

**Table 3.** Relative abundance of microbial populations and amount of rRNA extracted from ruminal, inoculum and fermenter (96, 120, 144 and 168 h) samples.

Population	Rumen	Inoculum	Fermenter <sup>a</sup>				SEM <sup>b</sup>
			96 h	120 h	144 h	168 h	
$\mu\text{g g}^{-1}$ sample							
Total SSU rRNA <sup>c</sup>	124.1	79.4	174.9	154.8	274.1	180.7	46.5
% of total SSU rRNA							
Bacteria <sup>c,d,e</sup>	48.0	52.3	84.0	84.2	86.7	83.0	4.4
Eukarya <sup>f,g</sup>	52.2	70.7	1.7	1.1	2.0	2.5	8.6
Archaea <sup>d</sup>	1.3	1.8	2.3	2.1	1.8	2.1	0.2
Gram-positive bacteria <sup>d</sup>	28.0	24.4	39.6	33.8	37.5	38.0	4.0
<i>Fibrobacter</i>	2.2	2.8	2.2	3.4	2.2	2.5	0.3
% of <i>Fibrobacter</i> SSU rRNA							
<i>Fibrobacter succinogenes</i>	90.6	67.4	83.7	89.0	92.5	75.8	5.7
<i>Fibrobacter intestinalis</i> <sup>f</sup>	2.1	2.7	0.4	0.9	0.6	0.3	0.5
<i>F. succinogenes</i> subgroup 1 <sup>f,g</sup>	28.4	29.7	7.9	9.4	9.0	6.5	3.6
<i>F. succinogenes</i> subgroup 3	25.3	46.5	13.5	39.6	21.5	9.3	9.2

a. Average of samples from four fermenters after 96, 120, 144, and 168 h of operation.

b. SEM = standard error of the mean.

c. Relative abundance of Bacteria includes *Fibrobacter* and Gram-positive bacteria.

d. Values for fermenter samples significantly greater than inoculum samples. Based on paired *t*-test,  $P \geq 0.05$ .

e. Values for fermenter samples significantly greater than ruminal samples. Based on paired *t*-test,  $P \geq 0.05$ .

f. Values for fermenter samples significantly less than ruminal samples. Based on paired *t*-test,  $P \geq 0.05$ .

g. Values for fermenter samples significantly less than inoculum samples. Based on paired *t*-test,  $P \geq 0.05$ .