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SELECTION OF DIFFERENTIALLY EXPRESSED GENES IN *CENTAURIUM ERYTHRAEA* RAFN. DURING *IN VITRO* SOMATIC EMBRYOGENESIS

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Abstract

Centaurium erythraea Rafn. (Gentianaceae) represents a well-known medicinal plant rich in secondary metabolites and an appropriate model system for studying developmental biology due to its great developmental plasticity in vitro. One of the most unique manifestations of this characteristic in plants is somatic embryogenesis (SE), the development of embryos from somatic cells. SE initiation and progressing of the embryo through different developmental stages involves gene reprogramming and differential expression of numerous genes. Our current research focuses on characterizing novel SE-related genes in centaury tissues using next-generation RNA sequencing data and quantitative real-time PCR (qPCR). Six different centaury tissues, including embryogenic calli, globular and cotiledonary somatic embryos were subjected to ultra-high-throughput sequencing on an Illumina HiSeq 2500 platform, followed by de novo transcriptome assembly. FPKM (fragments per kilobase of exon model per million reads mapped) was used to evaluate in silico expression of functionally annotated transcripts. The generated transcriptome data were subsequently used for discovering genes with potential roles in centaury SE. Potential SE markers were excavated focusing on transcripts with greater than eight fold change in FPKM values in embryogenic tissues compared to non-embryogenic ones. Based on these criteria, twenty transcripts were chosen, four with completely unknown function. Expression analysis of selected genes was carried out by qPCR using specific primers in different embryogenic and non-embryogenic centaury tissues. Identified genes with differential expression during SE will be further characterized by overexpression and silencing in centaury.

Keywords: somatic embryogenesis, marker genes, gene expression, RNAseq.

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