

**TITLE: MICROBIAL ANALYSIS OF RUMENAL BACTERIA IN SHEEP EXPERIMENTALLY FEED WITH *Brachiaria decumbens***

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**ABSTRACT:**

Among the Brazilian economic activities, the livestock activity is highlighted, due to the importance in the composition of the Gross Domestic Product (GDP). Pasture represents the main component in cattle, sheep, equines and goats feeding, with *Brachiaria* spp. The most used forage in pasture formation in Brazil, being present in all Brazilian regions. Intoxication cases have been described in ruminants and equidae, causing economic losses. The clinical signs observed in intoxication are secondary photosensitization with alterations in liver characterized with presence of macrophages with foamy cytoplasm in the sinusoids and obstruction of the lumen of the bile ducts. It was suggested that the saponins, a component of *Brachiaria*, itself were responsible for intoxication. Saponins are composed of low molecular weight secondary metabolites, identified in several plant families, being associated with protection against herbivory and pathogens. It is assumed that the saponins found in *Brachiaria* spp. It is assumed that the saponins found in *Brachiaria* spp are not able to promote intoxication and that activity of ruminal microbiome plays important role in its occurrence, since healthy animals infused with rumen fluid from intoxicated animals developed photosensitization. The aim of this work was to evaluate the rumenal diversity of sheep through new generation sequencing. Ruminal content (solid and liquid) in three periods (0d, 4d and 30d) of five sheep were collected using nasogastric tube. After extraction, DNA was amplified with multiplex oligonucleotides "Barcode" with the modified 3' region encoding the 16S rDNA region (V4-V5). Samples were sequenced using the Ion Torrent Genome Machine. The sequences were processed using Ion Torrent platform-specific pipeline software Torrent Suite v4.1 and 16S profiling analysis pipeline (Brazilian Microbiome Project) to generate the readings, removal of the adapters, denoising, chimera detection and taxonomic assignment with RDP database. The analysis of alpha diversity of ruminal bacteria presented a lower diversity of operational taxonomic units (OTU) before *B. decumbens* consumption when compared to the post-consumption periods. Diversity profile analysis showed 389 OTU with different abundance. Archea, Erysipelotrichaceae and Clostriales were more abundant after (4d and 30d), and Ruminococcaceae and Bacteroidales (0d) before. *Brachiaria* consumption in sheep associated to high saponin contents alters bacterial rumen profile that could modify susceptibility to intoxication.

**Keywords:** Microbiome, Rumen, *Brachiaria decumbens*, Intoxication

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