

Associations between rumen and faecal microbiota and inflammatory status in transition dairy cows

Jeyanathan Jeyamalar, Heirbaut Stijn, Zhang Q Mingqi, Girma Muluken, Hertogs Karolien, Stevens Els, Aernouts Ben, Vandaele Leen, Fievez Veerle



Background

The transition period around calving is critical for dairy cows, due to the significant physiological, metabolic, and nutritional challenges. The variability among individual cows in adapting to these changes may be linked to differences in their gastrointestinal microbial communities.

Aim: To investigate the potential links between rumen & gut (faecal) microbial composition and the blood inflammatory biomarkers of dairy cows during the period between 7 days prior and 21 days after calving.

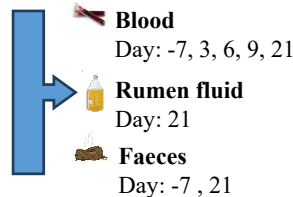
Method

Monitored during D-7 to D21 postpartum

Farm 1: 99 cows (117 lactations)
Farm 2: 65 cows (86 lactations)



Farm 1: 40 cows
Farm 2: 20 cows



Metabolic & inflammatory variables

β-hydroxybutyrate (BHBA), Non-esterified fatty acids (NEFA), Glucose, Insulin, Haptoglobin (HP), Serum amyloid A (SAA) & Albumin:Globulin (A:G)



Composition of microbes (Metataxonomic)

Bacteria, archaea, protozoa and fungi



Data analysis

Inflammatory status-based clusters: using SAA, HP and A:G
dbRDA analysis- Bray-Curtis distances of microbial composition in relation to blood metabolic and inflammatory variables.

Results

Inflammation-based clusters

- A. Acute phase response + diseased cows (APR⁺, n=20)
- B. Non- acute phase response cows (Non-APR, n=34)

Significant Farm Effect: Rumen & Faecal microbes

APR⁺ vs Non-APR: Rumen (D21) microbes

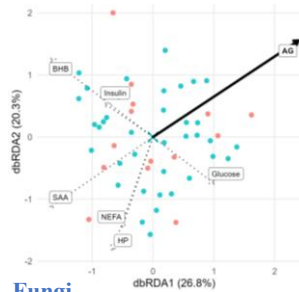
Beta diversity

Differentially abundant bacteria

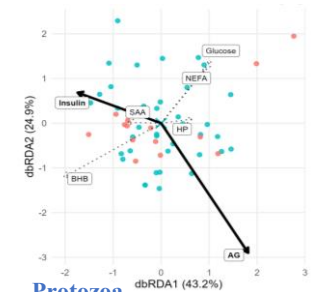
Target	P-value	Tax. level	Taxa
Bacteria	0.07	ASV	Uncul_Prevotella
Archaea	0.16	Genus	UMGS1994
Protozoa	0.03	Genus	Uncul_RFP12
Fungi	0.37		

dbRDA analysis rumen samples

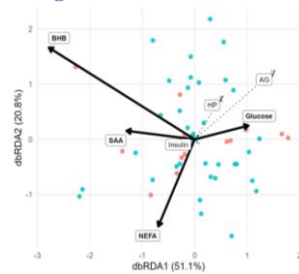
Bacteria



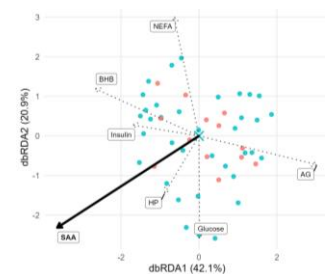
Archaea



Fungi



Protozoa



** Blood variables with significant association (P<0.05) are highlighted

Conclusion

- Farm significantly influenced rumen and faecal microbiota.
- At three weeks postpartum, inflammation was associated with shifts in the rumen but not faecal microbiota.
- Despite farm effects, rumen microbiota were linked to blood inflammatory variables, suggesting host-microbiome interplay in transition dairy cows.