

Assessment on Rumen Microbial Diversity of Bali Cattle Using 16S rRNA Sequencing

Authors : Asmuddin Natsir, A. Mujnisa, Syahriani Syahrir, Marhamah Nadir, Nurul Purnomo

Abstract : Bacteria, protozoa, Archaea, and fungi are the dominant microorganisms found in the rumen ecosystem that has an important role in converting feed ingredients into components that can be digested and utilized by the livestock host. This study was conducted to assess the diversity of rumen bacteria of bali cattle raised under traditional farming condition. Three adult bali cattle were used in this experiment. The rumen fluid samples from the three experimental animals were obtained by the Stomach Tube method before the morning feeding. The results of study indicated that the Illumina sequencing was successful in identifying 301,589 sequences, averaging 100,533 sequences, from three rumen fluid samples of three cattle. Furthermore, based on the SILVA taxonomic database, there were 19 kinds of phyla that had been successfully identified. Of the 19 phyla, there were only two dominant groups across the three samples, namely Bacteroidetes and Firmicutes, with an average percentage of 83.68% and 13.43%, respectively. Other groups such as Synergistetes, Spirochaetae, Planctomycetes can also be identified but in relatively small percentage. At the genus level, there were 157 sequences obtained from all three samples. Of this number, the most dominant group was Prevotella 1 with a percentage of 71.82% followed by 6.94% of Christensenellaceae R-7 group. Other groups such as Prevotellaceae UCG-001, Ruminococcaceae NK4A214 group, Sphaerochaeta, Ruminococcus 2, Rikenellaceae RC9 gut group, Quinella were also identified but with very low percentages. The sequencing results were able to detect the presence of 3.06% and 3.92% respectively for uncultured rumen bacterium and uncultured bacterium. In conclusion, the results of this experiment can provide an opportunity for a better understanding of the rumen bacterial diversity of the bali cattle raised under traditional farming condition and insight regarding the uncultured rumen bacterium and uncultured bacterium that need to be further explored.

Keywords : 16S rRNA sequencing, bali cattle, rumen microbial diversity, uncultured rumen bacterium

Conference Title : ICVBR 2017 : International Conference on Veterinary Bacteriology and Research

Conference Location : Melbourne, Australia

Conference Dates : November 29-30, 2017