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TOWARDS THE MODELING OF TOMATO-FORL INTERACTION

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FORL, cytochrome P450, ethylene, glucosinolate

In recent years models have been widely used to study pathogenicity mechanisms thanks to the availability of high throughput sequence data and computational resources. Gene expression approaches constitute a starting point from which to determine the best strategy for building a biological model of a plant –pathogen system. A common strategy in gene expression analysis is to identify a set of genes of interest following their expression profile in different hosts and/or treated tissues. *Fusarium oxysporum* f. sp. *radicis lycopersici* (FORL) is one of the most destructive pathogen of tomato plants. This pathogen is responsible of the crow and roots rot until to determinate the plant's death. Large-scale microarray analysis has been performed on infected and non-infected root samples of resistance (Momor) and susceptible (Monalbo) tomato genotypes. The differential expression of cytochrome gene family in compatible and incompatible reaction helped us to generate hypotheses about its behavior in susceptible and for resistance response to FORL. The results showed that in the incompatible reaction there is an activation of the metabolic pathway of tryptophan whilst in the compatible reaction was detected the activation of the ethylene synthesis. Previous studies showed that the production of glucosinolate compounds are involved in the defense plant and that ethylene suppresses the action of the cytochrome P450. Although still fragmented genes expression network helped us to formulate a hypothesis that provides a overview of the tomato-FORL interaction process. Proteomic techniques as well as data mining and functional genomics tools available nowadays will help us to refine the current model.