

GENOMIC AND TRANSCRIPTOMIC INVESTIGATION ABOUT FUSARIUM OXYSPORUM F. SP. MELONGENAE RESISTANCE IN '305E40' EGGPLANT LINE

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Domesticated eggplant (*S. melongena* L.) is severely affected by soil borne diseases, including *Fusarium oxysporum* f. sp. *melongenae* (Fom), causing heavy yield loss both in field and greenhouse cultivation. The development of lines carrying resistance traits as well as the identification of genetic factors underlying plant responses are among the eco-friendlier alternative to chemical treatments. In this work, we focused on '305E40', an eggplant doubled haploid line obtained from somatic hybrid with *S. aethiopicum*. '305E40' carries a fully resistance trait on chromosome 02, in an introgressed fragment from the allied species not yet fully characterized. A mapping approach based on a segregating Recombinant Inbred Lines (RILs) population from the cross between '305E40' x '67/3' lines allowed the identification of a major QTL associated with the resistance trait on CH02. ONT sequencing was exploited to assemble *de novo* a line-specific genome of '305E40' that was annotated and employed as high-quality reference for the deep characterization of the introgressed fragment with the aim to identify the candidate gene(s) responsible of the resistance. Genome comparison with the *S. melongena* reference '67/3' line confirmed the presence of a large introgression of the allied genome in the CH02 of the '305E40' line. Moreover, unique *S. aethiopicum* specific portions were identified which are absent in the reference genome of line '67/3'. A targeted next-generation sequencing-based BSA-Seq approach was employed thus highlighting, within the introgressed fragment, differentially

enriched regions between pools of resistant/susceptible RILs. Among these regions, by combining different approaches as evaluation of differential reads coverage and annotation sources, 33 promising candidate genes were identified. To further provide evidence of their involvement in *Fom* resistance, a differential expression analysis by RNASeq was performed after inoculation with *Fom* on roots from the lines '305E40' and 'Tal1/1' (eggplant line completely sensitive to the pathogen, employed as recurrent to obtain '305E40'). Among the genes lying on CH02, relevant DEGs (differentially expressed genes) with very low or absent expression in the sensitive line were identified. The achieved results were consistent with BSA-seq prediction and led to the identification of a panel of nearly ten best candidate genes putatively involved in biotic stress resistance deserving of functional analysis for the identification of the resistance gene.