

232W Predicting dispensable chromosomes(scaffolds) in newly sequenced *Fusarium* species. A. Salamov¹, W. Andreopoulos¹, L.-J. Ma², J. Coleman³, I. Grigoriev¹ 1) DOE Joint Genome Institute, Walnut Creek, CA; 2) Department of Biochemistry and Molecular Biology, University of Massachusetts Amherst, Amherst, MA, 01003, USA; 3) Department of Entomology and Plant Pathology, Auburn University, Auburn, AL, 36849, USA.

Many *Fusarium* species have dispensable (or lineage-specific) chromosomes which are not required for normal growth, but may control host-specific pathogenicity of these species. For newly sequenced species from *F. solani* and *F. oxysporum* species complexes we investigate the possibility of predicting dispensable chromosomes (scaffolds) based on genomes sequence features and similarity to two reference genomes of *F. oxysporum* f.sp. *lycopersici* and *Nectria haematococca* with experimentally determined dispensable chromosomes. We have found that when new strains are close enough to the reference genomes, dispensable chromosomes can be reliably predicted based on combination of genome alignments and mapping of proteins from reference genomes to new sequences. We also built Hidden Markov Models for gene families, specific for dispensable chromosomes of reference genomes, which in combination with other features, such as repeat content, sparsity of genes with known functional domains, codon usage, and GC content can be used for prediction of dispensable chromosomes in more distant species.

233T Genomic comparison of a dispensable chromosome within the *Fusarium fujikuroi* complex. L. De Vos¹, E.T. Steenkamp², M.A. van der Nest¹, W.-Y. Chan², S. van Wyk², B.D. Wingfield¹ 1) Department of Genetics, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa; 2) Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa.

Species within the *Fusarium fujikuroi* complex (FFC) are considered important pathogens of commercially planted plants and trees. Members of this complex typically have 12 chromosomes, of which the 12th chromosome is the smallest and considered to be part of the accessory genome. This hypothesis is based on low sequence similarity among the corresponding chromosome from different species, and the apparently dispensable nature of this chromosome within the FFC. In this study, we investigated this hypothesis by making use of a comparative genomic approach. For this purpose, whole genome sequence data available for representatives of the FFC (i.e., *F. circinatum*, *F. subglutinans*, *F. nygamai*, *F. fujikuroi* and *F. temperatum*) were used. From these data, sequences for chromosome 12 of *F. fujikuroi* and *F. temperatum* were used to assemble the corresponding chromosome in the other three species. Chromosome 12 comparisons within the FFC showed that the density and average size of genes encoded on this molecule were lower when compared to whole-genome data. Assignment of gene functions revealed genes primarily involved in oxidation-reduction and macromolecule metabolic processes, cation and nucleoside phosphate binding, and as intrinsic components of membranes. Phylogenetic analyses also showed that the genes of chromosome 12 had diverse and non-orthologous origins, with only a small proportion apparently sharing an evolutionary trajectory similar to those of the species harbouring them. Taken together, these findings therefore suggest that the ancestor of the FFC likely harboured a version of chromosome 12. Also, consistent with being part of the accessory genome, the evolution of chromosome 12 involved the acquisition of genes from sources outside the FFC. Future research should seek to determine the processes encoded by chromosome 12 and the biological properties this molecule might confer to the species harbouring it.

234F Genome mining, pathogenicity and secondary metabolism of three strains of *Fusarium fujikuroi*, the causal agent of bakanae disease on rice. E. Piombo^{1,2}, H. Banani^{1,2}, I. Siciliano¹, P. Abbruscato³, A. Acquadro², M.L. Gullino^{1,2}, D. Spadaro^{1,2} 1) Università degli Studi di Torino, Centro AGROINNOVA; 2) Università degli Studi di Torino, DISAFA; 3) Bioeconomy Unit, Parco Tecnologico Padano.

Bakanae is an important seedborne disease of rice, caused by *Fusarium fujikuroi*. This pathogen can produce a wide range of secondary metabolites, including fumonisins and gibberellins. In order to gain insight into secondary metabolites (SM) synthesis in *F. fujikuroi*, the genomes of the 3 strains *Augusto2*, *CSV1* and *I1.3* were sequenced to identify the allelic variants in the genes responsible for SM production, and compare the virulence on rice and the SM production *in vitro* and on rice. Sequence analysis was conducted by *de novo* and *reference guided* genome assembly. Three genomes of 42.8 Mb on average were obtained. The gene clusters responsible for fumonisin and gibberellin production, formed respectively by 15 and 7 genes, were analyzed and aminoacidic differences were predicted for *fum1*, *fum13* and *fum21*. The 3 strains also exhibited distinct differences in colony morphology and growth kinetics. The virulence and fumonisin production of the three strains on cultivar "Galileo" of rice were compared. At 3 weeks post germination *I1.3* showed statistically higher virulence compared to *Augusto2* and *CSV1*. *Augusto2* was the major producer of fumonisins both *in vitro* and *in vivo*, followed by *CSV1*, while *I1.3* was unable to produce fumonisins either *in vivo* or *in vitro*. The lack of fumonisin production in *I1.3* is probably caused by a number of identified mutations in the sequence of key genes (*fum1* and *fum21*) in the fumonisin gene cluster, while the difference in the production between *Augusto2* and *CSV1* might be due to a mutation in the gene *VeA*, regulator of SM biosynthesis, including fumonisins. *CSV1* was unable to produce gibberellins *in vivo* and *in vitro* on Petri dish, confirming the different symptomatology of *CSV1* on rice, characterized by dwarfing and chlorosis, but lack of stem elongation. This study showed how *F. fujikuroi* can present a great deal of intra-species variation, both in the induced symptoms and in SM production.

235W Quantitative mapping of pathogenicity factors in the *Fusarium fujikuroi* complex with an interspecific genetic cross. Wei Yue¹, Christopher Toomajian¹, Nik Mohd Izham Mohamed Nor^{1,2}, John F. Leslie¹ 1) Dept Plant Pathology, Kansas State Univ, Manhattan, KS, USA; 2) School of Biological Sciences, Science University of Malaysia, Penang, Malaysia.

The *Fusarium fujikuroi* species complex contains agronomically important plant pathogens that produce secondary metabolites such as mycotoxins and gibberellic acids (GAs) that are involved in pathogen virulence. Two members of this species complex, *F. proliferatum* (*Fp*) and *F. fujikuroi* (*Ff*), are closely related phylogenetically but have different host specificity and produce different mycotoxins. Our long-term aim is to explore the genetic bases behind these differences, and we have begun by conducting QTL analyses of progeny from an interspecific cross. Using the R/qtl software package, we constructed a high density genetic map with data from 6,381 high quality Genotyping-by-Sequencing (GBS) markers and 253 progeny from the cross. The final genetic map consisted of 12 linkage groups, which correspond to the 12 chromosomes present in each species, and had a length of over 1900 cM with only 4 gaps greater than 20 cM. In parallel, we generated next generation sequence data from the *Fp* parent of this cross and performed a draft genome assembly. Our sequence-based markers allowed us to anchor 97.8% (42.2 Mb) of the total assembly onto the 12 linkage groups. Not surprisingly for an