

USING A BESPOKE 'OMICS' APPROACH TO DEVISE A FLEXIBLE NEW WAY TO CONTROL *Fusarium* IN WHEAT

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Fusarium head blight (FHB) disease has re-emerged as a major problem in most cereal growing regions and now threatens global food security. New ways to control FHB disease are urgently required. Here, we are using a bespoke genome, transcriptome and reverse genetics guided approach to understand and pinpoint the *Fusarium* genes and pathways required to cause disease in wheat heads. Our intention is to identify a new suite of target genes for intervention, enabling the development of flexible new ways to control FHB disease. The genome analyses: The completed *F. graminearum* (*Fg*) genome for the North American reference isolate PH-1 became available in 2015. To predict the core *Fg* proteome prevalent in one of the most severely FHB affected regions of the world, namely Brazil, the genomes of eight well characterised *Fg* isolates from Rio Grande do Sul were sequenced using Illumina and PacBio technologies. The annotated core *Fg* proteome was then inter-compared with the new genomes of two closely related species, *F. culmorum* (a wheat pathogen) and *F. venenatum* (a non-pathogen), to identify to core proteome involved in pathogenicity. The *in planta* transcriptome analyses: During compatible wheat-*Fg* interactions, the advancing *Fg* hyphae colonise the extracellular spaces in wheat tissue without causing macroscopic symptoms. Later, hyphal penetration of wheat cells coincides with the induction of host cell death. By using both RNAseq and *Fg* Affymetrix analyses, we have characterised the early *Fg* transcriptome during symptomless wheat infection. Over 3,000 genes coding for the core *Fg* proteome were found to be either rapidly up-regulated or down-regulated post-infection, revealing candidate gene targets that may be involved in the establishment of infection. Host-induced gene silencing (HIGS): Two recently published independent studies have revealed that transgenic plants expressing RNAi silencing constructs that specifically target *Fg* genes, such as cytochrome P450 lanosterol C-14 α -demethylase (CYP51) or chitin synthase, display high levels of resistance to this pathogen. Using the predicting sub-set of genes coding for the core *Fg* proteome that were expressed during symptomless infection, we are now in a position to target additional *Fg* genes that may be essential and/ or required for virulence towards wheat. Transgenic wheat plants harbouring specific RNAi gene combinations have been generated and these will be functionally characterised in the T₁ and T₂ generations, revealing the efficacy of this novel HIGS approach aimed at combatting FHB in Brazil.

Keywords: genome-wide analyses; transcriptomics; *Fusarium venenatum*; *Fusarium culmorum*; host induced gene silencing