

Table S1. Comparisons of the average food intake, water intake, and body weight gains before and after intervention among different animal groups

Groups	Before intervention (days 0-14)	After intervention (days 15-25)
Daily food intake (g/day)		
Normal control	25.19 ± 0.42 ^a	25.43 ± 0.58 ^a
Negative control	24.12 ± 0.13 ^a	22.37 ± 1.32 ^a
BC	25.84 ± 0.70 ^a	22.05 ± 1.23 ^b
FOS	24.21 ± 0.45 ^a	22.39 ± 0.48 ^b
FB	24.68 ± 1.02 ^a	21.56 ± 0.70 ^b
GOS	25.13 ± 1.12 ^a	22.49 ± 0.39 ^b
GB	25.38 ± 0.60 ^a	22.54 ± 0.85 ^b
Daily water intake (g/day)		
Normal control	38.24 ± 1.04 ^a	37.70 ± 0.79 ^a
Negative control	34.38 ± 3.56 ^a	34.98 ± 1.40 ^a
BC	34.47 ± 1.02 ^a	33.42 ± 0.57 ^a
FOS	33.57 ± 0.80 ^a	34.07 ± 0.99 ^a
FB	32.02 ± 2.18 ^a	31.89 ± 2.87 ^a
GOS	37.23 ± 1.48 ^a	37.05 ± 2.12 ^a
GB	34.53 ± 0.89 ^a	32.83 ± 1.97 ^a
Body weight gains (g/day)		
Normal control	2.69 ± 1.07 ^a	2.73 ± 1.03 ^a
Negative control	2.61 ± 0.57 ^a	1.60 ± 0.78 ^b
BC	2.48 ± 0.62 ^a	1.59 ± 0.68 ^b
FOS	2.49 ± 0.47 ^a	1.54 ± 0.34 ^b
FB	2.49 ± 0.76 ^a	1.64 ± 0.25 ^b
GOS	2.32 ± 0.42 ^a	1.50 ± 0.32 ^b
GB	2.51 ± 0.55 ^a	2.10 ± 0.36 ^a

^{a-b} Values (mean ± SD, n = 6) with different superscripts in the same row significantly different ($p < 0.05$).

Table S2A. The concentrations of acetic acid ($\mu\text{mol/g}$) in fecal samples collected at different time points

Groups	Day 14 (Before antibiotic intervention)	Day 19 (After <i>Salmonella</i> infection)	Day 25 (Recovery period)
Normal control	53.8 \pm 11.7 ^{aA}	65.5 \pm 20.4 ^{cA}	49.6 \pm 10.0 ^{aA}
Negative control	59.3 \pm 10.4 ^{aB}	30.1 \pm 10.4 ^{aA}	59.9 \pm 20.2 ^{abB}
BC	114.3 \pm 16.0 ^{cC}	52.9 \pm 9.6 ^{bcA}	76.6 \pm 12.0 ^{bcB}
FOS	98.9 \pm 12.1 ^{bcC}	37.6 \pm 8.9 ^{abA}	77.1 \pm 11.7 ^{bcB}
GOS	101.4 \pm 6.1 ^{bcB}	48.2 \pm 17.2 ^{abcA}	98.3 \pm 22.4 ^{cB}
FB	100.5 \pm 4.8 ^{bcB}	42.9 \pm 18.4 ^{abA}	85.4 \pm 26.4 ^{cB}
GB	133.0 \pm 14.5 ^{dB}	62.5 \pm 9.6 ^{cA}	122.3 \pm 14.0 ^{dB}

^{a-d} Different lower-case superscripts in the same column indicate significant differences among different groups, $p < 0.05$.

^{A-C} Different capital superscripts in the same row indicate significant differences within the same group, $p < 0.05$.

Table S2B. The concentrations of propionic acid ($\mu\text{mol/g}$) in fecal samples collected at different time points

Groups	Day 14 (Before antibiotic intervention)	Day 19 (After <i>Salmonella</i> infection)	Day 25 (Recovery period)
Normal control	22.5 \pm 4.8 ^{aA}	29.4 \pm 15.5 ^{abA}	17.5 \pm 5.5 ^{aA}
Negative control	28.3 \pm 5.8 ^{aA}	16.7 \pm 12.1 ^{abA}	21.8 \pm 11.4 ^{aA}
BC	49.1 \pm 10.7 ^{dA}	33.7 \pm 17.1 ^{bA}	36.3 \pm 5.9 ^{bA}
FOS	40.9 \pm 7.0 ^{bcdAB}	53.5 \pm 19.3 ^{cB}	26.7 \pm 6.2 ^{abA}
GOS	36.6 \pm 2.1 ^{bB}	12.4 \pm 8.7 ^{aA}	35.4 \pm 16.7 ^{bB}
FB	40.0 \pm 2.3 ^{bcB}	18.8 \pm 2.6 ^{abA}	38.2 \pm 1.4 ^{bB}
GB	46.6 \pm 10.6 ^{cdB}	55.9 \pm 18.2 ^{cB}	26.1 \pm 13.1 ^{abA}

^{a-d} Different lower-case superscripts in the same column indicate significant differences among different groups, $p < 0.05$.

^{A-B} Different capital superscripts in the same row indicate significant differences within the same group, $p < 0.05$.

Table S2C. The concentrations of butyric acid ($\mu\text{mol/g}$) in fecal samples collected at different time points

Groups	Day 14 (Before antibiotic intervention)	Day 19 (After <i>Salmonella</i> infection)	Day 25 (Recovery period)
Normal control	$38.7 \pm 18.4^{\text{bcA}}$	$42.9 \pm 18.0^{\text{bA}}$	$35.3 \pm 10.2^{\text{bA}}$
Negative control	$36.5 \pm 18.3^{\text{abcB}}$	$5.6 \pm 2.2^{\text{aA}}$	$13.1 \pm 6.8^{\text{aA}}$
BC	$26.2 \pm 2.5^{\text{abB}}$	$5.6 \pm 2.8^{\text{aA}}$	$32.5 \pm 10.9^{\text{bB}}$
FOS	$30.2 \pm 18.5^{\text{abB}}$	$3.7 \pm 0.7^{\text{aA}}$	$19.4 \pm 8.9^{\text{aB}}$
GOS	$20.6 \pm 5.7^{\text{aB}}$	$9.3 \pm 3.2^{\text{aA}}$	$13.7 \pm 4.0^{\text{aA}}$
FB	$82.5 \pm 11.1^{\text{dC}}$	$5.4 \pm 4.4^{\text{aA}}$	$22.0 \pm 8.6^{\text{aB}}$
GB	$52.8 \pm 12.6^{\text{cC}}$	$3.1 \pm 1.0^{\text{aA}}$	$33.8 \pm 2.6^{\text{bB}}$

^{a-d} Different lower-case superscripts in the same column indicate significant differences among different groups, $p < 0.05$.

^{A-C} Different capital superscripts in the same row indicate significant differences within the same group, $p < 0.05$.

Table S3. Primers used for 16S rRNA gene analysis

Primer	Sequence	Reference
fD1	5'-AGAGTTTGATCCTGGCTCAG-3'	[1]
rP1	5'-ACGGTTACCTTGTTACGACTT-3'	[1]

Figure S1. Agarose gel electrophoresis of the amplified target of 16S rRNA gene. (A) *Bacillus coagulans* BACO-17, (B) *Salmonella enterica* subsp. *enterica* BCRC 10747.

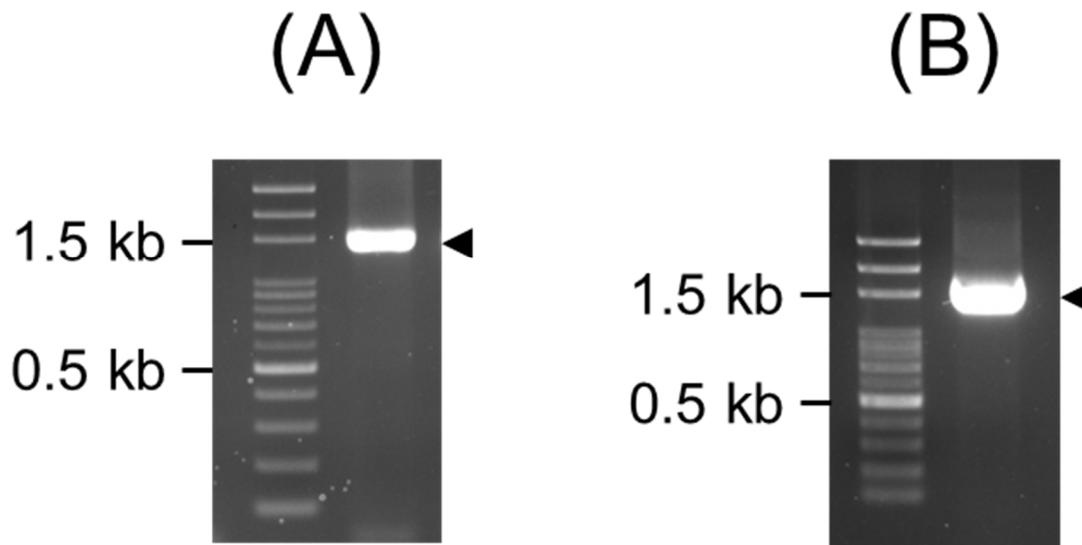


Figure S2. Partial sequence of 16S rRNA gene and top listed BLAST results. (A) *Bacillus coagulans* BACO-17, (B) *Salmonella enterica* subsp. *enterica* BCRC 10747.

(A)

GCTTGCTTTTAAAAGGTTAGCGGCGGACGGGTGAGTAACACGTGGGCAACCTGC
 CTGTAAGATCGGGATAACGCCGGGAAACCGGGGCTAATACCGGATAGTTTTTTC
 CTCCGCATGGAGGAAAAAGGAAAGACGGCTTTTGTCTGTCACCTACAGATGGGCC
 CGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCTCACCAAGGCAACGATGCGTA
 GCCGACCTGAGAGGGTGATCGGCCACATTGGGACTGAGACACGGCCAAACTCC
 TACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCA
 ACGCCGCGTGAGTGAAGAAGGCCTTCGGGTCGTA AAAACTCTGTTGCCGGGGAAG
 AACAAGTGCCGTTGAAACAGGGCGGCGCCTTGACGGTACCCGGCCAGAAAGCCA
 CGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCG
 GAATTATTGGGCGTAAAGCGCGCGCAGGCGGCTTCTTAAGTCTGATGTGAAATCT
 TGCGGCTCAACCGCAAGCGGTCATTGGAAACTGGGAGGCTTGAGTGCAGAAGAG
 GAGAGTGGAATCCACGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAACACC
 AGTGCGAAAGGCGGCTCTCTGGTCTGTA ACTGACGCTGAGGCGCGAAAGCGT

Sequences producing significant alignments									
Download Select columns Show 100									
select all 100 sequences selected									
GenBank Graphics Distance tree of results MSA Viewer									
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession	
Weizmannia coagulans strain 1906 16S ribosomal RNA gene, partial sequence	Weizmannia coagulans	1295	1295	100%	0.0	100.00%	1459	MT626077.1	
Weizmannia coagulans strain 3326 16S ribosomal RNA gene, partial sequence	Weizmannia coagulans	1295	1295	100%	0.0	100.00%	1461	MT613620.1	
Weizmannia coagulans strain 3247 16S ribosomal RNA gene, partial sequence	Weizmannia coagulans	1295	1295	100%	0.0	100.00%	1460	MT613576.1	
Weizmannia coagulans strain 2854 16S ribosomal RNA gene, partial sequence	Weizmannia coagulans	1295	1295	100%	0.0	100.00%	1458	MT611821.1	
Weizmannia coagulans strain 2538 16S ribosomal RNA gene, partial sequence	Weizmannia coagulans	1295	1295	100%	0.0	100.00%	1428	MT611570.1	
Weizmannia coagulans strain 2190 16S ribosomal RNA gene, partial sequence	Weizmannia coagulans	1295	1295	100%	0.0	100.00%	1456	MT604689.1	
Weizmannia coagulans strain 2102 16S ribosomal RNA gene, partial sequence	Weizmannia coagulans	1295	1295	100%	0.0	100.00%	1459	MT604650.1	
Weizmannia coagulans strain 2021 16S ribosomal RNA gene, partial sequence	Weizmannia coagulans	1295	1295	100%	0.0	100.00%	1462	MT604614.1	
Weizmannia coagulans strain 2019 16S ribosomal RNA gene, partial sequence	Weizmannia coagulans	1295	1295	100%	0.0	100.00%	1457	MT604612.1	
Weizmannia coagulans strain 1986 16S ribosomal RNA gene, partial sequence	Weizmannia coagulans	1295	1295	100%	0.0	100.00%	1459	MT597790.1	

note: *Weizmannia coagulans* is the new name of *Bacillus coagulans* [2].

(B)

TGCAGTCGAACGGTAACAGGAAGCAGCTTGCTGCTTCGCTGACGAGTGGCGGAC
 GGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACG
 GTGGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCT
 TGCCATCAGATGTGCCAGATGGGATTAGCTTGTGGTGGAGGTAACGGCTCACCA
 AGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGA ACTGAGA

CACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGC
AAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTA
CTTTCAGCGGGGAGGAAGGTGTTGTGGTTAATAACCGCAGCAATTGACGTTACCC
GCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTG
CAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTCAAGT
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TGAGTCTTGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGA
TCTGGAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAG
GTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTA
AACGATGTCTACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCG
TTAAGTAGACCGCC

Sequences producing significant alignments Download Select columns Show 100

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	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Salmonella enterica subsp. enterica strain JK.KSWS8 16S ribosomal...	Salmonell...	1528	1528	100%	0.0	100.00%	1408	MN192076.1
<input checked="" type="checkbox"/>	Salmonella enterica subsp. enterica strain JK.KSWS6 16S ribosomal...	Salmonell...	1528	1528	100%	0.0	100.00%	1408	MN192073.1
<input checked="" type="checkbox"/>	Salmonella enterica subsp. enterica serovar Enteritidis strain RM_AS...	Salmonell...	1528	1528	100%	0.0	100.00%	1433	MK809230.1
<input checked="" type="checkbox"/>	Salmonella enterica subsp. enterica serovar Enteritidis strain RM_AS...	Salmonell...	1528	1528	100%	0.0	100.00%	1432	MK809229.1
<input checked="" type="checkbox"/>	Salmonella enterica subsp. enterica serovar Enteritidis strain RM_AS...	Salmonell...	1528	1528	100%	0.0	100.00%	1431	MK809228.1
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<input checked="" type="checkbox"/>	Salmonella enterica subsp. enterica serovar Indiana strain RM_AST...	Salmonell...	1528	1528	100%	0.0	100.00%	1397	MK809215.1
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<input checked="" type="checkbox"/>	Salmonella enterica subsp. enterica serovar Indiana strain RM_AST...	Salmonell...	1528	1528	100%	0.0	100.00%	1427	MK809211.1

References

1. Weisburg, W. G.; Barns, S. M.; Pelletier, D. A.; Lane, D. J. 16S ribosomal DNA amplification for phylogenetic study. *J. Bacteriol.* **1991**, *173*, 697-703, doi: 10.1128/jb.173.2.697-703.1991.
2. Gupta, R. S.; Patel, S.; Saini, N.; Chen, S. Robust demarcation of 17 distinct *Bacillus* species clades, proposed as novel *Bacillaceae* genera, by phylogenomics and comparative genomic analyses: Description of *Robertmurraya kyonggiensis* sp. nov. and proposal for an emended genus *Bacillus* limiting it only to the members of the Subtilis and Cereus clades of species. *Int. J. Syst. Evol. Microbiol.* **2020**, *70*, 5753-5798, doi: 10.1099/ijsem.0.004475.