

CONSTRUINDO SABERES, FORMANDO PESSOAS E TRANSFORMANDO A PRODUÇÃO ANIMAL

FIBROLYTIC AND NONFIBROLYTIC RUMEN BACTERIA IN FEEDLOT CATTLE DURING TRANSITION FROM FORAGE TO CONCENTRATE DIETS

Leni Rodrigues LIMA*¹, Mircéia Angele MOMBACH¹, Daniela Cristina FERREIRA¹, Bruno Carneiro e PEDREIRA², Perivaldo de CARVALHO¹, Karitha Regiane Ribeiro de AMORIM¹, Luciano da Silva CABRAL¹

¹Federal University of Mato Grosso, Cuiabá, Mato Grosso, Brazil

²EMBRAPA Agrossilvipastoril, Sinop, Mato Grosso, Brazil

*leni_rlima@hotmail.com

The intensification of beef cattle production systems has been adopted for many farmers in Brazil, specially in Midwest region, as a way to increase the productivity by unit of land used as well as to increase the profit and decrease the Greenhouse Gas (GHG) emissions. In this way, feedlot is a major strategy used in order to increase the land productivity, where cattle from grazing systems are rapidly changed to high grains diets, what increases the risk of nutritional diseases to occurring as acidosis and lameness. The objective of this study was to assess the effect of dietary levels of concentrate on microbial population in cattle. Four rumen fitted Nellore male cattle were used in this study from which rumen samples (solid and fluid) three hours after feeding were taken when those animals were fed to diets containing only forage (*Brachiaria brizantha* grass pasture) or when the diet had 50, 60, 70, 80 and 90% of concentrate on dry matter basis. Each level of concentrate in the diet was increased weekly in order to reduce ruminal disturbances. In the lab, rumen samples were submitted to DNA microbial isolation protocol, which used beads, phenol and chloroform in order to get high amount and high quality DNA. The DNA of rumen microbial population was then amplified with specie specific primers for fibrolytic (*Fibrobacter succinogenes* and *Ruminococcus albus*) and nonfibrolytic bacteria (*Prevotella ruminicola*, *Selenomonas ruminantium* and *Streptococcus bovis*) by qPCR technique what permitted to calculate the genes copy numbers for each bacteria. The population of *F. succinogenes* decreased with higher level of concentrate (90%), while the *R. albus* numbers increased when concentrate levels were higher than 60% ($P < 0.05$). *Prevotella ruminicola* and *S. ruminantium* numbers decrease a little with concentrate levels among 60 and 70%, but increased again in function of more concentrate in the diets ($P < 0.05$). *S. bovis* were higher in animals fed with zero (forage) and 50% concentrate diets, have been observed the lower number in cattle fed more the 70% concentrate. The results indicate that higher amounts of concentrate in cattle diet decrease some type of fibrolytic bacteria and increased the others, while causes a lower effect on nonfibrolytic bacteria. These results also indicate that slow increase in concentrate in cattle diets cause a lower dramatic change in ruminal microbial population than do rapid changes, different what have been observed in other studies when the changes occur faster.

Keywords: amylolytic bacteria, cellulolytic bacteria, grains, ruminal microbial population

Promoção e Realização:



Apoio Institucional:



Organização:

