Transcriptomic Profiling Identifies Candidate Genes Involved in *Polyporus umbellatus* Sclerotial Formation Affected by Oxalic Acid

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Supplement Table S1. Primer sequences used in qRT-PCR amplification.

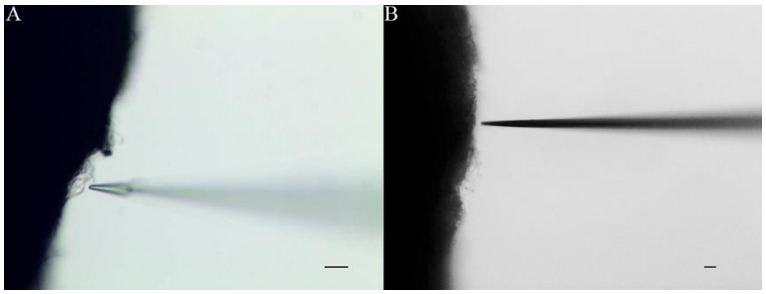
DEGs No.	Forward	Reverse
c43_g1	TGTATGAGCCCACCACATATTC	CACCGGTAGGAATTGCGATAA
c8987_g1	CATACCGCCATACGACACTTTA	GAAGGCCGAGACTTATCAGAAC
c8851_g1	CGGCTGGACATGACGAAATA	GCTGAAGGTGCTGAAGAAGA
c6769_g1	CGAGACGTTCTTGCAGGTATAA	CGACGATGGAGACGATAGAAAG
c9881_g2	GCGTTCTTGTTCCCTCATCT	CTCTTGCGTTCTACTAGCTTCC
c6055_g1	GCGCTACACTGATGAGACAA	GAAGTCTGCGAGGCTGTATTTA
c7209_g1	CATTCCCAGGTCAGTCATAGTG	CCTCCTGTCATTCCCAACAA
c8739_g2	CCCTCTTCGTCGGTGTTATTT	TCCTTCGGCTTGCTGTTT
c4703_g1	TGCAACAGGTGGATGATAAGG	TTGACTATGCCCGTGGAAAC
18S rRNA Previously identified	TGAGAAACGGCTACCACATC	TCCAATTATGAGACCCGAAAGAG

Supplementary Table S2. DEGs of Oxidase and dehydrogenase (partly).

Gene ID	Annotation of enzymes	Compared groups	adjusted p-value	Log_2Fold change	Up or down regulated
c8020_g1	Alcohol oxidase	CK *vs.* PU_SM	0.0096364	1.47	down
c9373_g1	Alcohol oxidase	CK *vs.* PD_S	0.00066247	0.90	up
c7619_g2	Alcohol oxidase	CK *vs.* PD_S	0.029102	0.74	up
c7390_g2	Galactose oxidase	CK *vs.* PD_S	2.27E-5	1.11	up
c7941_g1	D-amino-acid oxidase	CK *vs.* PD_S	0.0081601	0.86	up
c7166_g1	L-gulonolactone/D-arabinono-1,4-lactone oxidase	CK *vs.* PD_S	0.01134	1.12	up
c1151_g1	cytochrome c oxidase subunit I	CK *vs.* PU_SM	1.048E-18	-lnf	down
c10530_g1	cytochrome c oxidase subunit 3	CK *vs.* PU_SM	2.12E-9	-lnf	down
c18027_g1	cytochrome c oxidase subunit 2	CK *vs.* PU_SM	3.66E-08	-lnf	down
c8341_g1	NAD-dependent glutamate dehydrogenase	CK *vs.* PU_SM	3.32E-06	-2.26	down
c8341_g2	glutamate dehydrogenase	CK *vs.* PU_SM	8.92E-05	-1.93	down
c8523_g1	NAD-aldehyde dehydrogenase	CK *vs.* PU_SM	0.000187	-1.87	down
c1893_g1	NADH dehydrogenase subunit 4	CK *vs.* PU_SM	0.000199	-lnf	down
c1946_g1	NADH dehydrogenase subunit 1	CK *vs.* PU_SM	0.000277	-lnf	down
c524_g1	NADH dehydrogenase subunit 4	CK *vs.* PD_S	2.3558E-22	lnf	up
c1758_g1	NADH dehydrogenase subunit 2	CK *vs.* PD_S	1.02E-08	Inf	up
c6419_g1	NADH dehydrogenase (ubiquinone) Fe-S protein 6	CK *vs.* PD_S	4.16E-05	1.04	up
c2305_g1	NADH dehydrogenase subunit 3	CK *vs.* PD_S	0.00027	Inf	up
c3247_g1	D-isomer specific 2-hydroxyacid dehydrogenase	CK *vs.* PD_S	2.60E-13	1.79	up
c7606_g1	D-xylose 1-dehydrogenase	CK *vs.* PD_S	7.37E-08	1.47	up
c7742_g1	Sorbitol dehydrogenase	CK *vs.* PD_S	9.22E-07	1.22	up
c14038_g1	Succinate dehydrogenase	CK *vs.* PD_S	8.14E-06	Inf	up
c7145_g1	D-arabinitol dehydrogenase ($NADP^+$)	CK *vs.* PD_S	2.28E-05	1.06	up
c10255_g1	acetaldehyde dehydrogenase	CK *vs.* PD_S	6.90E-05	Inf	up
c12085_g1	Alanine dehydrogenase	CK *vs.* PD_S	0.000394	Inf	up
c6369_g1	alcohol dehydrogenase	CK *vs.* PD_S	0.00085884	0.89	up
c19597_g1	Alanine dehydrogenase	CK *vs.* PD_S	5.37E-05	Inf	up
c5285_g1	glycerol 2-dehydrogenase	CK *vs.* PD_S	0.001855	1.04	up
c17591_g1	glyceraldehyde 3-phosphate dehydrogenase	CK *vs.* PD_S	0.003745	Inf	up

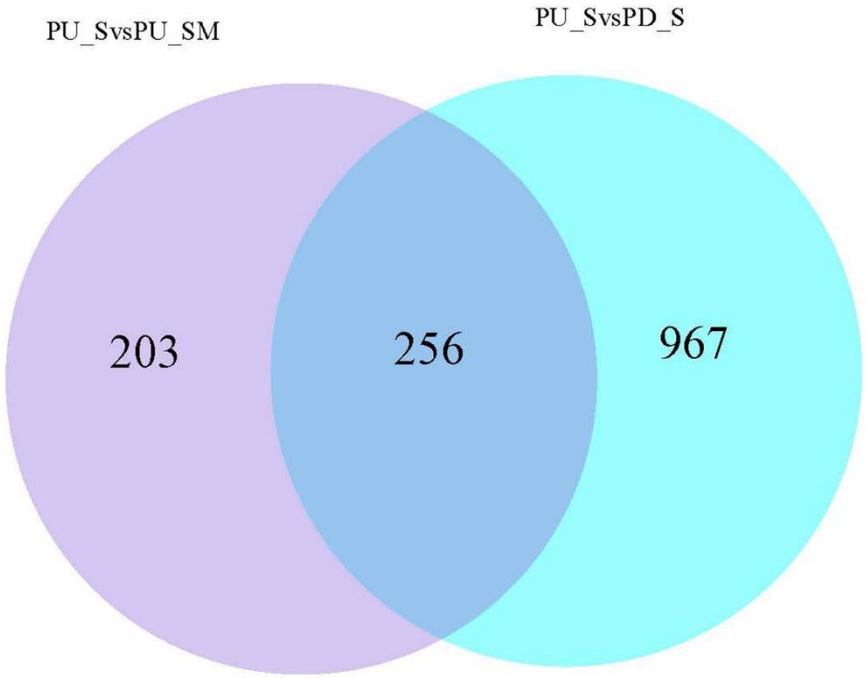
Supplementary Table S3. Reductases and glutathione S-transferase.

Gene ID	Annotation of enzymes	Compared groups	adjusted p-value	Log_2Fold change	Up or down regulated
c8217_g1	aldo/keto reductase	CK *vs.* PU_SM	0.043349	1.28	up
c9378_g1	aldo/keto reductase	CK *vs.* PD_S	1.56E-05	1.10	down
c9881_g2	aldo/keto reductase	CK *vs.* PU_SM	0.00084016	1.71	up
c8932_g1	quinone reductase	CK *vs.* PD_S	2.27E-5	1.38	up
c10001_g1	Nitrite reductase	CK *vs.* PU_SM	0.00067558	1.23	up
c16064_g1	cytochrome c reductase	CK *vs.* PD_S	9.12E-08	-Inf	down
c4751_g1	Cytochrome-b5 reductase	CK *vs.* PD_S	0.003188	0.81	down
c4563_g1	ribonucleotide reductase alpha subunit	CK *vs.* PD_S	2.28E-06	1.17	down
c5317_g1	gamma-glutamyl phosphate reductase	CK *vs.* PD_S	0.033067	0.65	down
c9468_g4	glutathione S-transferase	CK *vs.* PD_S	1.29E-34	4.27	down
c7959_g1	glutathione S-transferase	CK *vs.* PD_S	0.00051714	0.95	down
c6055_g1	glutathione S-transferase	CK *vs.* PU_SM	1.29E-34	2.79	down
c5235_g1	heme peroxidase	CK *vs.* PD_S	0.015399	0.89	down
c6600_gl	manganese peroxidase	CK *vs.* PD_S	1.13E-07	1.30	down
c6769_g1	manganese peroxidase	CK *vs.* PU_SM	0.00025727	2.62	up
c6329_g1	catalase	CK vs. PD_S	6.24E-05	1.20	down
c4316_g1	Glutathione peroxidase	CK vs. PD_S	0.00023161	-Inf	down



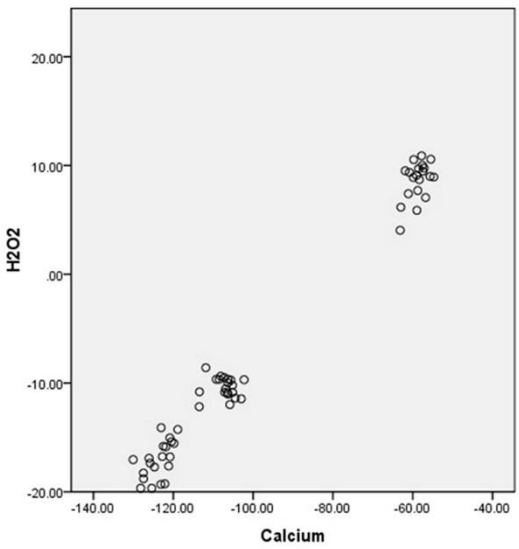
Supplement Figure 1 Sample detection images of real-time Ca^{2+} and H_2O_2 fluxes measurement of *P. umbellatus* mycelia using NMT

The primary position (M1) of Ca^{2+} (supplement Figure 1A) or ROS-sensitive microsensor (supplement Figure 1B) was placed 30 μm from *P. umbellatus* mycelial surface, and the further away position (M2) is 60 μm.



Supplement Figure 2 Venn diagram of PU_S vs PD_S and PU_S vs PU_SM

There are 1223 DEGs between the control group and the PD_S group, 459 DEGs between the control group and the PU_SM group, and among them there are 256 DEGs in common.



Supplement Figure 3 Correlation of real-time fluxes of calcium ion and H_2O_2.

Pearson's correlation coefficient (r=0.991, *P*<0.01) between both of the groups are presented, indicating a great significant positive correlation between the real-time fluxes measurement of calcium ion and H_2O_2.