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Transcriptomic Analysis for Differential Expression of Genes Involved in Secondary Metabolite Production in Narcissus Bulb and in vitro Callus

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Abstract : The Amaryllidaceae genus Narcissus contains secondary metabolites, which are important sources of bioactive compounds such as pharmaceuticals indicating that their biological activity extends from the native plant to humans. Transcriptome analysis (RNA-seq) is an effective platform for the identification and functional characterization of candidate genes as well as to identify genes encoding uncharacterized enzymes. The biotechnological production of secondary metabolites in plant cell or organ cultures has become a tempting alternative to the extraction of whole plant material. The biochemical pathways for the production of secondary metabolites require primary metabolites to undergo a series of modifications catalyzed by enzymes such as cytochrome P450s, methyltransferases, glycosyltransferases, and acyltransferases. Differential gene expression analysis of Narcissus was obtained from two conditions, i.e. field and in vitro callus. Callus was obtained from modified MS (Murashige and Skoog) media supplemented with growth regulators and twin-scale explants from Narcissus cv. Carlton bulb. A total of 2153 differentially expressed transcripts were detected in Narcissus bulb and in vitro callus, and 78.95% of those were annotated. It showed the expression of genes involved in the biosynthesis of alkaloids were present in both conditions i.e. cytochrome P450s, O-methyltransferase (OMTs), NADP/NADPH dehydrogenases or reductases, SAM-synthetases or decarboxylases, 3-ketoacyl-CoA, acyl-CoA, cinnamoyl-CoA, cinnamate 4-hydroxylase, alcohol dehydrogenase, caffeic acid, N-methyltransferase, and NADPH-cytochrome P450s. However, cytochrome P450s and OMTs involved in the later stage of Amaryllidaceae alkaloids biosynthesis were mainly up-regulated in field samples. Whereas, the enzymes involved in initial biosynthetic pathways i.e. fructose biphosphate adolase, aminotransferases, dehydrogenases, hydroxyl methyl glutarate and glutamate synthase leading to the biosynthesis of precursors; tyrosine, phenylalanine and tryptophan for secondary metabolites were up-regulated in callus. The knowledge of probable genes involved in secondary metabolism and their regulation in different tissues will provide insight into the Narcissus plant biology related to alkaloid production.

Keywords : narcissus, callus, transcriptomics, secondary metabolites
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