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Genome-wide identification of the Cytochrome P450 superfamily in *Trichoplusia ni* (cabbage looper) and in-silico expression of resistance against HDAC inhibitors

The cabbage looper, *Trichoplusia ni*, is a serious pest of cruciferous crops such as cauliflower, cabbage, broccoli, and Brussels and damages a significant amount. The previous chemical applications made insecticides resistant to most of them. This study aims to identify the Cytochrome-P450 (CYP450) gene family in *T. ni* to find out the resistance and metabolic detoxification genes that help them survive against various environmental stresses, including chemical stress. To find out the regulatory gene mechanism, two HDAC inhibitor insecticides (sulforaphane and Trichostatin A) were employed against this pest. The in-silico gene profiling of these HDAC inhibitors helps to find out the *CYP450* genes in *T. ni*. This investigation finds out the total of 19 *CYP450* genes that were renamed from *CYPTni1* to *CYPTni19*. The present study shows the phylogenetic relationship of *CYP450* genes, the number of exons present, gene structure, and functions that are regulated by mature microRNA (miRNA). The detailed information on genes presents on different chromosomes as well as the subcellular location of identified *CYP450* genes was crafted in this study. The physicochemical properties of these identified genes, such as molecular weight (Mw), isoelectric point value (pI), instability index (II), aliphatic index (AI), and grand average of hydropathy (GRAVY), were calculated to show the description and properties of the identified *CYPTni* genes. As a result of gene profiling, 3 genes were significantly up-regulated (*CYPTni3*, *CYPTni2*, and *CYPTni4*) when these HDAC inhibitors were applied as insecticides to control cabbage looper. These genes are responsible for resistance and metabolic detoxication mechanisms under the effects of HDAC inhibitor-induced chemical stressors.

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