

Supporting Information

Gut Bacteria Promote Phosphine Susceptibility of *Tribolium castaneum* by Aggravating Oxidative Stress and Fitness Costs

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Table S1 Primers used for qRT-PCR

Primer name	Primer sequence (5'-3')	Product size (bp)	Amplification efficiency (E%)	Coefficient of determination (R ²)	Usage
16S-27F	AGAGTTTGATCCTGGCTCAG	---	---	---	Bacterial identification
16S-1492R	GGTTACCTTGTACGACTT				
Tc- β -actin-F	TCCATCATGAAGTGCGATGT	228	99.2	1.00	Bacterial quantification
Tc- β -actin-R	CCACATCTGTTGGAATGTCG				
16S-F	TCGTTTGAAAATGTCCT	116	98.2	0.98	Bacterial quantification of
16S-R	GGCGTTGAACTTCCTAAT				<i>Brevibacterium</i> sp.
16S-F	AACAATCGAAACCGCATGGT	316	99.6	0.98	Bacterial quantification of
16S-R	TACCGTCAAGGGATGAACAGT				<i>Enterococcus</i> sp.
16S-F	TGGAAGAATTCGGTCAGGGAT	254	99.4	0.99	Bacterial quantification of
16S-R	ACTTTCGCTTCTTCCCTGCTA				<i>Microbacterium</i> sp.
16S-F	TGTGGGTGGGTGGAAAGTTTTT	291	97.4	0.99	Bacterial quantification of
16S-R	CCGGTACTTCTTCTGCAGGTA				<i>Micrococcus</i> sp.
16S-F	TGGGTGTTGGAAAGAATTCGGT	265	98.8	1.00	Bacterial quantification of
16S-R	CGTCACTTCGCTTCTTCCCTA				<i>Staphylococcus</i> sp.
Tc- <i>Atf2</i> -F	CCAAACTCCAACCAACACG	234	98.7	0.98	Gene expression
Tc- <i>Atf2</i> -R	TTCTCACTCGAACTGGGGCT				quantification
Tc- <i>CAT3</i> -F	ATCGCAACCCGGAAGACTAC	184	99.0	1.00	Gene expression
Tc- <i>CAT3</i> -R	TTGAAGGGACAGTTGACGGG				quantification
Tc- <i>DUOX</i> -F	CGATGAGAGTGCCGCTTTTT	250	100.4	0.99	Gene expression
Tc- <i>DUOX</i> -R	GCGATGATGTTTTGGACGGT				quantification
Tc- <i>IMD</i> -F	CAAGGGCGCTGGATTTCTCA	174	97.8	0.99	Gene expression
Tc- <i>IMD</i> -R	CGTCTTGCTGGTTTGTGTCC				quantification
Tc- <i>PLCβ</i> -F	AAAACCTGACCCAACGCAGC	190	100.7	0.99	Gene expression
Tc- <i>PLCβ</i> -R	TTGGGCTCGTATTGTGCGAT				quantification
Tc- <i>PRDX6</i> -F	GGACGAGAAGCGCGAATTG	192	98.5	1.00	Gene expression
Tc- <i>PRDX6</i> -R	TGGAGCGAATCAATGACCCT				quantification
Tc- <i>Rps18</i> -F	CGAAGAGGTCGAGAAAATCG	235	98.8	0.99	Gene expression
Tc- <i>Rps18</i> -R	CGTGGTCTTGGTGTGTTGAC				quantification
Tc- <i>SOD1a</i> -F	GCCATCGTGTGCCTCAAATC	238	97.9	0.99	Gene expression
Tc- <i>SOD1a</i> -R	TCCCGAGATCACCAACGTG				quantification
Tc- <i>SOD1b</i> -F	CCTCCACATTCACCAGTCGG	225	101.1	0.99	Gene expression
Tc- <i>SOD1b</i> -R	ACAATCGAACGGCCCAAT				quantification
Tc- <i>SOD1c</i> -F	TGTGTCCTAAACGGCGAAGT	241	97.3	1.00	Gene expression
Tc- <i>SOD1c</i> -R	CGATATCCCCAAATCCCCCA				quantification
Tc- <i>SOD2</i> -F	CTCGCTACAGCCCCCTTG	126	98.7	0.99	Gene expression
Tc- <i>SOD2</i> -R	GTGGTGTGTTGGAGTGGTGA				quantification
Tc- <i>Toll</i> -F	CATGCGTACCGCCAAAATACA	250	99.3	1.00	Gene expression
Tc- <i>Toll</i> -R	ACGCTTCGGGTAAAGTCTACAA				quantification

Figure S1 The neighbour-joining phylogenetic tree of five culturable gut bacteria isolated from adult *Tribolium castaneum*. The tree was constructed from 16S rDNA sequences (1422–1465 bp) using the generalized time-reversible model.

