

꽃 양귀비 전사체 다양성 분석

Transcriptome analysis in varieties of *Papaver nudicaule*

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ABSTRACT

In this study identify potentially new alkaloids predicted from transcription information will provide insight into the pathways and molecular regulation of alkaloid biosynthesis.

I. Introduction

Papaver nudicaule (syn. *Papaver croceum*, *P. miyabeianum*, [1] *P. amurense*, and *P. macounii*), the Iceland poppy, is a boreal flowering plant. Native to subpolar regions of Europe, Asia and North America, and the mountains of Central Asia (but not in Iceland), Iceland poppies are hardy but short-lived perennials, often grown as biennials, that yield large, papery, bowl-shaped, lightly fragrant flowers supported by hairy, one foot, curved stems among feathery blue-green foliage 1-6 inches long. They were first described by botanists in 1759. The wild species blooms in white or yellow.

II. Research

Several alkaloids of *Papaver nudicaule* have an efficacy for anti-cancer, anti-inflammatory and anti-pain. The expression of *P. nudicaule* genes involved in alkaloid biosynthesis, and expression during plant development remain unknown. Therefore, in this study, we investigated the genes involved in alkaloid biosynthesis and their expression during development. A transcriptome database of *P. nudicaule* Illumina mRNA. Sequencing of RNA complex samples collected from leaves (30, 60, 90 days) was performed. Trimmed 101bp paired-end read 11,331,806,100 bases

were newly assembled into 238,536 transcripts with an average length of 616.47 bp, of which 148,878 unigenes (39%) were annotated in 5 protein databases. Of the 400 putative unigenes involved in biosynthesis, 83 were identified as candidate genes involved in the biosynthesis of benzylisoquinoline alkaloid (BIAs). So far, we have reported only alkaloid type in *P. nudicaule*. Biosynthetic genes of BIA were highly upregulated in the overall pathway during plant development. Identification of alkaloid biosynthetic genes to initiate metabolic engineering to improve the yield of alkaloids of interest and to identify potentially new alkaloids predicted from transcription information will provide insight into the pathways and molecular regulation of alkaloid biosynthesis.

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References

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