عنوان مقاله:

Investigation in expression of key genes involved in sanguinarine biosynthetic pathway in Papaver genus under drought and salinity

محل انتشار:

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خلاصه مقاله:

The presence of morphine alkaloids, anti-microbial and anti-cancer metabolite, sanguinarine, in different species of Papaver genus has made it one of the most valuable plants in the pharmaceutical industry.With regard to the influence of drought and salinity on the increase of secondary metabolites, the present study attempted to investigate the effect of the mentioned stresses on the key genes expression involved in the sanguinarine biosynthetic pathway. Therefore, the expression of BBE۱, DIOX۲ and DBOX genes involved in the biosynthesis of sanguinarine was investigated under drought (۵۰% FC), salinity (۱۰۰ mM NaCl) and non-stress conditions in four species of P. somniferum, P. bractateum, P. armeniacum and P. argemone in a factorial experiment based on a completely randomized design with three replications. Total RNA was extracted from leaves and roots of non-stressed and stressed plants, and then cDNA was synthesized and used for quantitative real-time PCR reactions. The results showed that, increases in the expression of BBE۱, DIOX۲ and DBOX genes in each of four species under drought condition were more pronounced than salinity. In addition, the level of gene transcripts in roots was more than leaves. The expression of each of the threegenes was higher in P. somniferum and P. bractateum compared to P. armeniacum and P. argemone; so that the highest transcription levels of BBE۱ (seven-fold), DIOX۲ (four-fold) and DBOX (six-fold) in P. bractateum were related to root under drought, leaf under salinity and root under drought stresses, respectively. BBE۱ expression in the studied species was more than DIOX۲ and DBOX genes, under the mentioned stresses. In fact, according to sanguinarine biosynthesis pathway, BBE۱ is a branching point gene and it seems that these species divert the biosynthesis pathway of benzylisoquinoline alkaloids towards the production of sanguinarine by increasing BBEI gene expression under stress conditions. In conclusion, our results support the idea that P. somniferum and P. bractateum could be used as suitable candidates for metabolite engineering and high yield extraction of sanguinarine.

کلمات کلیدی:

BBE۱, *DBOX*, *DIOX۲*, Gene expression, Sanguinarine

لینک ثابت مقاله در پایگاه سیویلیکا: