

acidosis by pH reduction (Mackie *et al.*, 1978). However, Singh and Kundu (2011) reported the dominance of entodiniomorph protozoa in the rumens of sheep fed tree and grass leaves at the ratio of 75 to 25, so the explanation of their abundance may be more complicated than that. Polyplastron, a large cellulolytic protozoan with greater endoglucanase and xylanase activity than genus Entodinium (Newbold *et al.*, 2015), and the second most predominant group of the protozoa present in the rumen of the Baluchi lambs were also reported in a similar study by Lin *et al.* (2015), followed by the holotrich genus Isotricha. Polyplastron spp. were also the closest protozoal group associated with concentrate intake in a global study (Henderson *et al.*, 2015).

Table 6. Archaeal community structure in the rumen of Baluchi lambs fed a high concentrate diet.

Group	Percent ± SE
<i>Methanobrevibacter gottschalkii</i> clade	53.32 ± 1.87
Methanomassiliicoccales	28.29 ± 5.23
<i>Methanobrevibacter wolinii</i> and relatives	8.49 ± 4.26
<i>Methanobrevibacter ruminantium</i> clade	6.23 ± 1.53
<i>Methanosphaera</i> spp.	3.65 ± 0.74
<i>Methanimicrococcus</i> spp.	0.02 ± 0.02

The number of good quality reads obtained for rumen archaea was 4433, and on average there were 1108 reads per sample. Six archaeal groups were detected in the rumens of the sheep (Table 6). More than half of the archaeal community (53.32 ± 1.87 %) was composed of members of the *Methanobrevibacter gottschalkii* clade. The second and third most dominant groups were Methanomassiliicoccales (28.29 ± 5.23 %) and *Methanobrevibacter wolinii* and its relatives (8.49 ± 4.26 %). Two other dominant archaeal groups with relative abundances greater than 0.1 % were the *Methanobrevibacter ruminantium* clade

and *Methanosphaera* spp. The abundance of members of the *Methanobrevibacter gottschalkii* clade of rumen methanogens observed in the present study is similar to that reported elsewhere (Henderson *et al.*, 2015; Lin *et al.*, 2015; Huang *et al.*, 2016). These methanogens use hydrogen plus carbon dioxide for their growth. Their major competitors would appear to be the physiologically similar members of the *Methanobrevibacter ruminantium* clade, but these were rare in the samples studied here. This pattern fits well with the global pattern of *M. gottschalkii* being more strongly favored in concentrate-rich diets and *M. ruminantium* being favored in forage-rich diets (Henderson *et al.*, 2015). Members of the order Methanomassiliicoccales are implicated in methane emissions in the rumen, possibly from methylamines (Poulsen *et al.*, 2013) and were found as major methanogens in the rumen of Australian sheep and small ruminants of Tibetan Plateau (Huang *et al.*, 2016).

3. Conclusion

In the present study, lambs of the indigenous Baluchi sheep were fed a ration commonly used in the nutrition of ruminants, and the microbial communities in their rumen studied using 454 pyrosequencing. The dominant microorganisms observed in the rumen of these lambs were similar to those previously reported from different species and breeds fed similar diets. This indicated that when an indigenous breed consumed conventional feeds, the effect of the diet determined the rumen microbial community structure. Knowledge of rumen microbial community function from other studies may therefore be applicable to these sheep. However, it remains to be determined how the rumen microbial community of such animals changes when they are grazing on natural pastures under dry and warm conditions, and if there are indications that this may be specialized to the diet or even the host.

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