

Supplementary Material

Physiological and transcriptome analysis of *Dendrobium officinale* under low nitrogen stress

Hangtao Wu^A, Jin Li^A, Qian Pu^A, Chunyi Mi^A, Guohong Zeng^A, Ying Chen^A, Dedong Kong^B, Xiaorong Zuo^C, Xiufang Hu^{A,*}, and Ou Li^{A,*}

^AZhejiang Province Key Laboratory of Plant Secondary Metabolism and Regulation, College of Life Science, Zhejiang Sci-Tech University, Hangzhou 310018, P. R. China.

^BInstitute of Digital Agriculture, Zhejiang Academy of Agricultural Sciences, Hangzhou 310018, P. R. China.

^CXi'an Ande Pharmaceutical Co., Ltd, Zhenping Branch, Xi'an 710000, P. R. China.

*Correspondence to: Xiufang Hu 928th Second Avenue, College of Life Science and Medicine, Zhejiang Sci-Tech University, Hangzhou 310018, P. R. China Email: huxiuf@sina.com; Ou Li 928th Second Avenue, College of Life Science and Medicine, Zhejiang Sci-Tech University, Hangzhou 310018, P. R. China Email: ouli@zstu.edu.cn

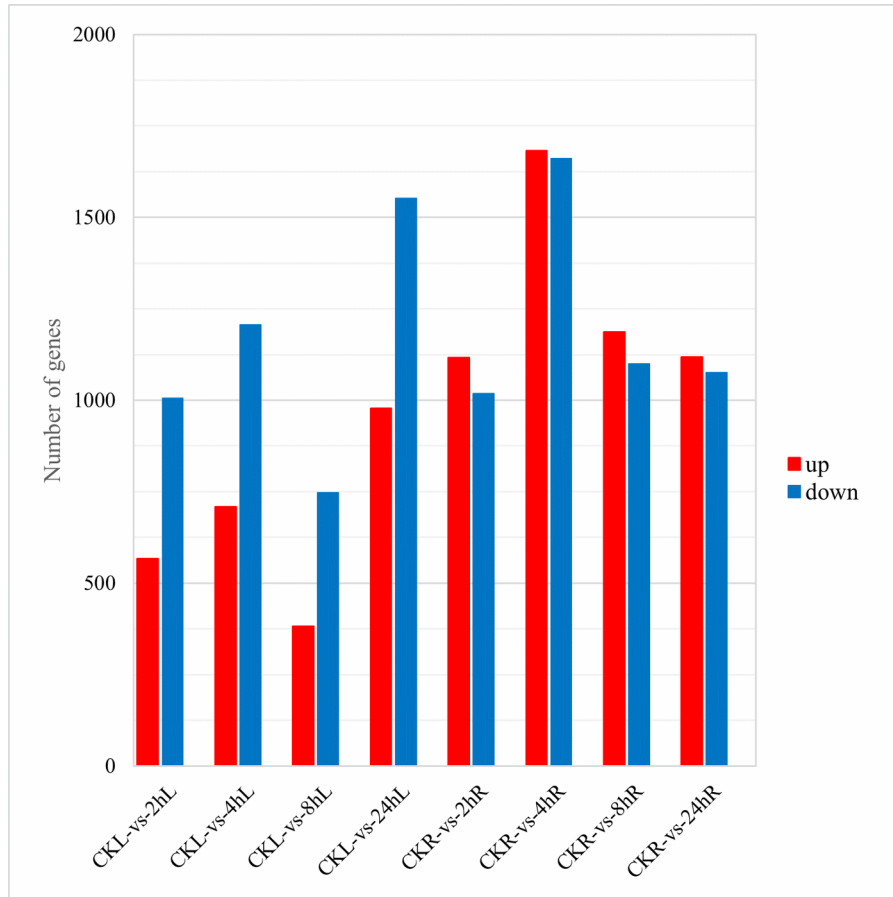


Fig. S1 The number of differentially expressed genes in *D. officinale*

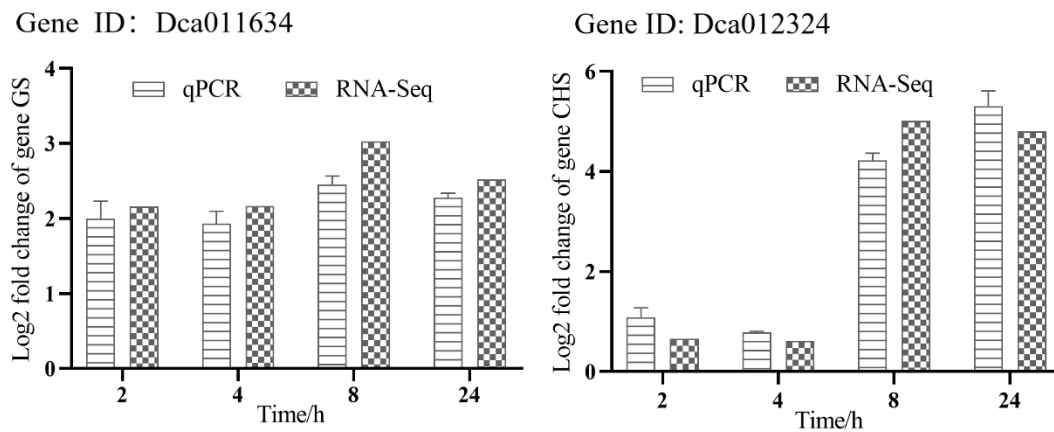


Fig. S2 Validation of RNA-Seq data using qRT-PCR

Table S1 KEGG pathway database from leaves of *D. officinale* transcriptome library

KEGG categories represented	Pathway ID	Unique sequences			
		2h	4h	8h	24h
Genetic information processing					
Ribosome	ko03010	18	21	19	31
Protein processing in endoplasmic reticulum	ko04141			5	
Base excision repair	ko03410			17	33
Environmental information processing					
Plant hormone signal transduction	ko04075			17	33
MAPK signaling pathway-plant	ko04016	13	17	12	21
Organismal systems					
Plant-pathogen interaction	ko04626	20	23	18	32
Cellular processes					
Endocytosis	ko04144		20		24
Metabolism					
Phenylpropanoid biosynthesis	ko00940	21	16	22	29
Starch and sucrose metabolism	ko00500	14	21	12	22
Glutathione metabolism	ko00480	10	14		
Amino sugar and nucleotide sugar metabolism	ko00520			12	
Alpha-linolenic acid metabolism	ko00592				12
Flavonoid biosynthesis	ko00941	8		9	10
Ascorbate and aldarate metabolism	ko00053	9			

Glycine, serine and threonine metabolism	ko00260	9			
Cyanoamino acid metabolism	ko00460	8	9	6	10
Inositol phosphate metabolism	ko00562		8		
Cysteine and methionine metabolism	ko00270	8		7	
Photosynthesis-antenna proteins	ko00196	7	7		
Alanine, aspartate and glutamate metabolism	ko00250	7			
Ubiquinone and other terpenoid-quinone biosynthesis	ko00130			7	
Galactose metabolism	ko00052			7	
Brassinosteroid biosynthesis	ko00905			7	6
Ether lipid metabolism	ko00565				6
Stilbenoid, diarylheptanoid and gingerol biosynthesis	ko00945	4		7	5
Nitrogen metabolism	ko00910	6		4	
Taurine and hypotaurine metabolism	ko00430		4		
Arachidonic acid metabolism	ko00590		3		
Anthocyanin biosynthesis	ko00942	2			2
Flavone and flavonol biosynthesis	ko00944		2		

a. A blank presented in the table means that there was no significant difference in gene expression

Table S2 KEGG pathway database from roots of *D. officinale* transcriptome library

KEGG categories represented	Pathway ID	Unique sequences			
		2h	4h	8h	24h
Genetic information processing					
Protein processing in endoplasmic reticulum	ko04141		44	35	43
Environmental information processing					
Plant hormone signal transduction	ko04075		39	32	31
MAPK signaling pathway-plant	ko04016		22		
Organismal systems					
Plant-pathogen interaction	ko04626				20
Metabolism					
Phenylpropanoid biosynthesis	ko00940	20	35	22	25
Alpha-linolenic acid metabolism	ko00592	13	20	9	19
Glycerolipid metabolism	ko00561	13	16	15	
Cysteine and methionine metabolism	ko00270	11	19	12	12
Arginine and proline metabolism	ko00330	12		11	
Beta-alanine metabolism	ko00410	11	12	11	
Glycine, serine and threonine metabolism	ko00260	10		10	
Fructose and mannose metabolism	ko00051				10
Cyanoamino acid metabolism	ko00460	9			9
Fatty acid degradation	ko00071	9			
Alanine, aspartate and glutamate metabolism	ko00250	7	10	9	

Nitrogen metabolism	ko00910		8	
Cutin, suberine and wax biosynthesis	ko00073		8	8
Arginine biosynthesis	ko00220		8	
Tryptophan metabolism	ko00380		8	
Fatty acid elongation	ko00062	7		
Sphingolipid metabolism	ko00600		7	
Porphyrin and chlorophyll metabolism	ko00860			7
Photosynthesis-antenna proteins	ko00196	5		8
Pantothenate and CoA biosynthesis	ko00770	6		
Linoleic acid metabolism	ko00591	6	7	4
Tropane, piperidine and pyridine alkaloid biosynthesis	ko00960	5		
Biosynthesis of unsaturated fatty acids	ko01040	5		
Mannose type O-glycan biosynthesis	ko00515		4	
Taurine and hypotaurine metabolism	ko00430	3		

a. A blank presented in the table means that there was no significant difference in gene expression

Table S3 The specific primer sequence of q-PCR gene

Primer	Sequences
GS-F	TGCGGAGACTACCATACTAT
GS-R	ATGACACGAGAATACCAATG
CHS-F	GTGCCGATTACCAACTCA
CHS-R	GGTCGTTCACTAGTCAAGT
EF1 α -F	TCAGGCTGACTGTGCTGTCT
EF1 α -R	GTGGTGGCGTCCATCTTGTT