

Microbiota and inflammation - do they tell the same story?

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Background and objective

Microbiota can tell much about the health of the individual. Even more so, when it is combined with inflammatory markers! The neonatal period is the foundation for future performance. In this study, we explore associations and possible effects of microbiota and inflammation during chronic cryptosporidiosis.

Statistics

Outcomes: haptoglobin (Hp), serum amyloid A (SAA), interleukin 6 (IL-6), calprotectin (cp), 3-month average daily weight gain (ADWG)

Predictors: 7, 10, 14 and 21-day microbiota, Shannon index

Analysis methods: stabiliser (elastic net), random forest

Materials & methods





One farm with chronic cryptosporidiosis

64 female dairy calves



Faecal and blood samples day 7, 10, 14 and 21



16S rRNA sequencing and ELISA

Results	Day 7 (n = 64)	Day 10 (n = 62)	Day 14 (n = 61)	Day 21 (n = 62)
SAA	Mitsuokella	Ruminococcus [torques] group	Gallibacterium	
		Peptostreptococcus		
Hp	Eubacterium [fissicatena] group	Lactobacillus, Megamonas, Cryptosporidium spp		Acidaminococcus, Lachnospiraceae NC2004 group, Acetitomaculum
		unclassified Muribaculaceae, Eysipelotrichaceae UCG-006		Succiniclasticum, Clostridium sensu stricto 1
ср	Unclassified Clostridia	Coprococcus	unclassified Ruminococcaceae	Megapshaera
IL-6	unclassified Coriobacteriales	Lactobacillus		
ADWG	Prevotella		Phascolarctobacterium	
Shannon index mean	2.21	2.57	2.97	3.2
Shannon index SD	0.37	0.34	0.31	0.39
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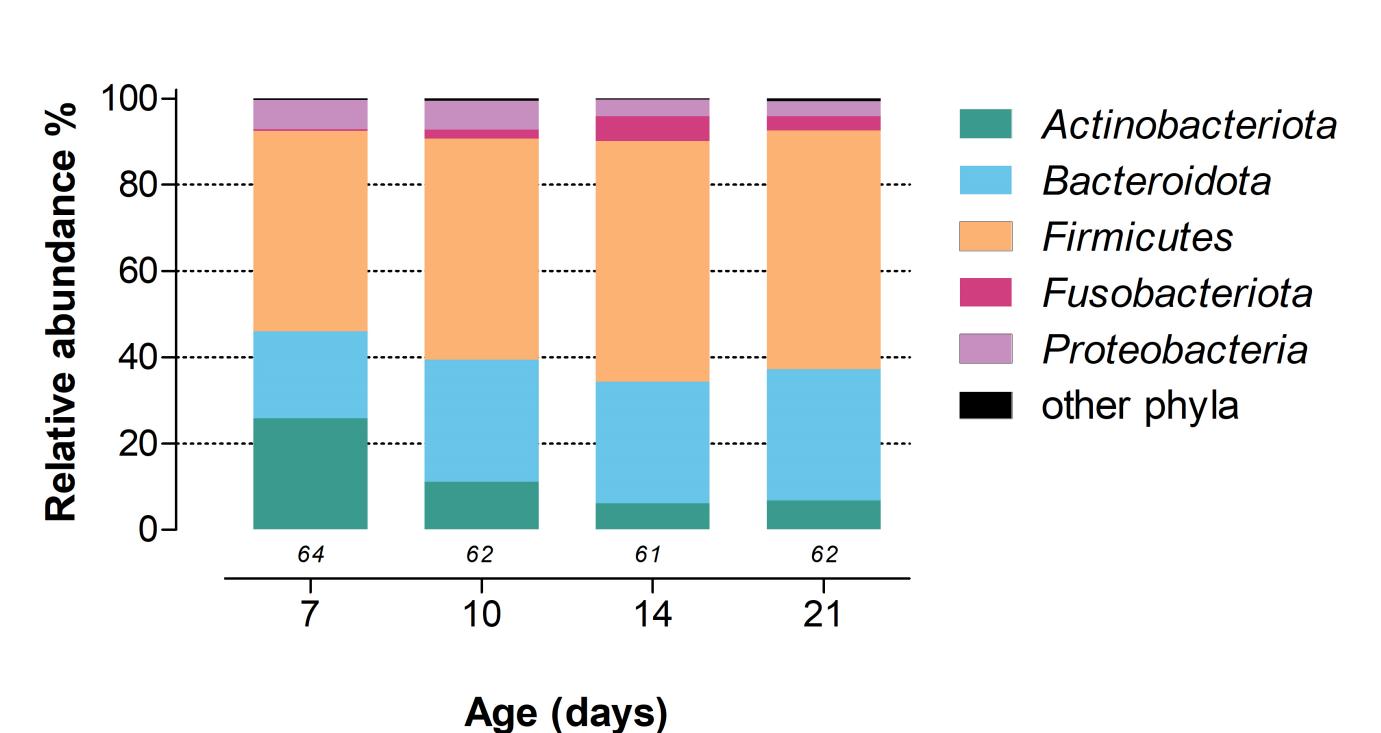


Figure 1: Composition of faecal microbiota of neonatal dairy calves at phylum level. Italic numbers above the x-axis indicate the number of samples.

Table 1: The green background indicates statistically significant positive association, purple indicates statistically significant negative association. Black text not in bold indicates trend toward the association in the respective background colour.

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Conclusions

Differs from other farm with acute cryptosporidiosis that caused deaths and was treated (Niine et al., 2018, Loch et al., 2023), although Peptostreptococcus showed a similar trend.

Relationships between microbiota, immune response, and performance depend on many factors, including farm, and results should be generalized with great caution.

Random forest and stabiliser identify the same genera.

