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SCREENING OF SOLANUM LYCOPERSICUM X SOLANUM PENNELLII INTROGRESSION LINES FOR THE RESISTANCE VERSUS THE PARASITIC WEED PHELIPANCHE RAMOSA: A STEP TOWARDS DUAL RNA-SEQUENCING AIMED AT STUDYING HOST/PARASITE CROSSTALK

FRUGGIERO C.*, AUFIERO G.*, CUCCURULLO A.**, YOENYAMA K.***, VURRO M.****, BARONE A.*, RIGANO M. M.*, NICOLIA A.**, D'AGOSTINO N.*

*) Department of Agricultural Sciences, University of Naples Federico II, Portici, Italy
**) CREA Research Centre for Vegetable and Ornamental Crops, Pontecagnano Faiano, Italy
***) Ehime University, Graduate School of Agriculture, Matsuyama, Ehime 790-8566, Japan
****) Institute of Sciences of Food Production (ISPA), National Research Council (CNR), Bari, Italy

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Broomrapes (Orobanche spp. and Phelipanche spp.) cause severe damages to crops every year around the world. Particularly, Phelipanche ramosa is a threat that severely affects tomato (Solanum lycopersicum L.) cultivation. One of the most effective approaches to control this pest is to develop resistant varieties through breeding. Unfortunately, within the cultivated tomato gene pool there are scarce sources of resistance, thus significantly impairing resistance versus this natural enemy. However, some preliminary and recent evidence indicates that Solanum pennellii, a close wild relative of S. lycopersicum, is resistant. Some S. lycopersicum x S. pennellii introgression lines (ILs) among those available may show considerable tolerance to parasitic weed infestations.

Interestingly, preliminary results on root exudates of S. pennellii showed the absence of the classical strigolactones usually found in cultivated tomatoes (i.e., orobanchol, solanacol and didehydro-orobanchol).

The screening for the resistance of ILs versus P. ramosa is ongoing. We are testing the ability of tomato plantlets to stimulate P. ramosa seed germination and induce the production of the haustoria and the development of the tubercles, by performing in vitro germination assays and plastic bag assays. The purpose of these experiments is to identify the most resistant and most susceptible ILs to be subjected to dual RNA-Sequencing. Indeed, host/parasite interaction determines large-scale reprogramming of transcriptomes in both organisms. The analysis of transcriptome dynamics and gene expression profiles is essential to reveal the molecular mechanisms that mediate host/parasite crosstalk and to eventually identify the key genes involved in the defense strategies implemented by the host.

In addition, some lines of evidence suggest that non-coding RNAs (ncRNAs) play an active role in the interaction between tomato and different pathogens and that in other species long ncRNAs are transferred bidirectionally through vascular connections acting as critical regulators in coordinating host/parasite interaction. Tomato root samples (3 biological replicates) and samples of P. ramosa at different stages of infection (pre-attachment, haustorium differentiation, tubercle development) will be collected, the total RNA extracted and then sequenced to simultaneously study both the evolution of the parasitic weed and the host response. The analysis of the coding and non-coding component (never investigated before) of the transcriptome could lead to expanding the panel of candidate genes useful as targets in future mutagenesis programs to obtain tomato varieties resistant to Orobanchaceae.