Discrepancies in microbiota composition along the pig gastro-intestinal tract between *in vivo* observations and an *in vitro* batch fermentation model

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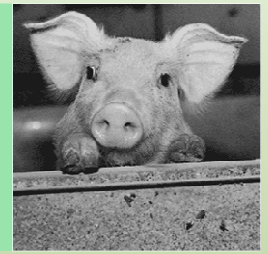


Introduction

In vitro fermentation models are increasingly used to assess prebiotic potential of novel indigestible carbohydrates (CHO)

However, the evolution of the microbiota during *in vitro* fermentation and along the gut intestinal tract *in vivo* have never been properly compared

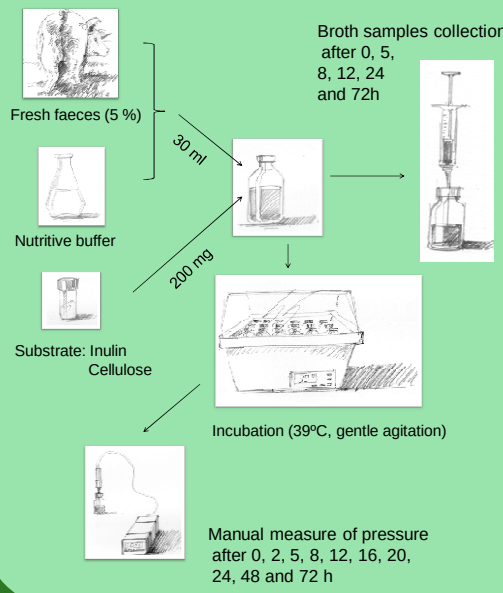
Material and Methods

***In vivo trial**: 3 X 4 pigs received 3 diets for 3 weeks :*

(i) Semi-purified diet + 5 % Inulin
(ii) Semi-purified diet + 5 % Cellulose
(iii) Semi-purified diet + 2.5 % Inulin + 2.5 % Cellulose

At slaughter: Digesta collected along the digestive tract (Jejunum, Ileum, Caecum and 3 parts of the Colon)

***In vitro trial**: gas fermentation with fresh faeces of the in vivo trial*



Analyzes

Fermentation Kinetics (modelisation)

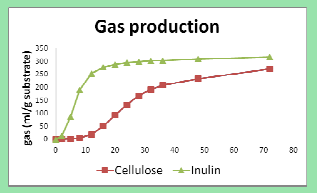
DNA Extraction on digesta and fermentation broth samples

Microflora quantification by qPCR *:*

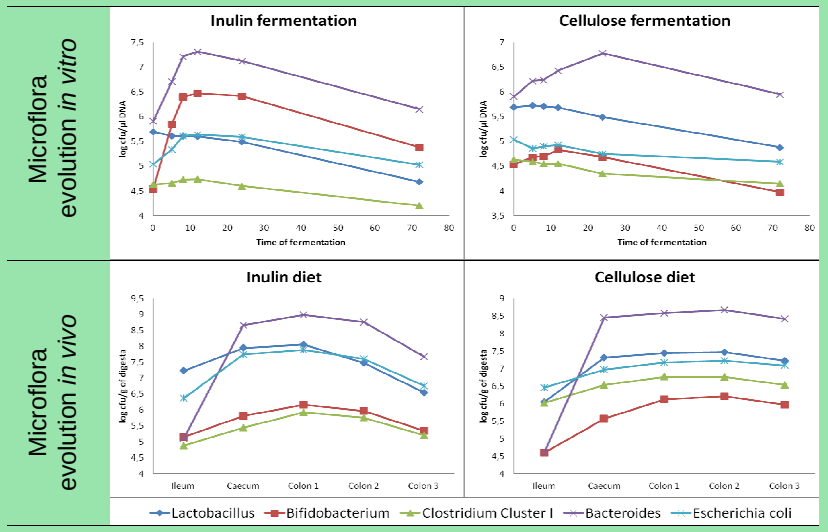
- ✓ *Lactobacillus sp.*
- ✓ *Bifidobacterium sp.*
- ✓ *Clostridium Cluster I*
- ✓ *Bacteroides*
- ✓ *Escherichia coli*

Results

Contrasted fermentation kinetics were observed for the 2 substrates *in vitro*



Microflora evolutions in both systems were consistent for *Bifidobacteria*, *Bacteroides* and *E. coli* in the first part of the digestive tract but not for *Lactobacillus* and *Clostridium* Cluster I.



Conclusions

Lactobacillus and _Clostridium CL I_ evolutions are different between both systems probably due to specific bacterial properties.

➔ Improves to the *in vitro* model are needed to assess properly prebiotic potential of new CHO.