

Faecal microbiota associations with serum immunoglobulin levels in neonatal dairy calves



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Materials & methods



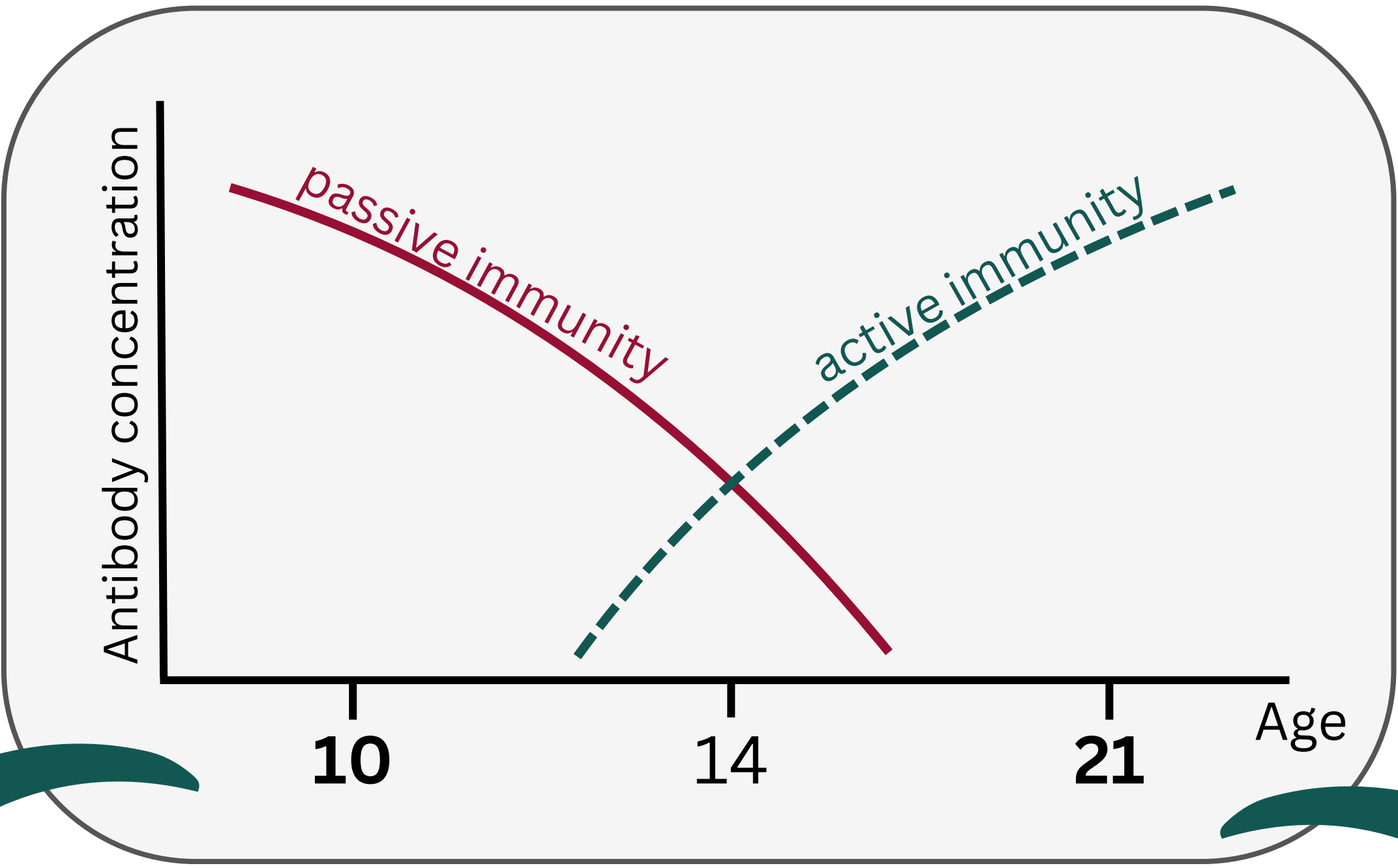
62 female dairy calves from one farm

Blood and faecal samples at day 10 and 21 of life

16S rRNA gene amplicon sequencing and ELISA

Background

The neonatal period is a critical window for the development of a capable immune system. Rapidly after birth, the intestines of newborns are colonized by bacteria, which may play a key role in shaping long-term health outcomes.



Objectives

This study investigates associations between faecal bacterial composition and immune reaction in dairy calves during their first weeks of life.

Table 1: Recurring bacterial families or genera are shown in bold.

Day 10	+	-	Day 21	+	-
IgG	<i>Mogibacterium</i> ***	<i>Ruminococcus torques</i>	IgG	<i>Ruminococcaceae</i>	<i>Peptoniphilus</i> ***
	<i>Allisonella</i> ^	<i>f. Lachnospiraceae</i> ***		<i>Catenisphaera</i> ***	<i>Phoceae</i> **
	<i>Escherichia-Shigella</i> ***	<i>Butyricicoccus</i> *		<i>Clostridium innocuum</i> ***	<i>f. Lachnospiraceae</i> *
	<i>Bacteroides</i> **			<i>Agathobacter</i> *	<i>Ruminococcus torques</i> ^
	<i>Holdemanella</i> ***				
SAA	<i>Bacteroides</i> *	<i>Erysipelotrichaceae</i> **	SAA	<i>Mitsuokella</i> ***	<i>Psychrobacter</i> ***
	<i>Peptostreptococcus</i> *	<i>Collinsella</i> **		<i>Campylobacter</i> *	<i>f. Lachnospiraceae</i> *
	<i>Escherichia-Shigella</i>	<i>f. Lachnospiraceae</i> ^		<i>Colidextribacter</i> **	
		<i>Mailhella</i> *		<i>Peptoclostridium</i> *	

p-value : < 0.001: three stars (***) / 0.001 to 0.01: two stars (**) / 0.01 to 0.05: one star (*) / 0.05 to 0.1: circumflex sign (^)

Conclusions

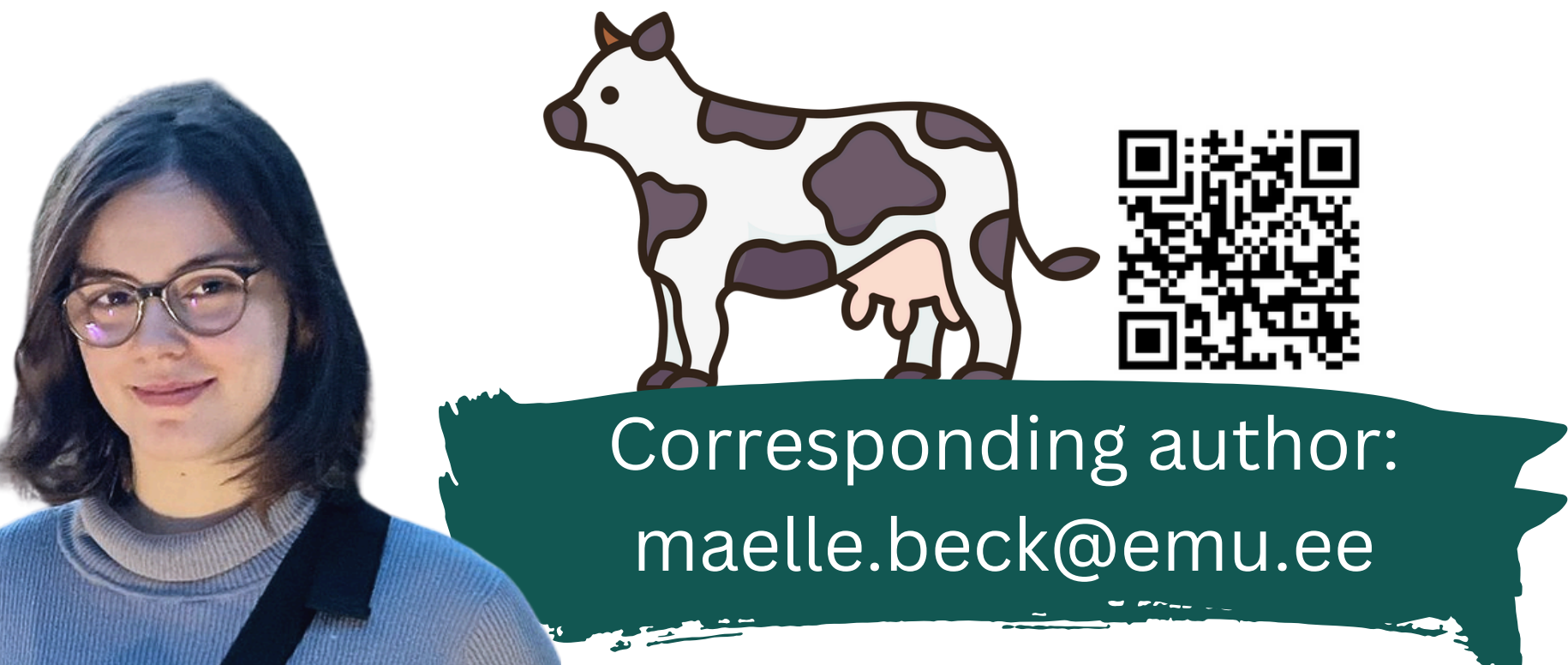
Fluctuations in IgG and SAA serum levels are associated with the changing microbiota before and after the window of low immune protection. Some bacterial families and genera remain consistent between day 10 and 21 of life, particularly those with a negative association to IgG.



Statistical analysis

First 10 most influential genera across 20 stabiliser runs were included into the regression model (GLM).

Backward stepwise method using Akaike Information Criterion (AIC) was implemented to select the best model explaining the IgG and SAA concentration changes by genera.



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