

## Rumen bacterial diversity associated with bloat - A metabolic disorder in steers grazing lush wheat forage

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Frothy bloat is a serious metabolic disorder that can cause reduced performance or mortality in 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. Rumen contents were collected from 6 animals (three steers with bloat score '2' and three steers with bloat score '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. Over 93% of variation in the bacterial communities of bloated and non-bloated animals was explained by a two-axis principal component analysis. 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. Members of Paraprevotellaceae and Porphyromonadaceae increased ( $P<0.05$ ) while Coriobacteriaceae and Lachnospiraceae decreased ( $P<0.05$ ) in bloated animals. Although, members in the phylum Tenericutes were present in lower counts, certain OTU's from the class Mollicutes were unique to bloated animals. Both assembled contigs and unassembled sequences from shotgun sequencing data revealed significant differences in functional capabilities between bloated and non-bloated animals ( $P<0.05$ ). The in vitro bloat assay (biofilm, viscosity and foam properties) results correlates with differences in bacterial diversity data between the two groups. It can be concluded that the bacterial community structure and metabolic fingerprint are substantially altered under moderate frothy bloat conditions.

### Biography

Dipti Pitta is the ruminant nutrition and microbiologist at the Center for Animal Health and Productivity (CAHP), School of Veterinary Medicine, UPenn. She completed her Ph.D. program in New Zealand in the field of Animal Science. Her 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.

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