content prepared from a high WSC perennial ryegrass (cv. Ba11353; HSGS) in a two period changeover experimental design. Liquid phase rumen samples were collected 2 h after feeding. Total and cellulolytic bacteria were estimated using a most-probable-numbers method and protozoa by direct counting. Bacterial and protozoal diversity in the samples was estimated by PCR-DGGE using, respectively, 16S and 18S ribosomal DNA specific primers. Cellulolytic bacteria numbers were lower (7.42 vs. 35.7 × $10^7 \cdot mL^{-1}$ respectively, $P = 0.004$) and total protozoa higher (13.2 vs. $8.12 \times 10^5 \cdot mL^{-1}$, $P = 0.025$) in the rumen fluid of animals fed the HSGS diet, however total bacteria were not significantly affected by the offered diet (3.71 vs. 2.41 × $10^9 \cdot mL^{-1}$). As expected the bacterial community displayed more diversity than the protozoal community as indicated by DGGE. Cluster analysis of DGGE band polymorphism showed that the experimental period explained most of the similarity in both bacteria and protozoa. However, within experimental periods, samples of amplified bacterial rDNA taken from animals fed the same diet shared the highest level of similarity, while no clear pattern was observed for rumen protozoa. Our results suggested that differences in silage WSC content can cause significant shifts in microbial community structure.

Effect of molasses diets on population profiles of rumen bacteria. M.X. Tolosa[a,b], T. Dinh Van[a], A.V. Klieve[b], D. Ouwerkerk[b], D.P. Poppi[a], S.R. McLennan[b] ([a] Schools of Animal Studies and Veterinary Science, University of Queensland, St Lucia QLD 4072, Australia; [b] Department of Primary Industries, Animal Research Institute, Yeerongpilly QLD 4105, Australia).

The objectives of this study were to obtain profiles of the predominant rumen bacterial species of beef cattle fed diets containing varying proportions of low-quality Pangola grass-hay and molasses. Four rumen-cannulated Brahman-cross steers were fed molasses as 0, 25, 50 and 75% of the diet once daily. Urea comprised 3% of the molasses. Steers were allocated to one of four diets in a 4 × 4 Latin square design with periods of 28 days. Following a 3-week adaptation period, rumen fluid samples were taken immediately prior to feeding and 8 h after feeding over two consecutive days. Total genomic DNA was extracted from the rumen fluid samples by bead beating. Subsequently, 16S rDNA was amplified by polymerase chain reaction with primers specific for the fragment between variable regions 2 and 3 (V2-V3) of the gene. The amplified V2-V3 products were analysed using DGGE. A comparison of two sets of four DNA samples, each set representing the two extreme dietary conditions (diets containing 0 and 75% molasses) belonging to two different animals, revealed the presence of dominant species in the rumen samples from the steer fed the highest molasses treatment that were not present in the samples obtained from the control steer. Furthermore, there were no differences in this steer between the DGGE banding pattern derived from the morning and afternoon, and between two consecutive days. Therefore, it can be concluded that predominant species of the rumen bacterial community appear to be particularly stable throughout the day and over at least a two-day period in animals fed a given diet. Further studies are being undertaken to identify those predominant species. A longer-term objective of this research is to investigate linkages between diet, rumen microbial populations and the efficiency of microbial protein production.

Differences in rumen microbial population induced by the quality of dietary forage. M. Fondevila[a], G. Muñoz[a], G. de la Fuente[a], M. Pérez-Quintana[b], J. Balcells[a] ([a] Departamento de Producción Animal y Ciencia de los Alimentos, Universidad de Zaragoza, Miguel Servet 177, 50013 Zaragoza, Spain; [b] Departamento de Química y Biología, Universidad de Matanzas, Matanzas, Cuba).

Previous studies showed that the lower the quality of dietary forage, the higher the degradation of poor quality roughages. Therefore, rumen bacterial and protozoal populations of sheep given alfalfa hay (AH), untreated (US) or ammonia-treated (TS) straw were studied. Four rumen cannulated sheep were adapted to diets for 14 days in three consecutive periods. Samples for bacterial and protozoal counts were taken just before the morning feed. In addition, pH and volatile fatty acid concentration (VFA) were determined 0, 4 and 8 h after feeding. Average pH ranked US > TS > AH (6.87; 6.60 and 6.33; $P < 0.05$). The proportion of acetate was lower