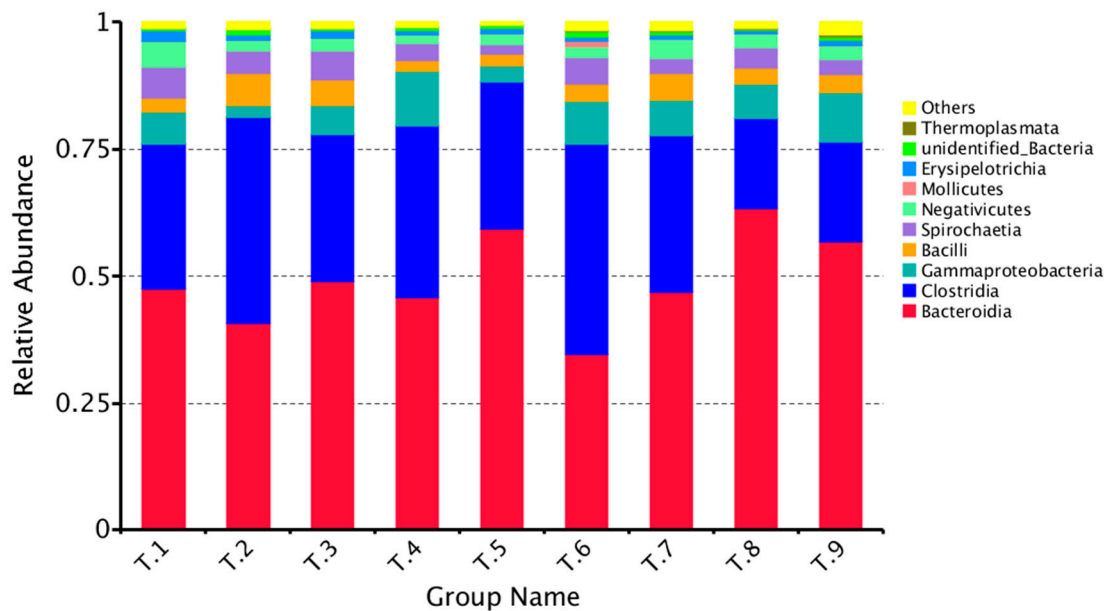
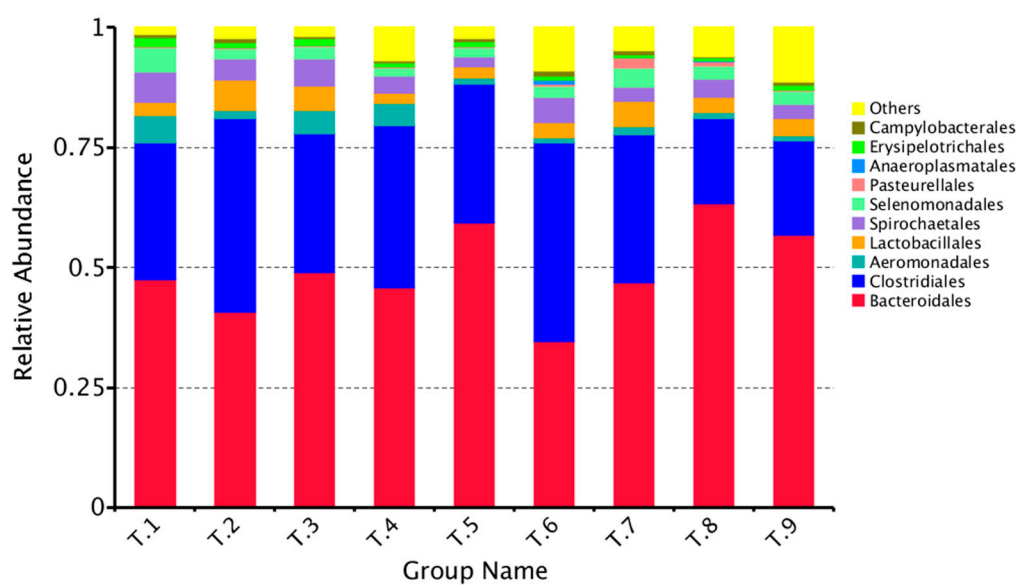


# Supplementary Material: The Optimal Combination of Dietary Starch, Non-Starch Polysaccharides and Mannan-Oligosaccharide Increases the Growth Performance and Improves Butyrate-Producing Bacteria of Weaned Pigs

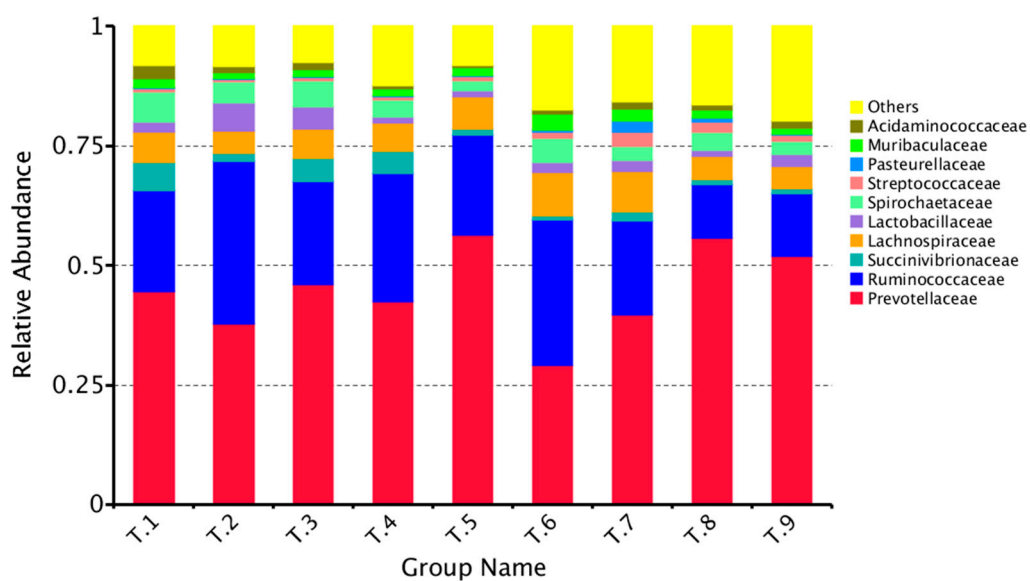
Hua Zhou, Bing Yu, Jun He, Xiangbing Mao, Ping Zheng, Jie Yu, Junqiu Luo, Yuheng Luo, Hui Yan and Daiwen Chen



**Figure S1.** Microbial community bar-plot of top 10 on the class level. The colonic digesta was used for 16S rRNA gene analysis.



**Figure S2.** Microbial community bar-plot of top 10 on the order level. The colonic digesta was used for 16S rRNA gene analysis.



**Figure S3.** Microbial community bar-plot of top 10 on the family level. The colonic digesta was used for 16S rRNA gene analysis.

**Table 1.** Effects of different combinations of starch, NSP and MOS on phyla level (top 10) in microbiota of weaned piglets based on16S rRNA gene.

Items	Different combinations of starch, NSP and MOS									SEM	<i>p</i> Values
	T1	T2	T3	T4	T5	T6	T7	T8	T9		
<i>Bacteroidetes</i>	0.4758 a,b,c,d	0.4079 c,d	0.4910 a,b,c,d	0.4578 b,c,d	0.5935 a,b	0.3473 d	0.4689 a,b,c,d	0.6334 a	0.5682 a,b,c	0.0376	<0.01
<i>Firmicutes</i>	0.3825 a,b,c	0.4777 a	0.3796 a,b,c	0.3846 a,b,c	0.3443 a,b,c	0.4791 a	0.4062 a,b	0.2446 c	0.2710 b,c	0.0346	<0.01
<i>Proteobacteria</i>	0.0681	0.0350	0.0633	0.1129	0.0368	0.0969	0.0807	0.0723	0.1076	0.0264	0.37
<i>Spirochaetes</i>	0.0631	0.0455	0.0556	0.0352	0.0200	0.0522	0.0300	0.0388	0.0278	0.0115	0.17
<i>Tenericutes</i>	0.0004	0.0002	0.0006	0.0003	0.0006	0.0091	0.0007	0.0005	0.0004	0.0029	0.41
<i>Cyanobacteria</i>	0.0075	0.0101	0.0073	0.0039	0.0027	0.0120	0.0043	0.0035	0.0149	0.0034	0.16
<i>Euryarchaeota</i>	0.0004	0.0009	0.0006	0.0009	0.0006	0.0012	0.0034	0.0020	0.0051	0.0013	0.19
<i>Fibrobacteres</i>	0.0003	0.0009	0.0009	0.0032	0.0006	0.0008	0.0028	0.0012	0.0025	0.0010	0.33
<i>Fusobacteria</i>	0.0000 b	0.0000 b	0.0000 b	0.0000 b	0.0000 b	0.0000 b	0.0007 b	0.0024 a	0.0009 b	0.0002 b	<0.01
<i>Actinobacteria</i>	0.0010	0.0007	0.0006	0.0004	0.0006	0.0005	0.0005	0.0003	0.0005	0.0002	0.26

NSP: non-starch polysaccharide; MOS: mannan-oligosaccharides. <sup>a-d</sup> Means within a row with different superscripts differ ( $p < 0.05$ ).

**Table S2.** Effects of different combinations of starch, NSP and MOS on class level (top 10) in microbiota of weaned piglets based on16S rRNA gene.

Items	Different combinations of starch, NSP and MOS									SEM	<i>p</i> Values
	T1	T2	T3	T4	T5	T6	T7	T8	T9		
<i>Bacteroidia</i>	0.4758 a,b,c,d	0.4079 c,d	0.4909 a,b,c,d	0.4578 b,c,d	0.5934 a,b	0.3472 d	0.4688 a,b,c,d	0.6334 a	0.5682 a,b,c	0.0376	<0.01
<i>Clostridia</i>	0.2844 a,b,c	0.4045 a	0.2875 a,b,c	0.3389 a,b	0.2895 a,b,c	0.4137 a	0.3084 a,b,c	0.1775 c	0.1952 b,c	0.0343	<0.01
<i>Gammaproteobacteria</i>	0.0621	0.0235	0.0558	0.1054	0.0298	0.0821	0.0654	0.0642	0.0918	0.0262	0.4254
<i>Bacilli</i>	0.0274	0.0622	0.0522	0.0208	0.0232	0.0332	0.0520	0.0324	0.0375	0.0113	0.1492
<i>Unidentified</i>	0.0631	0.0455	0.0556	0.0352	0.0201	0.0522	0.0300	0.0388	0.0278	0.0115	0.1769
<i>Spirochaetes</i>	0.0631	0.0455	0.0556	0.0352	0.0201	0.0522	0.0300	0.0388	0.0278	0.0115	0.1769
<i>Negativicutes</i>	0.0501 a	0.0212 b,c	0.0259 b,c	0.0167 c	0.0207 b,c	0.0228 b,c	0.0389 a,b	0.0282 b,c	0.0276 b,c	0.0044	<0.01

<i>Mollicutes</i>	0.0004	0.0002	0.0006	0.0003	0.0001	0.0091	0.0007	0.0005	0.0004	0.0028	0.4141
<i>Melainabacteria</i>	0.0075	0.0101	0.0073	0.0039	0.0027	0.0120	0.0043	0.0035	0.0149	0.0034	0.1652
<i>Erysipelotrichia</i>	0.0207 <sup>a</sup>	0.0098 <sup>a,b</sup>	0.0141 <sup>a,b</sup>	0.0081 <sup>b</sup>	0.0109 <sup>a,b</sup>	0.0095 <sup>a,b</sup>	0.0068 <sup>b</sup>	0.0065 <sup>b</sup>	0.0107 <sup>a,b</sup>	0.0025	<0.01
<i>Epsilonproteobacteria</i>	0.0045	0.0097	0.0049	0.0050	0.0047	0.0104	0.0068	0.0028	0.0065	0.0019	0.1229

NSP: non-starch polysaccharide; MOS: mannan-oligosaccharides. <sup>a-d</sup> Means within a row with different superscripts differ ( $p < 0.05$ ).

**Table S3.** Effects of different combinations of starch, NSP and MOS on order level (top 10) in microbiota of weaned piglets based on 16S rRNA gene.

Items	Different combinations of starch, NSP and MOS									SEM	<i>p</i> Values
	T1	T2	T3	T4	T5	T6	T7	T8	T9		
<i>Bacteroidales</i>	0.4755 <sup>a,b,c</sup>	0.4065 <sup>b,c</sup>	0.4902 <sup>a,b,c</sup>	0.4564 <sup>a,b,c</sup>	0.5929 <sup>a</sup>	0.3449 <sup>c</sup>	0.4663 <sup>a,b,c</sup>	0.6292 <sup>a</sup>	0.5583 <sup>a,b</sup>	0.0381	<0.01
<i>Clostridiales</i>	0.2843 <sup>a,b,c</sup>	0.4045 <sup>a</sup>	0.2875 <sup>a,b,c</sup>	0.3389 <sup>a,b</sup>	0.2895 <sup>a,b,c</sup>	0.4136 <sup>a</sup>	0.3083 <sup>a,b,c</sup>	0.1775 <sup>c</sup>	0.1951 <sup>b,c</sup>	0.0343	<0.01
<i>Aeromonadales</i>	0.0605	0.0220	0.0532	0.1025	0.0277	0.0779	0.0418	0.0548	0.0885	0.0262	0.4108
<i>Lactobacillales</i>	0.0274	0.0622	0.0522	0.0208	0.0232	0.0332	0.0520	0.0321	0.0370	0.0113	0.1488
<i>Spirochaetales</i>	0.0631	0.0455	0.0556	0.0352	0.0201	0.0522	0.0300	0.0388	0.0278	0.0115	0.1769
<i>Selenomonadales</i>	0.0501 <sup>a</sup>	0.0212 <sup>b,c</sup>	0.0259 <sup>b,c</sup>	0.0167 <sup>c</sup>	0.0207 <sup>b,c</sup>	0.0228 <sup>b,c</sup>	0.0389 <sup>a,b</sup>	0.0282 <sup>b,c</sup>	0.0276 <sup>b,c</sup>	0.0044	<0.01
<i>Pasteurellales</i>	0.0013	0.0011	0.0022	0.0023	0.0018	0.0035	0.0220	0.0084	0.0026	0.0047	0.0617
<i>Anaeroplasmatales</i>	0.0001	0.0000	0.0003	0.0002	0.0000	0.0088	0.0004	0.0001	0.0001	0.0028	0.4220
<i>Gastranaerophilales</i>	0.0075	0.0101	0.0073	0.0039	0.0027	0.0120	0.0043	0.0035	0.0149	0.0034	0.1652
<i>Erysipelotrichales</i>	0.0207 <sup>a</sup>	0.0098 <sup>a,b</sup>	0.0141 <sup>a,b</sup>	0.0081 <sup>b</sup>	0.0109 <sup>a,b</sup>	0.0095 <sup>a,b</sup>	0.0068 <sup>b</sup>	0.0065 <sup>b</sup>	0.0107 <sup>a,b</sup>	0.0025	<0.01

NSP: non-starch polysaccharide; MOS: mannan-oligosaccharides. <sup>a-c</sup> Means within a row with different superscripts differ ( $p < 0.05$ ).

**Table S4.** Effects of different combinations of starch, NSP and MOS on family level (top 10) in microbiota of weaned piglets based on 16S rRNA gene.

Items	Different combinations of starch, NSP and MOS									SEM	<i>p</i> Values
	T1	T2	T3	T4	T5	T6	T7	T8	T9		
<i>Prevotellaceae</i>	0.4450 <sup>a,b</sup>	0.3761 <sup>a,b</sup>	0.4590 <sup>a,b</sup>	0.4248 <sup>a,b</sup>	0.5617 <sup>a</sup>	0.2902 <sup>b</sup>	0.3975 <sup>a,b</sup>	0.5570 <sup>a</sup>	0.5190 <sup>a</sup>	0.0419	<0.01
<i>Ruminococcaceae</i>	0.2101 <sup>a,b,c</sup>	0.3422 <sup>a</sup>	0.2146 <sup>a,b,c</sup>	0.2663 <sup>a,b</sup>	0.2092 <sup>a,b,c</sup>	0.3043 <sup>a</sup>	0.1960 <sup>a,b,c</sup>	0.1110 <sup>c</sup>	0.1305 <sup>b,c</sup>	0.0326	<0.01

<i>Succinivibrionaceae</i>	0.0605	0.0220	0.0531	0.1025	0.0277	0.0779	0.0418	0.0546	0.0885	0.0262	0.4108
<i>Lachnospiraceae</i>	0.0645	0.0460	0.0612	0.0585	0.0675	0.0899	0.0855	0.0480	0.0463	0.0096	0.1448
<i>Lactobacillaceae</i>	0.0220 <sup>a,b</sup>	0.0578 <sup>a</sup>	0.0469 <sup>a,b</sup>	0.0130 <sup>b</sup>	0.0139 <sup>b</sup>	0.0206 <sup>a,b</sup>	0.0227 <sup>a,b</sup>	0.0126 <sup>b</sup>	0.0253 <sup>a,b</sup>	0.0094	0.0134
<i>Spirochaetaceae</i>	0.0631	0.0455	0.0556	0.0352	0.0201	0.0522	0.0300	0.0388	0.0278	0.0115	0.1769
<i>Streptococcaceae</i>	0.0054	0.0044	0.0053	0.0079	0.0093	0.0126	0.0293	0.0194	0.0116	0.0061	0.1117
<i>Pasteurellaceae</i>	0.0013	0.0011	0.0022	0.0023	0.0018	0.0035	0.0220	0.0084	0.0026	0.0047	0.0617
<i>Bacteroidales</i> _S24-7_group	0.0203	0.0136	0.0142	0.0149	0.0159	0.0332	0.0262	0.0262	0.0119	0.0053	0.0857
<i>Acidaminococcaceae</i>	0.0265 <sup>a</sup>	0.0130 <sup>a,b</sup>	0.0147 <sup>a,b</sup>	0.0055 <sup>b</sup>	0.0056 <sup>b</sup>	0.0100 <sup>b</sup>	0.0150 <sup>a,b</sup>	0.0118 <sup>a,b</sup>	0.0150 <sup>a,b</sup>	0.0032	<0.01

NSP: non-starch polysaccharide; MOS: mannan-oligosaccharides. <sup>a-c</sup>Means within a row with different superscripts differ ( $p < 0.05$ ).

**Table S5.** Effects of different combinations of starch, NSP and MOS on genus level (top 15) in microbiota of weaned piglets based on 16S rRNA gene.

Items	Different combinations of starch, NSP and MOS									SEM	<i>p</i> Values
	T1	T2	T3	T4	T5	T6	T7	T8	T9		
<i>Prevotella_9</i>	0.3197 <sup>a,b</sup>	0.2627 <sup>a,b</sup>	0.3015 <sup>a,b</sup>	0.2786 <sup>a,b</sup>	0.4073 <sup>a</sup>	0.1748 <sup>b</sup>	0.1736 <sup>b</sup>	0.2322 <sup>b</sup>	0.2793 <sup>a,b</sup>	0.0342	<0.01
<i>Ruminococcus_2</i>	0.1019 <sup>b,c</sup>	0.2656 <sup>a</sup>	0.1078 <sup>b,c</sup>	0.1966 <sup>a,b</sup>	0.1345 <sup>a,b,c</sup>	0.1923 <sup>a,b</sup>	0.0965 <sup>b,c</sup>	0.0478 <sup>c</sup>	0.0602 <sup>b,c</sup>	0.0309	<0.01
<i>Succinivibrionaceae</i> _UCG-002	0.0019	0.0056	0.0042	0.0554	0.0149	0.0685	0.0238	0.0427	0.0773	0.0204	0.07
<i>Alloprevotella</i>	0.0101 <sup>b</sup>	0.0103 <sup>b</sup>	0.0139 <sup>b</sup>	0.0228 <sup>b</sup>	0.0165 <sup>b</sup>	0.0214 <sup>b</sup>	0.0405 <sup>a,b</sup>	0.0677 <sup>a</sup>	0.0382 <sup>a,b</sup>	0.0084	<0.01
<i>Succinivibrio</i>	0.0585	0.0164	0.0488	0.0469	0.0127	0.0092	0.0179	0.0118	0.0111	0.0145	0.1
<i>Prevotellaceae_NK3</i> B31_group	0.0101 <sup>b</sup>	0.0097 <sup>b</sup>	0.0106 <sup>b</sup>	0.0174 <sup>b</sup>	0.0227 <sup>b</sup>	0.0120 <sup>b</sup>	0.0366 <sup>b</sup>	0.0817 <sup>a</sup>	0.0261 <sup>b</sup>	0.0079	<0.01
<i>Prevotella_2</i>	0.0229 <sup>c</sup>	0.0229 <sup>c</sup>	0.0316 <sup>b,c</sup>	0.0339 <sup>b,c</sup>	0.0317 <sup>b,c</sup>	0.0344 <sup>b,c</sup>	0.0560 <sup>a,b</sup>	0.0525 <sup>b,c</sup>	0.0879 <sup>a</sup>	0.0071	<0.01
<i>Lactobacillus</i>	0.0220 <sup>a,b</sup>	0.0578 <sup>a</sup>	0.0469 <sup>a,b</sup>	0.0130 <sup>b</sup>	0.0139 <sup>b</sup>	0.0206 <sup>a,b</sup>	0.0227 <sup>a,b</sup>	0.0126 <sup>b</sup>	0.0253 <sup>a,b</sup>	0.0094	<0.01
<i>Treponema_2</i>	0.0621	0.0439	0.0507	0.0336	0.0175	0.0494	0.0239	0.0244	0.0235	0.0115	0.1

<i>Prevotella_7</i>	0.0189	0.0157	0.0222	0.0196	0.0313	0.0132	0.0222	0.0415	0.0288	0.0073	0.2
<i>Streptococcus</i>	0.0054	0.0044	0.0053	0.0079	0.0093	0.0126	0.0293	0.01940	0.0116	0.0061	0.11
<i>Actinobacillus</i>	0.0013	0.0011	0.0022	0.0022	0.0017	0.0035	0.0219	0.0082	0.0026	0.0047	0.06
<i>Prevotella_1</i>	0.0032 <sup>b</sup>	0.0042 <sup>b</sup>	0.0036 <sup>b</sup>	0.0083 <sup>b</sup>	0.0063 <sup>b</sup>	0.0058 <sup>b</sup>	0.0276 <sup>a</sup>	0.0259 <sup>a</sup>	0.0151 <sup>a,b</sup>	0.0030	<0.01
<i>Succiniclasticum</i>	0.0188 <sup>a</sup>	0.0089 <sup>a,b</sup>	0.0111 <sup>a,b</sup>	0.0016 <sup>b</sup>	0.0015 <sup>b</sup>	0.0034 <sup>b</sup>	0.0008 <sup>b</sup>	0.0000 <sup>b</sup>	0.0038 <sup>b</sup>	0.0031	<0.01
<i>Anaeroplasma</i>	0.0001	0.0000	0.0003	0.0002	0.0000	0.0088	0.0004	0.0001	0.0001	0.0028	0.42

NSP: non-starch polysaccharide; MOS: mannan-oligosaccharides. <sup>a-c</sup>Means within a row with different superscripts differ ( $p < 0.05$ ).



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