

## UNRAVELLING THE GENETIC BASIS OF *FUSARIUM* RESISTANCE IN DIFFERENT MAIZE POPULATIONS

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*QTL mapping, GWAS, Fusarium ear rot, Zea mays*

Fungal infection by *Fusarium verticillioides* is cause of substantial reductions in maize yield and grain quality worldwide. Developing natural resistance in maize genotypes is an effective way to achieve sustainable control of *F. verticillioides* in the field, and breeding for resistance may be accelerated by identifying genes and loci responsible for natural disease resistance. Significant advances have been made in the development of transcriptomic, genetic and genomic information for maize, *F. verticillioides* moulds, and their interactions over recent years. Several quantitative trait loci (QTL) and single-nucleotide polymorphism markers for resistance to *Fusarium* deriving from QTL mapping and genome-wide association studies have been described in three different maize populations: 1. Bi-parental population; 2. Association mapping panel; 3. Multi-parent Advanced Generation Inter Crosses (MAGIC). To guide the identification of candidate genes within the identified QTL, transcriptomic and sequencing information have been exploited. Promising candidate genes associated with disease resistance and pathogen related-mechanisms at the *Fusarium* resistant loci have been identified on maize chromosomes 4, 5 and 7. Many of the identified candidates genes offer hints to key metabolic pathways that may have a significant effect on reducing *Fusarium* infection. Measuring *Fusarium* resistance in open field could confirm and support their direct use in maize breeding either through crosses or genome editing approaches.