

## Fun at the *Fusarium circinatum* Genome Annotation Jamboree (24 – 27 May 2010)

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*Fusarium circinatum* causes the serious disease of pines known as pitch canker (Fig. 1). The pathogen is believed to be native to Central America, possibly including the southeastern United States and the Caribbean region. *Fusarium circinatum* has caused tremendous damage to native *Pinus radiata* in California, where it first appeared in the early 1990's. Since then it has devastated pine plantation programmes in many countries where *Pinus* spp. are grown as non-natives. One example is found in South Africa where the pathogen first appeared in pine nurseries in 1990 and has come to be a major constraint to pine establishment in the country. It has also moved from the nursery environment to plantations in South Africa and it threatens the future of pine forestry in the country.



Fig. 1. Symptoms of pitch canker on matured pine trees. A: Die-back of branches and B: resinous cankers on the main stem.

Members of the research team of the Forestry and Agricultural Biotechnology Institute (FABI) and linked to the DST/NRF Centre of Excellence in Tree Health Biotechnology (CTHB) and the Tree Protection Co-operative Programme (CTHP) have studied various aspects of the taxonomy, biology and management of *F. circinatum* since it first appeared in South Africa. This work has developed to a point where knowledge of the genome of the pathogen has become desirable. To achieve this goal, the genome of *F. circinatum* was sequenced during the first semester of 2009 in a project led by Prof. Brenda Wingfield. Subsequently, she spent six months on sabbatical at the University of California, Davis as a guest of Prof. Ian Korf (<http://genomics.ucdavis.edu/>), where she and FABI Ph.D. student, Quentin Santana began the annotation process. This included a visit to the laboratory of Prof. Mark Yandell at Utah State University who specializes in comparative genomics and developing computer software for open reading frame predication and annotation (<http://www.yandell-lab.org/>).

The annotation of the *F. circinatum* genome was completed during a recently held Annotation Jamboree in Pretoria. The jamboree took place at FABI and among others utilized the computer laboratory of the University Bioinformatics Unit. During this event, annotators spent close to eight hours each day interrogating open reading frames (ORFs) generated from the MAKER genome annotation pipeline. The team of annotators included students and academic staff of the University of Pretoria and universities in the USA (Fig. 2).



Fig. 2 Genome annotators  
(from bottom row, left to right)

Prof. Brenda Wingfield, Mmatshapho Phasha, Chrizelle Beukes, Kershney Naidoo, Dr. Irene Barnes, René Sutherland, Simon Martin, Stefan Bam, Prof. Emma Steenkamp, Gerda Fourie, Lieschen de Vos, Melissa Simpson, Dr. Oleg Reva, Magriet van der Nest, Annie Chan, Albe van der Merwe, Prof. Fanus Venter, Alisa Postma, Dr. Martin Coetzee, Markus Wilken, Quentin Santana, Renate Zipfel, Stephanie Slinski, Prof. Mark Yandell, Darryl Herron

(Not in picture: Melanie Friend, Marija Kvas, Osmond Mlonyeni, Jan Nagel Prof. Bernard Slippers)

Prof. Mark Yandell of the Eccles Institute of Human Genetics, University of Utah assisted in the annotation jamboree. This was a special privilege and he and his team of computer scientists were responsible for developing MAKER, the genome annotation pipeline that was employed to predict the ORFs present in the *F. circinatum* genome. During his visit to the University of Pretoria, Mark presented a seminar, entitled "Next generation genomics" in which he discussed concepts behind MAKER and genome annotation. With assistance of his graduate student Carson Holt, Mark contributed significantly to the annotation jamboree by providing comparative analyses between the genomes of *F. circinatum*, *F. verticillioides* and other fungi for which genome data are available.

Prior to the jamboree, in January, annotators participated in a short course in genome annotation using the viewer and editor Apollo and presented by Brenda Wingfield. These annotations were completed during the jamboree. Nearly 15 000 protein coding genes have now been identified from the 44 Mb genome, many having an unknown function. Furthermore, results from comparative genome analyses have revealed that some genes have been lost and others gained during the evolution of this important pine pathogen.

By the end of the jamboree there were many red eyed and mentally exhausted annotators. It was, however, exciting to find that some of the participants had been inspired to further their careers in genomic research. However, the general consensus was that the whole event was "Great fun!" A summary of some of the early data emerging from the jamboree was presented at the International Mycological Congress in Edinburgh in August 2009 and the first publication presenting these data is being prepared.