

# Characterization of Bacterial Colonization in Large Intestine of Pre-weaned Dairy Calves Using Quantitative Real Time-PCR

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The mammalian hindgut is populated with a dynamic bacterial population, which has been suggested to associate with gut functions and host health. However, prior to this experiment, the microbiota composition in the hindgut of pre-weaned calves had not been studied. This study aimed to investigate population dynamics of total bacteria, *Bifidobacterium*, *E. coli*, *Faecalibacterium prausnitzii* and *Clostridium* cluster XIVa in the calf large intestine during the first 6 weeks of life. Tissues and digesta samples were collected from the cecum, colon and rectum of 18 Holstein bull calves at day 7 (n=6), day 21 (n=6), and day 42 (n=6), following euthanasia. Quantitative real time-PCR was used to estimate the copy number of 16S rRNA gene of total bacteria and selected bacterial groups associated with tissue and digesta. The density of large intestinal digesta-associated *E. coli* exhibited two and four-fold higher copy numbers on day 7 compared to that of day 21, and day 42, respectively. Similarly, the density of *E. coli* attached to cecum and colon tissue at day 7 was higher compared to day 21, and day 42. In contrast, the densities of butyrate producing beneficial bacteria *Clostridium* cluster XIVa and *F. prausnitzii* in colon tissue were highest on day 21. This study revealed that the prevalence of bacteria colonized in the large intestinal communities varied depending on calf age and intestinal region. Thus, detailed understanding of microbial colonization and their functions in the large intestine requires future studies based on sample type and region.