CLONING AND EXPRESSION OF DESOXYHEMIGOSSYPOL 6-O-METHYLTRANSFERASE FROM COTTON PLANT

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Abstract

Cotton contains a unique group of terpenoids including desoxyhemigossypol (dHG), hemigossypol (HG), gossypol (G), hemigossypolone (HGQ), and the heliocides that are part of the plant's defense system against pathogenic fungi and insects. Desoxyhemigossypol is the key intermediate in the biosynthesis of all of these compounds. These compounds are also accompanied by a group of related compounds in which the hydroxyl group at C-6 is methylated. The methylated terpenoids are unique in that they are less toxic to insects such as *H. virescens* larvae and to *V. dahliae* and *F. oxysporum f. sp. vasinfectum*. Previously we have purified and characterized an enzyme, desoxyhemigossypol 6-O-methyltransferase (dHG-6-OMT), which is responsible for specifically methylating the key intermediate dHG. The methylation of dHG may be the key step which lead to the biosynthesis of all of the methylated terpenoids and may be the cause of reduced effectiveness of the entire terpenoids defense system of cotton toward insects and fungal pathogens. Genetic engineering may allow us to down regulate the dHG-6-OMT gene and therefore to increase plant resistance. It is toward this goal, we present our work in the cloning and expression of dHG-6-OMT from cotton.

The sequence of dHG-6-OMT shares as high as 57% identity with an OMT from almond flower tissue at protein level. The deduced amino acid sequence includes all the dHG-6-OMT peptides that were sequenced, establishing its authenticity.

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