

IDENTIFICATION OF DIFFERENTIALLY EXPRESSED ESTs IN OLIVE AS A CONSEQUENCE OF THE OLIVE FRUIT FLY ATTACK

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differential expression, Olea europea, Bactrocera oleae, suppression subtractive hybridization

The olive fruit fly *Bactrocera oleae* (Rossi) is the most harmful pest of olives worldwide and it causes significant yield losses in almost all countries of the Mediterranean Basin. Indeed, the threshold for olive fly infestation of table olives is near zero, and slightly higher for oil olives (8 - 10%). In EU the standard control method is based on insecticidal bait sprays from ground. The damages caused by the olive fruit fly are firstly due to the egg laying punctures of early maturing fruits. It has been proposed that fruits easier to puncture will attract more flies. Secondly, to the feeding tunnels of the growing larva, which usually causes the fruit to drop off the tree.

It is likely that the olive response to these two damages are different and the aim of this study is the identification of clones differentially expressed in *B. oleae*-olive fruit interaction. Specifically, we want to investigate the fruit response to oviposition and to feeding larvae, using the suppression subtractive hybridization (SSH) technique.

We constructed two subtracted cDNA libraries, one from punctured fruits and one from fruits with developing larvae, from olives of the ‘Moraiolo’ cultivar. The nucleotide sequences and putative amino acids translations of clones of the two subtracted libraries were analyzed using tBLASTX and tBLASTN algorithms of the National Center for Biotechnology Information (NCBI). We then focus our attention to sequences with an e-value lower than 0.001. These ESTs were annotated and classified according to their biological function using Blast2GO.

The preliminary data suggest that olive response to puncture involves a number of genes that are different to those involved in the response to larva feeding. Furthermore, several biological classes of genes should be associated to the plant defense mechanisms, implying that the molecular response of olives is complex and involves numerous pathways.