

# XXI UANL Symposium

## “Cattle fattening in corral”

### October 2-3, 2018

Report written by:  
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# 2018 Symposium overview

- Aim: to provide updated information about the latest topics of interest to beef cattle producers
- Organized yearly since 1997!
- Sponsored by different companies and associations such as Bayer, Diamond V, KEMIN, Angus Mexico, ELANCO, Trouw Nutrition and others
- >550 assistants (beef cattle producers, representatives of Academia, students)
- “The best event on the topic of beef cattle in the world”

# Why talking about microbes?

- There are many reasons why we should talk about microbes in events like this
- More importantly: the gut microbiota of livestock is **strongly related to health and production**
- Interestingly, growing evidence suggests that the gut microbiota is related to feed efficiency in beef cattle and other livestock species



## **Linkage of microbial ecology to phenotype: correlation of rumen microbial ecology to cattle's feed efficiency.**

Guan LL, Nkrumah JD, Basarab JA, Moore SS.

### **Abstract**

Linkage of rumen microbial structure to host phenotypical traits may enhance the understanding of host-microbial interactions in livestock species. This study used culture-independent PCR-denaturing gradient gel electrophoresis (PCR-DGGE) to investigate the microbial profiles in the rumen of cattle differing in feed efficiency. The analysis of detectable bacterial PCR-DGGE profiles showed that the profiles generated from efficient steers clustered together and were clearly separated from those obtained from inefficient steers, indicating that specific bacterial groups may only inhabit in efficient steers. In addition, the bacterial profiles were more likely clustered within a certain breed, suggesting that host genetics may play an important role in rumen microbial structure. The correlations between the concentrations of volatile fatty acids and feed efficiency traits were also observed. Significantly higher concentrations of butyrate ( $P < 0.001$ ) and valerate ( $P = 0.006$ ) were detected in the efficient steers. Our results revealed potential associations between the detectable rumen microbiota and its fermentation parameters with the feed efficiency of cattle.

## **Assessment of the microbial ecology of ruminal methanogens in cattle with different feed efficiencies.**

Zhou M<sup>1</sup>, Hernandez-Sanabria E, Guan LL.

### **+ Author information**

#### **Abstract**

Cattle with high feed efficiencies (designated "efficient") produce less methane gas than those with low feed efficiencies (designated "inefficient"); however, the role of the methane producers in such difference is unknown. This study investigated whether the structures and populations of methanogens in the rumen were associated with differences in cattle feed efficiencies by using culture-independent methods. Two 16S rRNA libraries were constructed using approximately 800-bp amplicons generated from pooled total DNA isolated from efficient ( $n = 29$ ) and inefficient ( $n = 29$ ) animals. Sequence analysis of up to 490 randomly selected clones from each library showed that the methanogenic composition was variable: less species variation (22 operational taxonomic units [OTUs]) was detected in the rumens of efficient animals, compared to 27 OTUs in inefficient animals. The methanogenic communities in inefficient animals were more diverse than those in efficient ones, as revealed by the diversity indices of 0.84 and 0.42, respectively. Differences at the strain and genotype levels were also observed and found to be associated with feed efficiency in the host. No difference was detected in the total population of methanogens, but the prevalences of *Methanosphaera stadtmanae* and *Methanobrevibacter* sp. strain AbM4 were 1.92 ( $P < 0.05$ ) and 2.26 ( $P < 0.05$ ) times higher in inefficient animals, while *Methanobrevibacter* sp. strain AbM4 was reported for the first time to occur in the bovine rumen. Our data indicate that the methanogenic ecology at the species, strain, and/or genotype level in the rumen may play important roles in contributing to the difference in methane gas production between cattle with different feed efficiencies.



## **Analysis of the gut bacterial communities in beef cattle and their association with feed intake, growth, and efficiency.**

[Myer PR](#), [Freetly HC](#), [Wells JE](#), [Smith TPL](#), [Kuehn LA](#).

### **Abstract**

The impetus behind the global food security challenge is direct, with the necessity to feed almost 10 billion people by 2050. Developing a food-secure world, where people have access to a safe and sustainable food supply, is the principal goal of this challenge. To achieve this end, beef production enterprises must develop methods to produce more pounds of animal protein with less. Selection for feed-efficient beef cattle using genetic improvement technologies has helped to understand and improve the stayability and longevity of such traits within the herd. Yet genetic contributions to feed efficiency have been difficult to identify, and differing genetics, feed regimens, and environments among studies contribute to great variation and interpretation of results. With increasing evidence that hosts and their microbiomes interact in complex associations and networks, examining the gut microbial population variation in feed efficiency may lead to partially clarifying the considerable variation in the efficiency of feed utilization. The use of metagenomics and high-throughput sequencing has greatly impacted the study of the ruminant gut. The ability to interrogate these systems at great depth has permitted a greater understanding of the microbiological and molecular mechanisms involved in ruminant nutrition and health. Although the microbial communities of the reticulorumen have been well documented to date, our understanding of the populations within the gastrointestinal tract as a whole is limited. The composition and phylogenetic diversity of the gut microbial community are critical to the overall well-being of the host and must be determined to fully understand the relationship between the microbiomes within segments of the cattle gastrointestinal tract and feed efficiency, ADG, and ADFI. This review addresses recent research regarding the bacterial communities along the gastrointestinal tract of beef cattle; their association with ADG, ADFI, and feed efficiency; and the potential implications for beef production.

## Assessment of microbiome changes after rumen transfaunation: implications on improving feed efficiency in beef cattle.

Zhou M<sup>1</sup>, Peng YJ<sup>2</sup>, Chen Y<sup>1</sup>, Klinger CM<sup>1</sup>, Oba M<sup>1</sup>, Liu JX<sup>2</sup>, Guan LL<sup>3</sup>.

### ⊕ Author information

#### Abstract

**BACKGROUND:** Understanding the host impact on its symbiotic microbiota is important in redirecting the rumen microbiota and thus improving animal performance. The current study aimed to understand how rumen microbiota were altered and re-established after being emptied and receiving content from donor, thus to understand the impact of such process on rumen microbial fermentation and to explore the microbial phylotypes with higher manipulation potentials.

**RESULTS:** Individual animal had strong effect on the re-establishment of the bacterial community according to the observed profiles detected by both fingerprinting and pyrosequencing. Most of the bacterial profile recovery patterns and extents at genus level varied among steers; and each identified bacterial genus responded to transfaunation differently within each host. Coriobacteriaceae, Coprococcus, and Lactobacillus were found to be the most responsive and tunable genera by exchanging rumen content. Besides, the association of 18 bacterial phylotypes with host fermentation parameters suggest that these phylotypes should also be considered as the regulating targets in improving host feed efficiency. In addition, the archaeal community had different re-establishment patterns for each host as determined by fingerprint profiling: it was altered after receiving non-native microbiome in some animals, while it resumed its original status after the adaptation period in the other ones.

**CONCLUSIONS:** The highly individualized microbial re-establishment process suggested the importance of considering host genetics, microbial functional genomics, and host fermentation/performance assessment when developing effective and selective microbial manipulation methods for improving animal feed efficiency.





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¡Gracias!  
¿Preguntas?  
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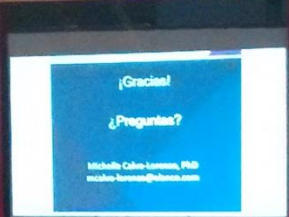
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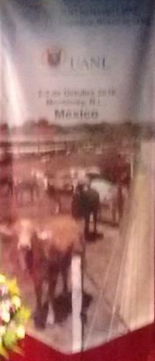
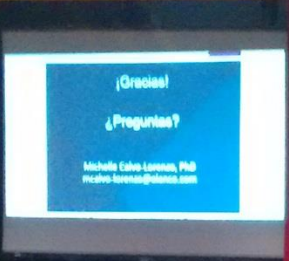
































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### Practices

- Bunk hay is a key tool for higher-risk and/or naive cattle
  - Purpose is an attractant, encourage eating new feeds
  - Typically not striving to obtain meaningful calories from it
  - Some nutritionists support the "low starch concept"
- Used more as an appetite regulator in healthy cattle that eat well









































Thank you ISME!

