Examination and identification of bacterial species present in the forestomach of the Alpaca (*Vicugna pacos*)

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ABSTRACT

The alpaca (*Vicugna pacos*), a South American domesticated camelid used for pack, fibre and meat, has substantially increased its popularity in the United States over the past two decades. The alpaca's diet is high in fiber and consists of a variety of grasses and pastures, trees, hay, and shrubs. Like ruminants, alpaca digestion is dependent upon its microbial consortium within its foregut to breakdown and ferment feeds. However, unlike ruminants, there is a lack of information available on the microbes resident in the foregut of alpacas. A recent study that examined the Australian camel foregut reported that 28.2% of the bacteria within the foregut are fibre-degrading bacteria, 19.3 % are lipid utilizing bacteria, 12.7% are lactic acid bacteria, and 39.8% are uncharacterized bacteria. Because alpacas are camelids, it is hypothesized that the bacterial percentages will be consistent with those listed above, but may differ slightly because of differences in geographical location and dietary preferences. The present study used bar-coded pyrosequencing to examine the bacterial microbiome within the foregut of five alpacas housed at the Hespe Garden in Berlin, VT, and will compare these results with ruminant livestock. Information from this study will provide a future bioresource of genetic information and bacterial diversity that could benefit future agriculture efforts to increase the efficiency of digestion of feeds in production animals.