

Transcriptional Analysis Revealing the Improvement of ϵ -Poly-L-lysine Production from Intracellular ROS Elevation after *Botrytis cinerea* Induction

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Table S1 Primer pairs sequences for quantitative real-time PCR (qRT-PCR) assay.

Target gene	Primer name	Primer sequence (5'-3')
16s rRNA	16s rRNA-forward	GCACAAGCAGCGGAGCAT
	16s rRNA -reverse	CCCAACATCTCACGACACGA
<i>zwf</i>	<i>zwf</i> -forward	CGTCCACGAGGTCTTCCC
	<i>zwf</i> -reverse	GGAGGAGGTGGTTCTGGATG
N1H47_01765	N1H47_01765 -forward	CTAACTCAGCAGGCACTGTGTC
	N1H47_01765 -reverse	GACGTGGTAGGCGTTCTCC
N1H47_21215	N1H47_21215 -forward	GTCCGCTCCTCCTTCTCG
	N1H47_21215 -reverse	CCGACGACCGTGACCTTC
N1H47_14640	N1H47_14640 -forward	GCCTTCAAGCAGGACATCAC
	N1H47_14640 -reverse	GGTTGTGGCTGTCCTGGTAG
N1H47_16885	N1H47_16885 -forward	GAGCTGTCCCAGACCATCG
	N1H47_16885 -reverse	GTTGGACCGGATGAAGACG
N1H47_34205	N1H47_34205 -forward	CCCTGTGGTCGTCGTTTCG
	N1H47_34205 -reverse	GAAGAGGTGGGTCTGCAGGA
N1H47_11760	N1H47_11760 -forward	ACCGTGTACTACAACTTCGCG
	N1H47_11760 -reverse	ACGTACAGCTGGGTGAGGG
N1H47_11815	N1H47_11815 -forward	AGGTGCTGCCCTGTCTGC
	N1H47_11815 -reverse	GTTCCGGGAGGCCATCAG
N1H47_25630	N1H47_25630 -forward	CACTACACCGCCGACGAA
	N1H47_25630 -reverse	AGGGTGTTGTAGACCGTGGC
N1H47_35560	N1H47_35560 -forward	CCTCATGGTGCTCGACGTC
	N1H47_35560 -reverse	CGGAAGGTAGTCGTCGGC

Table S2 Transcriptome analysis of genes coding for enzymes in ϵ -PL biosynthesis pathways among cells with different intracellular ROS levels.

Reaction	Gene ID	CK fpkm	LOS fpkm	HOS fpkm	Gene description
EMP					
1	<i>N1H47_30055</i>	35.68	76.51	86.51	Glucokinase
2	<i>pgi</i>	43.83	81.58	28.62	Glucose-6-phosphate isomerase
3	<i>N1H47_11860</i>	13.44	12.35	4.53	Phosphofructokinase
4	<i>fbaA</i>	32.76	30.24	31.22	Fructose-bisphosphate aldolase
5	<i>tpiA</i>	21.48	74.82	45.95	Triosephosphate isomerase
6	<i>gap</i>	38.84	122.32	83.42	Glyceraldehyde 3-phosphate dehydrogenase
7	<i>N1H47_10960</i>	39.26	112.01	90.60	Phosphoglycerate kinase
8	<i>N1H47_22570</i>	2287.06	2590.98	1256.65	Phosphoglycerate mutase
9	<i>eno</i>	51.85	71.29	36.87	Enolase
10	<i>pyk</i>	34.48	60.91	38.46	Pyruvate kinase
11	<i>N1H47_01765</i>	7.45	9.58	10.98	Phosphoenolpyruvate carboxylase
PPP					
12	<i>zwf</i>	123.19	232.08	295.68	Glucose-6-phosphate dehydrogenase
13	<i>pgl</i>	61.04	93.14	127.12	6-phosphogluconolactonase
14	<i>gndA</i>	676.42	838.07	400.21	Gluconate-6-phosphate dehydrogenase
15	<i>N1H47_14255</i>	745.10	1208.97	1255.08	Ribose 5-phosphate isomerase
16	<i>N1H47_16385</i>	38.30	34.64	37.65	Ribose-phosphate pyrophosphokinase
TCA cycle					
17	<i>N1H47_14640</i>	117.99	144.13	218.72	Citrate synthase
18	<i>acnA</i>	117.37	123.09	89.84	Aconitate hydratase
19	<i>N1H47_08375</i>	84.71	73.69	85.14	Isocitrate dehydrogenase

20	<i>N1H47_26000</i>	15.12	14.60	20.91	Oxoglutarate dehydrogenase E1 component
	<i>sucB</i>	29.74	29.21	24.00	Oxoglutarate dehydrogenase E2 component
	<i>lpdA</i>	148.34	194.07	127.39	Oxoglutarate dehydrogenase E3 component
21	<i>sucD</i>	261.14	320.37	320.12	Succinyl-CoA synthetase subunit alpha
	<i>sucC</i>	153.98	208.61	147.58	Succinyl-CoA synthetase subunit beta
22	<i>N1H47_11475</i>	68.92	100.37	87.38	Succinate dehydrogenase
23	<i>N1H47_24965</i>	36.56	35.02	37.94	Fumarate hydratase

DAp

26	<i>N1H47_21215</i>	58.99	93.25	60.88	Aspartate kinase
27	<i>N1H47_21220</i>	58.11	125.03	69.30	Aspartate-semialdehyde dehydrogenase
28	<i>dapA</i>	18.51	18.10	10.48	4-Hydroxy-tetrahydrodipicolinate synthase
29	<i>dapB</i>	57.58	67.08	98.66	4-Hydroxy-tetrahydrodipicolinate reductase
30	<i>dapC</i>	31.54	54.96	58.14	Diaminopimelate aminotransferase
31	<i>dapF</i>	42.09	28.64	27.39	Diaminopimelate epimerase
32	<i>lysA</i>	49.84	58.61	77.04	Diaminopimelate decarboxylase

ϵ -PL accumulation

33	<i>N1H47_34205</i>	23.66	41.01	22.83	ϵ -PL synthase
34	<i>N1H47_32795</i>	5.24	1.22	2.81	ϵ -PL degrading enzyme

Glutamate synthesis

35	<i>glbB</i>	55.94	115.84	120.83	Glutamate synthase subunit alpha
	<i>N1H47_11385</i>	167.98	212.73	250.29	Glutamate synthase subunit beta

Table S3 Influences of intracellular ROS levels on the genes' transcription concerning energy production.

Gene ID	CK fpkm	LOS fpkm	HOS fpkm	Gene description
Complex I				
<i>N1H47_17850</i>	55.30	39.53	3.62	NADH dehydrogenase subunit A
<i>N1H47_17990</i>	15.86	12.75	23.38	NADH dehydrogenase subunit B
<i>N1H47_18410</i>	2903.41	3248.27	4703.27	NADH dehydrogenase subunit C
<i>N1H47_17980</i>	9.94	7.97	10.00	NADH dehydrogenase subunit D
<i>nuoE</i>	22.86	19.61	26.97	NADH dehydrogenase subunit E
<i>nuoF</i>	85.38	79.65	163.66	NADH dehydrogenase subunit F
<i>N1H47_17965</i>	56.85	70.90	148.05	NADH dehydrogenase subunit G
<i>nuoI</i>	198.62	202.25	182.04	NADH dehydrogenase subunit I
<i>N1H47_17950</i>	114.09	132.22	159.97	NADH dehydrogenase subunit J
<i>nuoK</i>	496.33	373.54	565.08	NADH dehydrogenase subunit K
<i>nuoL</i>	98.61	81.28	122.15	NADH dehydrogenase subunit L
<i>N1H47_17935</i>	218.47	257.69	322.13	NADH dehydrogenase subunit M
<i>nuoN</i>	71.38	120.92	99.12	NADH dehydrogenase subunit N
<i>N1H47_17835</i>	140.44	172.43	139.43	NADH dehydrogenase subunit NuoH2
<i>N1H47_17830</i>	52.23	49.52	47.67	NADH dehydrogenase subunit NuoI2
Complex III				
<i>N1H47_11985</i>	1405.11	2187.52	1333.84	Ubiquinol-cytochrome C reductase iron-sulfur 'Rieske' subunit
<i>N1H47_11980</i>	29.44	48.86	57.38	Menaquinol-cytochrome C reductase cytochrome b subunit
Complex IV				
<i>ctaD</i>	58.72	74.40	53.18	Cytochrome c oxidase subunit I
<i>coxB</i>	3.32	8.55	11.75	Cytochrome c oxidase subunit II
<i>N1H47_11995</i>	2047.29	3098.15	3875.01	Cytochrome c oxidase subunit III
ATP synthase				
<i>atpA</i>	359.88	443.50	329.43	ATP synthase subunit alpha
<i>atpD</i>	9.79	9.80	6.84	ATP synthase subunit beta
<i>N1H47_26255</i>	3.69	6.14	0.97	ATP synthase subunit gamma
<i>N1H47_26245</i>	219.96	251.91	294.54	ATP synthase subunit delta
<i>N1H47_26265</i>	2.58	4.34	1.18	ATP synthase subunit epsilon
<i>atpB</i>	7.30	22.69	13.38	ATP synthase subunit A
<i>N1H47_26240</i>	57.00	72.40	95.18	ATP synthase subunit B
<i>atpE</i>	21.53	66.92	24.76	ATP synthase subunit C

Table S4 Influences of intracellular ROS levels on the genes' transcription concerning transcriptional regulator and secondary metabolites biosynthesis.

Gene ID	CK fpkm	LOS fpkm	HOS fpkm	Gene description
Transcriptional regulators				
<i>cynR</i>	508.97	895.42	784.97	Transcriptional regulator CynR
<i>N1H47_25630</i>	299.81	868.58	706.28	FurA family transcriptional regulator
<i>N1H47_11470</i>	422.80	832.65	702.49	LysR family transcriptional regulator
<i>N1H47_03465</i>	364.00	548.44	1124.80	LysR family transcriptional regulator
<i>N1H47_15470</i>	257.71	315.49	707.20	LysR family transcriptional regulator
<i>N1H47_21305</i>	35.57	54.10	100.45	LysR family transcriptional regulator
<i>N1H47_16885</i>	6.34	8.73	3.45	Sigma factor HrdD
<i>N1H47_11760</i>	17.20	101.83	8.70	TetR family transcriptional regulator
<i>N1H47_35560</i>	31.40	110.69	17.18	Transcriptional regulatory protein TcrA
<i>N1H47_11815</i>	34.19	177.38	17.65	MerR family transcriptional regulator
Biosynthesis of other secondary metabolites				
<i>N1H47_36795</i>	104.25	181.19	184.46	Erythromycin esterase family protein
<i>N1H47_05775</i>	306.07	486.94	471.45	Type I polyketide synthase
<i>N1H47_38515</i>	204.50	374.19	489.09	Type I polyketide synthase
<i>N1H47_05765</i>	178.15	232.59	212.45	Type I polyketide synthase
<i>N1H47_28655</i>	96.21	193.67	170.80	Type III polyketide synthase
<i>N1H47_05755</i>	150.89	250.20	187.16	Type I polyketide synthase
<i>N1H47_05780</i>	68.48	132.78	143.85	Type I polyketide synthase
<i>N1H47_38485</i>	21.01	2.70	4.96	Type I polyketide synthase
<i>N1H47_36780</i>	23.33	10.01	5.50	Polyketide synthase
<i>N1H47_01840</i>	10.05	1.44	2.64	Acyl transferase in polyketide synthase
<i>N1H47_31990</i>	14.80	7.97	4.47	Beta-ketoacyl synthase
<i>N1H47_00660</i>	37.93	16.92	11.33	Type I polyketide synthase