

Metabolites of *Camellia sinensis* (L.) from biotic-abiotic stresses and deciphering the molecular basis of *Helopeltis theivora* Waterhouse's infestation

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Abstract

Helopeltis theivora Waterhouse (Hemiptera: Miridae), commonly as tea mosquito bug (TMB), is an economic pest to the world tea industry and its resistance has been promoting for a novel management strategy. Moreover, to understand and explore the effect of such biotic factor i.e. TMB's sap-sucking and abiotic factor i.e. artificial mechanical injury on tea foliages, metabolomics is rapidly emerging as a one-step tool. Therefore, a comparative and qualitative HR-LCMS based metabolomic study is carried out on four young tea leaf samples viz. healthy (HTL), un-infested (UIP), infested (IP), and artificial spots (ACS). From a unique methodology, dynamic and selective hypersensitive (like) responses of tea are observed, for the TMB's sap-sucking and artificial mechanical injury. Interestingly under TMB's biotic stress, the UIP sample shows the expression (N=24) and suppression (N=27) of metabolites as compared to HTL sample. Whereas, the ACS sample from abiotic stress reveals unique metabolites (N=20) in comparison to the UIP and HTL samples. The IP sample from biotic stress surprisingly carries unique metabolites (N=9) in contrast to UIP, HTL, and ACS samples. Based on pharmacological and chemical properties, these nine secreted metabolites of TMB are hypothesized for the overall molecular mechanism of TMB's sap-sucking process.

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