

Supplementary tables

Table S1 The composition of experimental diet

D0-30			
Ingredient, %	CON	MCC	INU
Corn	40.41	40.41	40.41
Extruded soybean	6.00	6.00	6.00
Soybean meal	19.80	19.80	19.80
Fish meal	5.00	5.00	5.00
Whey powder	14.80	14.80	14.80
Soybean oil	1.15	1.15	1.15
Calcium phosphate	0.50	0.50	0.50
Limestone	1.03	1.03	1.03
Sodium chloride	0.50	0.50	0.50
DL-Methionine	0.10	0.10	0.10
L-lysine	0.40	0.40	0.40
L-Threonine	0.11	0.11	0.11
Sucrose	2.50	2.50	2.50
Glucose	2.50	2.50	2.50
Premix ¹	0.20	0.20	0.20
Cornstarch	5.00	-	-
Microcrystalline cellulose	-	5.00	-
Inulin	-	-	5.00
D31-72			
Ingredient, %	CON	MCC	INU
Corn	58.32	58.32	58.32
Soybean meal	28.47	28.47	28.47
Soybean oil	4.81	4.81	4.81
Calcium phosphate	1.37	1.37	1.37
Limestone	0.68	0.68	0.68
Sodium chloride	0.30	0.30	0.30
L-lysine	0.05	0.05	0.05
Premix ¹	1.00	1.00	1.00
Cornstarch	5.00	-	-
Microcrystalline cellulose	-	5.00	-
Inulin	-	-	5.00

1. All diets were formulated at Institute of Animal science, Chinese Academy of Agricultural Sciences.
2. Vitamin and mineral premixes were supplied per kg of diet as-fed: Mn ($\text{MnSO}_4 \cdot \text{H}_2\text{O}$), 25.0 mg; Zn (ZnSO_4), 100.0 mg; Cu ($\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$), 50.0 mg; Se (Na_2SeO_3), 0.15 mg; Fe (FeSO_4), 80.0 mg; I (KI), 0.5 mg; choline, 600.0 mg; vitamin A (all-trans retinyl acetate), 2.84 mg; vitamin D3, 0.22 mg; α -tocopherol, 40 mg; phylloquinone, 2.0 mg; thiamin, 1.0 mg; riboflavin, 5.0 mg; nicotinic acid, 15.0 mg; pantothenic acid, 15.0 mg; pyridoxine, 2.0 mg; vitamin B12, 0.025 mg; folic acid, 2 mg; biotin, 0.2 mg.

Table S2 Primer sequences used for qPCR

Gene	Accession number	Primer sequences (5'-3')	Product size/bp
<i>β-actin</i>	XM_003357928.4	F: GCGTAGCATTTGCTGCATGA R: GCGTGTGTGTAAGTAGGGGT	252
<i>GAPDH</i>	NM_001206359.1	F: CGTGTTCGGTTGTGGATCTGA R: TGACGAAGTGGTCGTTGAGG	209
<i>ZO-1</i>	XM_005659811.1	F: CTCCAGGCCCTTACCTTTCG R: GGGGTAGGGGTCCTTCCTAT	248
<i>Claudin-2</i>	NM_001161638.1	F: GCATCATTTCCCTCCCTGTT R: TCTTGGCTTTGGGTGGTT	156
<i>Occludin</i>	NM_001163647.2	F: CAGGTGCACCCTCCAGATTG R: TATGTCGTTGCTGGGTGCAT	168
<i>MUC2</i>	XM_021082584.1	F: CGCATGGATGGCTGTTTCTG R: ATTGCTCGCAGTTGTTGGTG	145
<i>TFF3</i>	NM_001243483.1	F: GGGAAAAAGCTCCCTGGCTA R: TCAAGGGTCACGGAAAGTGG	86
<i>GAL3ST1</i>	XM_005670826.3	F: AGGGACATGCCACCTGCTAT R: CACTGGGAAACAGGAACGCT	120
<i>GAL3ST2</i>	XM_021074665.1	F: GAAAGTCATGCCCAACGACA C R: GGAGGACTCGAGCTGGAAGA	70
<i>ST3Gal1</i>	XM_021088744.1	F: GCCTCAGATAGACAGCCACG R: GGGTACACGAAATGGTGGGT	105
<i>ST3Gal3</i>	XM_021093478.1	F: TGTCCCTCGCCAACAAGTCTC R:	130

<i>ST6GalNAC4</i>	XM_021080865.1	GGGGTAGGTGATGCGTAGTG	
		F: CATGGCAACCTTTGCACTCT	86
		R:	
		GACTCAGAGGTGGGACGAAC	

Table S3 Bacterial genera in ileal and colonic mucosa of pigs fed with MCC or INU diet

Taxa			
Phylum	Genus	Log ₂ FC	P value
Ileal mucosa			
MCC diet			
<i>Bacteroidetes</i>	<i>Bacteroides</i>	-5.8614	0.041
	<i>Prevotella_9</i>	1.7736	0.013
<i>Chlamydiae</i>	<i>Chlamydia</i>	-4.5537	<0.01
<i>Deferribacteres</i>	<i>Mucispirillum</i>	3.6142	<0.01
<i>Firmicutes</i>	<i>Fusicatenibacter</i>	-2.2621	0.015
	<i>Lactobacillus</i>	-1.3843	0.023
	<i>Ruminiclostridium_6</i>	-1.8962	0.049
	<i>Lachnospiraceae_AC2044_group</i>	5.2631	<0.01
	<i>Selenomonas_1</i>	4.014	0.014
<i>Proteobacteria</i>	<i>Lawsonia</i>	11.318	<0.01
	<i>Acinetobacter</i>	3.2482	0.019
	<i>Thalassospira</i>	2.6389	0.036
INU diet			
<i>Actinobacteria</i>	<i>Atopobium</i>	4.2958	0.010
<i>Bacteroidetes</i>	<i>Prevotellaceae_UCG_001</i>	-7.4012	0.014
	<i>Prevotella_1</i>	-1.8247	0.018
	<i>Prevotella_7</i>	3.1296	<0.01
	<i>Prevotella_9</i>	2.0182	0.011
<i>Firmicutes</i>	<i>Ruminococcus_2</i>	-2.2902	0.019
	<i>Ruminococcaceae_UCG_004</i>	-3.2884	0.035
	<i>Defluviitaleaceae_UCG_011</i>	-3.0018	0.042
	<i>Lachnospiraceae_UCG_005</i>	-2.7204	0.039
	<i>Coproccoccus_1</i>	-2.2925	0.042
	<i>Sharpea</i>	6.6057	<0.01
	<i>Erysipelotrichaceae_UCG_006</i>	4.4121	<0.01
	<i>Mitsuokella</i>	3.667	<0.01
	<i>Syntrophococcus</i>	5.279	<0.01
	<i>Pseudoramibacter</i>	5.2121	<0.01
	<i>Dialister</i>	2.9464	0.016
	<i>Megamonas</i>	4.6332	0.022
	<i>Solobacterium</i>	2.0059	0.043
	<i>Ruminiclostridium</i>	1.8036	0.046
	<i>Holdemanella</i>	1.8435	0.048
<i>Proteobacteria</i>	<i>Moraxella</i>	3.365	<0.01
	<i>Acinetobacter</i>	3.1534	0.010
	<i>Lawsonia</i>	4.3761	0.011
<i>Synergistetes</i>	<i>Pyramidobacter</i>	-3.1846	0.022

Colonic mucosa**MCC diet**

<i>Acidobacteria</i>	<i>Blastocatella</i>	-3.7745	0.045
	<i>norank</i>	-2.9585	<0.01
	<i>Corynebacterium_1</i>	-7.4136	<0.01
	<i>Propionibacterium</i>	-7.3891	<0.01
	<i>Rothia</i>	-5.5015	0.001
	<i>Kocuria</i>	-5.3835	<0.01
	<i>Lysinimonas</i>	-5.3829	<0.01
	<i>Mycobacterium</i>	-4.2995	0.032
	<i>Collinsella</i>	-2.9083	<0.01
<i>Bacteroidetes</i>	<i>Barnesiella</i>	-6.1607	<0.01
	<i>Bacteroides</i>	-4.8426	<0.01
	<i>Myroides</i>	-4.1455	<0.01
	<i>dgA_11_gut_group</i>	-2.933	0.025
	<i>Empedobacter</i>	1.4229	0.010
	<i>Chryseobacterium</i>	1.7878	<0.01
	<i>Flavobacterium</i>	1.9496	<0.01
	<i>Prevotella_7</i>	3.1875	0.027
<i>Cyanobacteria</i>	<i>Synechococcus</i>	-4.0551	0.024
<i>Firmicutes</i>	<i>Candidatus_Arthromitus</i>	-6.258	0.021
	<i>Exiguobacterium</i>	-4.7811	<0.01
	<i>Staphylococcus</i>	-4.1305	<0.01
	<i>Hungatella</i>	-3.8685	0.045
	<i>Tyzzarella_3</i>	-3.4872	0.016
	<i>Kurthia</i>	-3.2541	<0.01
	<i>Lachnoclostridium</i>	-3.0492	0.014
	<i>Eubacterium_hallii_group</i>	-2.7633	0.030
	<i>Lachnospiraceae_NK4A136_group</i>	-2.2061	<0.01
	<i>Christensenellaceae_R_7_group</i>	-2.1478	0.022
	<i>Brochothrix</i>	1.4802	0.016
	<i>Bacillus</i>	1.6135	<0.01
	<i>Lactococcus</i>	1.6473	<0.01
	<i>Carnobacterium</i>	1.7454	0.049
	<i>Lachnospira</i>	1.9212	0.015
	<i>Fusicatenibacter</i>	2.2066	0.010
	<i>Veillonella</i>	3.3763	<0.01
	<i>Streptococcus</i>	3.9855	<0.01
	<i>Ruminiclostridium_5</i>	5.2682	0.025
<i>Fusobacteria</i>	<i>Cetobacterium</i>	-8.0038	<0.01
<i>Planctomycetes</i>	<i>SM1A02</i>	-5.4344	0.024
<i>Proteobacteria</i>	<i>Aquitalea</i>	-7.5957	<0.01
	<i>Woodsholea</i>	-6.7507	<0.01

	<i>Hyphomicrobium</i>	-6.3061	<0.01
	<i>Pseudoalteromonas</i>	-6.0137	<0.01
	<i>Thauera</i>	-5.7683	<0.01
	<i>Burkholderia</i>	-5.6992	<0.01
	<i>Pseudoxanthomonas</i>	-5.3414	<0.01
	<i>Ochrobactrum</i>	-5.0946	<0.01
	<i>Rhodobacter</i>	-5.0732	<0.01
	<i>Massilia</i>	-4.9998	<0.01
	<i>Colwellia</i>	-4.4116	0.014
	<i>Reyranella</i>	-4.3948	0.025
	<i>Cupriavidus</i>	-4.3877	<0.01
	<i>Mesorhizobium</i>	-3.8427	0.048
	<i>Methylobacterium</i>	-3.8292	<0.01
	<i>Bradyrhizobium</i>	-3.629	<0.01
	<i>Parasutterella</i>	-3.2834	0.044
	<i>Bosea</i>	1.6027	0.013
	<i>Psychrobacter</i>	1.6079	0.016
	<i>Aquabacterium</i>	1.6955	<0.01
	<i>Moraxella</i>	1.7111	<0.01
	<i>Brevundimonas</i>	1.7331	<0.01
	<i>Ralstonia</i>	1.7791	<0.01
	<i>Stenotrophomonas</i>	1.8698	<0.01
	<i>Dechloromonas</i>	1.9984	<0.01
	<i>Sphingopyxis</i>	2.0147	0.013
	<i>Janthinobacterium</i>	2.0924	<0.01
	<i>Pelomonas</i>	2.2155	<0.01
<i>Verrucomicrobia</i>	<i>Akkermansia</i>	5.7748	<0.01
INU diet			
<i>Acidobacteria</i>	<i>norank</i>	-1.5654	0.028
<i>Actinobacteria</i>	<i>Rothia</i>	-6.1491	<0.01
	<i>Corynebacterium_1</i>	-6.1223	<0.01
	<i>Propionibacterium</i>	-5.8889	<0.01
	<i>Alpinimonas</i>	-5.0183	0.025
	<i>Illumatobacter</i>	-3.9955	0.025
	<i>Kocuria</i>	-3.9499	<0.01
	<i>Collinsella</i>	-2.8262	0.016
<i>Bacteroidetes</i>	<i>Myroides</i>	-5.5596	<0.01
	<i>Barnesiella</i>	-5.3763	0.010
	<i>Prevotellaceae_Ga6A1_group</i>	-3.913	0.031
	<i>Bacteroides</i>	-3.7492	<0.01
	<i>Parabacteroides</i>	-2.7827	<0.01
	<i>Porphyromonas</i>	1.9053	0.023
	<i>Prevotella_7</i>	4.0051	<0.01
<i>Cyanobacteria</i>	<i>Synechococcus</i>	-3.3448	0.045

<i>Firmicutes</i>	<i>Exiguobacterium</i>	-5.2448	<0.01
	<i>Staphylococcus</i>	-4.1854	<0.01
	<i>Megamonas</i>	-4.046	<0.01
	<i>Anaerostipes</i>	-3.8444	0.011
	<i>Hungatella</i>	-2.9426	0.047
	<i>Kurthia</i>	-2.9051	<0.01
	<i>Lachnoclostridium</i>	-2.5287	0.015
	<i>Bacillus</i>	1.0384	0.021
	<i>Lactococcus</i>	1.2609	0.018
	<i>Dialister</i>	2.3513	0.019
	<i>Ruminiclostridium_5</i>	7.9737	<0.01
	<i>Ruminococcaceae_UCG_013</i>	-3.2432	0.011
	<i>Eubacterium_hallii_group</i>	-3.2192	0.028
	<i>Ruminococcus_2</i>	-1.8954	0.031
	<i>Faecalibacterium</i>	2.4745	0.012
<i>Fusobacteria</i>	<i>Cetobacterium</i>	-6.9853	<0.01
<i>Planctomycetes</i>	<i>SM1A02</i>	-5.4418	0.017
<i>Proteobacteria</i>	<i>Thauera</i>	-5.8882	<0.01
	<i>Hyphomicrobium</i>	-5.8528	<0.01
	<i>Woodsholea</i>	-5.5444	<0.01
	<i>Pseudoxanthomonas</i>	-5.4367	<0.01
	<i>Rhodobacter</i>	-5.2728	<0.01
	<i>Burkholderia</i>	-5.0607	<0.01
	<i>Pseudoalteromonas</i>	-4.5849	0.011
	<i>Reyranella</i>	-4.4826	0.013
	<i>Ochrobactrum</i>	-4.1809	<0.01
	<i>Colwellia</i>	-4.1588	0.022
	<i>Cupriavidus</i>	-3.9327	0.011
	<i>Methylobacterium</i>	-3.2248	<0.01
	<i>Moraxella</i>	1.2888	0.024
	<i>Sphingopyxis</i>	1.3166	0.033
	<i>Aquabacterium</i>	1.5067	<0.01
	<i>Stenotrophomonas</i>	1.5244	<0.01
	<i>Dechloromonas</i>	1.5645	0.018
	<i>Brevundimonas</i>	1.6023	<0.01
	<i>Helicobacter</i>	2.2149	0.044
	<i>Caulobacter</i>	2.6356	<0.01
	<i>Citrobacter</i>	3.2107	0.011
	<i>Parasutterella</i>	-4.3136	0.020
	<i>Aquitalea</i>	-7.589	<0.01
<i>Verrucomicrobia</i>	<i>Akkermansia</i>	-5.4732	<0.01

Supplementary information

Figure S1 Effects of DFs on the growth performance.

(A) Body weight, (B) ADG, ADFI, and (C) FCR of pigs. CON: control; MCC: microcrystalline cellulose; INU: inulin (n=6). ADG: average daily gain; ADFI: average daily feed intake; FCR: feed conversion ratio. Data are expressed as min to max.

Figure S2 Effects of DFs on bacterial community diversities in the ileum and colon of pigs.

Alpha diversity index of bacteria, include the (A and D) Chao1, (B and E) Shannon, and (C and F) Simpson in the ileum and colon. CON: control; MCC: microcrystalline cellulose; INU: inulin (n=6). Data are expressed as min to max. Groups with different letters are statistically significant ($P < 0.05$).

Figure S3 Effect of DFs administration on the ileal (A) and colonic (B) microbiome composition at the phylum level.