



Identification of potential WRKY transcription factors as negative regulators of tomato defense against *Pseudomonas syringae* pv. *tomato*

Panel

Genética y Biología Molecular de Plantas

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The tomato (*Solanum lycopersicum* L.) is a major crop of agronomic and economic relevance, severely affected by the bacterial speck disease caused by *Pseudomonas syringae* pv. *tomato* (*Pst*). While several transcription factors (TFs) have been implicated in tomato defense, the role of WRKY TFs acting as negative regulators of basal resistance remains poorly understood. Evidence from *Arabidopsis thaliana* indicates that members such as WRKY7, WRKY11, and WRKY17 act as repressors of defense responses, with no detectable impact on plant growth or development. However, their functional counterparts in tomato plants remain to be evaluated. This study aims to identify potential WRKY transcription factors in tomato which may negatively regulate defense against *Pst*. To this end, we constructed a curated database of WRKY genes reported in tomato and *Arabidopsis* and performed comparative phylogenetic analyses to identify putative tomato homologs of known negative regulators. Based on sequence homology and domain conservation, we selected a preliminary set of candidate genes for downstream validation. Additionally, we evaluated available transcriptomic datasets from tomato plants challenged with *Pst* to prioritize candidate genes for further experimental analysis. Specific primers were designed for expression profiling of these candidates in tomato cultivar Moneymaker challenged with *Pst* DC3000. Preliminary analyses revealed several WRKY candidates clustering with *Arabidopsis* repressors of basal immunity. Ongoing expression

analyses are expected to provide insights into the transcriptional behavior of these candidates during *Pst* infection, representing a step toward evaluating their potential role as negative regulators of tomato defense. Overall, this work contributes to filling a critical knowledge gap on WRKY-mediated repression of immunity in tomato plants. Identifying such genes is an essential step toward functional validation and, ultimately, the development of novel tomato varieties with enhanced resistance through gene-editing approaches.

Palabras Clave

(1) *Solanum lycopersicum*, (2) WRKY transcription factors, (3) *Pseudomonas syringae* pv. tomato, (4) Plant immunity.

Financiamiento:

This research was supported by ANID-Fondecyt Postdoctorado N°3250059 and Fondecyt Regular N°1240785.