

Researchers study microbes in cattle to unlock metabolic disease mysteries

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Switching from warm-season grasses to cool-season forages can give livestock a belly ache, in some cases a deadly one, according to Texas AgriLife Research scientists.

Dr. Bill Pinchak, Texas AgriLife Research animal nutritionist at Vernon, is leading a team of scientists who are using state-of-the-art technology - metagenomics - to determine how changes in diet affect microbial communities in the digestive tract of cattle and how these changes may increase risk of disease.

Metagenomics is a field of molecular microbiology where the presence of a microbe is determined by identifying its DNA in a sample rather than trying to grow the organism in culture, said Dr. Jason Osterstock, AgriLife Research ruminant animal health scientist in Amarillo and part of the team.

Pinchak, who is head of the Bloat Research Project, said they want to understand the role of rumen microbial communities in metabolic disease, specifically frothy bloat of cattle grazing winter wheat pastures. Bloat is a costly and sometimes fatal disease of cattle, with an estimated \$400 million negative impact on the [beef cattle](#) industry.

Their goal is to determine the interactions among rumen microbes that lead to the onset and duration of disease, he said.

Studying individual microbial genus or species in the rumen only

provides part of the story, Osterstock said. In fact, the rumen is a complex microbial system comprised of bacteria, protozoa and fungi where the impact of a specific microbial species is dependent upon the activity of other microbes in the system.

Metagenomics is an ideal approach to studying these [microbial communities](#) because less than 10 percent of rumen microbes can be grown in culture using routine anaerobic methods, Osterstock said.

The team's current work has focused on bacterial populations in the rumen using sequencing methods and bioinformatics to classify which bacterial genera are present under different dietary conditions.

The bloat team recently completed the first genomics-based characterization of bacterial populations from steers associated with changing from a warm-season grass hay diet to a cool-season grazed forage diet. Their study included 14 steers sampled at two time points, the largest study of its kind to date, the scientists said.

During their research, the scientists found that the distribution of bacterial genera changes dramatically when stocker cattle transition from Bermuda grass hay to winter wheat forage diets, Pinchak said. In addition, analyses determined that bacterial communities were clearly different in the fiber, liquid and whole rumen fractions within the rumen, he said.

Overall, more groups of different bacteria occurred on Bermuda grass hay than wheat forage diets, which is consistent with the increased rumen retention time of the less digestible Bermuda grass hay, Pinchak said.

During the study, they found that specific bacterial groups would increase, decrease, appear or disappear from one diet to the other,

highlighting the complexity, plasticity and specificity of rumen bacterial populations, he said.

These results point toward the potential to use deeper metagenomic sequencing, including characterization of non-bacterial microbes, to gain better resolution and begin to unravel more complex relationships in future studies, Pinchak said.

Pinchak and Osterstock are joined on the research team by Dr. Dipti Pitta, an AgriLife Research post-doctoral research associate in Vernon; and Dr. Scot Dowd, director of the Research and Testing Laboratory in Lubbock.

The Bloat Research Project team recently formed a consortium with scientists at the Borlaug Institute at Texas A&M University; the J. Craig Venter Institute, a leader in genomic research in Rockville, Md.; and the University of Illinois.

Pinchak said metagenomics also can be used to study how cattle adapt to diets containing bioenergy co-products, discover novel enzymes for biofuel production, or to help understand how microbial community dynamics affect food safety pathogen prevalence, feed efficiency and greenhouse gas emissions.

Provided by Texas A&M AgriLife Communications

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