *P. chrysogenum*. We have used these metabolic networks for gaining novel insight into the metabolic functions of these organism through integrative analysis of different kinds of data, e.g. data from genome-wide transcription analysis. Among the processes studied are carbohydrate metabolism (use of different carbon sources like glucose, xylose and glycerol), enzyme production and penicillin production.

Monday 2 April

Plenary session 5: Genomes

PL5.1

Population genomics uncovers the *Verticillium dahliae* effector that is recognized by the tomato Ve1 immune receptor

Bart P.H.J. Thomma

Laboratory of Phytopathology, Wageningen University, Droevendaalsesteeg 1, 6708 PB Wageningen, The Netherlands

Cell surface receptors, generally referred to as pattern recognition receptors (PRR), detect conserved microbial molecules, generally referred to as microbe-associated molecular patterns (MAMPs), to activate MAMP-triggered immunity (MTI). Successful plant pathogens overcome MTI by the use of secreted effectors which perturb host immunity in a pro-active manner. An example is provided by LysM effectors that are secreted by various fungal plant pathogens during infection to sequester fungal cell wall-derived MAMPs to prevent detection by the host and activation of MAMP-triggered immunity. To overcome effector-triggered susceptibility, plants in turn evolved immune receptors that monitor the presence or activity of particular effectors to re-install immunity.

The tomato immune receptor Ve1 governs resistance to race 1 strains of the soil-borne vascular wilt fungus *Verticillium*, while race 2 strains are not recognized. Thus far, the *Verticillium* effector that is monitored by Ve1 remained unknown. By high-throughput population genome sequencing, we identified a sequence stretch that only occurs in race 1 strains, and that is absent from race 2 strains. Within this region the *Ave1* (for *Avirulence on Ve1 tomato*) gene was identified. Functional analyses confirmed that Ave1 activates Ve1-mediated resistance and demonstrated that Ave1 contributes to fungal virulence. Interestingly, Ave1 is homologous to a widespread family of plant proteins. Besides plants, homologous proteins were also found in few plant pathogenic fungi, including the fungal pathogens *Colletotrichum higginsianum* and *Fusarium oxysporum* f. sp. *lycopersici*. Remarkably, some of these Ave1 homologs can activate Ve1-mediated resistance in tomato as well.

PL5.2

Interacting with plants: lessons from fungal genomes

Marc-Henri Lebrun

Bioger,INRA, Thiverval-Grignon, URGI, INRA, Versailles, France. With the help of many fungal genome consortia and the Cazy database

Fungi display contrasting interactions with plants (symbiotic *vs* pathogenic; biotrophic *vs* hemi-biotrophic/necrotrophic; large *vs* restricted host range). Analysis of the increasing number of fungal genomes may help understanding how fungi have evolved towards such diverse infection strategies. Comparison of related species that differ in their infection strategies is a powerful approach to uncover such trends. This is illustrated by the related Leotiomycetes *Blumeria graminis (Bg),* and *Botrytis cinerea* (*Bc*), which are either necrotrophic (*Bc*) or biotrophic (*Bg*). *Bg* has a large genome (120 Mb) extensively invaded by transposons (70% genome) with few protein-coding genes (6000). These genomic features differ significantly from those of *Bc* (38 Mb, 4% transposons, 14270 genes), but are shared by other Erysiphales, suggesting that this type of genome evolution is a hallmark of this family. This evolutionary trend may help define minimal gene sets required for infection. Indeed, Bg has only one functional secondary metabolism key gene encoding a polyketide synthase likely involved in pigment biosynthesis. Likewise, the ascomycete symbiont *Tuber melanosporum* also has a very restricted set of secondary metabolism genes. This contrasts with the large number of such genes found in other plant pathogens (38 in *Bc*, 49 in *Magnaporthe grisea*). This suggests that biotrophic pathogens and symbionts have lost most secondary metabolism pathways except those needed for survival. Similarly, these biotrophic and symbiotic species have reduced numbers of genes encoding plant cell wall-degrading enzymes, suggesting that functions harmful to the host plant have been counter-selected during evolution towards biotrophy and symbiosis. In contrast, biotrophic fungi have similar numbers of transporters and effectors as other plant pathogenic fungi. These selective gene losses in biotrophs and symbionts suggest that repertoires of genes encoding secondary metabolism enzymes, plant cell wall-degrading enzymes and effectors, as well as their *in planta* expression patterns, can provide useful signatures of fungal infection strategies. The analysis of these signatures in genomes of other plant pathogenic fungi will be presented.

PL5.2 continued…

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PL5.3

Genome dynamics of the *Fusarium oxysporum* species complex

Li-Jun Ma [1,2] Shiguo Zhou [3] Liane R. Gale [4] Terry Shea [2] Sarah Young [2] H Corby Kistler [3]
[1]University of Massachusetts at Amherst, Amherst, Massachusetts USA 01003 [2] Broad Institute, Cambridge, Massachusetts USA 02142 [3] University of Wisconsin-Madison, Madison, Wisconsin USA 53706 [4] USDA ARS, University of Minnesota, St. Paul, Minnesota, USA 55108.

The *Fusarium* comparative genomes of *F. graminearum*, *F. verticillioides* and *F. oxysporum* revealed greatly expanded lineage-specific (LS) chromosomes in *F. oxysporum f*. sp. *lycopersici*. These LS chromosomes contribute to the organism pathogenicity and host–specificity, providing explanation for the polyphyletic origin of host specificity and the emergence of new pathogenic lineages in the *F. oxysporum* species complex (FOSC). In this presentation, I will describe the comparative study including one human isolate and 11 plant pathogenic isolates that represent 8 forma specialis, selected from *F. oxysporum* species complex. The optical maps confirmed that LS chromosomes exist in all the strains we have examined. Different races of the same forma specialis share the determinant pathogenicity chromosomes and effectors encoded in these chromosomes. Our preliminary analysis of the genome assemblies using only the illumine data indicates these *de novo* assemblies capture the effectors that determine the host-specificity. The genomic data also reveals the power in detecting genome-wide mutation pattern in short evolutionary divergent time, while RNA-seq data shows great promise in detecting novel genes encoded in the LS chromosomes and studying the gene expression under different conditions.

Monday 2 April

Plenary session 6: Regulation and Development

PL6.1
Coordination of fungal development and secondary metabolism
Gerhard H. Braus
Molekulare Mikrobiologie und Genetik, Georg-August-Universität Göttingen, D-37077 Göttingen, Germany

Differentiation and secondary metabolism are correlated processes in fungi that respond to various abiotic or biotic external triggers. The velvet family of regulatory proteins plays a key role in coordinating secondary metabolism and differentiation processes as asexual or sexual sporulation and sclerotia or fruiting body formation. The velvet family shares a protein domain that is present in most parts of the fungal kingdom from chytrids to basidiomycetes. The structure of this domain will be discussed. The heterotrimeric *velvet* complex VelB/VeA/LaeA which includes the velvet domain proteins VelB and VeA as well as the conserved eight subunit COP9 signalosome complex are required for the link between secondary metabolism and developmental programs. The current state of the work in the laboratory will be presented.

PL6.2
Tipping the balance. What turns a mutualist into a pathogen?
Barry Scott, Daigo Takemoto, Aiko Tanaka, Yvonne Becker, Matthias Becker, Carla Eaton, Gemma Cartwright
Massey University,NZ 2. Nagoya University, Japan

Epichloë festucae is a biotrophic fungus of the family Clavicipitaceae that forms a mutualistic symbiotic interaction with *Lolium* and *Festuca* temperate grass species. This fungal symbiont forms an interconnected hyphal network that extends throughout the aerial tissues of the grass including the leaf surface. Hyphal apical and intercalary growth within the host is highly regulated and coordinated with leaf growth. Fungal synthesis of reactive oxygen species, by a specific NADPH oxidase (Nox) complex, is a crucial signalling mechanism for maintaining a stable symbiotic association. Additional components of the Nox complex include a regulatory subunit NoxR, the small GTPase, RacA and homologues of the yeast polarity proteins Bem1, a scaffold protein, and Cdc24, a known guanine nucleotide exchange factor (GEF) for Rac. Disruption of any one of these genes leads to a breakdown in the symbiotic interaction resulting in dramatic changes in hyphal morphology and growth as well as plant development. Surprisingly, disruption of the *E. festucae* guanine nucleotide dissociation inhibitor (RhoGDI) or the p21-activated kinase, PakA/Cla4 had no obvious effect on the symbiotic interaction even though both mutants had severe culture growth phenotypes. We have also been examining the role of oxidative stress signalling systems in culture and in the symbiotic interaction through a functional analysis of the *E. festucae* homologues of the *S. cerevisiae* GPX3/YAP1 and *S. pombe* TPX1/PAP1 redox relay systems. Insights into our current understanding of what controls the balance between mutualism and pathogenicity will be presented.

PL6.3

Novel Intrinsically disordered proteins assemble at septal pores and regulate diverse aspects of hyphal homeostasis

Gregory Jedd

Temasek Life Sciences Laboratory, and Department of Biological Sciences, National University of Singapore, Singapore 117604

Like animals and plants, multicellular fungal hyphae possess cell-to-cell channels that allow intercellular cooperation, and communication. Using a combination of mass spectrometry of Neurospora Woronin body associated proteins, and a bioinformatics approach that identifies related proteins based on composition and character, we have identified 17 septal pore associated (SPA) proteins that localize in rings around the pore, and in pore-centered foci. SPA proteins are not homologous at the primary sequence level, but share overall physical properties with intrinsically disordered proteins. Some SPA proteins form aggregates at the septal pore, and in vitro assembly assays suggest self-assembly through a novel non-amyloidal mechanism involving mainly random coil structural moieties. SPA loss-of-function phenotypes include excessive septation, septal pore degeneration, and uncontrolled Woronin body activation. These data identify a new family of disordered proteins that control cell-to-cell communication, and diverse aspects of septal homeostasis.