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Transcriptomic profiling of shallots (*Allium cepa* var. *aggregatum*) reveals differential gene expression patterns under nitrogen deficiency

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Electronic Supplementary Material (ESM)

The authors are fully responsible for both the content and the formal aspects of the electronic supplementary material. No editorial adjustments were made.

Table S1. Primers names and sequence used for quantitative real-time polymerase chain reaction (qRT-PCR)

Actin-F	GAGAATATGATGAGTCGGGG
Actin-R	TGGACCTTAAGCAAATCCAA
UCH_1F	TGGCTTGAATTATGGTGAGGG
UCH_1R	TCTATCGCTTCCTCTACCTCTAC
PLATF	TGACGCAGTGATAACCATACTTG
PLATR	ATCTGGATGAGGCAAACCTGAG
P450F	TGTTTTTCCTAGTGCAGTCCTAC
P450R	AACATCTTCCGCCCGATAC
LRRNT_2F	CAGCAACGGTAGAGTAATCGG
LRRNT_2R	TTATGGATGAAGGAATGGAGCC
Ion_transF	TGGAGCAGTGGAATACAGAAC
Ion_transR	AGCTCCTAATTCACCGAACG
GATase_6F	GTTGGATTGATGGCTTGAAGG
GATase_6R	GTGTGGGTAAATGTGTTCTGC
EMP70F	GAAAGAGGAACAGGATGGAGAG
EMP70R	GGTTAGGAAAGTCAGGCCAAAAG
DUF212F	ACCTGTAATCTCAACCGTTCG
DUF212R	GCATATTAGGGAAGGTGACTGG
Bet_v_1F	CGTCGACCAGTCACTTCAAG
Bet_v_1R	CTGCCTTAATGTGACCAACG
RbcSF	CACTGGACTTGACGAACATTG
RbcSR	ATGGGCGATACTGGACAATG
PL4F	TCCAACCATCAACAGCCAG
PL4R	CTCCGTTCAGCATCAGATCC
LTP_2F	GTGCGACGGTCAGTACTATG
LTP_2R	TGGATGCGAGTTTGAGGAAG
GH9F	GGACCTGATGCCTACGATAAC
GH9R	CTCTGCCCTCTGTTAAGTCG
FAE1_CUT1_RppAF	CACAGAGGCGTATCGTTATCC
FAE1_CUT1_RppAR	ATGAGGCTGAGTACGAACAAG
Chloroa_b-bindF	TCGCTCAACTCCATTCTCTAAC
Chloroa_b-bindR	GGCTTACCTTCTCTACCTTC

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Table S2. Top 10 down-regulated differential expressed gene in nitrogen-stress plants compared to control plants of the same shallot cultivars

Row	Treatment group	Control group	logFC	P-value	FDR
TRINITY_GG_37958_c0_g1_i4	nitrogen-stressed	control	-7.9531	1.08×10^{-18}	4.26×10^{-14}
TRINITY_GG_53082_c0_g1_i1	nitrogen-stressed	control	-5.7367	1.09×10^{-12}	7.20×10^{-09}
TRINITY_GG_74176_c0_g1_i1	nitrogen-stressed	control	-5.3954	8.01×10^{-12}	3.17×10^{-08}
TRINITY_GG_35587_c7_g1_i1	nitrogen-stressed	control	-5.4991	9.11×10^{-12}	3.28×10^{-08}
TRINITY_GG_42483_c0_g1_i1	nitrogen-stressed	control	-5.3372	2.69×10^{-11}	7.61×10^{-08}
TRINITY_GG_71854_c0_g1_i1	nitrogen-stressed	control	-5.6294	3.29×10^{-11}	8.69×10^{-08}
TRINITY_GG_49598_c0_g1_i2	nitrogen-stressed	control	-5.0026	1.65×10^{-10}	3.29×10^{-07}
TRINITY_GG_34472_c0_g1_i1	nitrogen-stressed	control	-5.3373	1.66×10^{-10}	3.29×10^{-07}
TRINITY_GG_23180_c8_g1_i1	nitrogen-stressed	control	-4.7600	7.95×10^{-10}	1.26×10^{-06}
TRINITY_GG_6750_c0_g1_i1	nitrogen-stressed	control	-4.9725	1.08×10^{-09}	1.59×10^{-06}

\log_2FC – \log_2 fold change; FDR – false discovery rate

Table S3. Top 10 up regulated differential expressed gene in in nitrogen-stress plants compared to control plants of the same shallot cultivars

Row	Treatment group	Control group	logFC	P-value	FDR
TRINITY_GG_14147_c0_g1_i1	nitrogen-stressed	control	7.3284	2.31×10^{-16}	4.58×10^{-12}
TRINITY_GG_76810_c0_g1_i1	nitrogen-stressed	control	5.8811	7.89×10^{-13}	6.25×10^{-09}
TRINITY_GG_21380_c0_g1_i1	nitrogen-stressed	control	5.7524	2.16×10^{-12}	1.22×10^{-08}
TRINITY_GG_20731_c0_g1_i1	nitrogen-stressed	control	5.6462	5.70×10^{-12}	2.51×10^{-08}
TRINITY_GG_38162_c0_g1_i1	nitrogen-stressed	control	5.1584	5.11×10^{-11}	1.27×10^{-07}
TRINITY_GG_51834_c0_g1_i1	nitrogen-stressed	control	5.1682	5.50×10^{-11}	1.28×10^{-07}
TRINITY_GG_25113_c1_g1_i1	nitrogen-stressed	control	5.0370	1.24×10^{-10}	2.72×10^{-07}
TRINITY_GG_43220_c1_g1_i1	nitrogen-stressed	control	4.9320	2.05×10^{-10}	3.86×10^{-07}
TRINITY_GG_65174_c0_g1_i2	nitrogen-stressed	control	4.9624	4.26×10^{-10}	7.34×10^{-07}
TRINITY_GG_9251_c0_g1_i1	nitrogen-stressed	control	4.7733	6.75×10^{-10}	1.11×10^{-06}

\log_2FC – \log_2 fold change; FDR – false discovery rate

Table S4. List of top 10 biological processes with gene ontology (GO) IDs that are overrepresented in differentially expressed genes (DEGs)

Sr. No.	GO IDs	GO name	P-value (over-represented)
1	GO: 0005975	carbohydrate metabolic process	1.71×10^{-10}
2	GO: 0009409	response to cold	5.46×10^{-09}
3	GO: 0019253	reductive pentose-phosphate cycle	7.05×10^{-09}
4	GO: 0019685	photosynthesis, dark reaction	7.05×10^{-09}
5	GO: 1901568	fatty acid derivative metabolic process	7.86×10^{-09}
6	GO: 0045229	external encapsulating structure organization	1.84×10^{-08}
7	GO: 0071554	cell wall organization or biogenesis	2.60×10^{-08}
8	GO: 0015979	photosynthesis	2.71×10^{-08}
9	GO: 0071555	cell wall organization	3.32×10^{-08}
10	GO: 0008610	lipid biosynthetic process	3.26×10^{-07}

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Table S5. List of top 10 cellular component with gene ontology (GO) IDs that are overrepresented in differentially expressed genes (DEGs)

Sr. No.	GO IDs	GO name	P-value (over-represented)
1	GO: 0005576	extracellular region	2.63×10^{-24}
2	GO: 0048046	apoplast	7.13×10^{-15}
3	GO: 0031977	thylakoid lumen	5.98×10^{-09}
4	GO: 0009543	chloroplast thylakoid lumen	2.27×10^{-08}
5	GO: 0031978	plastid thylakoid lumen	2.27×10^{-08}
6	GO: 0009654	photosystem II oxygen evolving complex	3.71×10^{-08}
7	GO: 0009523	photosystem II	4.40×10^{-08}
8	GO: 0009579	thylakoid	8.63×10^{-08}
9	GO: 0005575	cellular_component	1.51×10^{-07}
10	GO: 0009521	photosystem	4.45×10^{-07}

Table S6. List of top 10 molecular function with gene ontology (GO) IDs that are overrepresented in differentially expressed genes (DEGs)

Sr. No.	GO IDs	GO name	P-value (over-represented)
1	GO: 0016491	oxidoreductase activity	8.15×10^{-09}
2	GO: 0140825	lactoperoxidase activity	3.72×10^{-08}
3	GO: 0003824	catalytic activity	4.35×10^{-07}
4	GO: 0016829	lyase activity	6.85×10^{-07}
5	GO: 0009924	octadecanal decarboxylase activity	1.11×10^{-06}
6	GO: 0071771	aldehyde decarboxylase activity	1.11×10^{-06}
7	GO: 1990465	aldehyde oxygenase (deformylating) activity	1.11×10^{-06}
8	GO: 0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	2.40×10^{-06}
9	GO: 0016984	ribulose-bisphosphate carboxylase activity	4.55×10^{-06}
10	GO: 0005506	iron ion binding	5.52×10^{-06}

Table S7. Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analysis top 10 pathways

ID	Description	Gene ratio	Bg ratio	Adjusted P-value	Gene ID
ko00195	photosynthesis	5/56	63/13 850	0.00058235	K08901/K02717/K03542/ K08903/K02639
ko00710	carbon fixation in photosynthetic organisms	4/56	36/13 850	0.00070526	K03841/K00855/ K01602/K05298
ko00010	glycolysis/gluconeogenesis	4/56	106/13 850	0.0321521	K03841/K00002/ K00001/K01792
ko00053	ascorbate and aldarate metabolism	3/56	62/13 850	0.05500166	K00434/K00002/K08679
ko00040	pentose and glucuronate interconversions	3/56	89/13 850	0.10845536	K00002/K01051/K01728
ko00561	glycerolipid metabolism	3/56	91/13 850	0.10845536	K00002/K06119/K13508
ko00100	steroid biosynthesis	2/56	34/13 850	0.11751572	K09828/K01052
ko00630	glyoxylate and dicarboxylate metabolism	3/56	104/13 850	0.11751572	K02437/K01602/K01915
ko00051	fructose and mannose metabolism	3/56	112/13 850	0.12781094	K03841/K19355/K00847

Bg – background