

A genomic approach for characterization of QTLs underlying partial and full resistance to *Fusarium oxysporum* by means of eggplant RIL population

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Eggplant (*S. melongena* L.) is susceptible to many diseases, often caused by soil-borne pathogens, including *Fusarium oxysporum* f. sp. *melongenae* (*Fom*). An intraspecific RIL population derived from the cross between '305E40' x '67/3', two eggplant lines highly contrasting for many key agronomic traits, was used for the development of a high-quality GBS-based map and identification of QTLs affecting key breeding traits including the resistance/tolerance to *Fom*. The female parental line 305E40 is a dihaploid line from the somatic hybrid between eggplant and *S. aethiopicum* and carries the introgressed resistance locus *Rfo-sa1* conferring complete resistance to *Fom* while '67/3' (whose high-quality genome sequence was recently released) is an F8 selection partially resistant to *Fom*. Data of replicated inoculation of each RIL with *Fom* were successfully employed to identify two major QTLs on chromosomes E02 (*Fom2.1*) and E11 (*Fom11.1*) associated with complete and partial resistance, respectively. By exploiting the 35X and 5X Illumina sequencing data available, respectively, for 305E40 and each RIL progeny, we investigated the chromosomal regions underlying QTLs and spotted polymorphisms between the two parental lines. RILs sequencing data were grouped according to the disease score and aligned to the reference genome to identify differentially enriched regions within the confidence intervals of the QTLs. For *Fom 11.1*, pooled sequence reads of partially resistant and sensible RILs were aligned to the 67/3 reference and allowed the identification of 4 differentially enriched regions containing 9 candidate genes. HRM markers for each region were designed and will be used for a fine mapping of the region. Regarding *Fom2.1* QTL, a *de novo* assembly of the 35X sequences from 305E40 allowed to build 5 Mbp of unique scaffolds of 305E40 which were used as reference for the alignment of the two pools of 28 Resistant and 21 sensible RILs, thus enabling the identification of differentially-enriched regions and 11 candidate genes. Characterization of all resistant available RILs, revealed 5 fully resistant lines displaying reduced portions of the QTL on CH2. For this reason, will be submitted to resequencing with the purpose to narrow the chromosomal region underlying the QTL. Twelve RILs miming a fully resistant phenotype did not display the *Fom2.1* QTL, but do have the 67/3 haplotype of the region below the *Fom11.1* QTL, resulting therefore the best lines carrying the partial resistance trait. The best performing RILs displaying full and/or high partial resistance traits will be employed for breeding purposes to introgress and pyramiding the two *Fusarium* resistance QTLs into elite cultivars of eggplant.

Keywords: *Solanum melongena*, *Fusarium oxysporum*, QTL mapping.