

TERPENOIDS AND THE EXPRESSION OF TERPENE SYNTHASE GENES ARE COHERENTLY AND SELECTIVELY MODULATED IN CALABRIAN PINE (*PINUS NIGRA* SUBS. *LARICIO*) IN RESPONSE TO PINE PROCESSIONARY MOTH (*THAUMETOPOEA PITYOCAMPA*) INFESTATION

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The pine processionary moth (PPM) is a severe defoliating pest that has recently increased its spread on the *Pinus* species in response to global warming, causing serious economic and ecological losses as well as severe allergic reactions in humans and other mammals. This prompts researchers and stakeholders involved in forest biology and management to look more closely at biological control methods, which primarily necessitate paying attention to and learning about the tri-trophic interactions that occur in natural environments between the plant host, the attacking insect, and its natural enemies. Because terpenoids may play important roles in both defence and chemical communication in such natural interactions, we investigated the production of terpenoid metabolites and their possible relationship with the transcriptional regulation of the terpene synthase genes in saplings of the non-model conifer *Pinus nigra* subsp. *laricio* (Calabrian black pine) facing PPM caterpillar attack under semi-natural conditions. By keeping in mind the progression of the PPM life cycle, pine needles were sampled after 0, 21, 84, and 195 days after induced infestation (AI), to monitor the expression profiles of mono- and di-

terpene synthase genes (*MTPSs* and *DTPSs*, respectively) and the quantities of the corresponding mono- and di-terpenoids. The 21 days AI correspond to the larval stage (LS) 2 in which larvae spend most of their time inside the nests with scarce and sporadic feeding on pine needles. The 84 days AI correspond to LS4 in which there is the maximal trophic activity of the larvae. Finally, the 195 days AI coincide with the LS5, when there is little or no defoliation activity and the beginning of the “subsidence” of the insect underground, which is preceded by the well-known “procession” of the PPM caterpillars. During PPM infestation, changes in the relative transcript abundances of six *MTPSs* and four *DTPSs*, previously isolated and characterised in *Pinus nigra* subs. *laricio*, were found to always match the quantitative changes of their putative corresponding metabolites, i.e., respectively, fourteen monoterpenes and nine diterpene resin acids. The extent and sign of such changes during the course of PPM infestation were found to be remarkably variable, depending on the gene/metabolite considered. Taken together, obtained results suggest a rather complex, selective and fine modulation of terpenoids biosynthesis in Calabrian pine needles in response to PPM infestation. Furthermore, because some of the observed changes occur prior to the establishment of the full trophic activity of the PPM larvae, it is tempting to speculate that, in addition to being involved in damage/compensation/defence responses, certain of the studied terpenoids and their biosynthetic genes may also participate in the chemical communication between the infested plant and its biotic and abiotic environment, such as alerting conspecific individuals and/or recruiting PPM natural enemies.