

Changes in the Rumen Bacterial Community in Steers Fed with Supplemented Tropical Pasture

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A major factor determining live weight gain (LWG) in beef cattle consuming tropical pastures in Northern Australia, is the microbial crude protein (MCP) supply and the efficiency of MCP production (eMCP). Native tropical pastures are typically of low nutritive value and the eMCP of cattle grazed on these pastures rarely exceeds 130gMCP/kgDOM, which is marginal for productive growth (NRC 1996). However, Panjaitan (2008) demonstrated that supplementation with spirulina (*Spirulina platensis*) increased eMCP to 166gMCP/kgDOM.

It is hypothesised that spirulina may produce changes in bacterial community composition which is associated with the increase in the eMCP. The substantial increase in eMCP in spirulina supplemented steers offers a unique opportunity to study whether changes occur in rumen bacterial community profiles.

Nine crossbred cannulated steers were used in a 9 x 3 incomplete latin square design which included nine treatments over three, 30 day periods. The treatments were Mitchell Grass hay (*Astrelba spp.*) (control), control + urea and ammonium sulfate (90, 130, 170 and 210 g rumen digestible protein (RDP/kgDOM)), control + spirulina (90, 130, 170 and 290 g RDP/kgDOM). Rumen digesta was collected at the end of each period and the liquid (planktonic) fraction extracted. Total genomic DNA was extracted using a bead-beating protocol and the V2V3 region of the 16S rRNA gene 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. Differences in banding-patterns between animals and diets were identified using BioNumerics 5.1 (Applied Maths, Saint-Martens Latem, Belgium).

A dendrogram illustrating similarities among all animals over the three runs was created from two gels. This dendrogram shows a tendency for individual animals to cluster over the three runs regardless of treatment. The similarity in the majority of these animal clusters was greater than the 80% threshold denoting effectively identical profiles. Exceptions of within animal clustering were those animals fed the control basal diet (very low eMCP values) and animals supplemented with the highest level of spirulina (very high eMCP values). It appears that at very high eMCP values (>150gMCP/kgDOM) or very low eMCP values (<60gMCP/kgDOM), profiles tended to cluster as a treatment and separately but were not similar within treatments (<70%). The dendrogram also reveals that in steers fed low to medium levels of either supplement the rumen bacterial community profiles were very similar.

These results show that the fundamental bacterial profiles were most similar between samples from individual animals over time thus individual animal's genetics or physiology exerted the dominant influence on the rumen's bacterial ecosystem. In specific cases where either very high or low levels of nitrogen (N) supplementation were imposed, the intrinsic animal effect appeared to be over-ridden by the effect of the diet. The profiles at high and low levels of N supplementation appeared to cluster relative to high and low eMCP values suggesting a correlation between bacterial community profile and eMCP at the extremities of the range.

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Yu Z., Forster R.J. (Eds) (2005) 'Nucleic Acid Extraction, Oligonucleotide Probes and PCR Methods.' (IAEA: Netherlands).

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