

IS4-1

Bovine Gut Microbiome

Jin-Woo Bae

Department of Biology, Kyung Hee University

In beef cattle, male castration in young period results in later onset of obese phenotype and increased meat tenderness of the carcass. However, the knowledge of the effect(s) of male castration, followed by hypogonadism, on host metabolism is scarce. In the current study, metagenomics and metabolomics approaches were used to evaluate the intestinal microbiota and host metabolism of male, castrated male (CtM), and female Korean brown cattle (n = 30), the Hanwoo, and Holstein Friesian cattle (n = 15). In postpubescent CtM cattle, the serum testosterone level was low, and the animals possessed distinct rectal microbial and serum metabolic profiles, with significantly higher levels of serum branched-chain amino acids (BCAAs) than age-matched male controls. Microbial and metabolic profiling of the different intestinal compartments of adult CtM Hanwoo (n = 10) revealed a strong positive correlation of the serum BCAA levels and the presence of bacteria representing two unclassified genera from the family Peptostreptococcaceae, and the genera *Butyrivibrio*, *Acetivibrio*, and *Atopobium*, in the small intestine. Fresh striploin meat from CtM carcasses (n = 5 for each) was characterized by higher intramuscular fat accumulation, with significantly higher levels of several amino acids (including BCAAs) and ketone body (i.e., β -hydroxybutyrate) than male carcasses. Thus, the data suggest a link between male castration, alterations of the intestinal microbiota, and systemic amino acid metabolism in ruminants.