

Biochemical conversion and microbial community in response to ternary pH buffer system during anaerobic digestion of swine manure

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Table S1

The diversity indexes of the bacterial community concerned in the study

Samples		Seq_num	OTU_num	Shannon_index	ACE_index	Chao1_index	Coverage	Simpson
Manure		35616	713	3.30	970.64	993.56	0.99	0.15
Inocula		35521	903	4.01	1483.50	1210.22	0.99	0.07
TS-4	D7	35556	1021	4.44	1681.21	1393.02	0.99	0.06
	D35	35593	805	4.23	1171.15	1149.40	0.99	0.04
	D63	35594	897	4.16	1551.14	1317.81	0.99	0.07
TS-8	D77	35606	902	4.08	1279.10	1236.93	0.99	0.08
	D7	35641	962	3.85	1810.85	1457.37	0.99	0.10
	D35	35628	819	3.55	1525.32	1222.22	0.99	0.13
	D63	35618	753	3.53	1573.54	1252.04	0.99	0.11
	D77	35660	642	3.62	1443.90	1102.70	0.99	0.06
	D98	35672	635	3.67	1139.51	977.01	0.99	0.08
	D112	35626	649	3.54	1252.73	984.84	0.99	0.09
TS-11	D144	35635	698	3.63	1283.37	1049.56	0.99	0.09
	D7	35601	890	3.65	1941.76	1442.47	0.99	0.11
	D35	35664	748	3.37	1658.64	1273.98	0.99	0.10
	D63	35636	718	3.42	1377.11	1165.00	0.99	0.09
	D77	35610	727	3.58	1591.18	1186.10	0.99	0.09
	D98	35610	634	3.76	1152.04	967.49	0.99	0.07
	D112	35653	481	3.24	897.30	776.02	0.99	0.10
TS-14	D144	35632	486	3.14	889.48	735.56	0.99	0.12
	D7	35612	732	3.31	1610.28	1209.79	0.99	0.14
	D35	35682	677	3.03	1423.95	1127.01	0.99	0.15
	D63	35639	614	3.19	1479.97	1095.79	0.99	0.11
	D77	35665	609	3.37	1153.82	909.71	0.99	0.10
	D98	35670	593	3.48	1231.48	891.90	0.99	0.08
	D112	35686	587	3.50	1058.73	880.33	0.99	0.08
	D144	35657	526	3.25	1178.51	939.88	0.99	0.09

Fig. S1

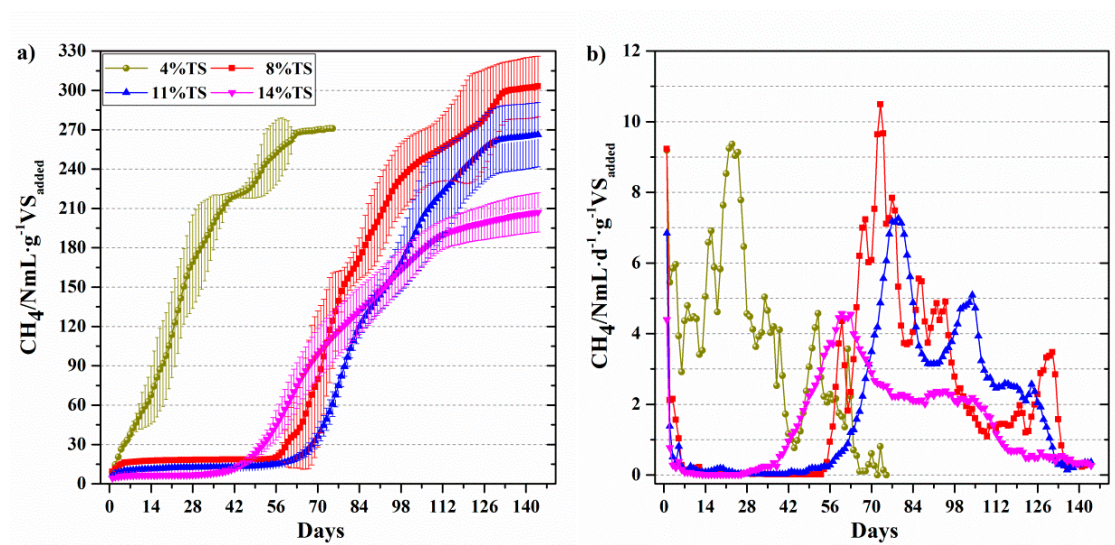


Fig. S1 Methane production from swine manure along with the digestion time at increasing TS contents

(a) Cumulative methane yields of VS added; (b) Daily methane yields of VS added

Fig. S2

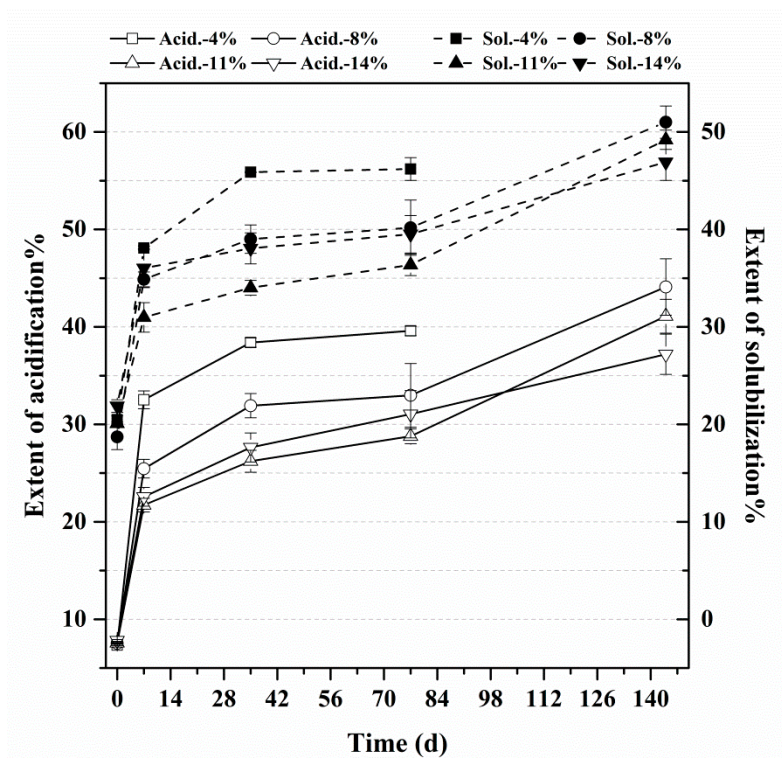


Fig. S2 Extent of solubilization (dashed line) and acidification (solid line) during the AD process

Fig. S3

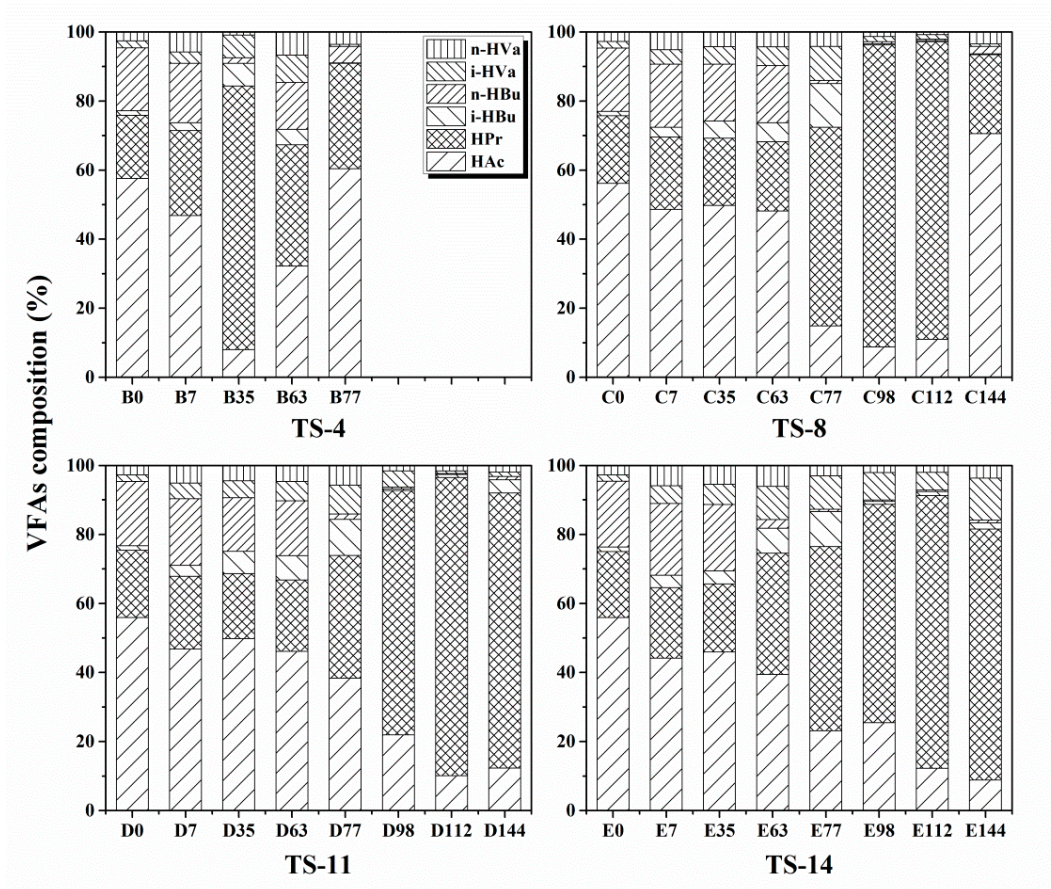


Fig. S3 Changes of VFAs composition (calculated via mole) along with AD at different TS

Fig. S4

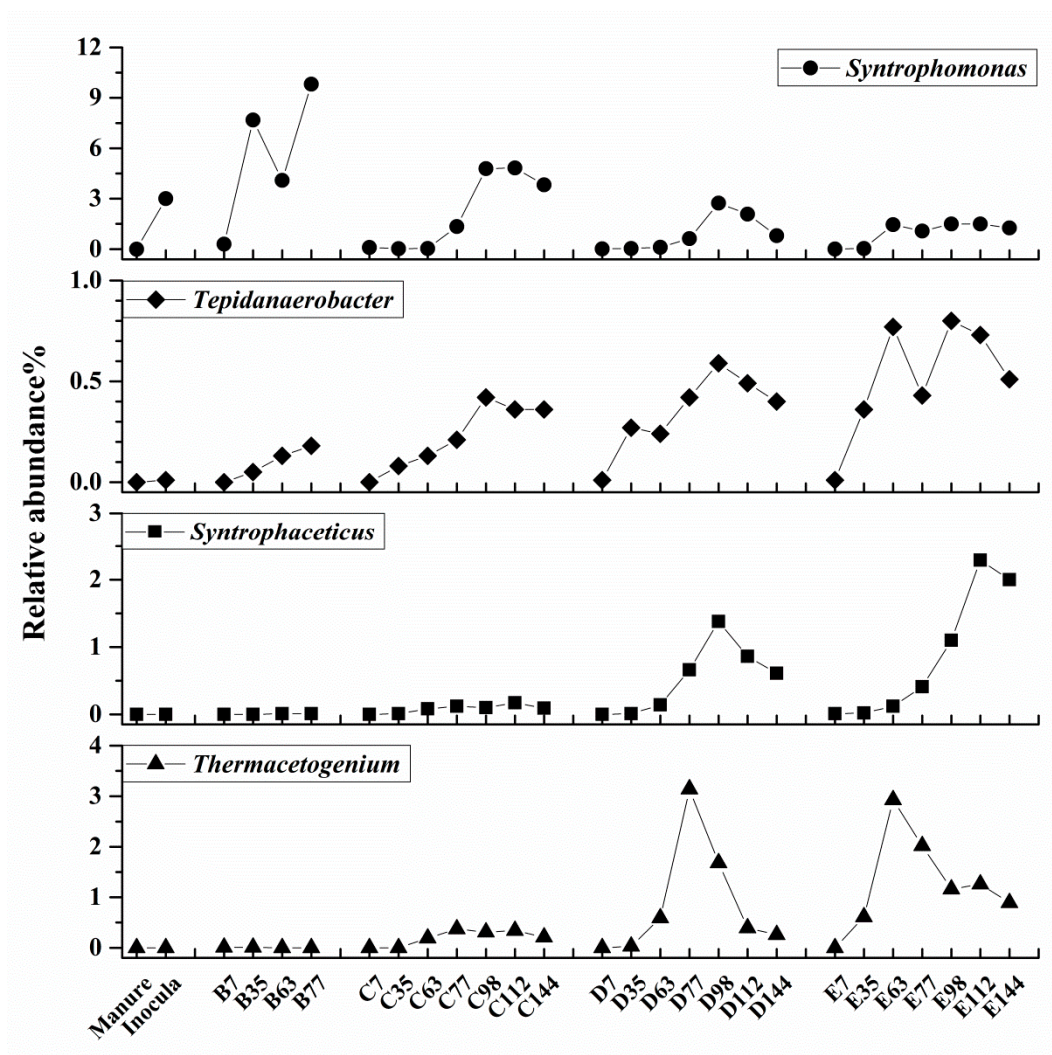


Fig. S4 Relative abundance of *Syntrophomonas* and three kinds of syntrophic acetate oxidizing bacteria

(SAOB) detected in this study

Fig. S5

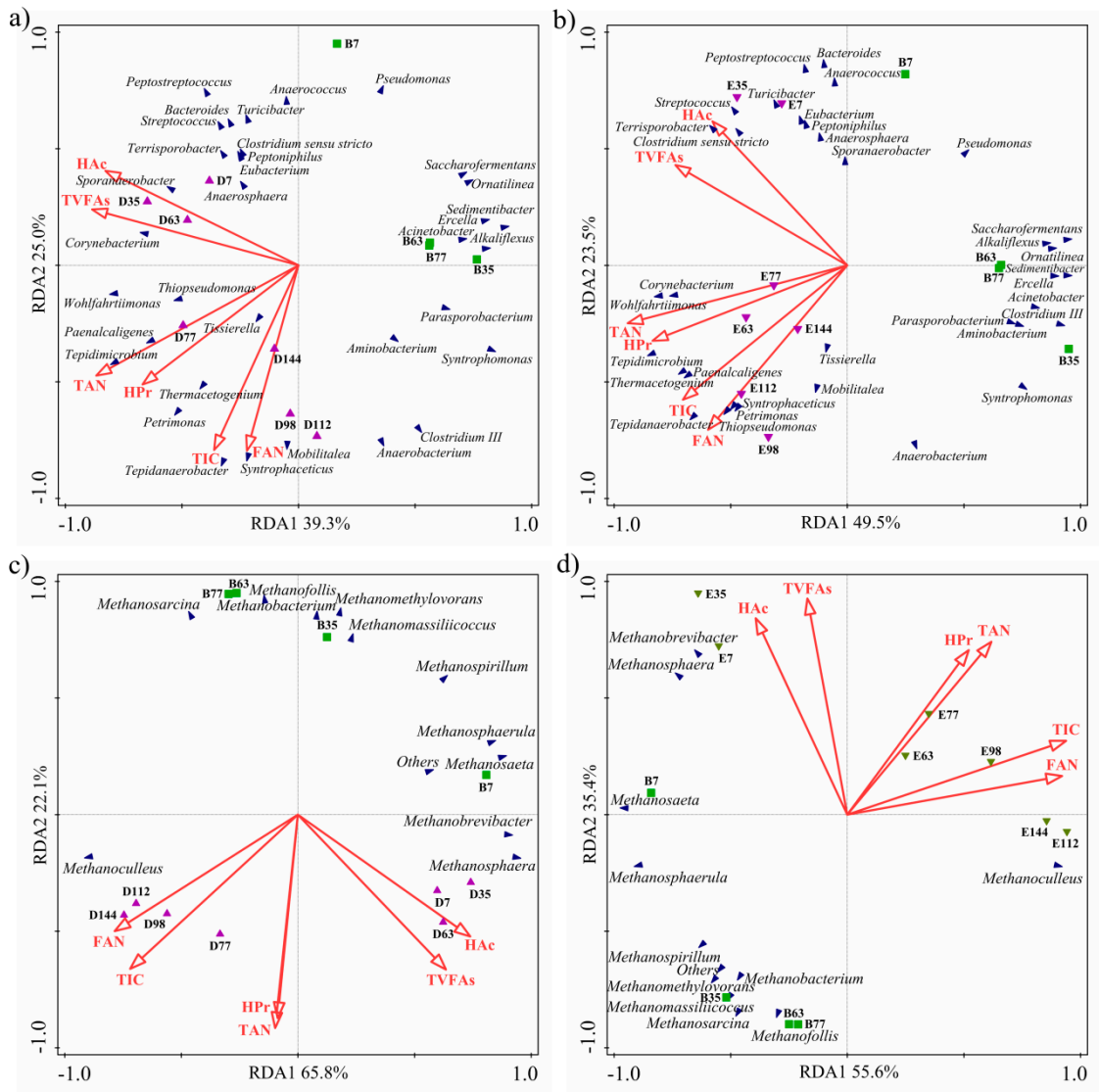


Fig. S5 The redundancy analysis (RDA) revealing the relationship between microbial community and

ammonia as well as VFAs at 11% (a, b) and 14% TS (c, d)