Session 28 – Feeding horses with forage based diets

Fatty acid composition of liquid and solid associated bacteria in the cecum and colon of horses

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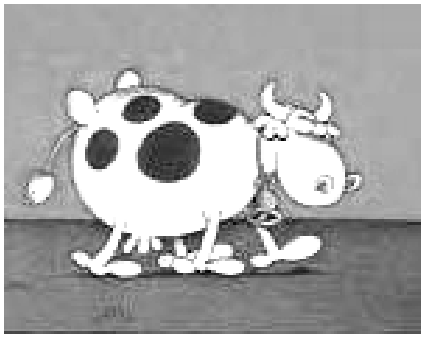
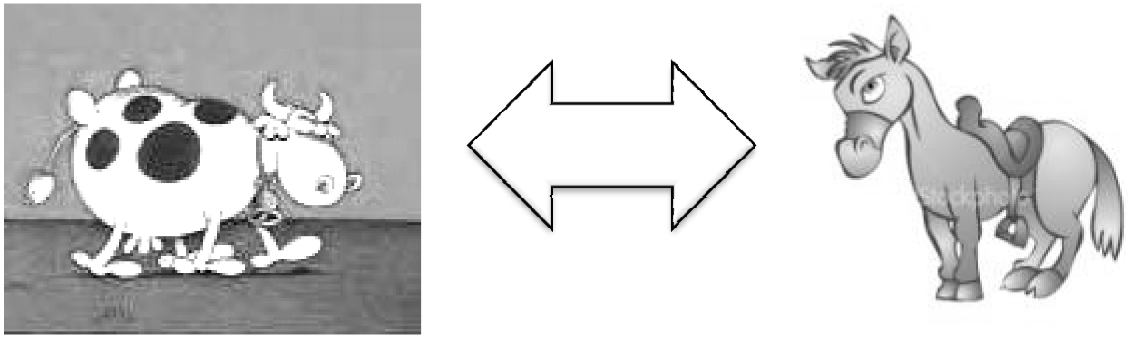


The ruminal microbial ecosystem has been the most thoroughly studied gut system, particularly the quantitative aspects and the contribution of the rumen to the host's nutrition

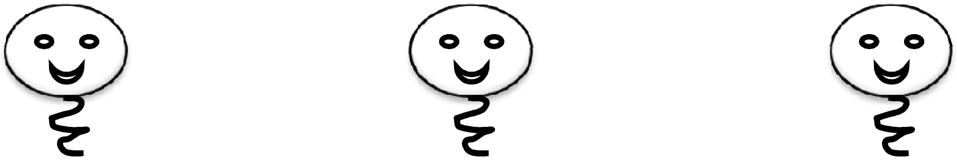
Despite the anatomical and placement differences…

comparison between the rumen and the hindgut of horses is, some times, inevitable…



Potential of odd and branched chain fatty acids (OBCFA) as markers to:

- Quantify bacterial matter leaving the rumen (Vlaeminck *et al.*, 2005)
- Provide a qualitative description of the proportions of different classes of bacteria in the rumen (Vlaeminck *et al.*, 2006)
- Predict rumen ratios of volatile fatty acids (Vlaeminck *et al.*, 2006)



The OBCFA of rumen bacteria

Fatty acid synthetase of the bacteria

Physiological and culture conditions

variations in the profile of OBCFA from the rumen are mainly a reflection of changes in the relative abundance of specific bacterial populations

The fatty acid composition of rumen bacteria:

large proportion of OBCFA in their membrane lipids - C15:0, *iso* C15:0, *ante-iso* C15:0, C17:0, *iso* C17:0, *ante-iso* C17:0 and C17:1 (Kaneda, 1991).

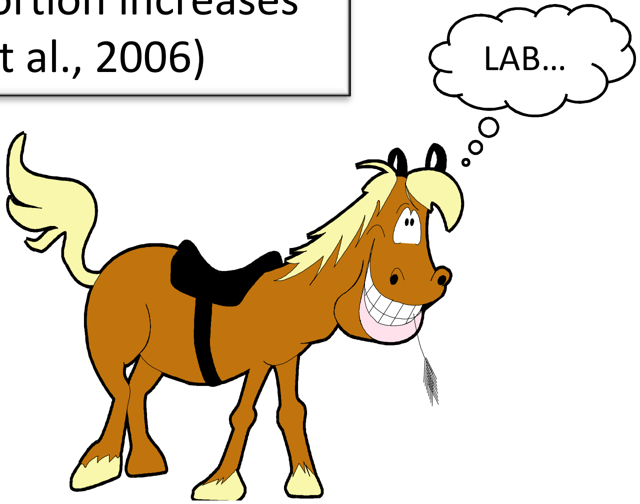
In the rumen, we can clearly divide the microbial population under two distinct ecological sites:

1) liquid phase colonized by bacteria and zoospores (Liquid Associated Bacteria, LAB)
2) bacteria associated to feed particles, mainly responsible for hydrolysis of cellular wall polysaccharides (Solid Associated Bacteria, SAB)

SAB are enriched in fibrolitic bacteria (Faichney, 1980; Merry and McAllan, 1983)

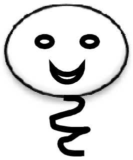
LAB are enriched in amylolityc bacteria (Dehority and Orpin, 1998, Vlaeminck et al., 2006).

Increasing the concentrate proportion increases the LAB phase (Vlaeminck et al., 2006)



Fatty acid composition of LAB and SAB are different

What's the big difference?

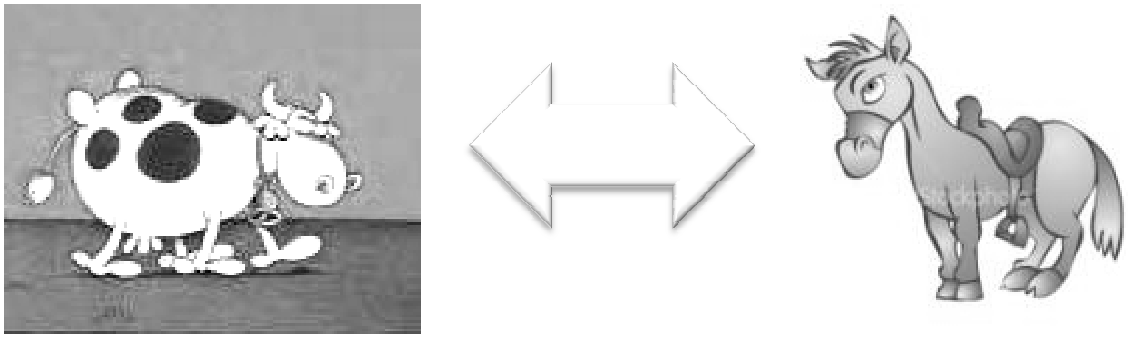


Total fatty acid content of SAB is higher than that in LAB.

Fibrolytic bacteria: high amounts of iso-fatty acids with *Ruminococcus flavefaciens* enriched in odd-chain iso-fatty acids and *Ruminococcus albus* in even-chain iso-fatty acids.

Amylolytic bacteria: low levels of branched-chain fatty acids and relatively enriched in linear odd-chain fatty acids,

Differences in the OBCFA profile observed among rumen bacteria suggest that they are useful in assessing the composition of, or shifts, in the rumen microbial population comparison between the rumen and the hindgut of horses is, some times, inevitable…

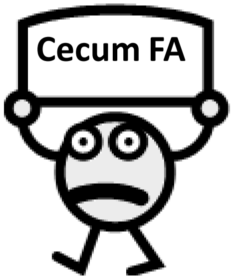


- * What is the fatty acid profile of cecum and colon bacteria?
- * Is there differences, as in the rumen, between LAB and SAB?
- * Can the FA profile be used as a marker for bacterial biomass and/or bacterial activity?

Objectives

* Test the methodology to isolate bacteria both from the liquid and the solid phase (LAB and SAB);

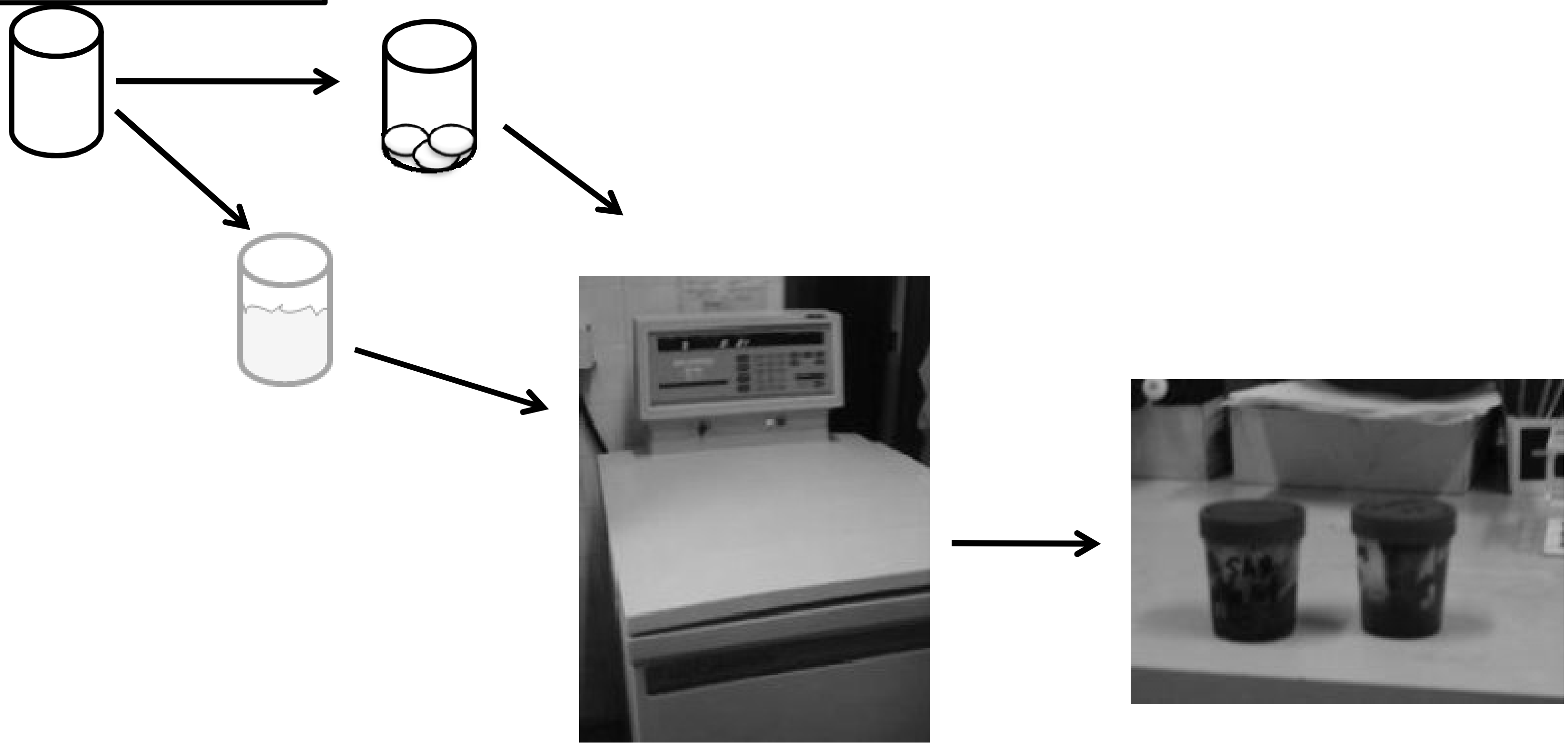
* Describe the FA profile of LAB and SAB from cecal and colon contents;



Materials and Methods

Cecal and colonic contents → 5 adult horses immediately after slaughter

Cecal and colonic contents



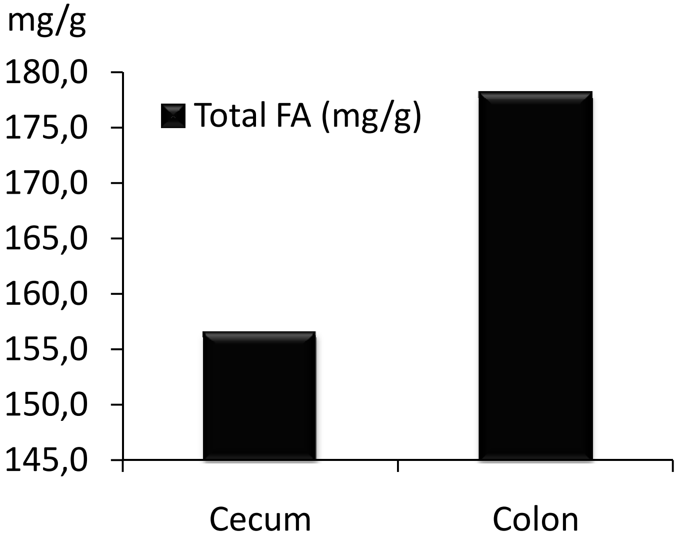
Bacterial pellets were freeze-dried, grinded and analysed for FA

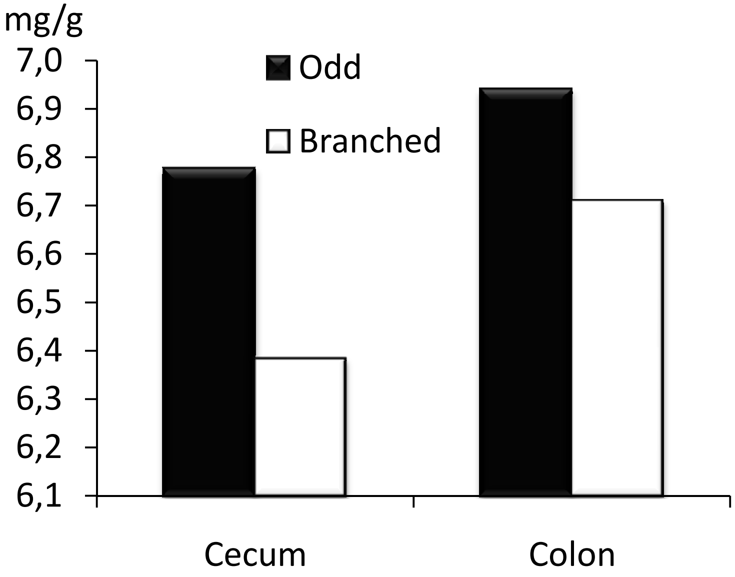
Results and Discussion

* The mean FA concentration in bacteria was 167mg/gDM

* 52% were C18 FA

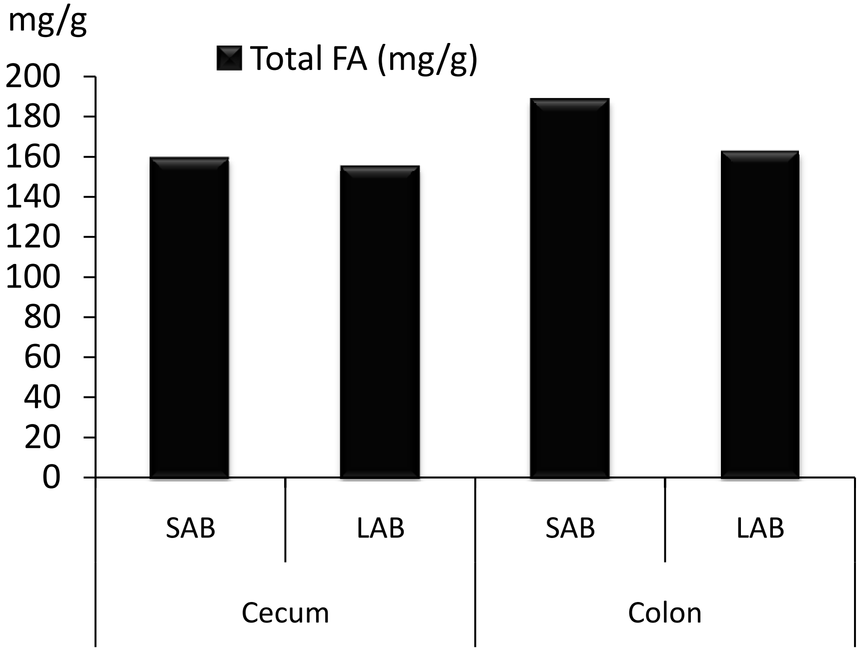
* 13.5% were odd and/or branched chain FA.

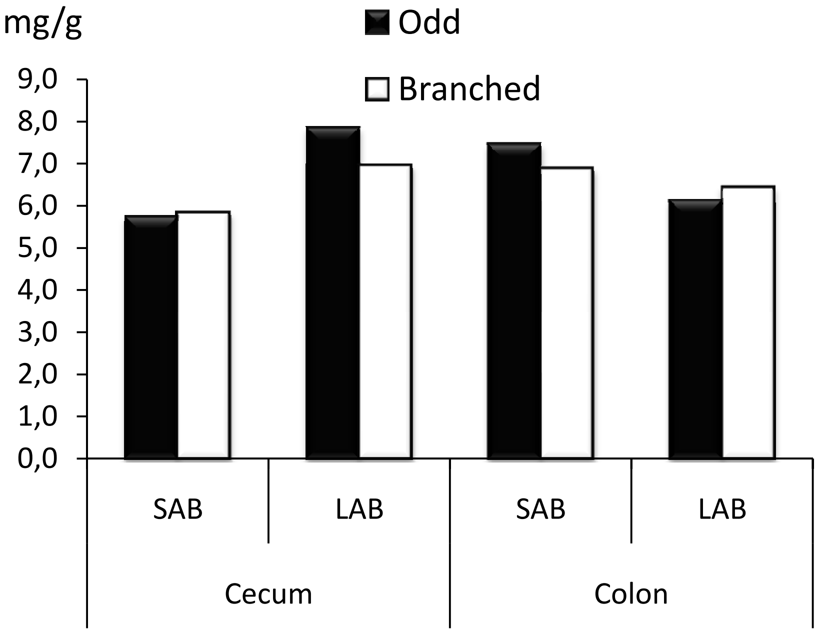




* No statistical differences were found between compartments

Results and Discussion





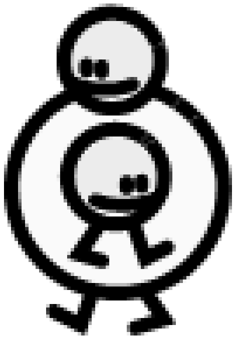
* No differences between LAB and SAB were found for either total FA, odd or branched chain FA for bacteria population

Results and Discussion

Cecum bacteria presented higher ($P<0.05$) C18:2n-6, C18:3n-3, **C18:1 trans isomers than colon bacteria ;** Usually reported for rumen **SAB.**

✓ Can be related to a greater biohydrogenation activity in cecum particles by SAB;

✓ Incorporation of exogenous FA instead of *de novo* synthesis.



Conclusions

* The methodology used to isolate LAB and SAB in rumen contents can be easily applied to cecum and colon contents;

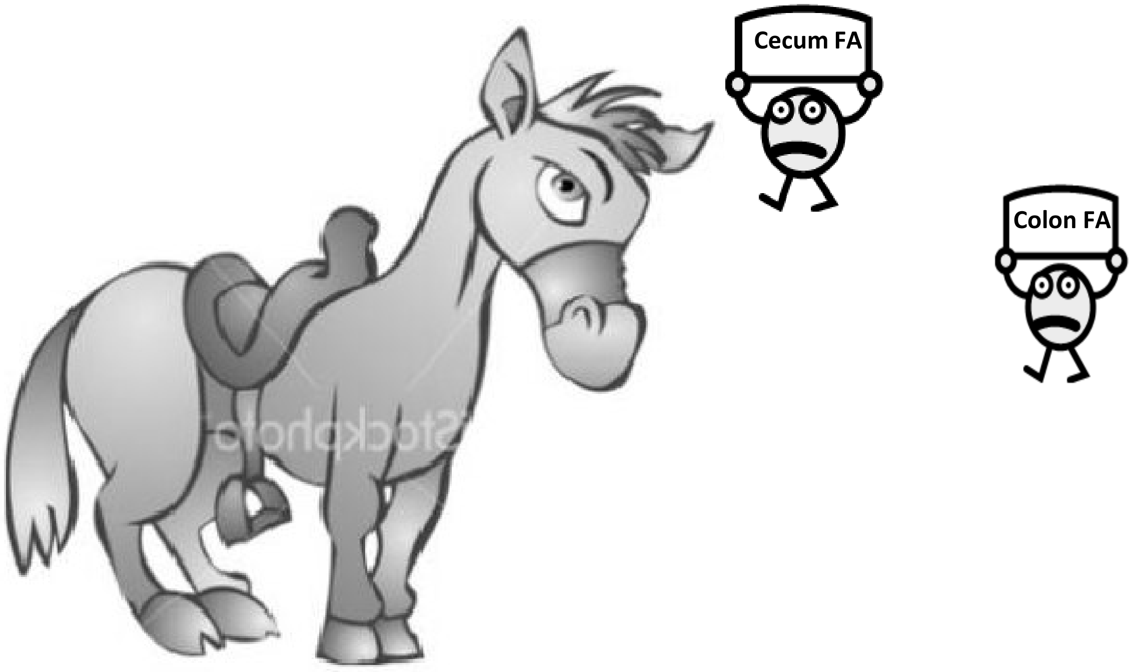
* Contrarily to what is reported for rumen bacteria, no differences between LAB and SAB were found for either total FA and FA profile;

* Cecum bacteria presented higher **C18:1 trans isomers** eventually indicating a higher SAB activity/population;

* The odd and branched chain FA did not differ between all bacteria population ;

* OBCFA may not be suitable for discriminate between bacterial sub-populations but might be useful as a global microbial marker in equine ceco-colonic ecosystem.

THANK YOU FOR YOUR ATTENTION!!!



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