toxins

Supplementary Materials: Mechanism Underlying *Bacillus subtilis* BS-Z15 Metabolite-Induced Prevention of Grain Contamination by *Aspergillus flavus*

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Table S1. Statistics of sequencing data.

Samples	Clean reads	Clean bases	GC Content	%≥Q30
CK1	22,386,295	6,696,520,678	52.06%	94.39%
CK2	21,582,670	6,456,964,878	52.08%	94.21%
CK3	20,967,620	6,278,301,228	51.37%	94.19%
H201	20,606,012	6,171,415,484	52.45%	93.71%
H202	21,298,436	6,375,798,960	52.65%	93.79%
H203	22,341,048	6,689,538,538	52.56%	94.67%
H31	20,345,623	6,091,658,234	52.51%	94.48%
H32	20,661,009	6,187,646,738	52.60%	94.12%
H33	21,387,432	6,397,095,262	52.79%	94.18%
L201	21,148,316	6,332,071,044	52.59%	94.46%
L202	21,727,698	6,504,578,288	52.59%	94.30%
L203	20,762,266	6,217,574,048	52.29%	93.96%
L31	20,600,728	6,167,592,962	52.70%	94.14%
L32	21,167,586	6,334,672,286	52.72%	94.38%
L33	21,034,646	6,297,696,836	52.61%	94.21%

Note: H201-H203 is 20μg/mL 12h; H31-H33 is 20μg/mL 3h; L201-L203 is 4μg/mL 12h; L31-L33 is 4μg/mL 3h

Table S2. Specific primer sequences used in qRT-PCR.

Primer name	Primer sequences(5′-3′)
18S	F：GCTCTTTTGGGTCTCGTAATTGG
	R:CGCTATTGGAGCTGGAATTACC
aflR	F: CCTTTCTCACTACTCGGGTTT
	R:GCAGGTAATCAATAATGTCGG
aflT	F:GATTCTATTGCCTTGATTTTGG
	R:GGCGTAGTGCCCTGTCTTAT
aflP(omtA)	F:CACGCTTTCAGAGCAGGTAA
	R:TTCGGTGGAGGAGGGAGTT

Table S3. Fluorescence quantitative PCR reaction system.

Composition	50μL System
2xSuperReal PreMix Plus	25μL
50×ROX Reference Dye	1.0μL
Forward primers	1.5μL
Reverse Primers	1.5μL
RNA template	5μL
RNase-Free ddH_2O	Add to 50μL

Table S4. Real-time PCR reaction program.

Circulation	Stage	Temperature	Time	Contents
1×	Pre-mutability	95℃	15min	Pre-mutability
40×	PCR reactions	95℃	10sec	Gender reassignment
		50-60℃	20sec	Annealing
		72℃	30sec	Extension

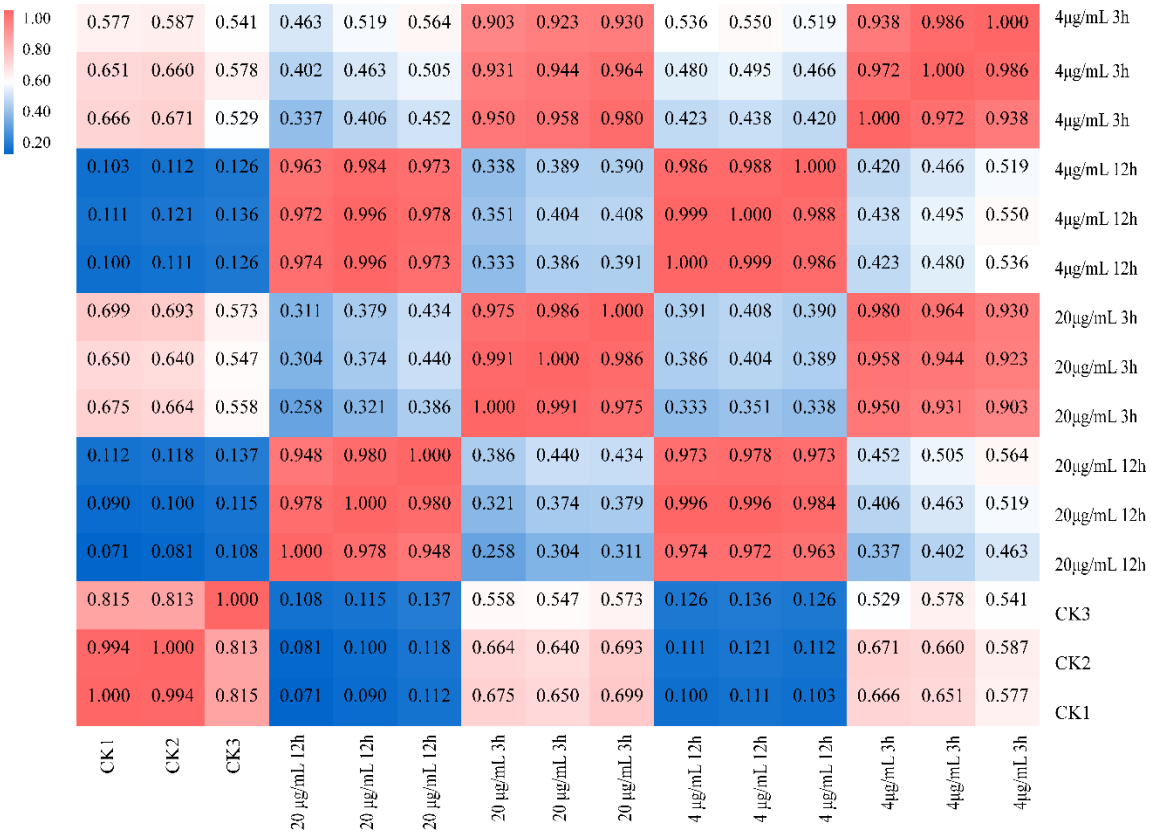

Figure S1. Correlation heat map between the control group and Myco treatment group.