

**Table 1.** Relative abundance of microbial populations and amount of rRNA extracted from ruminal and dual-flow continuous culture fermenter samples.

Population	Rumen	Fermenter <sup>a</sup>		SD <sup>c</sup>	Rumen	Fermenter		SD
	μg SSU rRNA g <sup>-1</sup> sample	0 h <sup>b</sup>	240 h		% of total SSU rRNA	0 h	240 h	
Total	212.8	163.5	113.9	51.1				
Bacteria <sup>d, e</sup>	74.3	55.9	93.2	62.4	34.9	33.9	80.9	9.2
Eukarya <sup>f, g</sup>	127.9	63.8	6.3	12.8	60.1	39.0	6.1	3.5
Archaea <sup>f</sup>	14.4	4.9	5.3	2.9	6.8	3.0	5.1	1.2
<i>Fibrobacter</i>	20.3	7.3	6.8	5.1	9.5	4.5	6.6	3.3

a. Value is the mean of four fermenters.

b. Time of fermenter operation (h).

c. Standard deviation.

d. Amount and relative abundance of Bacteria include *Fibrobacter*.

e. Relative abundance greater in 240 h fermenter samples than in ruminal,  $P \leq 0.05$ .

f. Amount of SSU rRNA extracted lower in 0 and 240 h fermenter samples than in ruminal,  $P \leq 0.05$ .

g. Relative abundance lower in 0 and 240 h fermenter samples than in ruminal,  $P \leq 0.05$ .