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QTL MAPPING FOR *FUSARIUM* EAR ROT RESISTANCE IN THE MAGIC MAIZE POPULATION

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Fusarium ear rot (FER), caused by *Fusarium verticillioides*, is a prevalent disease in maize causing substantial reductions in yield and grain quality worldwide. The development of resistant genotypes is the most effective way for the sustainable control of FER. Quantitative trait loci (QTL) mapping allows the identification of genomic loci responsible for natural disease resistance. A Multi-parent Advance Generation Intercross (MAGIC) population in maize was recently developed, providing the means to conduct high-definition QTL mapping on a set of highly diverse recombinant lines. We performed an *in vitro* assay for FER resistance using a rolled towel method on a set of 400 MAGIC maize recombinant inbred lines (RIL). For each RIL, 20 kernels as control and 20 kernels inoculated with *F. verticillioides* conidia were germinated for seven days. We measured infection severity level (SEV), seedling weight (PW), and seedling length (PL). QTL analysis was performed on RIL whose haplotypes were reconstructed from 50K single-nucleotide polymorphism data. In total, we identified 8 high confidence QTL for the considered traits and we detected two QTL on chromosome 4 and one QTL on chromosome 5 for SEV (p-value 0.05 from permutation test), indicating that FER resistance is controlled by multiple loci with low effect. To guide the identification of candidate genes within the identified QTL, we exploited transcriptomic and sequencing information generated on the founder lines. The differential expression of genes were tested in the QTL confidence intervals matching the founder effects at the QTL as estimated by the mapping model and we identified 32 suggestive candidates for the three traits. In addition, we performed a GWAS analysis to further improve candidate genes identification by imputing the genome sequence of the founder lines on the reconstructed RIL haplotypes in the QTL interval. We conclude that the rolled towel assay applied on the MAGIC maize population provides a fast and cost-effective method to identify QTL and candidate genes for disease resistance in maize.