



# Full Abstracts

**Fungal Genetics Conference  
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## POSTER SESSION ABSTRACTS

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**596. Segregation distortion in the progeny of an interspecific cross between *Fusarium circinatum* and *F. temperatum*: nuclear-cytoplasmic incompatibility and hybrid breakdown.** G. Fourie<sup>1</sup>, L. De Vos<sup>2</sup>, B.D. Wingfield<sup>2</sup>, N.A. van der Merwe<sup>2</sup>, M.J. Wingfield<sup>1</sup>, E.T. Steenkamp<sup>1</sup>. 1) Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa; 2) Department of Genetics, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa.

Natural selection and divergence due to mutation and drift are major drivers of speciation. However, the emergence of new species is mostly also dependent on reproductive isolation through pre- or post-zygotic mechanisms to prevent the development of hybrids. Although little is known about the nature and function of genes involved in reproductive isolation in fungi, the analysis of hybrid progeny from experimental crosses will likely hold valuable clues regarding molecular mechanisms underpinning the process. For example, hybridization between *Fusarium circinatum* and *F. temperatum* has previously been associated with high levels of genetic transmission ratio distortion (TRD), and it is likely that the genes associated with this phenomenon are also involved in reproductive isolation and ultimately speciation. Since segregation in the *F. circinatum* X *F. temperatum* progeny were skewed towards the maternal parent our hypothesis was that the observed TRD was caused by genetic incompatibilities where the presence of the *F. temperatum* mitochondrion influenced the genetic makeup of the hybrid progeny's nuclear component. To test this hypothesis we identified, characterized and mapped nuclear-encoded mitochondrial genes to the chromosomes of *F. circinatum* and *F. temperatum*. Of the 86 genes identified, 50% were positioned within TRD genomic regions or were located near markers that displayed TRD, which significantly deviated from what was expected purely by chance. Our results thus suggest that the observed TRD can indeed be attributed to limited interaction between products encoded by the nuclear and mitochondrial genomes of the hybrid progeny. Our future research will investigate the extent to which such nuclear-cytoplasmic incompatibility mechanisms could potentially drive the evolution of *F. circinatum*, *F. temperatum* and related fungi.

**597. Contemporary fungicide applications sign for selection in *Botrytis cinerea* populations collected in the Champagne vineyard (France).** Anne Sophie WALKER<sup>1</sup>, Adrien RIEUX<sup>2</sup>, Virginie Ravigné<sup>3</sup>, Elisabeth Fournier<sup>3</sup>. 1) BIOGER, INRA, THIVERVAL-GRIGON, France; 2) UCL Genetics Institute, London, United-Kingdom; 3) CIRAD, UMR BGPI, F-34398 Montpellier, France.

Populations of fungal pathogens may be subject to many selective pressures in agricultural environments. Among them, fungicides constitute one of the most powerful determinants of population adaptation acting in a short time span. Here, we investigated whether fungicides sprays applied yearly in the Champagne vineyard to control the grey mold causal agent *Botrytis cinerea* could shape population structure and evolution. We carried out a 2-year survey (4 collection dates) on three treated/untreated pairs of plots. We found that fungicides treatments had no or little impact on population subdivision at neutral loci, as well as on diversity or reproduction mode. Nevertheless, we found evidence of stronger genetic drift in some treated plots, consistent with the regular application of fungicides. Moreover, we observed spatial structure in resistance frequency for two loci under contemporary selective pressure, as reflected by cline patterns. At last, using a modeling approach, we estimated fitness costs of resistance to fungicides, responsible for resistance frequency decay during winter. Further work helped estimating parameters of positive selection and migration exerted on *B. cinerea* populations, and disentangling the relative effect of the evolutionary forces at work.

**Keywords :** *Botrytis cinerea*, population structure, selection, migration, resistance cost, fungicides, diversity, cline, vineyard.

**598. Maternal effects vary across sexual reproductive development in *Neurospora crassa*.** Kolea Zimmerman<sup>1</sup>, Daniel Levitis<sup>2</sup>, Anne Pringle<sup>3</sup>. 1) Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA; 2) Max-Planck Odense Center on the Biodemography of Aging, University of Southern Denmark, Odense M, Denmark; 3) Harvard Forest, Harvard University, Petersham, MA.

A large portion of mortality occurs in the form of offspring inviability or non-development, closely tying mortality to fertility. In this study, we tested the hypothesis that maternal effects on offspring production and quality are greater than paternal effects in both offspring number (fertility) and offspring viability (mortality). We designed a fully crossed reciprocal mating scheme using 11 mat-A and 11 mat-a *Neurospora crassa* strains chosen from a set of 24 mat-A and 24 mat-a strains from North America, the Caribbean, and Africa that were genotyped previously (Ellison, Hall, & Kowbel 2011). Precise genetic distances between mating pairs were calculated to control for the effects of crossing distance on offspring production. We performed reciprocal crosses of all 121 strain pairings and collected data on perithecial production, ascospore (sexual spore) production, and various ascospore characteristics. Mixed effects models of these data show that the female parent accounts for the majority of variation in perithecial production, number of spores produced, and spore germination. Surprisingly, both sexes equally influence the percentage of spores that are pigmented. In this fungus, pigmented spores are viable and unpigmented spores are inviable. These results show that while both parents influence all these traits, maternal influence is strongest on both fertility and mortality traits until the spores are physiologically independent of the maternal cytoplasm within the ascus.

**599. The origin, distribution and evolution of Type A trichothecenes in the *Fusarium graminearum* species complex.** Amy Kelly<sup>1</sup>, H. Corby Kistler<sup>2</sup>, Robert Proctor<sup>1</sup>, Todd Ward<sup>1</sup>. 1) NCAUR, USDA-ARS, Peoria, IL; 2) Cereal Disease Laboratory, USDA-ARS, St. Paul, MN.

Members of the *Fusarium graminearum* species complex (FGSC) are the major cause of Fusarium Head Blight (FHB) of cereal crops worldwide. FGSC strains typically produce one of three B trichothecenes (3ADON, 15ADON, NIV), which can contaminate grain and have toxic effects in animals and humans. Production of a novel Type A trichothecene (NX-2) by some strains of *F. graminearum* from the US was recently discovered. This unexpected trichothecene diversity is the result of polymorphisms in *TRII*, a cytochrome P450 enzyme that contributes to structural differences in Type A and Type B trichothecenes. To understand the geographic and phylogenetic distribution of the NX-2 toxin type, we developed and used several DNA sequence-based approaches to screen 1,475 isolates from 22 different countries for the NX-2 allele at *TRII*. Our data indicate that NX-2 production may currently be limited to *F. graminearum* isolates from Canada and the US (ND, SD, MN, CT), and that the distribution of NX-2 alleles mirrors that of the novel 3ADON population in North