Prediction of Solanum Lycopersicum Genome Encoded microRNAs Targeting Tomato Spotted Wilt Virus

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Abstract : Tomato spotted wilt virus (TSWV) belongs to the genus Tospoviruses (family Bunyaviridae). It is one of the most devastating pathogens of tomato (Solanum Lycopersicum) and heavily damages the crop yield each year around the globe. In this study, we retrieved 329 mature miRNA sequences from two microRNA databases (miRBase and miRSoldb) and checked the putative target sites in the downloaded-genome sequence of TSWV. A consensus of three miRNA target prediction tools (RNA22, miRanda and psRNATarget) was used to screen the false-positive microRNAs targeting sites in the TSWV genome. These tools calculated different target sites by calculating minimum free energy (mfe), site-complementarity, minimum folding energy and other microRNA-mRNA binding factors. R language was used to plot the predicted target-site data. All the genes having possible target sites for different miRNAs were screened by building a consensus table. Out of these 329 mature miRNAs predicted by three algorithms, only eight miRNAs met all the criteria/threshold specifications. MC-Fold and MC-Sym were used to predict three-dimensional structures of miRNAs and further analyzed in USCF chimera to visualize the structural and conformational changes before and after microRNA-mRNA interactions. The results of the current study show that the predicted eight miRNAs could further be evaluated by in vitro experiments to develop TSWV-resistant transgenic tomato plants in the future.

Keywords : tomato spotted wild virus (TSWV), Solanum lycopersicum, plant virus, miRNAs, microRNA target prediction, mRNA
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