Table S1. Primer sequences of *L. monosytogenes* and *A. flavus* genes and respective amplicons sizes used for the gene expression assay

Genes	Primers	Sequence	Concentration (μM)	Amplicon size (bp)	PCR efficiency	Reference
L. monocytogenes						
Reference genes						
IGS	IGS_f	GGCCTATAGCTCAGCTGGTTA	1.2	135	2.03	[1]
	IGS_r	GCTGAGCTAAGGCCCCGTAAA	1.2			
rpob	Rpob_f	CCGCGATGCGAAAACAAT	0.9	69	2.04	[2]
	Rpob_r	CCWACAGAGATACGGTTATCRAATGC	0.9			
16S	16S_f	GATGCATAGCCGACCTGAGA	0.9	114	2.05	[3]
	16S_r	CTCCGTCAGACTTTCGTCCA	0.9			[4]
Virulence- associated						
prfA	prfA_f	CTATTTGCGGTCAACTTTTAATCCT	0.9	100	2.09	[2]
	prfA_r	CCTAACTCCTGCATTGTTAAATTATCC	0.9			
sigB	sigB_f	CCAAGAAAATGGCGATCAAGAC	1.2	166	2.13	[1]
	sigB_r	CGTTGCATCATATCTTCTAATAGCT	1.2			
plcA	plcA_f	CTAGAAGCAGGAATACGGTACA	1.2	115	1.94	[1]
	plcA_r	ATTGAGTAATCGTTTCTAAT	1.2			
plcB	plcB_f	CAGGCTACCACTGTGCATATGAA	0.9	72	2.00	[2]
	plcB_r	CCATGTCTTCYGTTGCTTGATAATTG	0.9			
hly	hly_f	TACATTAGTGGAAAGATGG	1.2	153	1.98	[2]
	hly_r	ACATTCAAGCTATTATTTACA	1.2			
inlA	inlA_f	AATGCTCAGGCAGCTACAMTTACA	0.9	114	2.12	[2]
	inlA_r	CGTGTCTGTTACRTTCGTTTTTCC	0.9			
inlB	inlB_f	AAGCAMGATTTCATGGGAGAGT	0.9	78	2.04	[2]
	inlB_r	TTACCGTTCCATCAACATCATAACTT	0.9			
inlC	InlC_f	ACTGGTCAGAAATGTGTGAATGA	0.9	80	2.06	[4]
	inlC_r	CCATCTGGGTCTTTGACAGT	0.9			
inlJ	inlJ_f	TGCGTAAATGCTCACATCCAAG	0.9	81	2.03	[4]
	inlJ_r	TTGCCCTTCAGCATCCAAGT	0.9			
Fatty acid biosynthesis						
murE	murE_f	GCCACAACCAACAACGACAA	0.9	85	1.97	[5]
	murE_r	TCATACTCCAGACGGCTTGC	0.9			
accA	accA_f	GCGGTCAAAGTGAAGCCATT	0.9	94	1.99	[5]
	accA_r	CCACTTCCACCTTCACCGAT	0.9			
acpP	acpP_f	TGAAGACGAGTTCGGAGTTGA	0.9	91	2.05	[5]
	acpP_r	TGCGTTCGCCTCTATGTACT	0.9			
Peptidoglycan biosynthesis						
fapR	fapR_f	CGCCGTCATCCCAAATGAAA	0.9	88	2.02	[5]
	fapR_r	TGCGATGATGCGTTCTCCTT	0.9			
A. flavus						
Reference genes						
18S	18S_f	GCAAATTACCCAATCCCGACAC	0.2	32	1.97	[6]
	18S_r	GAATTACCGCGGCTGCTG	0.2			
cal	cal_f	CTTCCCCGAATTCCTTACC	0.2	89	2.02	[7]
	cal_r	TCACGGATCATCTCATCGAC	0.2			
Tub-β	tubβ_f	CGCATGAACGTCTACTTCAACGAG	0.2	28	1.94	[8]
	tubβ_r	AGTTGTTACCAGCAGCGGACT	0.2			
Biosynthesis						
aflM	aflM_f	AAGTTAATGGCGGAGACG	0.2	72	2.02	[9]
	aflM_r	TCTACCTGCTCATCGGTGA	0.2			
aflD	aflD_f	GCGCAAGTTCCACTTTGAGA	0.2	42	1.99	[10]
	aflD_r	CCTTGGTCGCCCATATCAGT	0.2			
aflP	aflP_f	AGCCCCGAAGACCATAAAC	0.2	70	1.91	[9]
	aflP_r	CCGAATGTCATGCTCCATC	0.2			
Regulatory						
aflR	aflR_f	CGGCACAGCTTGTTCTGAGT	0.2	8	1.92	[10]
	aflR_r	GCATCGTCTCCACCTTCTTG	0.2			
aflS	aflR_f	CTGGCAAAACTTGGGAATGG	0.2	63	2.05	[10]
	aflR_r	CACGAGGAAACGGAGTGATG	0.2			

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