

Electronic supplementary materials

Title:

Integrated Analysis of Metabolome and Transcriptome Reveals Key Candidate Genes Involved in Flavonoid Biosynthesis in *Pinellia ternata* under Heat Stress

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Table S1 Assembly statistics of transcriptome data from *Pinellia ternata* samples under high temperature stress.

length range/bp	Transcript		Unigene	
	Number	Percentage/%	Number	Percentage/%
300~500	123624	37.58	54726	44.93
500~1000	120215	36.55	39671	32.57
1000~2000	62615	19.04	19685	16.16
> 2000	22457	6.83	7730	6.34
Total	328911	-	121812	-
Total length	283651496	-	98409778	-
Mean length	862	-	808	-
Length of N50	1079	-	1015	-
Length of N90	414	-	383	-

Table S2 Primers used for RT-qPCR analysis.

Gene	NCBI Accession No.	Organism	Forward primer (5'-3')	Reverse primer (5'-3')
<i>GAPDH</i>	OMO60415.1	<i>Corchorus capsularis</i>	TGCTGGGAATGATGTTGAATG	TTGGCATTGTTGAGGGTTTG
<i>CYP73A</i>	XP_006850963.1	<i>Amborella trichopoda</i>	AGAAAGACCCGTCGGAGTTC	CAATGTGGAGGCAAGAACCG
<i>HCT</i>	RWR97947.1	<i>Cinnamomum micranthum</i>	CTTCTCCTTGAGCTTGCCGA	GAGTTCCGGCGCCATGTTAG
<i>CCoAOMT</i>	AEV43321.1	<i>Acacia auriculiformis</i>	GACGCCCTGTACCAATACATCT	GGGGAGTTGGCAGATCTTGA
<i>DFR1</i>	RWR80738.1	<i>Cinnamomum micranthum</i>	GCTGGATTCTGTGGCTTCCTAT	TGGATCAGATCGGACGGTG
<i>DFR2</i>	XP_010926084.1	<i>Elaeis guineensis</i>	AGCAAGTTTGAACGGGGAGT	ACCAGTTGGACAAAGTGACAGA

Table S3 The fpkm of the five differentially expressed genes (DEGs) in *Pinellia ternata* tuber under heat stress.

Genes	Fpkm Value	
	CK	HT
<i>CYP73A</i>	0.45	6.70
<i>HCT</i>	27.28	2.07
<i>CCoAOMT</i>	22.68	0
<i>DFR1</i>	11.84	1.49
<i>DFR2</i>	7.09	0.72

Table S4 Relative content of differentially accumulated metabolites (DAMs) in *Pinellia ternata* tuber under heat stress.

Index	Compounds	CK1	CK2	CK3	CK4	CK5	CK6	HT1	HT2	HT3	HT4	HT5	HT6
Com_5980	Naringenin	5.64E+06	6.78E+06	5.84E+06	6.10E+06	5.71E+06	5.89E+06	1.00E+06	8.63E+05	8.44E+05	9.07E+05	1.03E+06	9.31E+05
Com_2634	Pelargonidin	2.76E+07	2.86E+07	2.77E+07	2.65E+07	2.88E+07	2.66E+07	5.55E+06	5.90E+06	5.97E+06	5.72E+06	5.73E+06	5.66E+06
Com_1993	Vitexin	4.04E+07	4.23E+07	4.30E+07	4.09E+07	4.30E+07	4.09E+07	9.97E+06	9.14E+06	8.89E+06	8.51E+06	8.18E+06	8.72E+06
Com_4640	Apigenin	1.03E+07	1.05E+07	9.98E+06	1.07E+07	1.05E+07	1.02E+07	2.40E+06	2.70E+06	2.85E+06	2.56E+06	2.53E+06	2.93E+06
Com_2428	Chlorogenic acid	3.11E+07	2.76E+07	3.07E+07	2.83E+07	2.69E+07	3.31E+07	8.23E+06	7.75E+06	7.88E+06	7.48E+06	7.39E+06	7.89E+06
Com_10546	Naringenin chalcone	1.63E+06	1.79E+06	1.58E+06	1.73E+06	1.48E+06	1.58E+06	4.48E+05	5.73E+05	3.84E+05	4.09E+05	4.16E+05	4.40E+05
Com_5211	Naringin	8.42E+06	7.97E+06	7.69E+06	8.10E+06	7.56E+06	8.70E+06	2.68E+06	2.88E+06	2.74E+06	2.61E+06	2.55E+06	2.31E+06
Com_7999	Prunin	3.33E+06	3.63E+06	3.24E+06	3.61E+06	3.30E+06	3.17E+06	1.42E+06	1.32E+06	1.22E+06	1.27E+06	1.17E+06	1.09E+06
Com_1544	Hesperetin	6.03E+07	5.99E+07	5.18E+07	6.12E+07	5.81E+07	6.01E+07	2.62E+07	2.35E+07	2.41E+07	2.29E+07	2.39E+07	2.31E+07
Com_3251	Cyanidin	1.32E+07	2.02E+07	1.58E+07	1.92E+07	1.69E+07	1.47E+07	7.02E+06	7.57E+06	9.85E+06	8.18E+06	7.64E+06	9.02E+06
Com_4216	(-)-Epigallocatechin	1.09E+07	1.21E+07	1.26E+07	1.18E+07	1.20E+07	1.27E+07	7.80E+06	7.52E+06	8.69E+06	6.44E+06	7.64E+06	8.08E+06

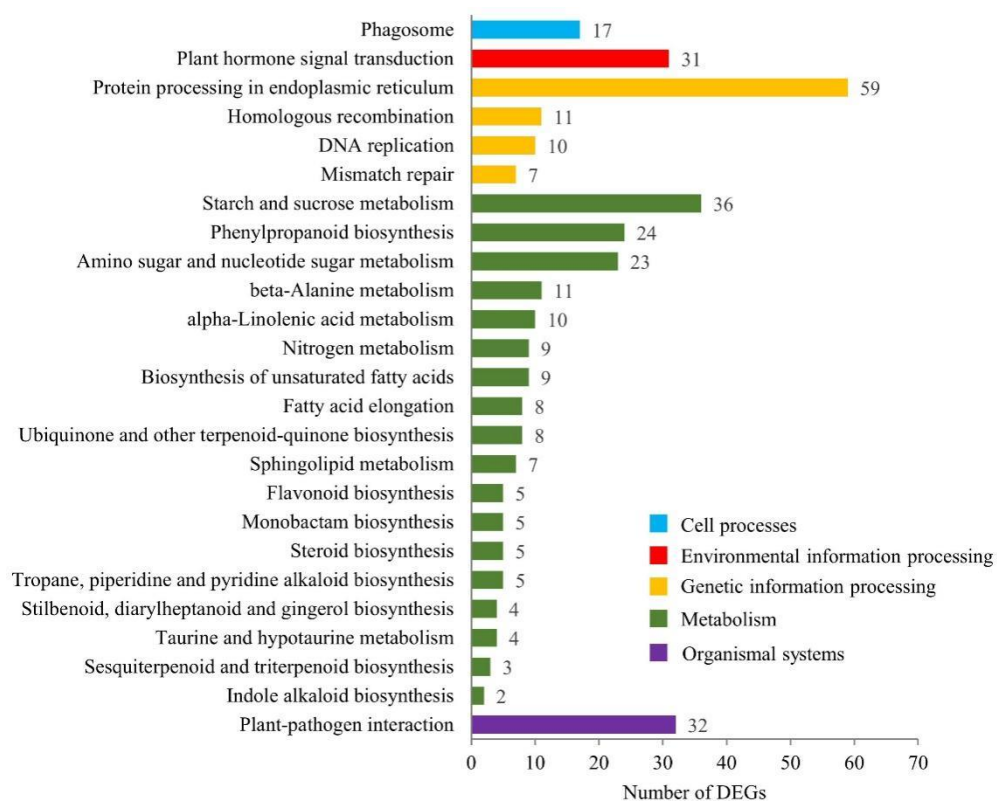


Fig. S1 Top 25 of metabolic pathways enriched for differentially expressed genes (DEGs) under high temperature stress treatment.

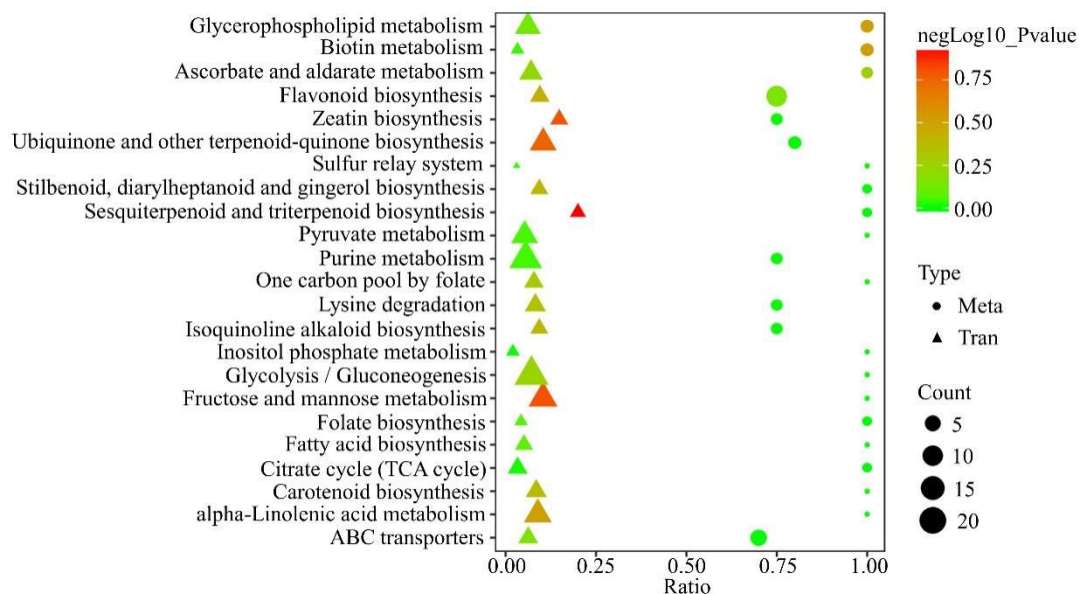


Fig. S2 KEGG enrichment analysis of differentially accumulated metabolites (DAMs) and differentially expressed genes (DEGs) under high temperature stress. Each count represents the number of DAMs or DEGs in the enriched pathway. The size of each dot or triangle represents the number of DAMs or DEGs, respectively. The abscissa represents the ratio of the number of differential DAMs or DEGs enriched in the pathway to the number of metabolites or genes annotated in the pathway.