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From the Editors

The importance of microbiota in ruminant production

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Ruminant production practices have changed greatly over the last century. For example, modern intensive dairy and beef systems can now produce an equivalent amount of milk and beef with far fewer animals, land, water, and feed compared with more than 30 years ago (Capper et al., 2009, 2011). Despite improvements in the efficiency of these systems, the world faces serious agricultural challenges in the coming decades. By 2050, global production and use of meat will almost double and is expected to reach 455 million tonnes per year (Alexandratos and Bruinsma, 2012). This will be a result of both an increase in human population, which is estimated to be 9 billion in 2050, and changes in dietary habits as rising incomes in developing nations increase demand for animal protein (Alexandratos and Bruinsma, 2012).

Meeting these demands in a sustainable manner will be challenging, as farmers will need to balance production with social, economic, and environmental issues. These issues include increased levels of: competition between livestock and humans for resources, such as water or plants used in ethanol production (Alexandratos and Bruinsma, 2012); greenhouse gas and manure production (Gerber et al., 2013), the latter which can be a source of food-borne pathogens; antimicrobial use as farms shift towards more intensive production systems (Van Boeckel et al., 2015); and animal health and welfare issues that may result from more intensive production, larger farms, and efforts to enhance feed utilization (Shields and Orme-Evans, 2015). How can we improve ruminant production efficiency to meet these pressures of a growing human population?

Articles in this issue of *Animal Frontiers* discuss how "microbiomes in ruminant production systems" are being studied and optimized to address the sustainability of ruminant production systems. It is becoming increasingly clear how the collective microorganisms of the ruminant host (microbiota) and their genomes (microbiome) play critical roles in animal digestion, health, and immunity (Backhed et al., 2005). Specifically, the

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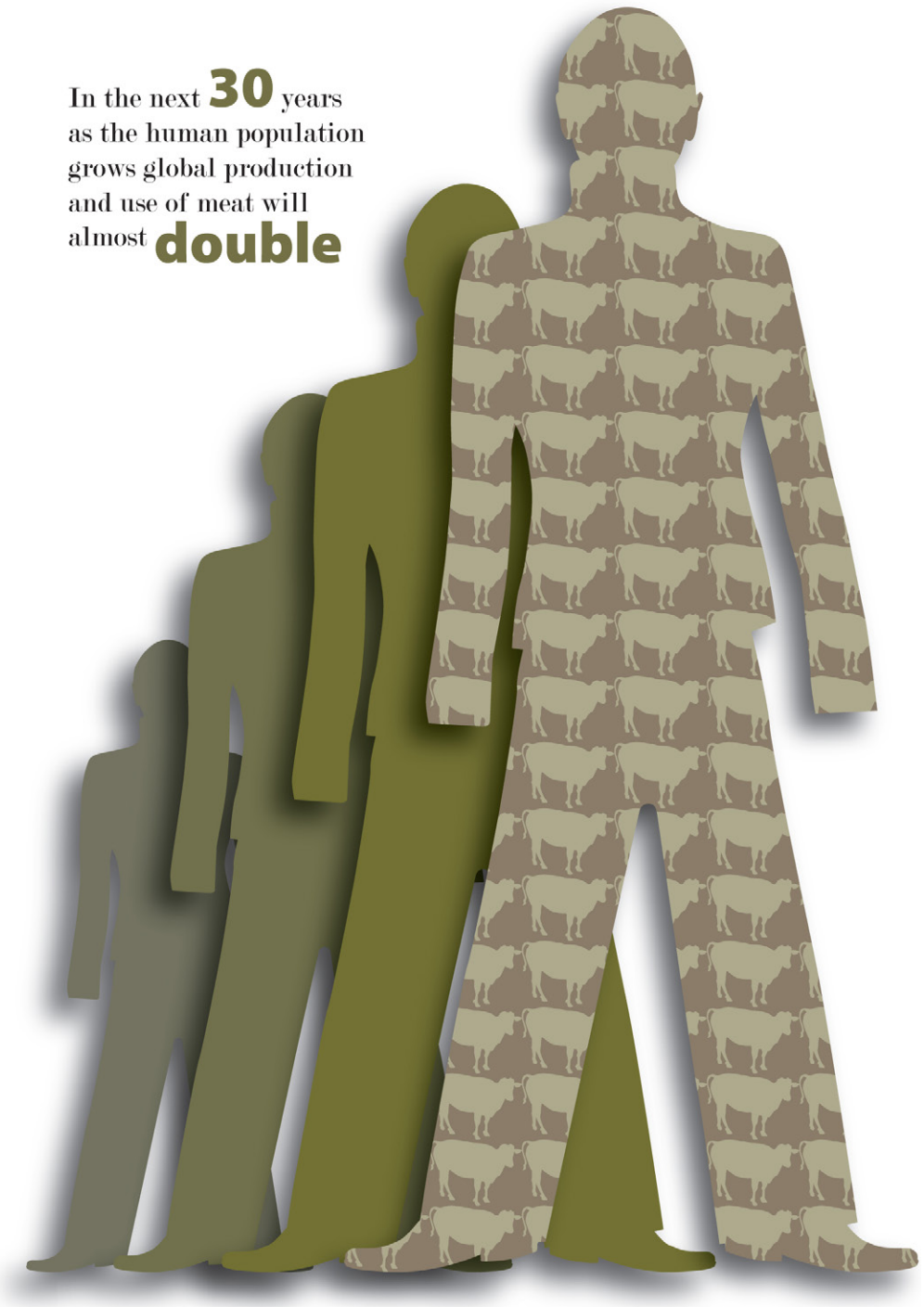
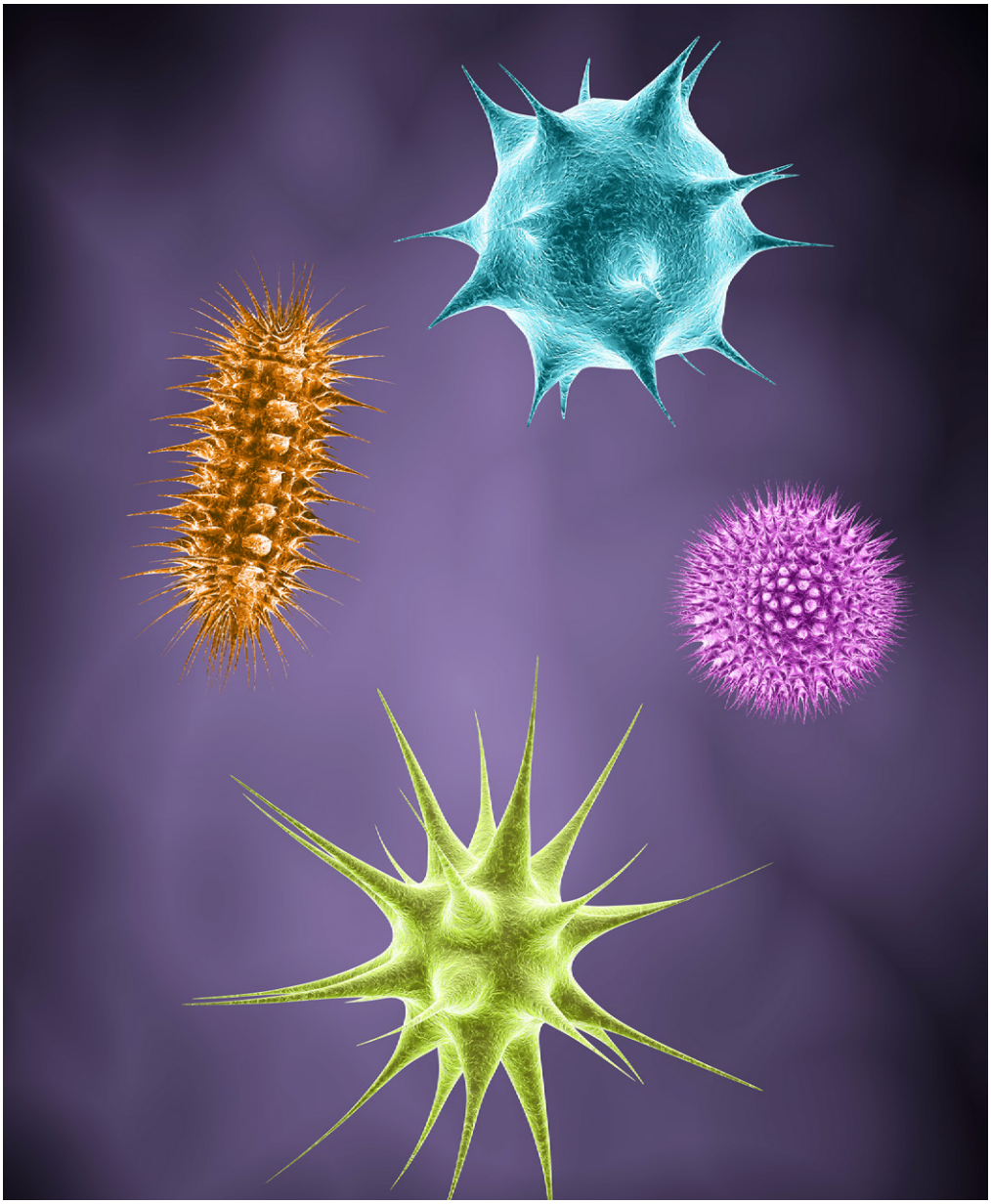
gut microbiota have been described as a microbial organ that provides metabolic capabilities to digest plant material that are missing in the host ruminant animal (Yoon et al., 2015). These microbiota are also a source of potential human and veterinary pathogens. Thus, manipulating the ruminant microbiome has the potential to enhance animal performance and health as well as reduce environmental pollution. So far, this has been a difficult task as technologies were lacking to study this microbiome comprehensively. However, decreasing costs of DNA sequencing technologies have allowed for studying the ruminant microbiome in unprecedented form in the last 10 years. This has led to an improved understanding of microbial genetic information and population dynamics in ruminants. Although knowledge on the functions of the microbiome is still relatively unknown, it is anticipated that this will become clearer in the future and that modification of the microbiota to enhance its functionality represents an opportunity to improve ruminant production systems.

We start with Malmuthuge and Guan (2016) where the authors provide an overview of the different technical strategies to study the microbiota of the ruminant digestive tract. They describe how the sequencing of genes that decipher taxonomic composition can be used to define what microorganisms are present in an environment. In contrast, analysis of community genomic DNA (metagenome), RNA (metatranscriptome), protein (metaproteome), and metabolites (meta-metabolome) lend to functional-based information. Utilizing a combination of these techniques is important to study the microbiome as studies have shown that low-abundant taxa can have important roles in host physiology. At the same time, genes that are present in high abundance do not necessarily correlate with expression and functional activity. The authors describe how certain microbial markers have been associated with disease susceptibility and efficiency. Changes in microbial populations may, therefore, create different phenotypes within a population. Altering the microbiome (e.g., through administration of probiotics), and therefore ruminant phenotype, is presented as a goal of future research.

The impact of feeding high-grain diets to ruminant livestock was described by Khafipour et al. (2016). The high-energy requirements of highly productive ruminant livestock necessitate the feeding of these diets. However, molecular-based sequencing technologies that have recently become available have shown how high-grain diets can adversely affect the composition and functionality, including the richness and diversity, of the microbiota in the reticulo-rumen and the hindgut. As a result, excessive grain feeding jeopardizes the health and production of the animals as well as the environmental sustainability of ruminant production systems. A challenge in determining how much grain feeding is excessive is that the grains and grain-processing techniques vary in their impact on gut health and the ruminants vary in their susceptibility to the adverse effects of high-grain feeding. These adverse effects can be attenuated by the use of supplements, such as buffers, yeasts, yeast culture products, direct-fed microbials and probiotics, and by microbiota engineering. However, in order to develop efficient strategies, their effects on the composition and functionality of





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microbiota in the digestive tract need to be better understood. In particular, more research on the effects of these strategies on the functionality of gut microbiota is needed as changes in this functionality are still difficult to predict from changes in the composition of these microbiota.

Ribeiro et al. (2016) focus on the rumen as a reservoir of plant-digesting enzymes that has resulted from the evolution of symbiotic microbiota and the host over millions of years. The rumen microbial community is specialized in degrading lignocellulosic material, which benefits the host through the production of end-products (e.g., volatile fatty acids) that can be used for growth and maintenance. Despite this, less than 50% of carbohydrates in low quality forages can be digested. Thus, as the authors suggest, enhancing digestion of low quality forages provides an opportunity to improve feed efficiency. To this end, feed enzymes have been utilized, but their initial development was not specific to rumen digestion, which may limit their efficacy. The authors describe how metagenomic and metatranscriptomic technologies are being used to characterize rate-limiting steps in the deconstruction of plant cell walls and the identification of novel enzymes that are tailored towards rumen fermentation. Combined, this may lead to development of rumen-specific feed enzymes with greater efficacy than the currently available varieties.

Wadhwa and colleagues (2006) described that in non-intensive ruminant husbandry systems, rumen function and productivity of ruminant livestock is often held back by poor forage quality and the resulting nutrient deficiencies. This can be overcome by supplementation with deficient nutrients, enzymes, and probiotics. However, the effects of these supplementations have so far been inconsistent. In order to develop efficient supplementation strategies, the effects of these strategies on the composition and functionality of microbial communities in the rumen, and the interactions between these communities and the host animal, must be understood. The recent advances in molecular-based techniques for the identification, quantification, and gene expression of microbiota allow for the generation of this information. In addition, these advances may allow the development of immunizations against selective microorganisms to enhance nitrogen utilization and reduce methane production in the rumen.

Conrad et al. (2016) describe the importance of the Shiga toxin-producing *Escherichia coli* (STEC), which are responsible for worldwide foodborne outbreaks and sporadic illnesses. The authors detail how horizontal gene transfer has led to the evolution of STEC through acquisition of virulence genes and mobile genetic elements. Ruminants are the main reservoir of STEC although they are asymptomatic carriers. Importantly, manure applied to land or in catchment basins acts as a source of STEC, which can then be transmitted to surface and groundwater during heavy periods of rain. Thus, increased manure production, as a result of livestock intensification, will need to be carefully managed in order to limit potential pathogen spread. It is a challenge to rapidly identify and source-track strains of STEC with the currently available technologies, but such efforts are critical for epidemiological studies and outbreak investigations. It is anticipated that genome sequencing and metagenomic analysis of environmental DNA will improve the speed at which STEC strains can be identified, but these technologies will only become more routinely applied when costs associated with their use decrease.

In the final paper of this issue, Timsit et al. (2016) focus on the microbiome of the bovine respiratory tract. Bacterial bronchopneumonia

can affect ruminants under all production practices, but it is especially devastating to the feedlot industry. The authors provide an overview of risk factors that predispose beef cattle to bronchopneumonia and also the pathogenesis of the disease. Despite research for more than 40 years, rates of bacterial bronchopneumonia have not decreased in feedlot cattle. Most studies on ruminant respiratory bacteria have focussed on pathogens using culture-based methods. However, recent microbiome studies suggest that the structure of the nasopharyngeal microbiota of cattle, including commensal bacteria, may also be related to the development of pneumonia. For example, after shipment to feedlots, the bacterial microbiota of the nasopharynx abruptly changes, and this coincides with the time cattle are most susceptible to bronchopneumonia. The use of metagenomic studies to better characterize the respiratory microbiota throughout beef production systems will help in the development of alternatives to antibiotics, which are currently used to both prevent and treat bacterial bronchopneumonia. Specifically, the authors propose that analysis of the respiratory microbiome may identify commensal bacteria that can be used as nasal-delivered probiotics to mitigate respiratory pathogens through direct inhibition and host immunomodulation.

In summary, demands for ruminant products will increase significantly in the next 30 years as the human population grows and a greater number of people can afford animal protein. Unless the sustainability issues that producers face today are addressed, meeting the needs of a growing population will be challenging for ruminant livestock sectors. As seen by the brief summary of papers in this issue of *Animal Frontiers*, studies of the ruminant microbiome are being conducted in several areas to address feed efficiency, animal health, food safety, and environmental concerns. Much of the work done to date has consisted of analyzing microbial populations in the ruminant digestive and respiratory tracts, and several authors indicate that functional research on their microbiome is the next step to many research goals for improving ruminant health and performance. With this will come the difficulties of the analysis and interpretation of the generated data. The depth of nucleotide sequence generation is ever-increasing, and the costs of the technologies are decreasing. Large sets of data can therefore be produced, but bioinformatic pipelines to analyze the data, though available, have not kept up with sequencing platforms in the form of user access and incorporation into research laboratory protocols. Also, it has been recognized that changes in the functionality of ruminant microbiota are difficult to predict from changes in their composition. As software for handling data continues to become available, we will see even more research on ruminant microbiomes. This will allow a continued shift from measuring what microorganisms are there to measuring what their functions are, how we can modify the microbiota structure, and what the result after modification will be. These are important questions that will lead microbiome research in the future. A combination of "omics" technologies may be needed to obtain the answers to these questions.

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