**RRES Press Release 7/2/23 Probing for weakness in wheat Septoria genomes**

*Identifying fixed DNA sequences across multiple strains may offer clues to disease control*

A new study comparing genomes across 18 strains of the Septoria leaf blotch fungus Zymoseptoria tritici has revealed a core set of genes that may offer clues for improved control of this important disease.

These “core biology” gene sets are present and functional in all strains of the fungus, unlike other “flexible biology” sections which appear to mutate and evolve rapidly.

The core set comprised 9807 sequences which were present more-or-less unchanged in all samples.  That left a large accessory genome, consisting of 45% of the total genes where the sequences could be highly variable.

The wheat-pathogenic fungus Zymoseptoria is one of the most rapidly evolving threats to global food security. Like many crop diseases, it can quickly adapt making it resistant to pesticides.  Severe epidemics of the disease have decreased wheat yields by up to 50%.

The core set coded for proteins required for essential functions including virulence. Both core and accessory genomes encoded many small proteins that likely interact with plant immunity.

However, the researchers were unable to identify the genes that induced the characteristic brown patches that are typical of the disease.

“We also identified a non-pathogenic strain lacking 5 of the core genes. Just by restoring a single carefully chosen gene full virulence was regained.” said Rothamsted’s Dr Jason Rudd who led the study.

“This hints at the huge potential for using genomic techniques to control crop diseases that can evolve rapidly, making them quickly resistant to herbicides or other treatments”

Publication

Chen, H., King, R., Smith, D. *et al.* Combined pangenomics and transcriptomics reveals core and redundant virulence processes in a rapidly evolving fungal plant pathogen. *BMC Biol* **21**, 24 (2023). https://doi.org/10.1186/s12915-023-01520-6