Supplement Materials-Linarin ameliorates dextran sulfate sodium-induced colitis in C57BL/6J mice via the improvement of intestinal barrier, suppression of inflammatory responses and modulation of gut microbiota

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Table S1 Primer sequences used for QRT-PCR analysis

Gene	Forward primer (5′-3′)	Reverse primer (5′-3′)	NCBI reference sequence
GAPDH	AGGTCGGTGTGAACGGATTTG	TGTAGACCATGTAGTTGAGGTCA	NM_001289726.1
Muc2	GCTGACGAGTGGTTGGTGAATG	GATGAGGTGGCAGACAGGAGAC	NM_023566.4
Occludin	ACGGACCCTGACCACTATGA	TCAGCAGCAGCCATGTACTC	NM_001360538.1
ZO-1	GCGAACAGAAGGAGCGAGAAGAG	GCTTTGCGGGCTGACTGGAG	NM_009386.2
Claudin-1	GCTGGGTTTCATCCTGGCTTCTC	CCTGAGCGGTCACGATGTTGTC	NM_016674.4
IL-1β	ACTCATTGTGGCTGTGGAGA	TTGTTCATCTCGGAGCCTGT	NM_008361.4
TNF-α	GCGACGTGGAACTGGCAGAAG	GCCACAAGCAGGAATGAGAAGAGG	NM_001278601.1
IL-6	AGAGGAGACTTCACAGAGGATACC	AATCAGAATTGCCATTGCACAAC	NM_001314054.1
IFN-γ	CTGGAGGAACTGGCAAAAGGATGG	GACGCTTATGTTGTTGCTGATGGC	NM_008337.4
IL-10	TTCTTTCAAACAAAGGACCAGC	GCAACCCAAGTAACCCTTAAAG	NM_010548.2

**Table S2** Relative abundances of differential taxa based at the phylum level [A]

Bacterial taxa information	NC	DSS	Lin-H
Firmicutes	37.616 ± 10.772 [a]	42.345 ± 9.379 [a]	32.325 ± 14.229 [a]
Bacteroidota	33.379 ± 5.896 [a]	29.359 ± 10.431 [a]	31.129 ± 12.406 [a]
Verrucomicrobiota	16.415 ± 14.884 [a]	22.779 ± 2.915 [a]	21.531 ± 7.052 [a]
Proteobacteria	9.527 ± 10.271 [a]	3.443 ± 2.518 [a]	12.805 ± 13.308 [a]
Desulfobacterota	1.457 ± 0.592 [a]	0.873 ± 0.742 [a]	0.892 ± 1.085 [a]
Campylobacterota	0.540 ± 0.577 [a]	0.419 ± 0.421 [a]	0.371 ± 0.274 [a]
Firmicutes/Bacteroidota ratio	100 ± 33.635 [a]	141.152 ± 60.06 [a]	117.966 ± 97.983 [a]

[A] Different lowercase letters in each line represent significant differences ($p < 0.05$).

Table S3 Relative abundances of differential taxa based at the genus level [A]

Bacterial taxa information	NC	DSS	Lin-H
Akkermansia	16.401 ± 14.897 [a]	22.777 ± 2.912 [a]	21.512 ± 7.057 [a]
Muribaculaceae_norank	21.563 ± 9.571 [a]	9.184 ± 3.94 [b]	6.800 ± 6.519 [b]
Bacteroides	6.761 ± 8.504 [a]	10.783 ± 6.689 [a]	14.510 ± 17.633 [a]
Lachnospiraceae NK4A136 group	5.869 ± 6.369 [a]	6.656 ± 3.402 [a]	2.618 ± 3.193 [a]
Clostridia UCG-014_norank	1.091 ± 1.332 [b]	10.910 ± 9.199 [a]	1.548 ± 1.41 [b]
Blautia	7.956 ± 9.735 [a]	0.401 ± 0.266 [a]	3.531 ± 5.429 [a]
Escherichia-Shigella	0.202 ± 0.248 [b]	1.348 ± 1.853 [b]	7.944 ± 9.673 [a]
[Ruminococcus] torques group	0.461 ± 0.593 [b]	4.330 ± 1.198 [a]	3.257 ± 3.424 [a]
Lachnospiraceae_uncultured	4.817 ± 2.314 [a]	1.279 ± 1.309 [b]	1.874 ± 1.519 [b]
Dubosiella	1.462 ± 1.948 [a]	4.048 ± 4.016 [a]	1.061 ± 1.447 [a]
Prevotellaceae UCG-001	0.151 ± 0.218 [b]	3.888 ± 2.855 [a]	2.210 ± 3.062 [ab]
Rikenellaceae RC9 gut group	0.019 ± 0.015 [a]	2.238 ± 1.828 [a]	3.600 ± 5.917 [a]
Romboutsia	0.007 ± 0.013 [b]	2.206 ± 1.440 [ab]	3.644 ± 3.525 [a]
Parabacteroides	2.625 ± 3.196 [a]	0.732 ± 0.827 [a]	1.904 ± 2.829 [a]
Parasutterella	1.828 ± 1.443 [a]	1.763 ± 0.975 [a]	1.077 ± 1.336 [a]
Turicibacter	0.030 ± 0.038 [b]	2.243 ± 1.962 [a]	2.352 ± 2.024 [a]
Ligilactobacillus	1.534 ± 1.638 [a]	0.586 ± 0.504 [a]	2.389 ± 3.083 [a]
Klebsiella	2.298 ± 3.105 [a]	0.025 ± 0.028 [a]	1.351 ± 2.070 [a]
Citrobacter	2.597 ± 3.400 [a]	0.002 ± 0.006 [a]	0.938 ± 2.168 [a]
RF39_norank	0.287 ± 0.525 [a]	1.138 ± 1.823 [a]	1.803 ± 2.589 [a]
Desulfovibrio	1.297 ± 0.461 [a]	0.825 ± 0.712 [a]	0.843 ± 1.074 [a]
Lachnoclostridium	1.457 ± 0.778 [a]	0.202 ± 0.095 [b]	0.253 ± 0.255 [b]
Paraprevotella	0.005 ± 0.012 [b]	0.232 ± 0.432 [ab]	1.650 ± 2.155 [a]
Eubacterium	0.009 ± 0.016 [a]	0.000 ± 0.000 [a]	0.005 ± 0.008 [a]
Faecalibaculum	1.485 ± 1.482 [a]	0.290 ± 0.334 [b]	0.023 ± 0.029 [b]
Lactobacillus	1.443 ± 1.504 [a]	0.088 ± 0.088 [b]	0.199 ± 0.364 [b]
Morganella	1.617 ± 2.027 [a]	0.000 ± 0.000 [b]	0.021 ± 0.036 [b]
Alistipes	0.102 ± 0.098 [b]	1.212 ± 0.297 [a]	0.310 ± 0.328 [b]
Erysipelatoclostridium	0.176 ± 0.151 [b]	0.204 ± 0.125 [b]	1.179 ± 1.111[a]
Alloprevotella	1.263 ± 0.807 [a]	0.000 ± 0.000 [b]	0.000 ± 0.000 [b]
Rikenella	0.060 ± 0.069 [b]	1.059 ± 0.732 [a]	0.074 ± 0.099 [b]
Roseburia	1.006 ± 1.119 [a]	0.000 ± 0.000 [b]	0.007 ± 0.013 [b]

[A] Different lowercase letters in each line represent significant differences ($p < 0.05$).
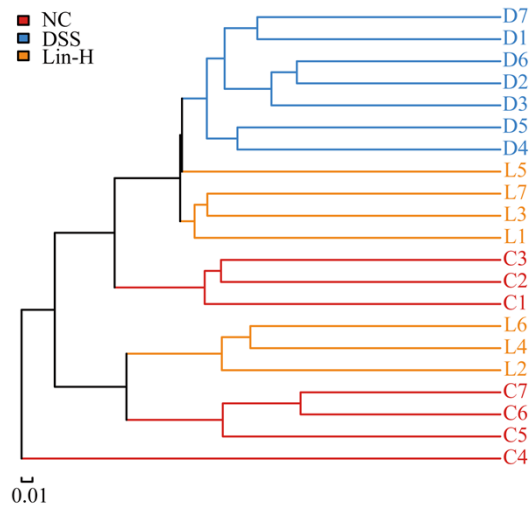
Fig. S1 Effect of linarin on the gut microbiota structure in DSS-treated mice. Samples cluster tree based on Bray-Curtis distance matrix.