

Chopping roughage length improved rumen development of weaned calves as revealed by rumen fermentation and bacterial community

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Supplementary Table S1

Effects of roughage length on the phylum (as a percentage of the total sequences) of the ruminal bacterial community.

Item	Diet			SEM	P-value	
	SL	ML	LL		Linear	Quadratic
<i>Bacteroidetes</i>	46.10	48.64	52.17	3.299	0.201	0.458
<i>Firmicutes</i>	37.18	33.76	33.80	2.125	0.274	0.458
<i>Proteobacteria</i>	5.47	5.40	4.12	0.763	0.229	0.411
<i>Tenericutes</i>	1.82	1.88	2.15	0.296	0.436	0.718
<i>Saccharibacteria</i>	1.61	1.67	1.72	0.271	0.759	0.956
<i>Fibrobacteres</i>	1.50	2.11	1.03	0.324	0.404	0.115
<i>Spirochaetae</i>	1.42	1.61	1.44	0.248	0.961	0.835
<i>Cyanobacteria</i>	1.34	1.62	0.73	0.420	0.335	0.351
<i>Verrucomicrobia</i>	1.15	1.08	0.74	0.276	0.297	0.549
<i>SR1_Absconditabacteria</i>	0.70	1.01	1.00	0.185	0.255	0.425
<i>Actinobacteria</i>	0.57	0.45	0.49	0.075	0.438	0.517
<i>Elusimicrobia</i>	0.41	0.26	0.19	0.100	0.139	0.331
<i>Lentisphaerae</i>	0.28	0.24	0.18	0.056	0.231	0.504
<i>Synergistetes</i>	0.23	0.14	0.10	0.029	0.010	0.036

SL, short length; ML, medium length; LL, long length.

Supplementary Table S2

Effects of roughage length on the genus (as a percentage of the total sequences) of the ruminal bacterial community.

Item	Diet			SEM	P-value	
	SL	ML	LL		Linear	Quadratic
Unidentified	25.86	24.38	23.55	1.951	0.400	0.709
<i>Prevotella_1</i>	16.52	23.94	25.16	3.903	0.138	0.288
<i>Rikenellaceae_RC9_gut_group</i>	6.42	4.20	4.53	0.860	0.159	0.199
<i>Christensenellaceae_R-7_group</i>	5.28	3.95	5.33	0.428	0.945	0.081
<i>Ruminococcaceae_NK4A214_group</i>	3.55	3.25	3.23	0.409	0.576	0.831
<i>Succiniclasticum</i>	2.39	3.39	2.68	0.556	0.724	0.453
<i>Prevotellaceae_UCG-001</i>	2.79	1.96	2.86	0.381	0.911	0.233
<i>Succinivibrionaceae_UCG-002</i>	2.95	2.29	2.29	0.449	0.303	0.511
<i>Prevotellaceae_UCG-003</i>	1.83	1.87	1.93	0.242	0.775	0.961
<i>Ruminococcus_2</i>	1.96	1.67	1.48	0.421	0.416	0.728
<i>Candidatus_Saccharimonas</i>	1.61	1.67	1.72	0.271	0.759	0.956
<i>Fibrobacter</i>	1.49	2.10	1.03	0.324	0.411	0.116
<i>Ruminococcaceae_UCG-014</i>	1.45	1.59	1.33	0.222	0.707	0.726
<i>Butyrivibrio_2</i>	1.45	1.14	1.58	0.205	0.689	0.342
<i>Treponema_2</i>	1.21	1.45	1.31	0.260	0.788	0.813
<i>Ruminococcaceae_UCG-005</i>	1.36	1.23	0.86	0.153	0.040	0.112
<i>Lachnospiraceae_NK3A20_group</i>	1.27	1.00	1.13	0.199	0.634	0.646
<i>Ruminococcus_1</i>	0.97	1.31	0.92	0.218	0.883	0.427

<i>Pseudobutyrvibrio</i>	0.79	0.68	1.12	0.170	0.214	0.217
<i>Anaeroplasma</i>	0.66	0.92	0.92	0.226	0.417	0.656
<i>Ruminococcaceae_UCG-010</i>	1.02	0.76	0.73	0.100	0.072	0.140
<i>Veillonellaceae_UCG-001</i>	0.78	0.77	0.72	0.122	0.715	0.932
<i>Saccharofermentans</i>	0.77	0.72	0.73	0.110	0.777	0.932
<i>Eubacterium_coprostanoligenes_group</i>	0.75	0.73	0.69	0.077	0.565	0.852
<i>Erysipelotrichaceae_UCG-004</i>	0.60	0.53	0.80	0.120	0.260	0.283
<i>Lachnospiraceae_XPB1014_group</i>	0.58	0.49	0.49	0.044	0.200	0.324
<i>Succinivibrio</i>	0.25	1.17	0.12	0.272	0.814	0.045
<i>Prevotellaceae_UCG-004</i>	0.77	0.33	0.36	0.111	0.037	0.036
<i>Acetitomaculum</i>	0.45	0.47	0.48	0.084	0.821	0.975
<i>Papillibacter</i>	0.60	0.42	0.31	0.082	0.025	0.089
<i>Prevotellaceae_NK3B31_group</i>	0.52	0.33	0.47	0.060	0.643	0.111
<i>Lachnospiraceae_AC2044_group</i>	0.43	0.46	0.36	0.089	0.581	0.753
<i>Unidentified_rumen_bacterium_RFN46</i>	0.72	0.21	0.31	0.230	0.246	0.306
<i>Ruminobacter</i>	0.50	0.35	0.29	0.124	0.244	0.503
<i>Lachnospiraceae_ND3007_group</i>	0.36	0.32	0.41	0.131	0.802	0.895
<i>Eubacterium_ruminantium_group</i>	0.32	0.36	0.37	0.055	0.503	0.792
<i>Moryella</i>	0.37	0.29	0.34	0.065	0.672	0.670
<i>Desulfovibrio</i>	0.39	0.26	0.31	0.045	0.312	0.181
<i>Ruminococcus_gauvreauii_group</i>	0.25	0.32	0.33	0.026	0.068	0.153
<i>Anaerovorax</i>	0.34	0.27	0.22	0.040	0.052	0.163
<i>Phocaeicola</i>	0.28	0.23	0.29	0.040	0.893	0.579
<i>Family_XIII_AD3011_group</i>	0.35	0.19	0.21	0.038	0.055	0.034
<i>Prevotellaceae_Ga6A1_group</i>	0.22	0.22	0.23	0.059	0.859	0.980
<i>Probable_genus_10</i>	0.16	0.20	0.20	0.044	0.525	0.786
<i>Anaerotruncus</i>	0.19	0.18	0.15	0.030	0.337	0.595
<i>Elusimicrobium</i>	0.24	0.16	0.09	0.074	0.166	0.403
<i>Ruminococcaceae_UCG-002</i>	0.19	0.15	0.14	0.036	0.345	0.613
<i>Selenomonas_1</i>	0.11	0.28	0.10	0.043	0.907	0.025
<i>Prevotellaceae_YAB2003_group</i>	0.11	0.19	0.17	0.054	0.439	0.555
<i>Senegalimassilia</i>	0.15	0.13	0.16	0.014	0.463	0.361
<i>Uncultured</i>	0.05	0.27	0.10	0.094	0.786	0.273
<i>Anaerovibrio</i>	0.17	0.11	0.13	0.026	0.269	0.305
<i>Oribacterium</i>	0.11	0.14	0.15	0.028	0.347	0.656
<i>Roseburia</i>	0.13	0.15	0.12	0.053	0.873	0.916
<i>Atopobium</i>	0.14	0.12	0.13	0.036	0.896	0.926
<i>Ruminococcaceae_UCG-013</i>	0.16	0.18	0.05	0.071	0.318	0.424
<i>Blautia</i>	0.11	0.11	0.17	0.020	0.099	0.119
<i>Defluviitaleaceae_UCG-011</i>	0.12	0.10	0.14	0.024	0.532	0.455
<i>Candidatus_Endomicrobium</i>	0.17	0.10	0.10	0.032	0.125	0.218
<i>Eubacterium_ventriosum_group</i>	0.14	0.08	0.13	0.018	0.648	0.121
<i>Olsenella</i>	0.14	0.11	0.10	0.029	0.355	0.658
<i>Eubacterium_hallii_group</i>	0.15	0.08	0.11	0.016	0.246	0.034

<i>Ruminiclostridium_6</i>	0.13	0.10	0.10	0.022	0.261	0.457
<i>Ruminococcaceae_V9D2013_group</i>	0.15	0.08	0.10	0.040	0.344	0.457
<i>Pyramidobacter</i>	0.15	0.11	0.06	0.018	0.005	0.024
<i>Mogibacterium</i>	0.14	0.06	0.12	0.016	0.613	0.014
<i>SP3-e08</i>	0.09	0.07	0.15	0.025	0.192	0.123
<i>Marvinbryantia</i>	0.12	0.08	0.11	0.019	0.965	0.352

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