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Development of gut microbiota through life in an Angus-Brahman multibreed herd

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Commensal bacteria in the intestinal tract provide energy for the host and inhibit pathogen colonization. In this study, we investigated the effects of age, host genetics, and environmental factors on the gut microbiota development in an Angus-Brahman multibreed (MAB) herd from birth through entire life. The MAB herd was kept on the pasture before weaning, and steers were transported to a feedlot after weaning, while heifers were still kept on the pasture. We collected fecal samples from 278 calves belonging to the herd at four time points (within 12 hours, 3, 12, and 18 months after birth), and analyzed their gut microbiota structure by using 16S rRNA gene sequencing. Gut microbiota structure was gradually changed, with increased bacterial richness and diversity until stabilized 12 months after birth. However, the gut microbiota was altered dramatically after calves were moved to the feedlot, with decreased bacterial richness and diversity. *Enterobacteriaceae* (50%) and *Clostridaceae* (18%) were most abundant bacterial families right after birth. *Ruminococcaceae* (24%) *and Bacteroidaceae* (13%) became predominant during growth on the pasture, while *Prevotellaceae* (14%) elevated to be the second most abundant family in calves kept in feedlot. The animal weight steadily increased after birth and the growth rate was accelerated in feedlot, which was associated with *Succinivibrionaceae* and *Spirochaetaceae* proportion. We identified relative abundance of numerous bacteria linearly correlated with breed composition during 3~18 months after birth. *Clostridium* showed constant negative correlations with Brahman proportion through life. Similar consistent negative correlations were observed between plasma IgG1 level and Brahman proportion. In conclusion, these results indicate the existence of associations between specific gut commensal bacteria and animal growth and immunity through life. Further studies are needed to uncover the underneath host-microbe interactions.