

Supplementary Materials: Dimethylformamide Inhibits Fungal Growth and Aflatoxin B₁ Biosynthesis in *Aspergillus flavus* by Down-regulating Glucose Metabolism and Amino Acid Biosynthesis

Lin Pan, Peng Chang, Jing Jin, Qingli Yang and Fuguo Xing

Table S1. Transcriptional activity of genes involved in *A. flavus* carbon metabolism.

Gene ID	CK* (FPKM)	D1* (FPKM)	Log ₂ D1/CK	Annotated Gene Function
AFLA_101470	1.44	0.040	-5.15	glyceraldehyde-3-phosphate dehydrogenase, putative
AFLA_041570	387.62	28.23	-3.78	conserved hypothetical protein
AFLA_052400	316.70	104.23	-1.60	isocitrate lyase AcuD
AFLA_028130	15.99	5.97	-1.42	thermoresistant gluconokinase family protein
AFLA_086400	402.88	178.47	-1.17	isocitrate dehydrogenase Idp1, putative
AFLA_085400	1255.25	582.91	-1.11	phosphoglycerate mutase, 2, 3-bisphosphoglycerate-independent
AFLA_069370	3560.94	1676.10	-1.09	phosphoglycerate kinase PgkA, putative
AFLA_119290	676.31	323.46	-1.06	Phosphofructokinase, putative
AFLA_047080	164.12	85.29	-0.94	cytosolic hydroxymethyltransferase, putative
AFLA_026470	263.66	141.33	-0.89	aspartate aminotransferase, putative
AFLA_041840	98.10	54.49	-0.85	glycine dehydrogenase
AFLA_046740	150.91	85.02	-0.83	NADP-dependent malic enzyme MaeA
AFLA_105320	166.68	98.79	-0.75	phosphoserine aminotransferase
AFLA_037910	678.05	414.33	-0.71	NAD ⁺ -isocitrate dehydrogenase subunit I
AFLA_027310	20.02	12.37	-0.69	fructose-1, 6-bisphosphatase Fbp1, putative
AFLA_073260	37.37	23.13	-0.69	Hexokinase, putative
AFLA_025100	9433.07	5907.44	-0.68	glyceraldehyde 3-phosphate dehydrogenase GpdA
AFLA_068840	48.32	30.87	-0.65	glycine cleavage system T protein
AFLA_091270	210.94	139.70	-0.59	fumarate hydratase, putative
AFLA_111650	78.81	52.66	-0.58	threonine dehydratase, biosynthetic
AFLA_085420	537.59	361.44	-0.57	serine hydroxymethyl transferase, putative
AFLA_049390	210.48	141.58	-0.57	malate synthase AcuE
AFLA_134130	47.00	31.73	-0.57	methylenetetrahydrofolate reductase, putative
AFLA_054750	738.72	501.26	-0.56	malate dehydrogenase, NAD-dependent
AFLA_007020	885.66	616.47	-0.52	citrate synthase (Cit1), putative
AFLA_067450	195.06	136.01	-0.52	glycine cleavage system H protein
AFLA_021700	99.45	69.65	-0.51	Aminotransferase, class V, putative
AFLA_100700	115.97	83.77	-0.47	phosphoserine phosphatase
AFLA_044820	488.47	354.15	-0.46	glucose-6-phosphate isomerase
AFLA_048020	188.81	137.94	-0.45	D-3-phosphoglycerate dehydrogenase
AFLA_034050	1139.95	847.92	-0.43	mitochondrial aconitate hydratase, putative
AFLA_048610	274.66	207.49	-0.40	succinyl-CoA synthetase alpha subunit, putative
AFLA_115170	385.52	291.89	-0.40	succinyl-CoA synthetase beta subunit, putative
AFLA_018850	390.74	302.65	-0.37	isocitrate dehydrogenase, NAD-dependent
AFLA_072370	0.08	0.06	-0.35	Hexokinase, putative

AFLA_083880	417.48	339.18	-0.30	succinate dehydrogenase subunit CybS, putative
AFLA_045020	150.27	122.81	-0.29	aspartate transaminase, putative
AFLA_090000	0.49	0.43	-0.20	conserved hypothetical protein
AFLA_059570	0.25	0.22	-0.16	conserved hypothetical protein

* CK=Control; D1=1% dimethylformamide.

Table S2. Transcriptional activity of genes involved in *A. flavus* MAPK pathway, Oxylipins, GPCRs and OSR.

Gene ID	gene	CK* (FPKM)	D1* (FPKM)	Log ₂ D1/CK	Annotated Gene Function
AFLA_062500	<i>maf1</i>	80.24	71.00	-0.17	mitogen-activated protein kinase MAF1
AFLA_083380	<i>pbs2</i>	49.22	44.29	-0.15	MAP kinase kinase (Pbs2), putative
AFLA_048880	<i>ste11</i>	16.98	15.66	-0.11	MAP kinase kinase kinase Ste11
AFLA_103480	<i>ste7</i>	21.33	20.04	-0.09	MAP kinase kinase Ste7
AFLA_034170	<i>fus3</i>	116.05	155.35	0.42	MAP kinase FUS3/KSS1
AFLA_035530	<i>ste20</i>	42.19	50.59	0.26	serine/threonine kinase Ste20
AFLA_073630	<i>ste20-like</i>	18.95	21.86	0.20	serine/threonine protein kinase, Ste20-like
AFLA_021030		24.99	22.37	-0.15	serine/threonine protein kinase, putative
AFLA_052570	<i>mpkA</i>	67.01	64.48	-0.05	MAP kinase MpkA
AFLA_051240	<i>mkk2</i>	99.25	77.87	-0.35	MAP kinase kinase (Mkk2), putative
AFLA_031560	<i>bck1</i>	17.71	18.20	0.03	MAP kinase kinase kinase (Bck1), putative
AFLA_100250	<i>cat</i>	1.39	0.72	-0.93	catalase Cat
AFLA_090690	<i>cat1</i>	500.21	555.65	0.15	mycelial catalase Cat1
AFLA_122110	<i>cat2</i>	12.65	17.77	0.48	bifunctional catalase-peroxidase Cat2
AFLA_056170	<i>catA</i>	47.28	108.67	1.20	spore-specific catalase CatA
AFLA_099000	<i>sod1</i>	311.11	209.12	-0.57	Cu, Zn superoxide dismutase SOD1
AFLA_033420	<i>mnSOD</i>	1844.59	2033.04	0.14	Mn superoxide dismutase MnSOD
AFLA_031340	<i>atfA</i>	68.74	52.93	-0.37	bZIP transcription factor (AtfA), putative
AFLA_094010	<i>atfB</i>	94.74	98.13	0.05	bZIP transcription factor (Atf21), putative
AFLA_129340	<i>ap-1</i>	172.52	103.13	-0.74	bZIP transcription factor AP-1
AFLA_110650	<i>msnA</i>	147.14	152.03	0.04	C ₂ H ₂ transcription factor (Seb1)
AFLA_091490	<i>mtfA</i>	42.87	81.01	0.91	C ₂ H ₂ finger domain protein
AFLA_030580	<i>pacC</i>	138.05	116.60	-0.24	C ₂ H ₂ transcription factor PacC
AFLA_034540	<i>srrA</i>	52.96	65.05	0.29	stress response transcription factor SrrA/Skn7, putative
AFLA_062210	<i>sskA</i>	42.65	41.37	-0.04	response regulator, putative
AFLA_068590	<i>sskB</i>	22.86	28.84	0.33	MAP kinase kinase kinase SskB, putative
AFLA_099500	<i>sakA1</i>	8.46	13.53	0.67	MAP kinase Saka
AFLA_061090	<i>sakA2</i>	11.34	40.50	1.83	MAP kinase Saka
AFLA_026790	<i>ppoA</i>	23.61	58.07	1.29	fatty acid oxygenase PpoA, putative
AFLA_120760	<i>ppoB</i>	0.00	0.00	Up	fatty acid oxygenase, putative
AFLA_030430	<i>ppoC</i>	1.74	4.36	1.32	fatty acid oxygenase PpoC, putative
AFLA_025100	<i>gpdA</i>	9433.07	5907.44	-0.67	glyceraldehyde 3-phosphate dehydrogenase GpdA
AFLA_046760	<i>gfdB</i>	29.62	10.94	-1.43	glycerol 3-phosphate dehydrogenase (GfdB), putative
AFLA_060740	<i>gprA</i>	6.13	5.61	-0.12	mating-type alpha-pheromone receptor PreB
AFLA_061620	<i>gprB</i>	9.84	11.96	0.28	a-pheromone receptor PreA

AFLA_074150	<i>gprC</i>	20.10	13.97	-0.52	conserved hypothetical protein
AFLA_135680	<i>gprD</i>	15.89	9.93	-0.67	G protein-coupled receptor GprD
AFLA_006880	<i>gprF</i>	29.26	33.18	0.18	PQ loop repeat protein
AFLA_067770	<i>gprG</i>	58.95	28.22	-1.06	PQ loop repeat protein
AFLA_006920	<i>gprH</i>	1.54	3.47	1.16	cAMP receptor-like protein
AFLA_127870	<i>gprJ</i>	37.85	32.38	-0.22	vacuolar membrane PQ loop repeat protein
AFLA_009790	<i>gprK</i>	0.08	0.40	2.26	conserved hypothetical protein
AFLA_075000	<i>gprM</i>	11.82	33.67	1.51	conserved hypothetical protein
AFLA_032130	<i>gprO</i>	40.56	42.44	0.06	hemolysin-III channel protein Izh2, putative
AFLA_088190	<i>gprP</i>	45.71	44.28	-0.04	IZH family channel protein (Izh3), putative
AFLA_023070	<i>gprR</i>	100.49	80.17	-0.32	integral membrane protein
AFLA_006320	<i>gprS</i>	40.64	34.30	-0.24	PQ loop repeat protein
AFLA_117970	<i>nopA</i>	1380.92	1261.75	-0.13	opsin, putative
AFLA_039130	<i>sln1</i>	189.95	235.23	0.30	sensor histidine kinase/response regulator TcsB/Sln1, putative
AFLA_045720	<i>mak10</i>	22.95	17.07	-0.42	amino-acid N-acetyltransferase subunit Mak10, putative
AFLA_112280	<i>mak11</i>	40.78	46.82	0.19	60S ribosome biogenesis protein Mak11, putative
AFLA_018940	<i>mak32</i>	13.76	16.96	0.30	PfkB family carbohydrate kinase (Mak32), putative
AFLA_106830	<i>tcsA</i>	16.58	19.07	0.20	sensor histidine kinase/response regulator Fos- 1/TcsA
AFLA_026290	<i>ypd1</i>	113.21	142.22	0.32	phosphotransmitter protein Ypd1, putative
AFLA_099770		27.69	22.64	-0.29	conserved hypothetical protein
AFLA_116790		3.46	3.40	-0.02	conserved hypothetical protein
AFLA_126140		0.27	0.30	0.15	conserved hypothetical protein
AFLA_050640		25.73	14.39	-0.83	dual specificity phosphatase catalytic domain protein
AFLA_134840	<i>tep1</i>	20.29	9.44	-1.10	phosphoinositide phosphatase Pten/Tep1, putative
AFLA_133310		34.00	30.07	-0.17	protein-tyrosine phosphatase, putative
AFLA_087770	<i>spc105</i>	16.23	14.73	-0.14	chromosome segregation protein Spc105, putative
AFLA_043340	<i>spc19</i>	43.75	42.86	-0.02	mitotic spindle biogenesis protein Spc19, putative
AFLA_086270	<i>msn5</i>	11.87	16.02	0.43	nuclear import and export protein Msn5, putative
AFLA_053070		27.66	33.94	0.29	Yapsin, putative
AFLA_021190		26.06	24.19	-0.10	PAP2 domain protein
AFLA_056030		38.60	36.91	-0.06	PAP2 domain protein
AFLA_084240		89.81	92.17	0.03	poly(A) polymerase Pap
AFLA_095910		27.53	31.57	0.19	PAP2 domain protein
AFLA_135870		37.63	54.54	0.53	PAPA-1-like conserved region protein
AFLA_048050	<i>nap1</i>	408.00	403.31	-0.01	nucleosome assembly protein Nap1, putative
AFLA_092040		23.44	25.05	0.09	NAP1-binding protein, putative

* CK=Control; D1=1% dimethylformamide.