GENETIC AND BIOCHEMICAL ANALYSES TO EVALUATE INTERACTIONS BETWEEN BACTROCERA OLEAE (ROSSI) AND OLEA EUROPAEA L.


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In the Mediterranean basin the olive fruit fly Bactrocera oleae (Rossi) is the most dangerous pest of olive crop production. It is an insect strictly associated with the genus Olea and most of the O. europaea cultivars show high levels of susceptibility.

This work aims to characterize the fruit metabolites involved in the B. oleae defence response and to evaluate the genes involved in the resistance/tolerance mechanisms.

A set of new olive genotypes derived from reciprocal crosses between ‘Picholine’ and other six cultivars, under evaluation for B. oleae resistance, were chosen for biochemical and genetic analyses. Two groups, characterized by high and low susceptibility to olive fly, were identified and evaluated for fruit metabolic profiles and differentially expressed genes.

Metabolic analyses have been conducted on olive fruits from field-growing plants collected at five ripening stages, from August to November. HPLC-DAD-MS analyses have allowed the identification of different classes of phenolic compounds specific to high and low susceptible olive genotypes. Metabolites common to all samples were quantified at 280 and 330 nm in order to identify quantitative differences between the two groups of genotypes.

cDNA-AFLP approach was used to identify differentially expressed transcripts between low and high susceptible genotypes and to identify genes putatively involved in insect-plant interactions. We isolated 109 transcript-derived fragments (TDF) that were sequenced and compared to the GeneBank database using BlastX. Among them, 43 TDFs showed high similarity to known proteins, some of them being involved in disease resistance, stress response and signal transduction in defence mechanisms.