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BOOK OF ABSTRACTS

IDENTIFICATION OF CANDIDATE GENES INVOLVED IN OLIVE RESPONSE TO ANTHRACNOSE FOR A SUSTAINABLE DISEASE MANAGEMENT.

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Anthracnose is a disease that affect the olive tree caused by fungi of the genus *Colletotrichum*. These fungi are responsible to premature fruit drop and a consequent decrease in the oil quality, and also cause defoliation of trees compromising the production of the following years. Currently the best control strategy is based on application of synthetic fungicides, with a regulatory pressure in agriculture worldwide to limit its use.

Looking for a sustainable disease management, the present study reports the transcriptional changes of olive genes that encode enzymes directly associated with the maintenance of the balance of oxidative oxygen species (ROS), in response to *Colletotrichum* sp. infection. The cultivar selected for the studies was 'Galega vulgar', known to be extremely susceptible to this disease. Plants used in the experiments were from *in vitro* culture (to warranty their healthy status), transplanted to pots and maintained under controlled conditions. Leaves of the olive plants were inoculated with a spore suspension of *Colletotrichum* sp., and leaf samples were collected before fungi inoculation (T0) and at 10 days (T1) and 35 days (T2) after inoculation. Confirmation of the presence of the fungi in inoculated plants was performed following a real-time qPCR approach. The selected target genes for expression analysis were Superoxide dismutase (*SOD*), Endochitinase_EP3-like (*CHI2*), Glutathione S-transferase L3-like (*TransFL3*), Glutathione peroxidase 2 (*PEROX2*), Glutathione S-transferase THETA 1 (*THETA*), Glutathione S-transferase DHAR2-like (*TransfDHAR*), Glutathione peroxidase 5 (*PEROX5*) and Glutathione peroxidase 8 (*PEROX8*). Following a qPCR approach, a general up-regulation of the target genes was detected, but only *CHI2* revealed a significantly up-regulation ($p < 0.005$) between T0 and T2 in response to *Colletotrichum* sp. infection, being a promising candidate to be later used in functional analysis. We emphasize the importance of this study for the identification of candidate genes to incorporate new sources of resistance of olive trees to anthracnose with the promotion of the development of sustainable management strategies.

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