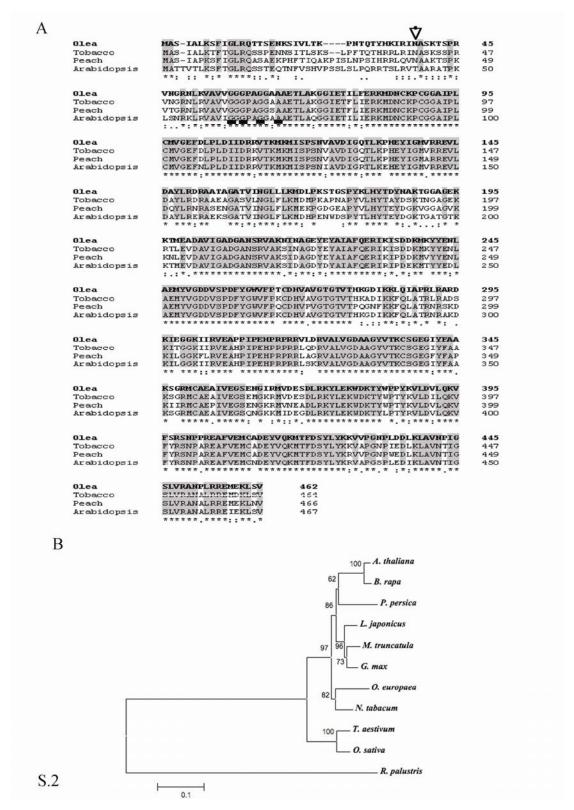
## **Accessory publication**

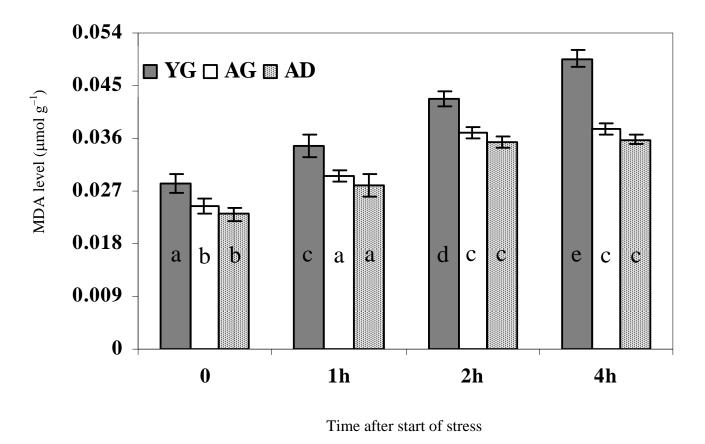


**Fig. S1.** Whole-drupe phenotype of *Olea europaea* L. infected by carpophagus larvae. Scale bars = 1cm.



**Fig. S2.** Features of the protein encoded by *OeCHLP*. (A) Amino acidic alignment of deduced protein *OeCHLP* in bold (accession no. DQ424963) with homologues from other plant species. Strictly conserved amino acids are boxed in grey. The residues of the motif necessary to bind NADPH are underlined. The black arrow indicates the editing site for the transit peptide. (B) OeCHLP within the phylogenetic tree of

CHLPs proteins. OeCHLP amino acid sequence was compared to the CHLPs proteins of dicotyledonous and monocotyledonous species available in database. The procedures for alignments and phylogenetic relationships are in the materials and methods; trees were rooted with the *Rhodopseudomonas palustris* has used to create an out-group. Bootstraps values (at the branching points) are given for major nodes only and were based on 1000 repetitions. The list of protein accession numbers is in the material and methods.



**Fig. S3.** Level of malondialdehyde ( $\mu$ mol g<sup>-1</sup>) in the leaves of cold-exposed plants evaluated through the thiobarbituric acid test at different times after start of stress. Values represent the means  $\pm$  s.e. of three independent biological replicates. Means signed with the same letters are not significantly different for P = 0.05 after ANOVA followed by *Bonferroni* post hoc test. AD, adult dark leaves up 6cm long; AG, adult green leaves up 6cm long; MDA, malondialdehyde; YG, young green leaves 2–4 cm long.