

Changes in the fecal Microbiome of Periparturient Dairy Cattle and Associations with the Onset of Salmonella Shedding

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Abstract : Non-typhoidal Salmonella enterica is a zoonotic pathogen with critical importance in animal and public health. The persistence of Salmonella on farms affects animal productivity and health, and represents a risk for food safety. The intestinal microbiota plays a fundamental role in the colonization and invasion of this ubiquitous microorganism. To overcome the colonization resistance imparted by the gut microbiome, Salmonella uses invasion strategies and the host inflammatory response to survive, proliferate, and establish infections with diverse clinical manifestations. Cattle serve as reservoirs of Salmonella, and periparturient cows have high prevalence of Salmonella shedding; however, to author`s best knowledge, little is known about the association between the gut microbiome and the onset of Salmonella shedding during the periparturient period. Thus, the objective of this study was to assess the association between changes in bacterial communities and the onset of Salmonella shedding in cattle approaching parturition. In a prospective cohort study, fecal samples from 98 dairy cows originating from four different farms were collected at four time points relative to calving (-3 wks, -1 wk, +1 wk, +3 wks). All 392 samples were cultured for Salmonella. Sequencing of the V4 region of the 16S rRNA gene using the Illumina platform was completed to evaluate the fecal microbiome in a selected sample subset. Analyses of microbial composition, diversity, and structure were performed according to time points, farm, and Salmonella onset status. Individual cow fecal microbiomes, predominated by Bacteroidetes, Firmicutes, Spirochaetes, and Proteobacteria phyla, significantly changed before and after parturition. Microbial communities from different farms were distinguishable based on multivariate analysis. Although there were significant differences in some bacterial taxa between Salmonella positive and negative samples, our results did not identify differences in the fecal microbial diversity or structure for cows with and without the onset of Salmonella shedding. These data suggest that determinants other than the significant changes in the fecal microbiome influence the periparturient onset of Salmonella shedding in dairy cattle.

Keywords : dairy cattle, microbiome, periparturient, Salmonella

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