

Title: BEING NOSY: CHARACTERIZATION OF THE UPPER RESPIRATORY TRACT BACTERIOME OF APPARENTLY HEALTHY DAIRY CALVES IN PEI, CANADA

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Background: Bovine respiratory disease (BRD) is a major health concern involving complex interactions between respiratory bacterial and viral communities. Although metagenomic studies have characterized respiratory microbiome in cattle, limited information exists for healthy dairy calves, particularly on Prince Edward Island (PEI).

Hypothesis: Healthy dairy calves share core bacterial taxa within the upper respiratory tract (URT), but relative abundances vary with calf age.

Objectives: Characterize bacterial communities within the URT of healthy dairy calves on PEI and compare organism abundance by calf age.

Methods: Twenty apparently healthy dairy calves from one PEI dairy farm were sampled using protected nasopharyngeal swabs. Bacterial DNA underwent 16S rRNA gene sequencing using the MK1B Oxford Nanopore platform, and taxonomic classification was performed with EPI2ME software based on the SILVA_138_1 database. Statistical analysis and visualization were performed in R.

Results: Calves aged 1-5 weeks had a lower relative abundance of host-associated commensal bacteria than older calves. Shannon and Simpson diversity indices did not differ significantly between age groups. However, observed richness was significantly different between younger and older calves. Beta diversity analysis indicated that age explained about 16% of the variation in community structure.

Conclusion: Colonization of the nasal mucosa of neonatal calves with host-associated commensal bacteria appears to be delayed, which increases the risk of the development of respiratory disease in this group. Future research should focus on large-scale respiratory microbiome studies and on strategies to promote the early establishment of a healthy microbiome in young calves, including the development of effective probiotics or prebiotics.

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