



***In silico* analysis of gene content in tomato genomic regions mapped to the *Ty-2* resistance gene**

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ABSTRACT. Tomato yellow leaf curl virus is one of the main diseases affecting tomato production worldwide. Previous studies have shown that *Ty-2* is an important resistance gene located between molecular markers C2_At2g28250 (82.3 cM) and T0302 (89.0 cM), and exhibits strong resistance to tomato yellow leaf curl virus in Asia. In this study, *Ty-2* candidate genes were subjected to bioinformatic analysis for the sequenced tomato genome. We identified 69 genes between molecular markers C2_At2g28250 and T0302, 22 of which were disease-related resistant genes, including nucleotide binding site-leucine-rich repeat disease resistance genes, protease genes (protein kinase, kinase receptor, and protein isomerase), cytochromes, and transcription factors. Expressed sequence tag analysis revealed that 77.3% (17/22) of candidate disease-resistance genes were expressed, involving 143 expressed sequence tags. Based on full-length cDNA sequence analysis, 7 candidate genes were found, 4 of which were involved in tomato responses to pathogens. Microarray ex-

pression analysis also showed that most candidate genes were involved in the tomato responses to multiple pathogens, including fungi, viruses, and bacteria. RNA-seq expression analysis revealed that all candidate genes participated in tomato growth and development.

Key words: Disease resistance; Expressed sequence tag; Tomato; *Ty-2*; Tomato yellow leaf curl virus