

Revealing the mechanism of aroma production driven by high salt stress in *Trichomonascus ciferrii*

WLW

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Supplementary Materials

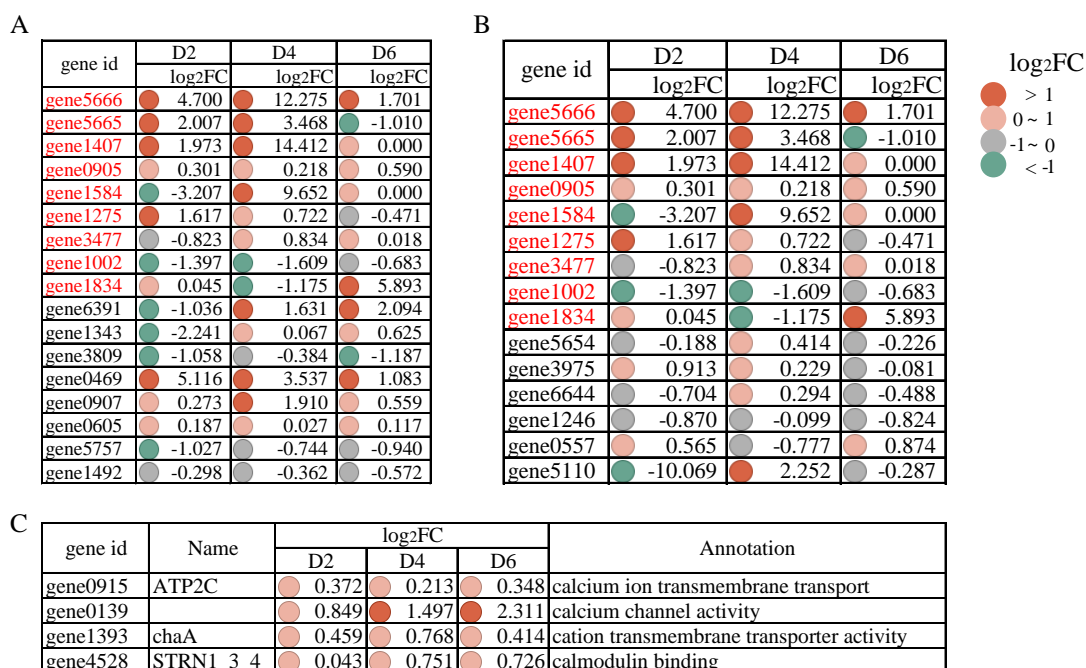


Figure S1. Difference in expression of genes related to iron and copper ion homeostasis. (A) Logarithmic difference multiple of iron ion homeostasis related genes; (B) Logarithmic difference multiple of copper ion homeostasis related genes; (C) Logarithmic difference multiple of calcium ion homeostasis related genes. (Note: Gene names highlighted in red indicate genes that are common to both iron and copper ion homeostasis.)

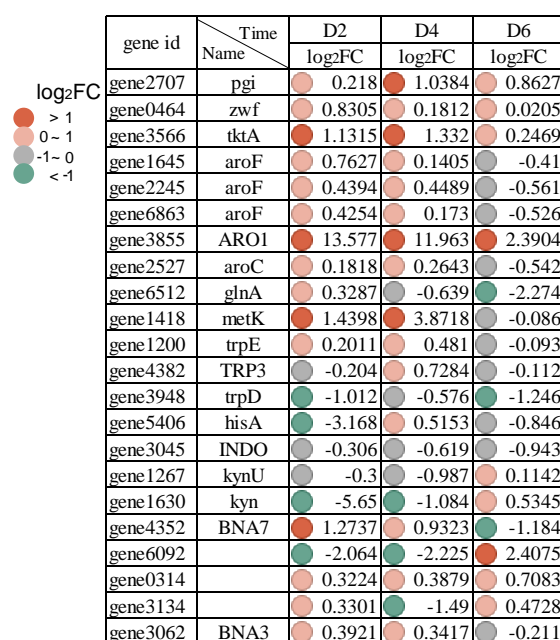


Figure S2. Differences in the timing of expression of key genes for MA synthesis.

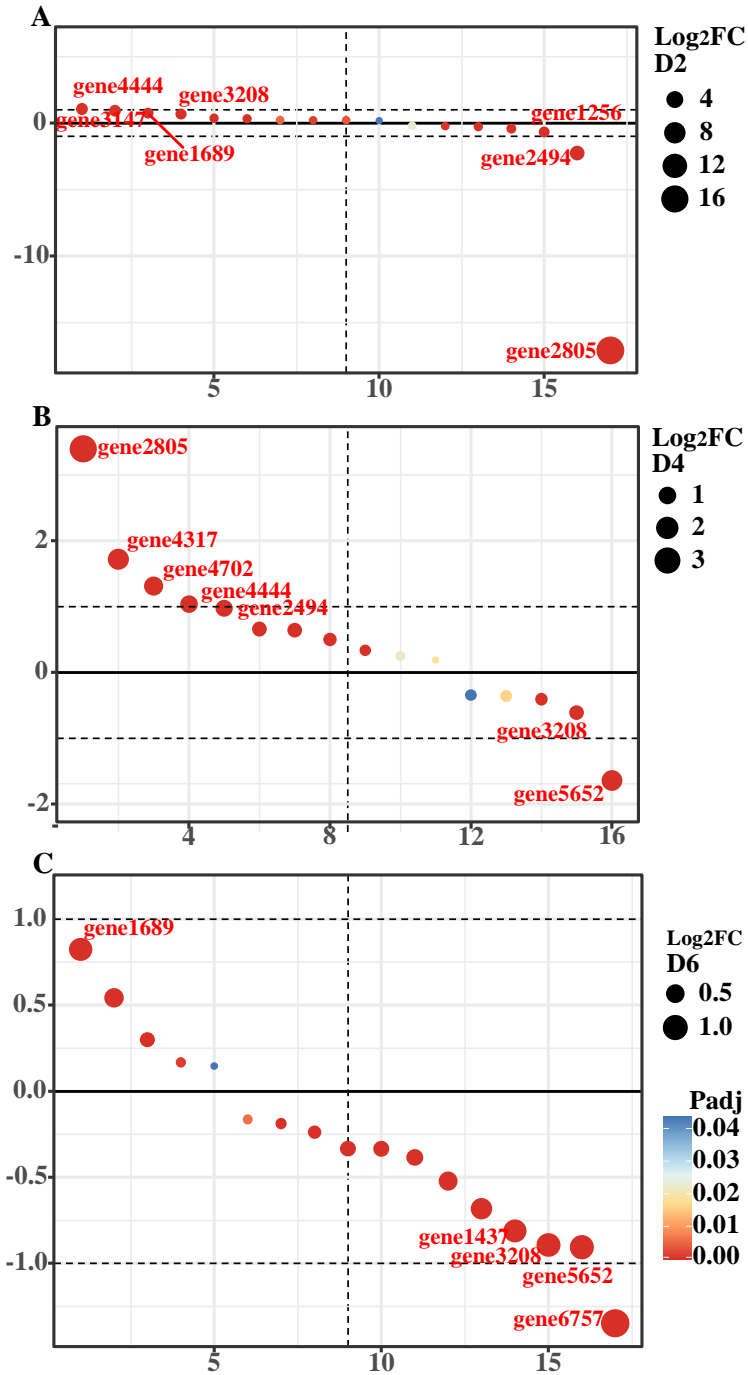


Figure S3. Bubble map of fold change order of the main different genes including in Citrate Cycle. A,B and C correspond to differential gene ordering on days 2, 4 and 6, respectively.

Table S1. Effect testing of generalized linear model based on the data from salt tolerance test

Source	Type III		
	Wald Square	df	Sig.
Intercept	48608.417	1	.000***
Concentration of NaCl (C _{NaCl})	15822.675	8	.000***
Time	349.975	2	.000***
C _{NaCl} * Time	590.451	16	.000***

***represent p value <0.001.

Table S2. Summary of trimming and read mapping results of the sequences generated from WLW yeast with or without salt condition. (Salt concentration for salty conditions is 10%)

Sample	Raw reads	Clean reads	Q20(%)	Q30(%)	GC content (%)	Total mapped	Mapped rate (%)
A1	46794622	46474868	98.74	95.97	52.94	45566560	98.05
A2	46639378	46217078	98.6	95.64	52.98	45442061	98.32
A3	51469228	5101383 4	98.46	95.23	52.85	50063335	98.14
A4	47618156	47056408	97.98	94.36	52.6	45651413	97.01
A5	48551412	47872646	98.14	94.8	52.94	46553567	97.24
A6	45684012	45123020	97.9	94.16	52.58	43739850	96.93
A7	40687686	40162444	98.26	94.88	52.5	39319240	97.9
A8	50053874	49497154	98.32	95.04	52.18	48383567	97.75
A9	45121422	44673092	98.41	95.24	52	43664380	97.74
B1	46855532	46529340	98.59	95.6	52.75	45522893	97.84
B2	48131568	47681486	98.31	94.89	52.91	46660258	97.86
B3	43480310	43040408	98.38	95	52.91	42188297	98.02
B4	53090626	52654106	98.54	95.48	52.42	51654328	98.1
B5	46273784	45948046	98.49	95.3	52.28	44969456	97.87
B6	54124588	53695254	98.5	95.34	52.35	52652124	98.06
B7	56401044	55814542	98.36	95.04	51.71	54664291	97.94
B8	44964352	44490480	98.32	94.94	51.82	43586203	97.97
B9	45526268	45034920	98.27	94.81	51.75	44113954	97.95

Table S3. Transcription factors predicted by JASPAR database

Transcript id	Gene id	TF name	Motif id	Family
rna_gene6782	gene6782	ASH1	MA0276.1	C4-GATA-related
rna_gene5591	gene5591	DAL80	MA0289.1	C4-GATA-related
rna_gene0729	gene0729	GAT1	MA0300.1	C4-GATA-related
rna_gene4672	gene4672	GAT1	MA0300.1	C4-GATA-related
rna_gene5591	gene5591	GAT1	MA0300.1	C4-GATA-related
rna_gene4672	gene4672	GLN3	MA0307.1	C4-GATA-related
rna_gene5591	gene5591	GZF3	MA0309.1	C4-GATA-related
rna_gene2471	gene2471	HAP2	MA0313.1	Heteromeric CCAAT-binding
rna_gene2847	gene2847	MIG1	MA0337.1	Other factors with up to three adjacent zinc fingers
MSTRG.2080.1	gene4502	SPT15	MA0386.1	TBP-related factors
rna_gene4502	gene4502	SPT15	MA0386.1	TBP-related factors
MSTRG.2511.1	gene4906	ARG81	MA0272.1	None
MSTRG.2511.2	gene4906	ARG81	MA0272.1	None
rna_gene3785	gene3785	ASG1	MA0275.1	None
MSTRG.1693.1	gene0100	CAT8	MA0280.1	None
rna_gene0100	gene0100	CAT8	MA0280.1	None
rna_gene5326	gene5326	MCM1	MA0331.1	None
rna_gene5878	gene5878	NHP10	MA0344.1	None
rna_gene5056	gene5056	ROX1	MA0371.1	None
rna_gene4572	gene4572	YHP1	MA0426.1	None
rna_gene4572	gene4572	YOX1	MA0433.1	None

Table S4. The main different genes including in Citrate Cycle.

Gene id	Gene name	KO id	Annotation in KEGG database
gene2805	gltA	K01647	Citrate synthase
gene5652	IDH3	K00030	Isocitrate dehydrogenase
gene6757	SDH1	K00234	Flavoprotein subunit of succinate dehydrogenase (ubiquinone)
gene1437	SDH4	K00237	Succinate dehydrogenase complex, Oxidative phosphorylation
gene4766	sucA	K00164	2-oxoglutarate dehydrogenase
gene4317	fumC	K01679	Fumarase
gene4444	MDH2	K00026	Malate dehydrogenase
gene4702	lpd	K00382	Dihydrolipoic acid dehydrogenase, redox activity
gene1256	LSC1	K01899	Succinate-CoA ligase complex
gene3147	ACLY	K01648	ATP citrate (pro-S)-lyase
gene3208	IDH3	K00030	Isocitrate dehydrogenase
gene1689	acnA	K01681	Aconitate hydratase
gene2494	pckA	K01610	Phosphoenolpyruvate carboxykinase, Flow from the TCA cycle to gluconeogenesis