NEWS AND VIEWS

Frontiers in ruminant nutrition: An ASAS-CSAS-WSASAS 2020 Symposium overview

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Introduction

The Frontiers in Ruminant Nutrition Symposium was recently held at the 2020 joint American Society of Animal Science (ASAS), Canadian Society of Animal Science (CSAS), and Western Section of the American Society of Animal Science (WSASAS) in virtual format. This symposium was designed to showcase specific areas of ruminant nutrition research that represent current and emerging research frontiers. The purpose of the symposium was to stimulate discussion, creative research, and scholarship activities within these critical areas through relevant presentations by leading scientists in specifically selected fields. Five presentations were selected for this year's "Frontiers in Ruminant Nutrition" symposium. The first was the 2020 American Feed Ingredient Association Ruminant Nutrition Award recipient presentation by Dr. Terry Engle (Engle, 2020), who presented "Effect of Trace Mineral Source on Rumen Fermentation and Trace Mineral Distribution in the Rumen." The second presentation was entitled "Micronutrients, One-Carbon Metabolism, and Epigenetics: Potential Developmental and Production Outcomes" was provided by Dr. Matthew Crouse (Crouse et al., 2020a). The third presentation was given by Drs. Shawn Archibeque, Jasmine Dillon, and Kristen Johnson (Archibeque et al., 2020) and focused on "Linking Nutrition, Production, and Environmental Aspects of Ruminant Livestock Production." Dr. T. G. Nagaraja (Nagaraja, 2020) gave the fourth presentation on "Nutrition and the Ruminant Microbiome: Emerging Frontiers from an Old Friend." The final presentation

was entitled "Past, Present and Future of Protein and N Metabolism in Ruminants" and was presented by Drs. Gerald Huntington and Joan Eisemann (Huntington and Eisemann, 2020).

Symposium Overview

Dr. Engle (Engle, 2020) reported that the trace elements Cu and Zn have critical roles in ruminal microbial fermentation and whole animal metabolism. For Cu and Zn to be accessible to ruminal microbes, they must be soluble. Recent research from Dr. Engle's laboratory (Caldera et al., 2019) indicate that hydroxy trace mineral (HTM) forms of Cu and Zn are relatively insoluble in the rumen and more of HTM remains associated with the ruminal insoluble fractions when compared to sulfate trace mineral (STM) sources. Dr. Engle's laboratory has also reported (Caldera et al., 2019) that highly soluble sources of supplemental Cu and Zn (STM) can decrease fiber digestion, reduce total VFA concentrations, and be more tightly bound to ruminal solid digesta compared with HTM (Caldera et al., 2019). Their data are interpreted to indicate that stronger binding of STM relative to HTM to the ruminal solid digesta fraction may reduce small intestinal trace mineral absorption. Future research investigating the flow and passage rate of different trace mineral sources through the abomasum into the duodenum and duodenal absorption efficiency of Cu and Zn is needed. Future research investigating trace element supply, demand,

and function will yield a greater understanding of critical roles that these micronutrients play in animal metabolism, growth, function, and wellbeing.

Micro-nutrients serving as one-carbon metabolites (OCM) are methyl donors and/or cofactors that directly participate in the one-carbon metabolism pathway and include choline, B₁₂, B₆, riboflavin, folate, cobalt, sulfur, methionine, serine, and glycine. Crouse et al., (2020) reported that the core one-carbon metabolic pathways connect directly to polyamine synthesis, nucleotide synthesis, redox metabolism, and the citric acid cycle. One-carbon metabolites participate biochemically as methyl donors for epigenetic mechanisms (Crouse et al., 2019a,b). Limited data are available investigating developmental consequences of OCM supplementation in ruminants. In dairy cows, OCM supplementation has increased calf birth weight and offspring performance. Furthermore, methyl deficient diets during pre-conception altered the fetal hepatic methylome at 90 days of gestation and body composition in male offspring at 22 mo of age. Cell culture studies with bovine embryonic fibroblasts supplemented with OCM had increased growth rates and mitochondrial respiration parameters. Research into one-carbon metabolism and the influence of OCM supplementation on postnatal function will provide new insight and likely lead to altered management practices and increased beef cattle production efficiency (NASEM, 2016; Crouse et al., 2020).

The relationship between nutrition, production and environmental aspects of ruminant livestock production systems is a complex and highly nuanced subject that has long suffered from oversimplification and assumptions associated within these practices (Archibeque et al., 2020). However, with the advent of new and evolving models and a growing understanding of these complexities and their interactions with each other, there has been a large and welcome growth in recent literature regarding new and emerging technologies, and insights that will allow for appropriate and impactful changes in livestock management that will affect overall change for the benefit of society as a whole. The primary means through which environmental impacts may be modified are separated into four distinct, but interconnected mechanisms, which include 1) improvements in use of dietary nutrients, 2) use of dietary additives that impact certain functions in the digestive tracts of the animal, 3) improvements in genetics, and 4) improvements in productive efficiency. While it is obvious that there are significant overlaps between these practices, it is imperative to consider all these aspects to prevent “leakage” of impacts to other industries and processes. Understanding the relationships between nutrition, production, and the environment are essential to livestock production and sustainable agroecosystems. Future research efforts in this area are essential to success and competitiveness of both the U.S. and global livestock production.

The ruminal microbial community is composed of bacteria, archaea, protozoa, fungi and viruses (Nagaraja 2020). Culture and/or microscope techniques have identified over 200 ruminal microbial species. Rapid advancements in community genetic material-based analysis of the microbiome, based on targeted amplicon sequencing and metagenomics, has significantly expanded our understanding of the vast diversity and complexity associated with the ruminal ecosystem. Genetic material-based methodologies have identified thousands of microbial species in the rumen and indicate that 75 to 85% of the ruminal microbiome has yet to be cultured and functionally identified. A core microbiome of ruminal bacterial and archaeal populations exists across global geographical

region; however, wide variations in diversity, abundance, and individual taxa are driven by diet and host genetics (Nagaraja 2020). Evidence also exists for a signature microbiome among individual ruminants consuming the same diet type within similar environments. Microbiome-wide association studies in relation to dietary changes, ruminal function and dysfunctions have begun to link and define the complexity of the host-microbe relationships. Translation of the potential of the microbiome analysis is supported by emerging evidences that specific microbiota can be linked to ruminal activity and productivity. The low percentage of ruminal microbes that have been functionally studied coupled with the unique niche that ruminants play in both agroecosystems and human food security creates rich opportunities for novel and relevant research.

Dr. Gerald Huntington provided the final presentation of the symposium and focused on the protein and N metabolisms in ruminants (Huntington and Eisemann, 2020). By 1900, research identified urea, ammonia, and protein as the basic components of N metabolism in ruminants. Energy and protein metabolic interactions were outlined, amino acids were individually recognized as constituents of protein molecules, and the concept of enzyme-catalyzed reactions was established. Research stations were publishing research results and feeding recommendations. By 2000, the National Research Council built on the work of Henry and Morrison to create and revise publications of nutrient requirements for various classes of ruminants. Use of surgically altered animals, isotopically labelled molecules, and standardized laboratory analyses created quantitative information on ingestion, digestion, absorption, and metabolism of N-containing compounds. Protein composition and structure as well as the role of protein turnover to determine the concentration of cellular proteins were elucidated. Hypothesis-driven, statistically valid experimental designs created quantitative information on protein and amino acid requirements. Methionine was identified as the likely first-limiting amino acid for several ruminant species and production states. The internet and the advent of international symposia provided links among researchers around the globe. Today, multidisciplinary research teams are needed to enlarge the data base, to describe proteomics and metabolomics, and to integrate “big data” into insightful and useful models. Those models currently use or estimate rates and daily amounts of ruminal (in)degradability of dietary protein, ammonia production, urea recycling, microbial protein synthesis, post-ruminal protein digestion, metabolic fecal nitrogen, and amino acid absorption and metabolism. They predict use of metabolizable amino acids for maintenance, milk yield, growth, and fetal growth. Directions of future research include integration of functional roles of amino acids into recommended dietary supply and requirements, and focus on solutions to challenges presented by climate change, (in)sustainability of livestock production, and changes in public perception of humans’ use of ruminants and other animals.

Conclusions

Future research investigating trace element supply, demand, and function will yield a greater understanding of critical roles that these micronutrients play in animal metabolism, growth, function, and wellbeing. Research into one-carbon metabolism and the influence of OCM supplementation on postnatal function will provide new insight and likely lead to altered management

practices and increased beef cattle production efficiency. The relationship between nutrition, production and environmental aspects of ruminant livestock production systems is a complex and highly nuanced subject that has long suffered from oversimplification and assumptions associated within these practices. Understanding the relationships between nutrition, production, and the environment are essential to livestock production and sustainable agroecosystems. Translation of the potential of the microbiome analysis is supported by emerging evidences that specific microbiota can be linked to ruminal activity and productivity. The low percentage of ruminal microbes that have been functionally studied coupled with the unique niche that ruminants play in both agroecosystems and human food security creates rich opportunities for novel and relevant research. Regarding protein and N metabolism in ruminants, future research directions should include integration of functional roles of amino acids into recommended dietary supply and requirements, and focus on solutions to challenges presented by climate change, (in)sustainability of livestock production, and changes in public perception of humans' use of ruminants and other animals. Robust research efforts in these and other critical areas of ruminant nutrition are essential to success and competitiveness of both the U.S. and global animal agriculture.

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