Bacterial Population Dynamics in Cattle Fed Pasture of Varying Nutritive Value

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In northern Australia the beef industry is largely reliant on native tropical grasses, typically of low nutritive value, for beef production. Ruminants derive between 66 – 75% of their protein requirements from microbial protein flowing from the rumen and therefore the microbial species in the rumen are the most important source of protein to a grazing ruminant but factors affecting production of microbial protein are poorly understood. This study was designed to identify and compare the dominant bacterial species in the rumen of \textit{Bos indicus} cattle consuming a wide range of forages of varying quality, including low quality hays of black spear grass (\textit{Heteropogon contortus}; 2.6% CP) and Mitchell/Flinders grasses (\textit{Astrebla spp}, \textit{Iseilema vaginoflorum}; 3.0% CP), mimicking mature tropical forages, the medium quality tropical pangola grass (\textit{Digitaria eriantha}; 7.6%CP) and the high quality temperate ryegrass (\textit{Lolium aristocrat}; 20.0 %CP). This experiment hypothesised that inherent nutritional differences between forage species may produce changes in bacterial community composition and the efficiency of microbial protein production.

Five rumen-cannulated \textit{Bos indicus} steers were fed four basal hay diets for three weeks prior to rumen sampling. Collected digesta from the rumen was separated into four fractions by a progressive process of both physical and chemical dissociation: the planktonic phase (liquid), the digesta associated phase (squeezed) and both the loosely (associated) and strongly attached (attached) phases. Following fractionation, total genomic DNA was extracted using a bead-beating protocol and the V2V3 region of 16S rDNA amplified by PCR (Yu and Forster, 2005). Denaturing gradient gel electrophoresis (DGGE) was used to generate bacterial community profiles of the amplified V2V3 PCR products. Dominant bands and differences in banding-patterns between animals and diets were then identified. A clone library of the 16S rRNA genes from a selected sample was established to enable DNA sequence to be obtained that corresponded to dominant bacterial species and the phylogenetic position of these bacteria to be determined.

DGGE results revealed a largely stable rumen bacterial community despite considerable variability in the nutritive value of the forage consumed. The majority of dominant bacterial species were stable across diets, and within and between animals within diets (Figures 1 and 2). A number of bands were identified as being specific to animal, diet or both but the overall stability of the community tended to overshadow these differences. Additionally, dominant bands observed in the particle associated phase were also present, although slightly less so, within the planktonic phase. DNA from the two most dominant, fibre associated, bands (arrowed in Figure 1) were sequenced and the nearest bacterial relatives both belonged within the Clostridiales family. Neither of these bands represent previously cultured species, and they were not related to previously documented cellulolytic or fibre associated bacteria. These bacteria could be of importance in the utilisation of plant fibre by \textit{Bos indicus} cattle in northern Australia given the dominance and ubiquitous presence in the rumen of the cattle in this study.

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