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after the administration and comparison of 4 different diets. Thirty-two growing pigs were randomly distributed into four treatments. The animals were fed ad libitum for 6 weeks with a commercial diet (15% barley, 28% soya 44, 54% corn and vegetable oil (basal diet, A). Fine-sized corn of basal diet (2.5 mm) was changed to 4 mm corn (B treatment), and sugar beet pulp (8%) or bran (10%) were added to the basal diet in treatment C and D respectively. After the experimental period, the animals were slaughtered and the GI tract was sampled. Digesta samples were diluted and fixed with formaldehyde prior to analysis. Fluorescent in situ hybridisation (FISH) was used to quantify bacterial populations by using five probes: EUB338, EREC482, RFLA729 plus RBRO730 and FPRA645 to quantify total bacteria and the predominant groups of low G+C Gram positive bacteria belonging to clusters IV and XIVa in samples of rectum digesta. Total bacteria were 1.98E11 ± 6.63E10 bacteria·g^{-1} fresh matter and cluster XIVa and ruminococci were the predominant bacterial groups in all treatments. *Faecalibacterium* spp. represented 1.3 ± 0.3% of the total bacterial population. The administration of these diets did not significantly change the bacterial populations of the pigs and each diet maintained high proportions of the cluster IV and XIVa groups.

Effect of dietary changes on the bacteriophage population in the rumen of sheep. R.A. Gilbert[a], J. Shepherd[b], A.V. Klieve[c], J.V. Nolan[d], C.J. Newbold[b], R.J. Wallace[b] ([a] CSIRO Livestock Industries, Queensland Bioscience Precinct, St Lucia, Qld 4067 Australia; [b] Rowett Research Institute, Bucksburn, Aberdeen AB21 9SB, UK; [c] Animal Research Institute, Queensland Department of Primary Industries, Moorooka, Queensland 4105, Australia; [d] University of New England, Armidale NSW 2351, Australia).

The effect of alternating the diet from a hay-based to a silage-based diet on the rumen phage population of four cannulated sheep was examined in a 2 × 2 factorial design experiment. Two animals were fed each diet during two 20 d feeding periods, each consisting of an initial 14 d feed adaptation period and 6 d monitoring period, in which rumen fluid samples were collected on days 15 and 20, immediately before feeding and again at 2 h and 6 h after feeding. Phage DNA extracted from rumen fluid samples was used to determine rumen phage concentration, and phage population diversity was determined by pulsed field gel electrophoresis separation of phage DNA. In addition, rumen bacteria and protozoa were enumerated and pH, and concentrations of volatile fatty acids, ammonia and L-lactate, were determined. No significant differences occurred in either the size or diversity of the rumen phage population between sheep fed silage or hay-based diets. These findings contrast with previous studies that have shown the size of the rumen phage population to vary dramatically between different dietary regimes. Other parameters of fermentation and microbial composition suggested that the rumen microbial population may not have altered significantly between the two diets and therefore did not cause major changes in the size and relative composition of the rumen phage population.

Functional and ecological characterization of newly isolated *Fibrobacter succinogenes* strains in relation to their phylogeny. T. Shinkai, N. Matsumoto, Y. Kobayashi (Graduate School of Agriculture, Hokkaido University, Sapporo 060-8589, Japan).

Fibrobacter succinogenes strains were newly isolated from the rumen of sheep receiving orchardgrass hay, orchardgrass pasturage, alfalfa hay or rice straw. Then, rumen solid, liquid and ruminally incubated forage stems were the bacterial sources. Thirty-three strains in total were obtained mainly from ruminally incubated forage stems. Most of these (29 of 33) were affiliated with group 1, based on their partial 16S rDNA sequences. Four strains were classified into group 2, and then two of these formed a novel sub-group, the branching of which was supported by an 82% bootstrap value. Only these two strains produced yellow pigments when cultured with Avicel. Group 1 strains showed faster growth to a higher extent than group 2 strains when cultured with Avicel. Although there were variations in number and molecular size of CMCases that were detected on SDS-polyacrylamide gel by activity staining, group 2 strains possessed 112kD CMCase as a common enzyme. Meanwhile, strains belonging to groups 1 and 2, when grown on Avicel, showed no particular