Olive Endochitinase EP3-like gene mediates plant response against Colletotrichum nymphaeae infection.

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One of the most economically important fruit trees in Mediterranean countries is the olive tree (*Olea europaea* L.). Foliar and fruit fungal pathogens are responsible for economically important diseases in most olive-growing areas. Within these pathogens, we highlight *Colletotrichum* spp., the causal agent of the serious anthracnose disease. Under favourable conditions, the disease can devastate entire production fields. Symptoms typically occur on fruits at maturation under wet autumn conditions causing severe quantitative and qualitative yield losses of olive oil and fruits. The best control strategy currently relies on the use of synthetic fungicides, but there is regulatory pressure in agriculture worldwide to limit their use.

In search of a sustainable approach to disease management, the present study reports the transcriptional changes of genes that encode enzymes actively involved in the olive tree's defence response to *C. nymphaeae* infection. 'Galega vulgar', an olive cultivar known to be highly susceptible to the disease, was selected for the studies. The plants used in the experiments were grown *in vitro* to ensure their health status, transplanted into pots, and grown under controlled conditions. Leaf samples were collected before fungi inoculation, and in different timepoints after inoculation with a spore suspension of *C. nymphaeae*. Transcriptomic studies revealed a general up-regulation of the selected target genes, but only *Endochitinase_EP3-like* (*CHI*), presented a significantly up-regulation in response to *C. nymphaeae* infection. *CHI* is a promising candidate to be later used in functional analysis. We stress the importance of this study for incorporation of new sources of resistance of olive trees to anthracnose for the promotion of sustainable management strategies.

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