

Supplementary Materials: Identification of the Anti-Aflatoxinogenic Activity of *Micromeria graeca* and Elucidation of its Molecular Mechanism in *Aspergillus flavus*

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Table S1. Gene expression ratio values of AFB₁ cluster genes upon hyssop addition. Ratios are obtained in comparison to control values.

Gene	Function of encoded protein	Gene expression ratio	SEM	Fold change	p-value
<i>AFB₁ cluster genes</i>					
<i>aflR</i>	Zn-finger transcription factor	0.31	0.053	3.2	<0.0001
<i>aflS</i>	AFLR co-activator	0.35	0.069	2.8	<0.0001
<i>aflT</i>	MFS-transporter	0.43	0.055	2.3	<0.0001
<i>aflA</i>	Fatty acid synthase	0.08	0.019	12.2	<0.0001
<i>aflB</i>	Fatty acid synthase	0.08	0.018	12.3	<0.0001
<i>aflC</i>	Polyketide synthase	0.07	0.029	14.7	0.00058
<i>hypC</i>	Noranthrone oxidase	0.01	0.003	167.2	<0.0001
<i>aflD</i>	Ketoreductase	0.06	0.022	16.8	<0.0001
<i>aflE</i>	Deshydrogenase	0.06	0.019	17.8	<0.0001
<i>aflG</i>	Cytochrome P-450 mono-oxygenase	0.11	0.042	9.3	<0.0001
<i>aflH</i>	Deshydrogenase	0.04	0.011	24.8	<0.0001
<i>aflI</i>	Flavin-dependent oxidoreductase	0.02	0.007	60.7	0.00043
<i>aflV</i>	Microsomal Cyt. P-450 mono-oxygenase	0.05	0.012	19.8	<0.0001
<i>aflJ</i>	Esterase	0.06	0.020	18.0	<0.0001
<i>aflK</i>	Cyclase	0.07	0.019	14.9	<0.0001
<i>aflL</i>	Desaturase	0.05	0.015	19.2	<0.0001
<i>aflM</i>	Ketoreductase	0.12	0.053	8.4	0.00120
<i>aflN</i>	Cytochrome P-450 mono-oxygenase	0.03	0.010	34.0	<0.0001
<i>aflX</i>	Oxidoreductase	0.02	0.008	50.4	<0.0001
<i>aflO</i>	O-methyl transferase (I)	0.00	0.000	468.8	<0.0001
<i>aflP</i>	O-methyl transferase (II)	0.03	0.010	29.7	<0.0001
<i>aflQ</i>	Cytochrome P-450 mono-oxygenase	0.07	0.027	13.4	<0.0001
<i>hypB</i>	Hypothetical protein	0.03	0.016	35.8	0.00085
<i>aflW</i>	Cytosolic mono-oxygenase	0.07	0.019	14.7	<0.0001
<i>aflY</i>	Baeyer-Villiger mono-oxygenase	0.02	0.009	45.8	<0.0001
<i>hypD</i>	Integral membrane protein	0.11	0.024	9.4	<0.0001
<i>hypE</i>	Hypothetical protein	0.05	0.011	18.5	0.00018

Table S1. Cont.

Gene	Function of encoded protein	Gene expression ratio	SEM	Fold change	p-value
<i>Secondary metabolism regulator genes</i>					
<i>abaA</i>	Developmental TF	0.63	0.17	1.58	0.23329
<i>ap-1</i>	bZIP TF (Oxidative stress response)	1.02	0.12	1.02	0.63484
<i>areA</i>	Environmental GATA TF (Nitrogen)	1.71	0.25	1.71	0.0215
<i>atfA</i>	bZIP TF (Oxidative stress response)	0.84	0.14	1.18	0.50247
<i>cat2</i>	Catalase (Oxidative stress response)	0.33	0.04	3.04	<0.0001
<i>catA</i>	Catalase (Oxidative stress response)	0.45	0.05	2.23	0.004
<i>creA</i>	Environmental Zn TF (Carbon)	2.50	0.90	2.50	0.09569
<i>brlA</i>	Developmental Zn finger TF	1.54	0.33	1.54	0.10605
<i>fadA</i>	G-protein signaling pathway	1.47	0.48	1.47	0.78896
<i>fcr3</i>	Global bZIP TF	0.82	0.06	1.22	0.05987
<i>flbA</i>	Developmental regulator	1.40	0.19	1.40	0.07493
<i>fluG</i>	Developmental regulator	0.77	0.12	1.30	0.27419
<i>gprA</i>	G-protein receptor	0.70	0.19	1.44	0.15496
<i>gprG</i>	G-protein receptor	1.33	0.18	1.33	0.09379
<i>gprH</i>	G-protein receptor	0.49	0.01	2.06	0.0006
<i>gprK</i>	G-protein receptor	2.00	0.17	2.00	<0.0001
<i>gprP</i>	G-protein receptor	1.19	0.07	1.19	0.23350
<i>laeA</i>	Velvet complex	1.10	0.18	1.10	0.53537
<i>meaB</i>	Environmental bZIP TF (Nitrogen)	1.14	0.14	1.14	0.31329
<i>mnsod</i>	Mn superoxide dismutase	0.49	0.09	2.04	0.0007
<i>msnA</i>	Zn finger TF (Oxidative stress response)	3.25	0.77	3.25	0.0126
<i>mtfA</i>	Zn finger TF (Oxidative stress response)	1.93	0.17	1.93	0.0001
<i>nsdC</i>	Global Zn finger TF	1.54	0.18	1.54	0.0122
<i>pacC</i>	Environmental Zn finger TF (pH)	1.64	0.11	1.64	<0.0001
<i>ppoA</i>	Oxylipin	0.87	0.05	1.15	0.19087
<i>ppoB</i>	Oxylipin	0.85	0.10	1.18	0.17278
<i>ppoC</i>	Oxylipin	1.50	0.14	1.50	0.003
<i>rasA</i>	Ras-family signaling pathway	2.36	0.65	2.36	0.05524
<i>sod1</i>	CuZn superoxide dismutase	0.60	0.05	1.67	0.013
<i>srrA</i>	bZIP TF (Oxidative stress response)	1.44	0.13	1.44	0.0017
<i>stuA</i>	Developmental factor	1.76	0.44	1.76	0.0012
<i>veA</i>	Velvet complex	3.76	0.44	3.76	<0.0001
<i>velB</i>	Velvet complex	1.03	0.10	1.03	0.63158
<i>vosA</i>	Velvet complex	0.85	0.14	1.05	0.87741