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Methane emission, microbiome and immune function in dairy cattle





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Background

- Low methane emissions were associated with higher feed efficiency
- Low methane emission is related to less efficient fiber digestion
 - Lack energy to sustain immune reponse
- How microbial community structure reflects low or high methane emissions?





Objective

• Delineate interactions between enteric methane (CH₄) emissions, rumen microbiome, and immune function in early and late lactating cows.





Research questions



Experimental design and results



Days in milk	Early lactation, 31 ± 7	End of lactation, 390 ± 80
Number of Holstein cows	N = 20	N = 14
2./3./4. lactation	14/6/0	9/4/1
Body weight, kg	650 ± 59	790 ± 76
Dry matter intake (DMI), kg	17 ± 4	16 ± 3
Energy-corrected milk (ECM), kg	41 ± 6	21 ± 3
ECM/DMI, kg/kg	2.5 ± 0.7	1.3 ± 0.3
DMI/BW, kg/kg	2.6 ± 0.7	2.0 ± 0.3
Methane (CH ₄), g/d	362 ± 54	404 ± 66
CH ₄ /DMI, g/kg	22 ± 4	26 ± 3
CH ₄ /BW, g/100 kg	56 ± 9	51 ± 7
CH₄/ECM, g/kg	9 ± 2	20 ± 4

• Statistics: regression analysis and paired t-test

Results





Low methane yield = low feed efficiency

 Cows producing less CH₄/DMI (g/kg) were characterized by a LOWER feed conversion efficiency FCE (ECM/DMI)













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Immune response and methane emission

- Peripheral blood mononuclear cells (PBMC) proliferation index (PI) to mitogens PHA and ConA
- TNF α concentration in whole blood incubations stimulated by lipopolysaccharide (LPS)
- CH₄/d, CH₄/DMI, CH₄/ECM and CH₄/BW were not related (p>0.1) to immune response (PI_PHA, PI_ConA)











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Immune response and methane emission

 Except that a trend was observed between TNFα concentration and methane yield in early lactation









Immune response and methane emission

- Retrospectively categorized into low and high CH₄/DMI emitting cows
- Low and high emitters in early lactation differ in immune response to ConA and TNF α (not shown), and tend to be different in response to PHA



Dilemma Low methane yield = climate friendly cow Low proliferative immune response = not resilient cow



Low methane yield reflected by rumen microbiome?





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- 16S rRNA sequence analysis for taxonomic identification and relative abundance of microbial populations (Kunath et al. 2018).
- Preliminary results obtained so far comparing lactation stages
- low and high emitters within lactation stage are not compared yet

Comparison of early and late lactation rumen microbes



	Early	Late	
Bacteroidetes; Prevotella 1 -	12.7	22	
Euryarchaeota; Methanobrevibacter -	11.5	7.7	
Firmicutes; Succiniclasticum -	6.6	7.4	
Firmicutes; Christensenellaceae R-7 group -	7.7	45	
Firmicutes; Lachnospiraceae NK3A20 group –	6.7	43	
Firmicutes; Ruminococcus 2 -	4	43	
Firmicutes; Ruminococcaceae NK4A214 group -	4.6	3.1	
Firmicutes; Acetitomaculum –	3.5	1.6	
Bacteroidetes; Rikenellaceae RC9 gut group -	1.8	2.4	
Actinobacteria; Bifidobacterium –	2.4	1.4	
Bacteroidetes; Prevotellaceae UCG-001 -	1.5	1.9	relative abundance (%)
Bacteroidetes; Prevotella 7 –	1.5	15	20
Firmicutes; Ruminococcaceae UCG-014 -	1.4	13	15
Firmicutes; Mogibacterium –	1.6	,	- 10
Firmicutes; [Ruminococcus] gauvreauii group –	1.2	12	5

11

• Heatmap of the 15 most abundant genera.

Comparison of early and late lactation rumen microbes



• Example of graphical output from LEfSe analysis



Comparison of early and late lactation rumen microbes





• **Principal component analysis (PCA):** identification of samples with similar microbial communities





Summary

 Results suggested that low methane emissions were related to lowered feed efficiency and decreased immune function

