

Article

Composition and Biosynthesis of Scent Compounds from Sterile Flowers of an Ornamental Plant *Clematis florida* cv. 'Kaiser'

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Supplementary Figures

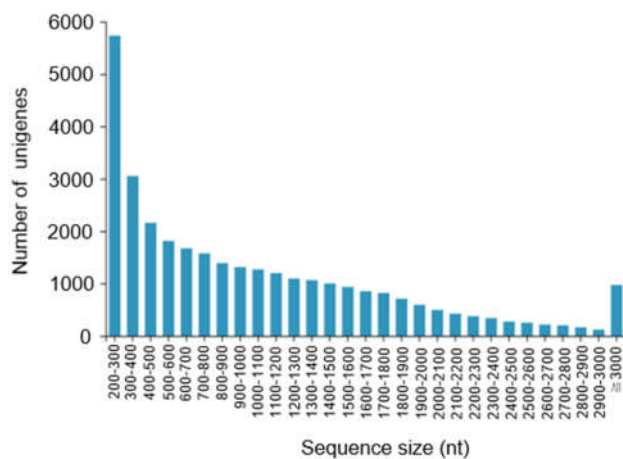


Figure 1. The length distribution of assembled unigenes from *C. florida* 'Kaiser'. The horizontal and vertical axis showed the size and the number of transcripts, respectively.

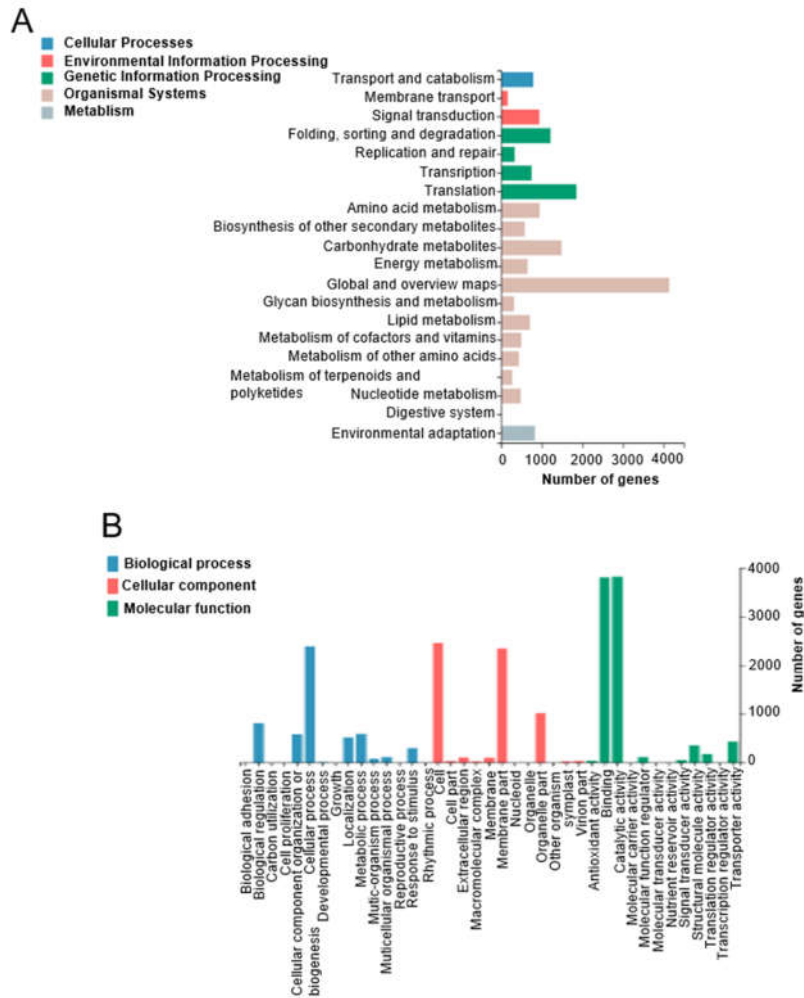


Figure S2. (A) KEGG annotation of putative proteins. The y-axis indicates the name of the KEGG metabolic pathway. The x-axis indicates the percentage of the number of unigenes annotated to the pathway out of the total number of unigenes annotated. The unigenes were divided into five branches according to the KEGG metabolic pathway: Cellular Processes, Environmental Information Processing, Genetic Information Processing, Metabolism and Organismal Systems. (B) GO classification of unigenes in *C. florida* 'Kaiser'. Gene Ontology terms are classified into three main categories: biological process (BP), cellular component (CC) and molecular function (MF).

Supplementary Tables

Table S1. The summary of the *Clematis florida* 'Kaiser' transcriptome.

	Transcript	Unigene
Total assembled bases		22038123
Total number of genes		32048
Max length of unigenes (bp)		11031
Min length of unigenes (bp)		297
N50 (bp)		1323
GC percentage (%)		44.68%

Table S2. The statistics of annotation on unigenes against public databases.

Database	Number of Annotated Unigenes	Percentage of Annotated Unigenes (%)
Nr	24939	77.82
Swiss-prot	18484	57.68
KOG	19429	60.62
KEGG	18981	59.23
GO	16150	50.39
Total	32048	100

Table S3. Primers of *CfTPS* used for qRT-PCR.

Gene No	Forward	Reverse
<i>CfTPS1</i>	CAGTCTCAACGCCTATCCATT	TGTTATCGCCAGCATCATCATT
<i>CfTPS2</i>	AGAATCCGTTTCAGCGACTAGA	GCGTCATAGGAGCCATAACATT
<i>CfTPS3</i>	CTTGCGTGGCTATCACTT	CCGTTCTCATCTGTACTTGTTG
<i>CfGAPDH</i>	AACCCTGAGGAGATTCCA	CACCACCCTCAAGTGAGCAG