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# A GENOMIC APPROACH TOWARDS IDENTIFICATION OF PARTIAL AND FULL RESISTANCE GENES TO FUSARIUM WILT IN EGGPLANT

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Eggplant (*S. melongena* L.) is susceptible to soil borne pathogens including the fungal wilt caused by *Fusarium oxysporum* f. sp. *melongenae* (Fom). A RIL mapping population of 170 lines from the intraspecific cross between '305E40' x '67/3' was produced, and a high-quality GBS-based map developed. '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 spot 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, two pools of 18 partially resistant and 21 sensible RILs were aligned on 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 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 enabling the identification of differentially-enriched regions and 11 candidate genes. The first candidate is being functionally characterized through RNAi.