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Rumen bacterial diversity in steers with frothy bloat

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Abstract

Frothy bloat is a serious metabolic disorder that can result causein reduced performance or mortality inamong stocker cattle grazing hard red winter wheat forage in the Southern Great Plains. We hypothesize a dysbiosis in the rumen microbiome when the animal is exposed to one or more factors such as higher protein content (>18%) in wheat forage, cold and wet weather conditions (frost and dew) and animal itself which ultimately culminates in bloat. The study included 12 ruminally cannulated steers maintained on wheat pasture in late winter/early spring of 2010. The animals were scored for bloat (BS range 0 to 3) every morning 09:00 am during the bloat prone period which lasted for 3 weeks. Although most animals succumbed to experiencedbloat, only 3 animals showed a BS >2 (moderate to severe) while the rest of the group had either no bloat incidence or had a BS of 0.5 or 1. During the bloat prone period, the CP content of wheat forage was between 18-23% and the total precipitation was 6 inches . Rumen contents were collected from 6 animals (three steers with BS 2 and three steers with BS 0) and analyzed for bacterial community composition using pyrosequencing(454/Roche) of 16s rRNA gene tags. The total number of sequences analyzed was 54,621 reads and the number of operational taxonomic units (OTU's) identified were 3952. Firmicutes was the most prevalent phylum (up to 95%) among all animals. that grazed wheat forage. Nearly, Variation among animals was compared based on presence-absence information for bacterial taxa (unweighted UniFrac) and percent abundance (weighted UniFrac). Both the unweighted and weighted UniFrac analysis showed no differences (P>0.05), however >93% of variation in the clustering of bacterial communities between the bloated and non-bloated animals was explained by principal component analysis.weighted UniFrac was explained by the principle component analysis and the bacterial communities in bloated and non-bloated animals appeared to cluster as distinct groups . Differences based on relative abundance of bacterial taxa between the two groups became apparent from order rank and lower in phylogeny. For example, Bacteroidales, Clostridiales, Erysipelotrichales were higher P<0.05) in bloated animals. Although, the members in the phylum Tenericutes were present in lower counts, certain OTU's from the class Mollicutes were unique to bloated animals. It can be concluded that the bacterial community structure gets altered under a typical frothy bloat situation but future work is warranted with multiple sample numbers to validate results.

Biography

Pitta is the ruminant nutrition and microbiologist at the Center for Animal Health and Productivity (CAHP), School of Veterinary Medicine, Upenn. She completed her PhD program in New Zealand in the field of Animal Science. Dr. Pitta's current research program is focused on utilizing deep sequencing technology to gain a better understanding of the gut microbiome in herbivores in their health and diseased conditions and also in different stages of production.