**Application**

The microbial, physiological, and immunological development of the calf in the first few hours of life will be influenced by the colostral microbiome, as evidenced by the diversity of community members and their possible functions. Colostrum quality and its timely intake are key to preventing diseases and ensuring optimum calf health.

**Introduction**

Once believed to be sterile, there is increasing evidence of a naturally occurring colostral microbiome. Recent work in other mammals provides evidence that an entero-mammary pathway that mobilizes gut microbes and transfers them to the mammary during colostrogenesis does exist (Derakhshani et al., 2018). The microbes present in colostrum are ingested by the calf, and are integral to calf gut microbiome and immune development (Messman and Lemley, 2023). During development, commensal gut microbiota and their metabolites function in conjunction with the host to improve mucosal barrier and immune function (Chase and Kaushik et al., 2019). The origins of the pioneering microbes that colonize the calf gut are still debated, with microbes being sourced maternally and environmentally (Messman and Lemley, 2023). One potential maternally driven source would be that of a colostral microbiome, which may be an evolutionary adaptation designed to aid in gut microbiome colonization and development in the calf. To better understand the potential implications of a colostral microbiome on calf health and development, it is important to identify the microbes present in fresh, unprocessed colostrum as this is what the calf would be consuming naturally. Thus, the study objective was to examine the core bacteria identified in fresh colostrum collected from a single, spring-calving herd of primi and multiparous Holstein-Friesian (n=17) and Jersey (n=10) cows.

**Materials and Methods**

Colostrum samples (10mL × 3) were collected from all four mammary gland quarters within 2h of parturition (n=27) and were immediately snap frozen and stored at -80°C. Prior to microbial DNA extraction 600µL EDTA per 10mL colostrum was added and centrifuged to generate a microbial pellet (Siebert et al., 2021). Microbial DNA was extracted via repeated bead beating and column purification using a Qiagen DNeasy® PowerSoil® Pro Kit and extracted DNA was sent to Macrogen for Illumina amplicon sequencing of the V4 region of the 16S rRNA gene. Sequencing data underwent PERMANOVA, α- and β-diversity, and core analysis using R packages DADA2, Phyloseq, and Microbiome. Core analysis was performed once sequencing data had been filtered for a relative abundance (RA) of >0.05%. Core bacteria was defined as those bacteria, which were present in abundance of greater than 0.05% in all samples analysed. Colostrum immunoglobulin (Ig) concentration was determined using single radial immunodiffusion.

**Results**

There were no effects of breed or parity on colostrum IgG concentrations. Colostrum was determined to be of excellent quality (mean IgG 150.59 (SE 6.60) mg/ml). Based on PERMANOVA analysis, breed and parity had no effect on α-diversity, nor an effect on microbial composition. Fresh colostrum was observed to harbour a diverse microbial community with homogenous microbial composition across samples. Twenty-six bacterial genera were observed to contribute to the core microbiota. Bacillota (39.05%; 17 core), Pseudomonadota (21.56%; 5 core), Actinomycetota (6.88%; 2 core) and Bacteroidota (2.52%; 2 core) were the major phyla observed to contribute to the colostral core bacterial community. Of these, Christensenellaceae R-7, Lachnospiraceae NK3A20, and Oscillospiraceae UCG-005 are regularly identified as bovine gut commensals. The archaeal genera with the greatest relative abundance (RA) were Methanobrevibacter (85.5%) and Methanosphaera (13.5%). Both of these have previously been reported to be the dominate archaea present in the neonatal calf hindgut, indicating that archaea present in colostrum may contribute to the pioneering archaeal community in the calf gut.

**Conclusions**

The core colostral bacterial community observed in this study was highly diverse, in not only genera but also potential function, including acetate, propionate, and butyrate producers. These short chain fatty acids are critical to the development of the mucosal immune system of the calf in early life. The presence of strict anaerobes like archaea and commensal gut bacteria lend support to the theory of an endogenous entero-mammary pathway in cattle and may be reflective of a naturally occurring colostral microbiota. Mechanisms behind the formation of a colostral microbiome in ruminants are still unclear. To fully comprehend how the colostral microbiome influences the calf's intestinal microbiome, more research is necessary.

**References**

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