

# THE RELATIONSHIP BETWEEN THE HINDGUT MICROBIOMES AND CARCASS MERIT IN ANGUS STEERS

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## I. OBJECTIVES

It is well known that microbial populations in the gastrointestinal tract of cattle contribute protein and energy to meet the host's nutrient requirements. These nutrients go on to influence animal performance and ultimately carcass composition. While the rumen is often accredited with the largest contribution of nutrients to requirements, recent research has suggested that the secondary fermentation occurring in the hindgut may also provide significant levels of nutrients that may explain portions of the variation seen in animal performance. Therefore, variation in carcass value, through the quality and quantity of beef produced, could be partially attributed to variation in the microbial fermentation occurring in the hindgut. The objective of this study was to determine whether dissimilarities in microbial taxa from the cecum and rectum contents of Angus steers could be correlated to differences in carcass lipid accretion in terms of intramuscular and subcutaneous fat deposition.

## II. MATERIALS AND METHODS

Twenty-four Angus steers were slaughtered to collect cecum contents, feces, *longissimus* muscle samples, and measurements for the calculation of carcass quality and yield grades. Cecal and fecal microbial DNA extraction and 16S ribosomal RNA gene sequencing were performed to determine microbial relative abundances. Proximate analysis was performed to determine chemical lipid content of *longissimus* muscle samples. A variety of correlation and regression analyses were performed to investigate the relationships between the cecal and fecal microbiomes and carcass traits.

## III. RESULTS

The relative abundance of the phylum Proteobacteria in the feces was negatively correlated to marbling score ( $P=0.009$ ) and *longissimus* lipid content ( $P=0.015$ ), indicating that lower abundances of bacteria within the phylum Proteobacteria may be linked to greater intramuscular adipose accumulation. The abundance of the family Succinivibrionaceae in the feces was negatively correlated to *longissimus* lipid content ( $P=0.017$ ), and within that family, the genus *Succinivibrio* was negatively correlated to *longissimus* lipid content ( $P=0.018$ ). In the feces, the abundance of the genus *Ruminococcus* was positively correlated to *longissimus* lipid content ( $P=0.031$ ). In the cecum, the abundance of the genus *Mycoplasma* was positively correlated to marbling score ( $P=0.029$ ). In contrast, the abundance of the genus *Methanosphaera* in the cecum was negatively correlated to marbling score ( $P=0.03$ ), suggesting that lower abundances of methane-producing bacteria in the cecum may be linked to greater marbling deposition through reductions in energy wasting in the hindgut. The genus *Bulleidia* was positively correlated to 12th rib adjusted backfat thickness ( $P=0.002$ ) and yield grade ( $P=0.019$ ), suggesting that greater abundances of bacteria within this genus in the cecum may be linked to increased subcutaneous fat deposition.

#### IV. CONCLUSION

No other bacterial taxa in the hindgut were correlated with 12th rib adjusted backfat thickness or yield grade, indicating that the hindgut microbiome may not play a substantial role in subcutaneous fat deposition. The hindgut microbiome may, however, influence intramuscular fat deposition through the fermentation end products of various microbial taxa. Overall, these results suggest that the microbiomes of the cecum and rectum impact adipose accumulation in the carcass via distinct mechanisms due to the lack of overlap in significant taxa.

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