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STUDY OF MOLECULAR BASES OF PLANT-APHID INTERACTION

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The development of an appropriate defence requires that plants recognize pests as early as possible. Consequently, plant responses are correlated to the mode of insect feeding and the degree of tissue damage at the feeding site. Although phloem-feeding pests, including aphids, cause extensive crop damage, only few data are available about how plants perceive these arthropods and activate endogenous defences.

Aphids are highly specialized in their mode of feeding and impose a complex stress on plants. Differently from herbivorous pests, the prolonged interaction of aphid stylets and plant tissue causes minimal mechanical damage and consequently, plants respond to aphids activating various defense mechanisms.

The potato aphid (*Macrosiphum euphorbiae* T.) is an important pest of tomato and other Solanaceae. Besides vectoring pathogenic viruses, this species causes physical damage to green tissues and removal of photoassimilates, which result in high yield loss when populations are high. Tomato (*Solanum lycopersicum*) transcriptional changes in response to aphids and molecular mechanisms associated with the development of symptoms are currently largely unexplored. To investigate tomato responses activated during a compatible interaction, we used a microarray analysis to monitor changes in host gene expression during *M. euphorbiae* attack.

We present a time series-based investigation of the tomato cv Microtom after *M. euphorbiae* infestation. Transcriptomic changes were studied 24h, 48h and 96h after infestation to monitor the progress of early induced responses. Transcriptional reconfiguration covered a broad range of biological processes, which include both primary and secondary metabolism. We also carried out a proteomic study 48h following aphid attacks to identify differentially expressed protein compared to uninfested control plants. About 87 differential expressed spot were identified and 49 out of them represented a single protein. These sequences were classified by Blast2go database and most of them were involved in functions highlighted by the transcriptomic analysis, e.g. primary and secondary metabolism of the plant, photosynthesis, oxidative and defence stress response.

This study showed how plant aphid response are complex and multifactorial. Because the modulation of endogenous defense may be a practicable strategy to improve plant resistance against

aphids, integrating transcriptomics and proteomics can greatly contribute to a systems-level understanding of host response.