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Microbial community dynamics in the rumen associated with feeding dryforage and concentrate in different proportions in Mehshana buffalo (Bubalis bubalis) using 454/Roche sequencing technology

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Abstract

We surveyed 72 microbial communities from the rumen of water buffalo using 454/Roche sequencing technology. Our objectives were to identify diet-induced shifts in the rumen microbiome and to investigate the depth of coverage of metabolically active bacteria from the buffalo rumen using different primer pairs. To assess reproducibility, we considered animal to animal variation in all phylogenetic and community comparisons. The experiment included four non-lactating water buffaloes (Mehshana breed) fed three different experimental diets for six weeks each; diets were M1 (50% concentrate: 50% dry roughage), M2 (25% concentrate: 75% dry roughage) and M3 (100% dry roughage). A total of 333, 851 pyrotags (pooled by primer, diet, fraction and animal) were analyzed. Phylogenetic analysis revealed significant differences in the rumen microbiome mediated by primer and diet ($P<0.05$). Variations in microbial communities due to primer, diet, fraction and animal were compared using two approaches- one based on presence/absence of bacterial populations (unweighted UniFrac) and the other based on relative abundance of bacterial populations (weighted UniFrac). Clustering of communities was largely explained by primer differences in both weighted and unweighted UniFrac analyses ($P<0.001$). In the weighted analysis, community clustering by diets were significant ($P<0.05$), clustering by fractions tended to be significant ($P<0.08$) while no inter-animal variation was observed ($P>0.05$). Overall, bacterial populations showed higher proportions of celluloytic populations such as Ruminococcus and Fibrobacter ($P<0.05$) when diet comprised 100% roughage while Prevotella dominated ($P<0.05$) when concentrate was available to the animals.

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.