عنوان مقاله:

Study of Cannabinoids Biosynthesis-Related Genes in Hemp (Cannabis sativa L.) under Drought Stress by In Vitro and In Silico Tools

محل انتشار:

تعداد صفحات اصل مقاله: 7

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خلاصه مقاله:

Introduction: Cannabinoids can be found as the specific secondary metabolites of hemp (Cannabis sativa L.), including Δ۹-tetrahydrocannabinol (THC), cannabidiol (CBD), and cannabichromene (CBC). There are many enzymes, particularly cannabichromene synthase, cannabidiolate synthase, and Δ۹-tetrahydrocannabinolate synthase, contributing to the biosynthesis of the cannabinoids. Environmental stress, particularly drought, can induce secondary metabolites. In the present study, we have tried to investigate and understand the key factors such as drouth-induced Transcriptional Factors (TFs) involving in the pathway by employing in vitro and in silico tools.Materials and Methods: After providing the genes' names and IDs from the National Center for Biotechnology Information (NCBI), Transcription Start Sites (TSS) and TATA-box were predicted by the TSS Plant website, as well as involved transcriptional factors. The expression of the genes was assayed under drought conditions by in silico and in vitro tools, R software, and Real-time PCR, respectively.Results: The findings identified all the genes contributing to biosynthesis cannabinoids in drought conditions. There were actually six TF sites and four TF sites for the gene of olivetolic acid cyclase and AAE۱, respectively.Conclusions: Drought stress can induce overexpression of the genes encoding B۳ domain-containing proteins, MLP۲۸, MYB binding site, transcriptional repressor OFP۷, and WAK۱ as TFs respond to biotic and abiotic stresses in Cannabis sativa plants.

کلمات کلیدی:

Cannabis sativa L, Δ۹-tetrahydrocannabinol, Cannabidol, Gene expression, R Program, Real-Time PCR

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