Microbiome and Feed Efficiency in Dairy Cows

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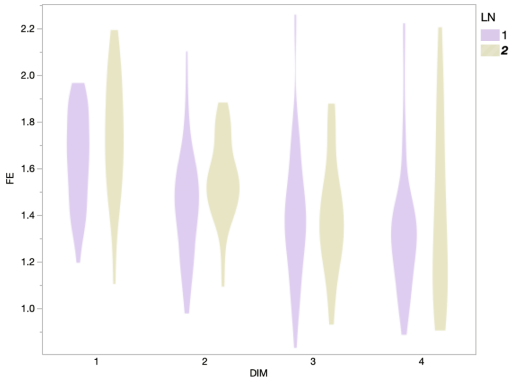
Introduction

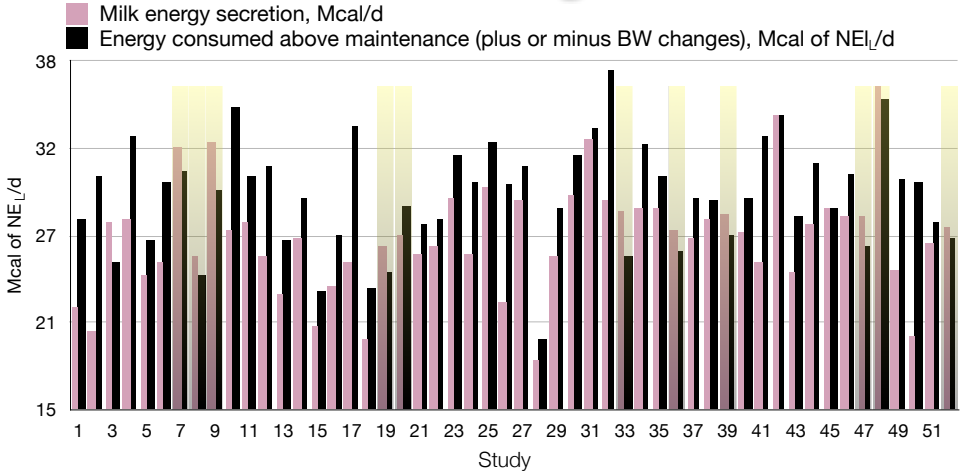
- Feed efficiency is of paramount importance for adequate use of natural resources
- Efficiency of milk production at the cow level can be decomposed in:
  - **1)** Physiological status of the cow
  - **2)** Digestive function
  - **3)** Metabolic partitioning
  - **4)** Genetics (ultimately dictating the two previous aspects)
  - **5)** Nutritional management

Physiological Status

- Parity
- Stage of lactation
- Health status
- Environmental conditions (both cold and heat)



Metabolic Partitioning



Metabolic Partitioning

- This discrepancy could be explained by:

1) A difference between DMI at which the NE_L content of the diet was calculated for and the actual DMI (i.e., overestimation of energy supply from the ingredients in the ration)

2) Underestimated maintenance needs

3) Potential changes in efficiency of use of energy for milk

Metabolic Partitioning

- Energy requirements for maintenance are calculated as:

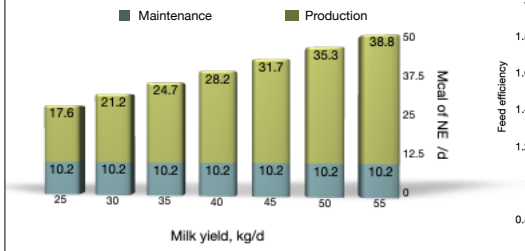
$$0.08 \times BW^{0.75}$$

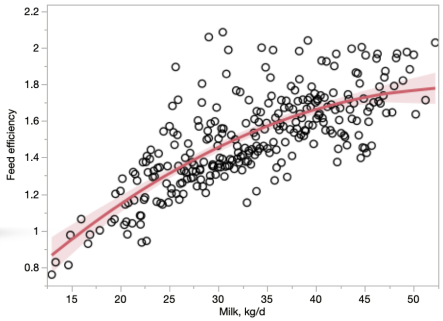
- Moraes et al. (2015) proposed that energy requirements for maintenance should be calculated using an α=0.086
- Bach et al. (2020) summarized 52 studies and inferred that it should be α=0.097

10.2 vs 11.1 Mcal (~1.3 kg of milk)

Genetics

- Despite the fact that FE has not been directly selected for in dairy cattle, it has doubled in the last 50 years
- Because the improvements in FE diminish with each marginal increase in milk yield, continued FE amelioration through more milk seems not plausible (VandeHaar et al., 2016)





Digestive Function

- Feed digestibility is a reflection of both inherent digestibility of the ingredients that compose a ration and the digestive ability of the animal
- External component:
  - Feeding highly digestible ingredients should result in improved FE
  - Particle size
- Inherent component:
  - Feeding behavior
  - Rumen (and hind gut) microbiome

Microbiome

- Bacteria are present:
  - 10^{10}–10^{14} cells/ml rumen fluid (O'Hara et al., 2020)
  - 10^{4} cells/ml in the small intestine (Frey et al., 2010)
  - 10^{10}–10^{14} cells/ml in the hind gut (especially colon) (Imai et al., 1981)

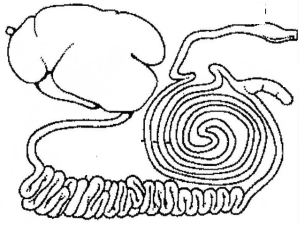
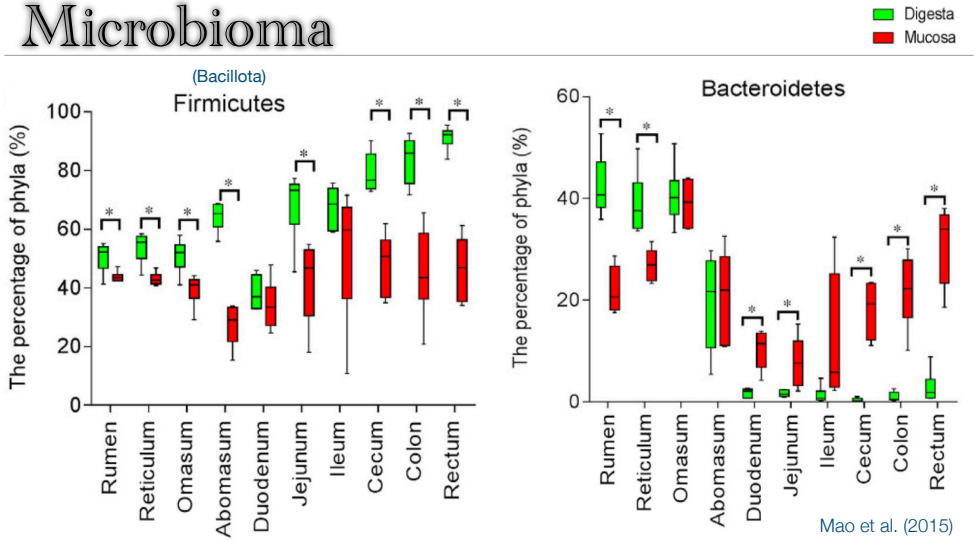


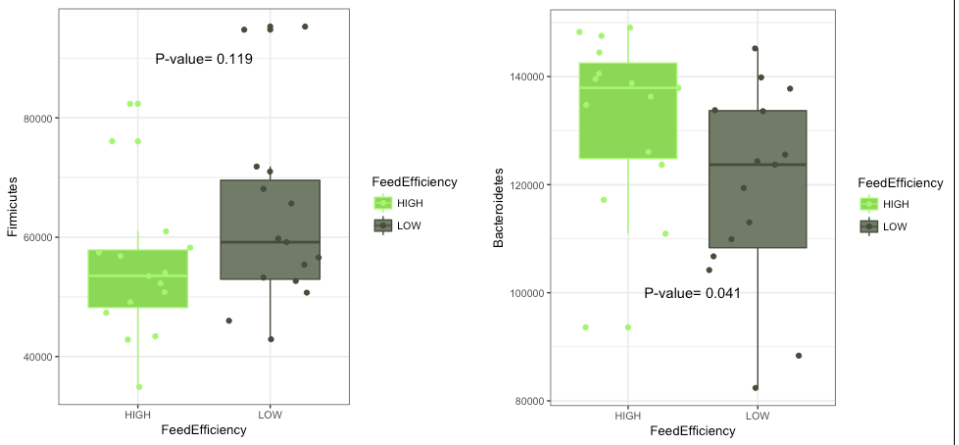
Image from: https://inspection.canada.ca/en/food-guidance-commodity/meat-products-and-food-animals/srm/appendix-c

Microbioma



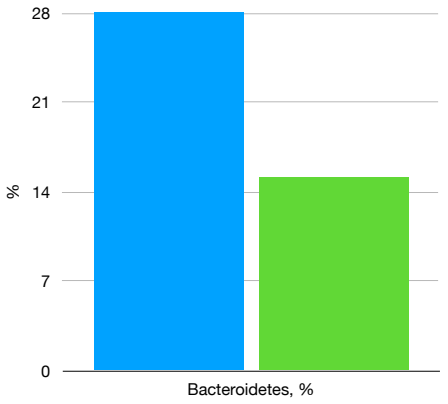
Mao et al. (2015)

Microbiome



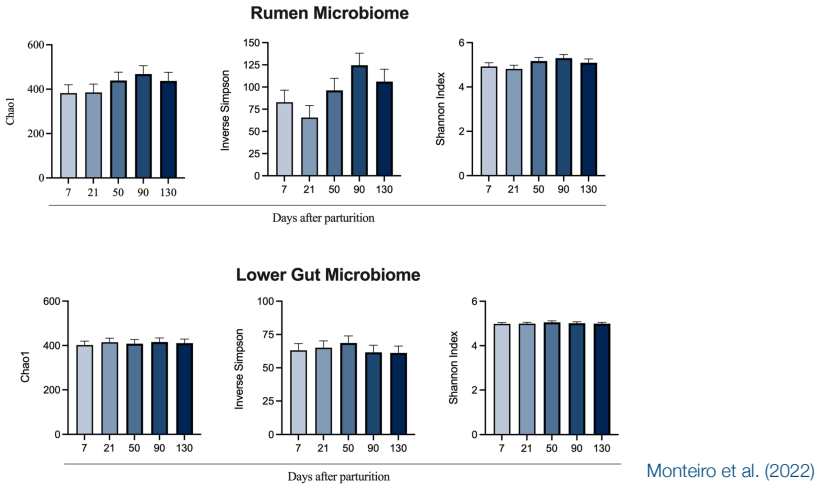
Delgado et al. (2019)

Microbiome



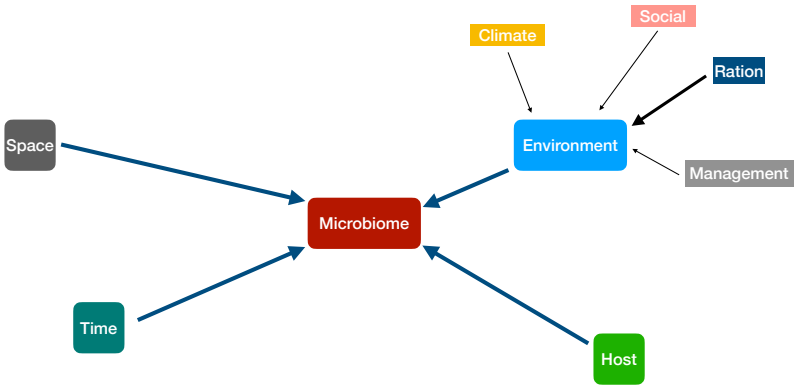
Khafipour et al. (2009)

Microbiome



Monteiro et al. (2022)

Microbiome



Direct fed microbials

- Which DFM?

Fungi
- *Aspergillus oryzae*
- *Saccharomyces cerevisiae*
- *S. boulardii*

Gram Negative
- *Butyrivibrio fibrisolvens*
- *Megasphaera elsdenii*
- *Prevotella bryantii*

Gram Positive
- *Lactobacillus acidophilus*
- *L. rhamnosus*
- *Lactococcus lactis*
- *Streptococcus bovis*
- *Enterococcus faecalis*
- *E. faecium*
- *Bifidobacterium bifidum*
- *B. ruminantium*
- *Bacillus toyonensis*
- *B. subitilis*

Rumen - Yeast

1. Scavenging of oxygen: 1.3 mg of yeast/ml of rumen liquid in Rusitec. That would be equivalent to 325 g of yeast per cow a day (Commercial use is 1 g/d)

2. *S. cerevisiae* was able to outcompete *S. bovis* for the utilization of sugars and limited the amount of lactate produced (Chaucheyras et al., 1996) (dose $1x10^7$ CFU/ml, much greater than what would be fed commercially ~10^4/ml)

3. Increased relative abundance of lactate-utilizing bacteria (*Megasphaera* and *Selenomonas*) as well as fibrolytic groups (*Fibrobacter* and *Ruminococcus*) ($5x10^{10}$ CFU/d)

Rumen - Yeast

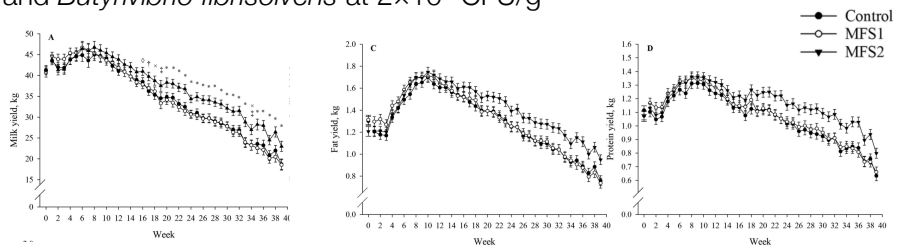
- Pre-conceived bias
- *In conclusion, supplementation of live yeast did not affect production performance or nutrient digestibility of high-producing cows in mid lactation. The reasons for the lack of effect are not clear, but an evaluation of interactions between yeast and rumen buffer supplementation is warranted.*

Ferreira (2019)

Rumen - Bacteria - Yeast

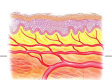
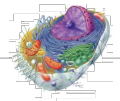
~6x10^6 CFU/d

- Mixtures of rumen-native microorganisms
- MFS1: 0.33 g/kg *Clostridium beijerinckii* and *Pichia kudriavzevii* at 2×10^7 CFU/g
- MFS2: 0.33 g/kg *C. beijerinckii*, *P. kudriavzevii*, *Ruminococcus bovis*, and *Butyrivibrio fibrisolvens* at 2×10^7 CFU/g



Valldecabres et al. (2022)

Intestine

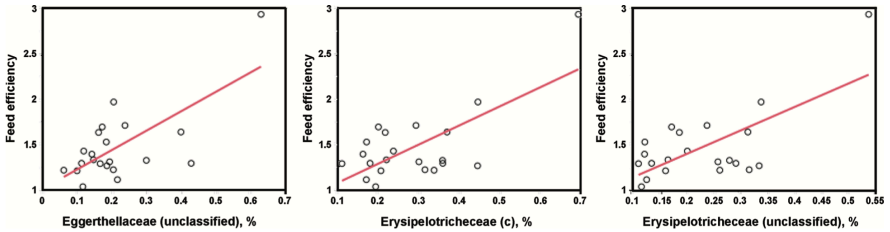
- Mice with a high-running capacity have a greater basal metabolic rate because they have a greater 'metabolic machinery' (Rolfe and Brown, 1997)
- In cattle, maintenance needs have increased as milk production has increased throughout the years (NRC, 2001; NASEM 2021)
- Maintaining gut length and absorptive surface is energy-requiring
- To ensure that the intestinal lengthening pays off, the energy needed to maintain the increased intestinal surface must by justified by promoting overall increase in the energy balance

Intestine

- Research involving probiotics targeting the intestine in dairy cattle:
  - Wu et al. (2024): A combination of encapsulated *Bacillus coagulans* and *Saccharomyces boulardii*. Tested on 3 cows per treatment
  - Chida et al. (2021): *Lactobacillus plantarum* in 5 transition cows (probiotic confounded with energy level of the diet -no control)

Intestine

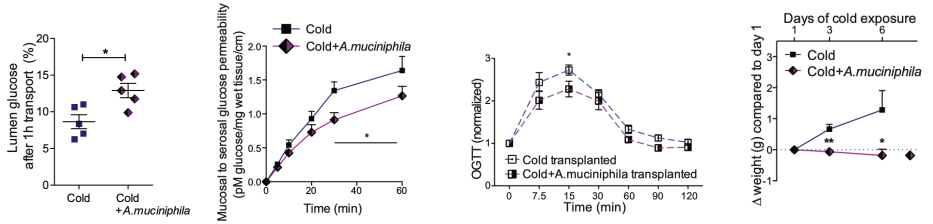
Correlation between the relative abundance (%) of selected genera in the colon 14 d before calving and feed efficiency after calving



Bach et al. (2018)

Intestine and beyond…

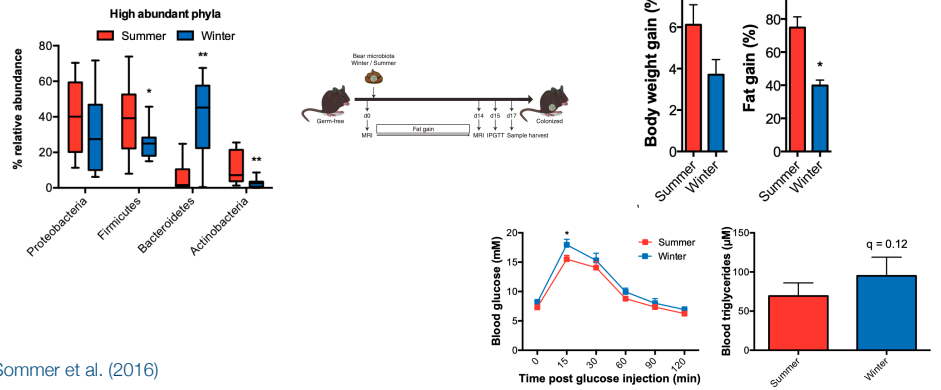
- Gut microbiota affects energy metabolism
- Under cold environments (when feed intake is increased), the decrease of the mucin-degrading bacterium *Akkermansia muciniphila* results in increased intestinal absorptive capacity



Chevalier et al. (2015)

Intestine and beyond…

- Bear microbiota composition and blood metabolites differ between hibernation and active phase



Sommer et al. (2016)

SUMMARY

- Feed efficiency is highly influenced by digestive and metabolic functions
- Both, ruminal and intestinal microbiomes play an important role in modulating digestion and metabolism
- Lots of research has explored the impact of supplementing DFM in the rumen (mainly yeast)
- Less research is available on bacteria
- In both cases, there is a need to identify the right strain, dose, and ration
- Open opportunity to explore both fungi- and bacteria-based DFM in the intestine


THANK YOU
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