

Abstract

Impalas are wild African ruminants that feed on wild browse which domestic cattle are incapable of utilizing because they lack the rumen microorganisms needed to breakdown these plants. Also, many of these plants contain toxins that the domesticated cattle are unable to detoxify and therefore become sick or die. By studying the bacteria within the rumen of impalas we can gain a better understanding of how they are able to utilize the toxic feed source. We can then apply this knowledge to improving the rumen of domesticated cattle so that they can develop the capability to digest such feeds and therefore become more efficient producers. Pyrosequencing was used to sequence the V1-V3 region of the bacteria 16S rRNA gene from the rumen of five adult impala from Pongola South Africa. MOTHUR and RDP Classifier were then used to analyze and classify the bacterial sequences down to family level.. Overall, the phylum Firmicutes was found to be the predominant bacterial group in all five impala samples, followed by the phylum Bacteroidetes in three of the five impala. Members of the Proteobacteria and Actinobacteria phyla were also present in percentages that were greater than those discovered in other ruminants such as the goat. A large percentage of the diversity within the rumen of all five impala samples were unclassified sequences. The presence of a large percentage of unclassified sequences may be explained by the limited studies done on the bacterial diversity of wild ruminants. The high concentrations of bacteria belonging to the Proteobacteria and Actinobacteria may explain how the impala can digest the toxic feed.