conferenceseries.com SciTechnol

Mohammad Sadegh Sabet et al., J Plant Physiol Pathol 2017, 5:5
DOI: 10.4172/2329-955X-C1-012

3rd Global Summit on

Plant Science

August 07-09, 2017 | Rome, Italy

Identification of gene sequences involved in chicoric acid biosynthesis pathway in *Echinacea purpurea* through RNA-SEQ transcriptome analysis

Mohammad Sadegh Sabet, Meisam Salmanzadeh and **Ahmad Moieni**
Tarbiat Modares University, Iran

Plant secondary metabolites are the sources for pharmaceuticals, food additives, stuffing, and industrially important biochemical substances. Chicoric acid is one of the important plant secondary metabolites that two percent of which is contributed by *Echinacea purpurea* roots. Retroviral integrase (IN) is an enzyme produced by a retrovirus (such as HIV) that enables its genetic material to be integrated into the DNA of the infected cell. Chicoric acid is able to inactive the integrase (IN inhibitor) and prevents the HIV virus spreading. Cichoric acid is a hydroxycinnamic acid and an organic compound of the phenylpropanoid class. Engineering of secondary metabolite biosynthesis is strongly related to the identification and isolation of genes involved and effective in the biosynthesis pathways. The known genes involved in chicoric acid biosynthesis are: PAL phenylalanine amino lyase, C4H cinnammate-4-hyroxylase, C3H p-coumarate-3-hydroxylase, 4CL 4-(hydroxyl) cinnamoyl CoA ligase, HTT hydroxycinnamoyl-CoA/tartaric acid hydroxycinnamoyl transferase. RNA-seq analysis based on the next generation sequencing technology was shown to be a potent method for identifying candidate genes encoding responsible enzymes in biosynthesis pathways in non-model plants. In this study, the sequences of important genes involved in chicoric acid biosynthesis pathway obtained, using transcriptome databases searching and *in silico* analysis. In order to identify the close plant species to *Echinacea purpurea* and to access to the corresponding genes, the BLASTn method (available at www.ncbi.nlm.nih.gov) was used based on identified gene sequences. SRA-BLAST was performed, using the close reference genome, and Sequence Read Archive (SRA) of target genes was made from the NCBI database. All short obtained reads were extracted and assembled via codon code aligner software to obtain the gene sequences. The verification of the extracted sequences was performed, using gene specific primers, designed with Oligo v. 7 software for each sequence, PCR reaction and agarose gel electrophoresis.

Biography

Mohammad Sadegh Sabet received a PhD in Plant Breeding (Molecular Genetics and Genetic Engineering) from Tabriz University, Tabriz, Iran in 2011. He is Assistant Professor in Department of Plant Breeding, Faculty of Agriculture, Tarbiat Modares University, Tehran, Iran. His research interest areas are Plant Molecular Genetics and Genetic Engineering.

ms.sabet@modares.ac.ir

Notes: