

## Supplementary Materials: Deciphering the Anti-Aflatoxinogenic Properties of Eugenol Using a Large-Scale q-PCR Approach

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**Table S1.** Gene expression values of regulatory factors that were not impacted upon Eugenol addition. Values are expressed in fold change and compared to a control fixed at 1.

Gene Name	Values	p-Value
<i>abaA</i>	1.13	0.8179
<i>ap-1</i>	1.12	0.4589
<i>areA</i>	1.29	0.4578
<i>atfA</i>	2.09	0.0537
<i>brlA</i>	0.77	0.1953
<i>cat2</i>	1.13	0.8072
<i>catA</i>	1.84	0.3623
<i>creA</i>	1.32	0.648
<i>fadA</i>	0.95	0.891
<i>fcr3</i>	0.73	0.0836
<i>flbA</i>	0.55	0.2958
<i>fluG</i>	1.11	0.5914
<i>gprG</i>	1.52	0.1591
<i>gprH</i>	0.84	0.3971
<i>gprP</i>	1.29	0.2462
<i>laeA</i>	1.05	0.7673
<i>meaB</i>	1.43	0.1367
<i>mnSOD</i>	0.84	0.3045
<i>ppoA</i>	1.26	0.2914
<i>ppoB</i>	0.77	0.4413
<i>ppoC</i>	0.89	0.6097
<i>rasA</i>	0.88	0.4225
<i>SOD1</i>	0.95	0.8985
<i>srrA</i>	1.69	0.2001
<i>velB</i>	1.43	0.3543
<i>vosA</i>	1.49	0.1905

Table S2. Primer sequences of the 62 designed genes.

Access Number	Gene	nM	Primers Sequences 5' to 3'	
AFLA_139380	<i>aflA</i>	300/900	F: CCAGTCGGTGGTGTGCAAAA	R: CGCAGCACCCAGAGCTT
AFLA_139370	<i>aflB</i>	300/300	F: GTCTGCGCAGGCCATTTC	R: AGCTCTGGCCTTCAACAGTCTC
AFLA_139410	<i>aflC</i>	300/300	F: CTGACCCCGGCATTTCG	R: TGCCAGATTCTCATATTCCCG
AFLA_139390	<i>aflD</i>	300/900	F: AGGCATCTGTGCTCGGATTG	R: TGCCCCGATGTAGTCTCCTTAGT
AFLA_139310	<i>aflE</i>	900/300	F: CTGCAACACTCGGCTAGAAACA	R: GAAGGGTTCGATCGGCTGT
AFLA_139260	<i>aflG</i>	900/900	F: CATGCAGAGTAACCGCATCGT	R: TTGTAGACCGACGGATGTCCC
AFLA_139330	<i>aflH</i>	900/900	F: CCAGCTCCACGGTCGG	R: CTTAAGGTCAAAGATTCCCTCGG
AFLA_139230	<i>aflI</i>	300/300	F: GATCGGCTCGTTTGAGGGA	R: GCAAAAATGATATTCAGCTGGTTGAC
AFLA_139320	<i>aflJ</i>	300/900	F: GCTCCGTGGCACCAGTT	R: TCGTCACGCTCTCATCGG
AFLA_139190	<i>aflK</i>	300/300	F: ACAGCGCGAAATGTTTTATATGC	R: GCGCCTTTCGAGCCTCTG
AFLA_139250	<i>aflL</i>	300/300	F: CCGATTCGTACCCGAAGAGAC	R: TCGGCAAAGTAGGTACCGAGAT
AFLA_139300	<i>aflM</i>	900/900	F: TCCTGGAGCCATTAAGACTGATATGT	R: GCCAAGCGGCGCACTC
AFLA_139280	<i>aflN</i>	300/300	F: CCAGGCTCGCCAGGAAGT	R: AGCTTGAAGTCTGGCATAGGAAGG
AFLA_139220	<i>aflO</i>	300/900	F: CCCAAGAGTATACCTCGAGTGC	R: AAGGTCCCGAGATGTCGAATAGTT
AFLA_139210	<i>aflP</i>	900/300	F: TATTCTACATGACTATCCCGATGCTG	R: GCGCGACTTGCTTGGGT
AFLA_139200	<i>aflQ</i>	900/900	F: GGGAGGATCGGACACGACA	R: CATGGCCACGAAAAGCTAGAC
AFLA_139360	<i>aflR</i>	900/900	F: GCGGCACAGCTTGTTCTGA	R: CCGGTATCCCTGCTGCATC
AFLA_139340	<i>aflS</i>	900/900	F: AACGGTCGTGCATGTGGG	R: CGGCCTTAGCTTCTGTCTGC
AFLA_139420	<i>aflT</i>	300/300	F: GTAGCATGCGCCTCCGTCT	R: GCGAATGGCTTGAACCAG
AFLA_139180	<i>aflV</i>	300/900	F: CCTGGTGGTTCCTCGCTGT	R: TGAAATATGCGGTTTGAAGAATCTTG
AFLA_139170	<i>aflW</i>	300/900	F: CGATGTCTTTGTGCGGACG	R: GTGTTGCCCGCTAGCACTC
AFLA_139160	<i>aflX</i>	900/900	F: GATCCACGCTACTGCCGT	R: GATCTCAGGATGCAATCGGTTT
AFLA_139150	<i>aflY</i>	300/300	F: GGTGTCCCTACGGTCTTAAATGAGT	R: CAATGGGTGGAGAAAGCCAGA
AFLA_139240	<i>hypB</i>	900/300	F: TCCTGCACTTCAAGCTACCGC	R: GACGCTCATCATGGCTCCG
AFLA_139400	<i>hypC</i>	900/900	F: GGTCTTTTTGACGGGAGCC	R: TCTCGATAAGAATGGGAATGGTGA
AFLA_139270	<i>hypD</i>	300/900	F: TTGCGTTTGCCGACGG	R: GCGCATAACTCCAATGTCCC
AFLA_139290	<i>hypE</i>	900/900	F: AAGTTCGACTTTCCCGC	R: CAAAGTTGATAATAGCAAATCCGTCATA
AFLA_029620	<i>abaA</i>	900/900	F: TACAAAATACTGGCAAAGGAGGTC	R: CCCGTACAAGCCTCTCCCA
AFLA_129340	<i>ap-1</i>	900/300	F: CTTGCACCAAGATTGGGACC	R: TCGTACGCAATTCGGAGCA
AFLA_049870	<i>areA</i>	300/900	F: CAGCCAATCCGCGAAC	R: CCCATTCCTGACTAGCCCCTT
AFLA_031340	<i>atfA</i>	900/900	F: GCAGTTACAGGCACCTTAACACATC	R: CGGCGCCTGGGAGTCTT
AFLA_082850	<i>brlA</i>	300/300	F: GCGTGCCTTCTCCCGC	R: GGAGTCCATCCGGTGTGAGTT
AFLA_068620	$\beta$ -tub	300/900	F: AACGTCTACTTCAACGAGGCCA	R: GTACCAGGCTCAAGATCAACGAG
AFLA_122110	<i>cat2</i>	300/900	F: TGGCAGCAGTGACGGAAAG	R: AGCCCAAGCGGCAACAA

Table S2. Cont.

AFLA_056170	<i>catA</i>	300/900	F: ATTAAGTTCCCGGATTTTGTCCA	R: GGTACCTCGTTGTGCGGCT
AFLA_134680	<i>creA</i>	300/900	F: CAGCCGGAAGGCCCC	R: CATATCTTGCACCGCGACCT
AFLA_018340	<i>fadA</i>	900/900	F: TACATCCTCAACCGCTTCGTG	R: GGTTCCTCTGGATGATGATGTCATT
AFLA_133560	<i>fcf3</i>	300/900	F: GGCACAGAACAGAGCAGCTCAA	R: GCACATGTCGCTCCTTTTCGTT
AFLA_134030	<i>flbA</i>	300/900	F: CTGGCTGCAGCATATGGTCTT	R: CATTGATTTCGTCATCCCCTACAG
AFLA_101920	<i>fluG</i>	300/300	F: CGCCGGTTACCTAGGCGT	R: TTGGCGGCATCGTGGA
AFLA_025100	<i>gpdA</i>	900/900	F: CGTGTGTTGACCTCATTGCCT	R: GGTGACCTGATAATCCGGGAAC
AFLA_060740	<i>gprA</i>	900/900	F: CTTCTGCAGTATCTTCATTATCAAGCTC	R: AATCGAAAGCAGCGCTGG
AFLA_067770	<i>gprG</i>	300/900	F: CCGCATTACAGCGAAACTT	R: GCGGTTAGGGTTTGTGAGGAG
AFLA_006920	<i>gprH</i>	300/900	F: TTGATTGTACCTGGGTTCTTTC	R: CATAGTTCAGAGCAAAGTTGTGGGA
AFLA_009790	<i>gprK</i>	300/900	F: CTGCCATGCAGGTAGTCAAC	R: TCCAAATGGACAGGCAAATCC
AFLA_088190	<i>gprP</i>	300/300	F: CGATGCAGTCTTTCTAAGGGTGG	R: GCCATCGATTGTACCATGTGTGA
AFLA_033290	<i>laeA</i>	900/900	F: TGCCAACAAATACCCAGACG	R: TCGCAATTCTTTGGGTGGTT
AFLA_031790	<i>meaB</i>	900/900	F: CCAAAGCACTATGATCAGCTTGAA	R: CCCACGGACGACTCATGC
AFLA_033420	<i>mnSOD</i>	300/300	F: GGTGGCTAATGGACCGGG	R: CATACGAGGCCTTGTTATTGAAGTACTG
AFLA_110650	<i>msnA</i>	900/900	F: GACGTCCATGCCGAGCTTT	R: AATTGGCGTTGATGAAGACAGG
AFLA_091490	<i>mtfA</i>	300/900	F: GCATCGACATATGCTGCAAAG	R: GGCGCAAAGGTGGAGTAGG
AFLA_131330	<i>nsdC</i>	300/900	F: TCCAGGACCACATGACTCCAA	R: GCTGTGCCCTTAAAGCAGCTACT
AFLA_030580	<i>pacC</i>	900/300	F: CAAGGATGTTCTGAGAAGTGTCCC	R: CGTTCGCAGACGTGCTCATA
AFLA_026790	<i>ppoA</i>	300/900	F: ATCAAGAGGCTGGCGAAGGT	R: GGGCGCCTTCCATGAAGTA
AFLA_120760	<i>ppoB</i>	300/900	F: AGTCTCTATGCGTTCCTATGACTTG	R: CGTCCCTTCCCAGGAAT
AFLA_030430	<i>ppoC</i>	300/300	F: GTTACAATCAGGCTCAAATGTTC	R: CAGGCAGTAGCGCATCAACTT
AFLA_132380	<i>rasA</i>	300/300	F: GCGAGCCGTCACAGTAGAAGAG	R: CGGATGTTTCGATAAATTTGCAG
AFLA_099000	<i>sod1</i>	900/300	F: CGAGAGCGTACTTGGCCGT	R: TCTTCTTGACTCCGGGTGTT
AFLA_034540	<i>srrA</i>	300/900	F: TGTCGTCAGATTGGCGGAA	R: GCCTCGAGTCCGTCGAAAG
AFLA_066460	<i>veA</i>	300/300	F: CGTCAGCCGGATCACTCG	R: GACGGTCCGCAGAGGACTT
AFLA_081490	<i>velB</i>	300/300	F: GGCTTCGGCGACAAGGAT	R: TCTGCGTTCCACAAGTCTACCA
AFLA_026900	<i>vosA</i>	300/900	F: GGGTGTTCAGATTATGCGATG	R: CCCGTTGAATCCCCGCTAG