

# Effect of Potato Vine and Leaf Mixed Silage to Whole Corn Crops on Rumen Fermentation and the Microbe of Fatten Angus Bulls

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Table S1. Buffer solution composition.

Solution	Component (1000ml)	Volume(ml)
Distilled water		2400
Trace element solution A	13.2g CaCl <sub>2</sub> ·2H <sub>2</sub> O,10g MnCl <sub>2</sub> ·4H <sub>2</sub> O,1g CoCl <sub>2</sub> ·6H <sub>2</sub> O, 8g FeCl <sub>2</sub> ·6H <sub>2</sub> O	0.6
Artificial saliva B	35g NaHCO <sub>3</sub> , 4g NH <sub>4</sub> HCO <sub>3</sub>	1200
Constant element solution C	5.7g Na <sub>2</sub> HPO <sub>4</sub> , 6.2g KH <sub>2</sub> PO <sub>4</sub> , 0.6g MgSO <sub>4</sub> ·7H <sub>2</sub> O	1200
Resazurin solution D	1g Resazurin	6
Reducing agent solution	6.25g Na <sub>2</sub> S·9H <sub>2</sub> O, 40 mL 1 M NaOH	240

Table S2. The diversity index of bacterial communities in the rumen in three different dietary silage groups.

Items	CS	PVS 1	PVS 2	SEM	<i>p</i> -value
ACE	639.65	629.90	669.70	12.16	0.459
Chao1	641.26	629.81	669.71	12.16	0.472
Simpson	1.00	0.99	1.00	0.0016	0.181
Shannon	8.54	8.48	8.67	0.08	0.654
PD whole tree	35.47	35.48	37.27	0.44	0.159
Coverage	1.000	1.000	0.9999		

**Table S3.** The relative abundance of dominant bacteria was  $\geq 0.1\%$  (phylum level).

Items	CS	PVS 1	PVS 2	SEM	<i>p</i> -value
Bacteroidota	52.0	53.4	50.0	1.63	0.711
Firmicutes	33.7	36.6	38.4	1.81	0.595
Proteobacteria	7.20 <sup>a</sup>	2.73 <sup>b</sup>	4.78 <sup>ab</sup>	0.708	0.034
Fibrobacterota	2.49	2.23	2.43	0.237	0.849
Patescibacteria	1.60	1.53	1.33	0.119	0.587
Verrucomicrobiota	1.07	1.84	1.36	0.206	0.630
Spirochaetota	0.881	0.270	0.357	0.113	0.057
Desulfobacterota	0.301	0.574	0.379	0.0640	0.202
Elusimicrobiota	0.144	0.220	0.160	0.0294	0.565
unclassified_Bacteria	0.0462	0.299	0.292	0.0665	0.135
Synergistota	0.0862	0.179	0.133	0.0185	0.077
Actinobacteriota	0.258	0.103	0.128	0.0527	0.751
Cyanobacteria	0.109	0.0350	0.178	0.0360	0.444
others	0.0628	0.0625	0.0737	0.0167	0.958

There is a significant difference between different groups marked with different lowercase letters within the same row in table.

**Table S4.** The relative abundance of dominant bacteria was  $\geq 1\%$  (family level).

Items	CS	PVS1	PVS2	SEM	<i>p</i> -value
<i>Prevotella</i>	29.8 <sup>a</sup>	19.3 <sup>b</sup>	21.5 <sup>b</sup>	1.43	0.001
<i>uncultured_rumen_bacterium</i>	6.32 <sup>b</sup>	9.06 <sup>a</sup>	7.52 <sup>ab</sup>	0.456	0.037
<i>Rikenellaceae_RC9_gut_group</i>	5.00	7.93	6.93	0.580	0.106
<i>Ruminococcus</i>	3.80	2.86	2.17	0.425	0.308
<i>Succiniclasicum</i>	3.62	3.35	2.84	0.283	0.676
<i>unclassified_F082</i>	3.01	7.35	5.54	0.768	0.064
<i>Prevotellaceae_UCG_001</i>	2.78	2.12	2.12	0.198	0.306
<i>Prevotellaceae_UCG_003</i>	2.60	2.77	2.01	0.196	0.148
<i>Fibrobacter</i>	2.49	2.23	2.43	2.380	0.849
<i>unclassified_Lachnospiraceae</i>	2.49	1.95	2.76	0.169	0.139
<i>Ruminobacter</i>	2.28	0.624	1.92	0.382	0.180
<i>Succinivibrionaceae_UCG_002</i>	2.25	0.816	1.21	0.328	0.189
<i>unclassified_Prevotellaceae</i>	2.18 <sup>a</sup>	1.69 <sup>ab</sup>	1.09 <sup>b</sup>	0.155	0.007
<i>Saccharofermentans</i>	1.85	2.19	2.27	0.129	0.382
<i>NK4A214_group</i>	1.69	3.01	2.78	0.278	0.114
<i>unclassified_Ruminococcaceae</i>	1.31	1.23	2.78	0.339	0.107
<i>unclassified_Bacteroidales_RF16_group</i>	1.17	0.821	1.03	0.115	0.738
<i>unclassified_Clostridia</i>	1.13	2.07	2.06	0.239	0.184
<i>Lachnospiraceae_XPB1014_group</i>	0.728 <sup>b</sup>	1.01 <sup>ab</sup>	1.35 <sup>a</sup>	0.104	0.040
<i>Bacteroidales_bacterium_Bact_22</i>	0.026 <sup>b</sup>	4.40 <sup>ab</sup>	3.18 <sup>a</sup>	1.42	0.013
Others	23.5	23.2	24.5	0.751	0.798

There is a significant difference between different groups marked with different lowercase letters within the same row in table.