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UNRAVELING THE GENETIC BASIS AND HETEROSIS OF FUSARIUM SEEDLING ROT RESISTANCE IN THE RECOMBINANT INBRED CROSSES OF MAGIC MAIZE POPULATION

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Climate change is aggravating the incidence of several maize diseases worldwide. *Fusarium verticillioides* is a prevalent fungal pathogen affecting all growth stages of maize, triggering several diseases including seedling rot and ear rot. Although several quantitative trait loci (QTL) for resistance have been mapped and some candidate genes have been identified in maize recombinant inbred lines (RILs), the genetic basis underlying *F. verticillioides* resistance remains unclear. Moreover, resistance should be addressed in heterozygous genetic material, since yield, growth performances and resistance to disease in maize all show heterotic effects in the cultivated hybrids. For this reason we produced a novel population of 400 recombinant inbred crosses (RIXs), by crossing 400 multi-parent advance generation intercross (MAGIC) RILs in a chain design. This RIX population is a panel of hybrid genotypes providing high genetic diversity and frequent recombination events that is particularly suited to identify heterotic QTL associated to Fusarium seedling rot (FSR) resistance. Phenotyping for FSR resistance was conducted with a rolled towel assay (RTA) allowing a fast screening to identify RIXs resistant to the *F. verticillioides* in the controlled condition. We measured infection severity level, seedling weight and seedling length. For each RIX, 10 seeds as control and 10 seeds inoculated with *F. verticillioides* conidia were germinated for seven days in two replicates. RTA showed high consistency and good reproducibility to phenotype FSR and seedling traits. Phenotypic analyses on 400 RIXs showed a wide distribution of disease severity levels. When compared to FSR values of RILs, RIXs appeared to be more resistant. We also observed that seedling length and seedling weight were higher in RIXs indicating the presence of hybrid vigor. The RIXs genomes were reconstructed from the haplotype composition of each pairs of RILs crosses to establish RIXs, and the distribution of heterozygosity across the genome was consequently estimated. This data will be used to identify heterotic QTL conferring resistance to Fusarium diseases both at the seedling stage and at the adult plant stage, resulting novel insights on heterosis and on the genetic basis of disease resistance that capable to accelerate the breeding effort to achieve maize resistance to Fusarium.