

# THE RELATIONSHIP BETWEEN THE RUMEN MICROBIOME AND CARCASS MERIT IN ANGUS STEERS

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## I. OBJECTIVES

Profitability in the beef industry is heavily influenced by the quality and quantity of end products. Therefore, opportunities to improve both the quality and yield grades of beef carcasses at the producer level should be fully explored. The ruminal microbial ecosystem has a significant impact on overall host energetic status and nutrient availability, and thus alterations in the microbial populations in the rumen could impact energy partitioning and subsequent carcass composition. The objective of this study was to explore the relationships between ruminal microbial populations and adipose accumulation in Angus steers that were divergent in carcass merit.

## II. MATERIALS AND METHODS

Twenty-four Angus steers were slaughtered, and ruminal contents and carcass data were collected. Microbial DNA extraction and 16S ribosomal RNA gene sequencing were performed on the ruminal contents to determine microbial relative abundances, estimate microbial diversity, and to predict microbial metabolic pathways. *Longissimus* muscle samples were collected 48 h postmortem for proximate analysis to determine chemical lipid content. A variety of correlation analyses and one-way analysis of variance were performed to investigate the relationships between the rumen microbiome and carcass traits. For the analysis of variance, steers were grouped into high- and low-marbling classes ( $n = 10$  steers/class) with average marbling scores of 760 (low Prime) and 579 (average Choice), respectively.

## III. RESULTS

Marbling score and *longissimus* lipid content were positively correlated to both Chao1 richness index ( $P = 0.001$  and  $P = 0.009$ ) and the number of operational taxonomic units ( $P = 0.017$  and  $P = 0.043$ ), respectively, suggesting that increased intramuscular fat was associated with increased numbers of ruminal microbial species. The phyla Tenericutes and TM7 were negatively correlated ( $P \leq 0.05$ ) to marbling score and *longissimus* lipid content, indicating that lower abundances of these phyla in the rumen were linked to improvements in intramuscular fat content. Greater abundances of the bacterial family S24-7 in the rumen were positively correlated ( $P = 0.002$ ) to marbling score. Analysis by marbling classification revealed differences in microbial richness ( $P \leq 0.063$ ), diversity ( $P = 0.044$ ), and S24-7 abundances ( $P < 0.001$ ), such that the high-marbling steers had greater microbial richness, diversity, and abundance of bacteria within the family S24-7 in their rumen compared to the low-marbling steers. However, computational prediction of the microbial metabolic pathways revealed no differences ( $P \geq 0.05$ ) in metabolic function between steers in the high- and low-marbling classes. No estimates of microbial richness, evenness, or diversity were correlated ( $P \geq 0.05$ ) to 12th rib adjusted backfat thickness or yield grade. Several phyla, families, and genera, however, were correlated ( $P \leq 0.05$ ) to both 12th rib adjusted backfat thickness and yield

grade, each in a positive nature, suggesting that increased abundances of bacteria within these taxa were associated with increased subcutaneous fat deposition.

#### IV. CONCLUSION

Collectively, our results imply that differences in ruminal microbial abundances and diversity are linked to differing performance in carcass adipose traits. Overall, most of the bacterial taxa correlated to the intramuscular and subcutaneous fat depots did not overlap, suggesting that the microbial population impacted adipose accumulation largely via separate biological mechanisms within the host animal.

Keywords: lipid, marbling, rumen microbiome, subcutaneous fat, yield grade