Impact of weaning age on the gut microbiota composition in piglets.

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Weaning is one of the most important period of pig life.

- 3rd and 4th week of age
- switch from highly digestible liquid milk to a less-digestible more-complex solid feed
- move from maternity building to a post-weaning unit
- social change owing to the separation from the mother and by mixing piglets from different litters

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INTRODUCTION

Weaning is one of the most important period of pig life

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- switch from highly digestible liquid milk to a less-digestible more-complex solid feed
- move from maternity building to a post-weaning unit
- social change owing to the separation from the mother and by mixing piglets from different litters

Piglets during the weaning are susceptible to diarrhea:

- Dysbiosis
- Colonization of enteric pathogens
The gastrointestinal microbiota is dynamic and subject to changes based on environment, age, exposure to microbes and diet.

The gut microbiota is mostly stressed at weaning.

The main debated parameter is the age at weaning and few studies have been performed about how early-life establishment of the swine gut microbiota may contribute during the weaning period to the individual’s robustness.

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➢ AIMS

✓ To characterize the gut microbiota composition at different weaned ages, ranging from ultra-early weaning (14 days) to organic-like weaning (42 days), in antibiotic-free piglets

✓ To evaluate the effect of weaning age on the later composition of the gut microbiota (day 60)
### ANIMAL DESIGN

<table>
<thead>
<tr>
<th>N. piglets</th>
<th>Weaned at (d0)</th>
<th>Birth (d0)</th>
<th>d14</th>
<th>d21</th>
<th>d28</th>
<th>d35</th>
<th>d42</th>
<th>d49</th>
<th>d60</th>
</tr>
</thead>
<tbody>
<tr>
<td>12</td>
<td>14 days</td>
<td>Faeces</td>
<td>Faeces (12 pigs)</td>
<td>Faeces (12 pigs)</td>
<td>Faeces (12 pigs)</td>
<td>Faeces (6 pigs)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>12</td>
<td>21 days</td>
<td>Faeces</td>
<td>Faeces (12 pigs)</td>
<td>Faeces (12 pigs)</td>
<td>Faeces (6 pigs)</td>
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<td></td>
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<td></td>
</tr>
<tr>
<td>12</td>
<td>28 days</td>
<td>Faeces</td>
<td>Faeces (12 pigs)</td>
<td>Faeces (12 pigs)</td>
<td>Faeces (6 pigs)</td>
<td></td>
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<td></td>
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</tr>
<tr>
<td>12</td>
<td>42 days</td>
<td>Faeces</td>
<td>Faeces (12 pigs)</td>
<td>Faeces (12 pigs)</td>
<td>Faeces (6 pigs)</td>
<td></td>
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</tr>
</tbody>
</table>

✓ Animals were recorded for growth and diarrhea

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MATERIALS AND METHODS

- DNA extraction
- 16S sequencing using the Illumina system
- Bioinformatics data analyses using QIIME (v1.9.1)
  - Samples < 10,000 post-quality reads were removed from the analysis
- Biostatistical analyses using R software
  - PhyloSeq
  - Vegan
  - MetagenomeSeq

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RESULTS

GROWTH
Impact of weaning on growth rate decreased with weaning age, and for W42 the ADG was stable and increased.

DIARRHEA
Weaning at younger ages increased diarrhea, which was not observed in W42 group.

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➢ RESULTS – Diversity analysis

Alpha diversity

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The group weaned at 42 days old has a higher alpha diversity during the pre-weaning, post-weaning and until the day 60.

These animals having a richer microbiota can be more resistant to the enteric diseases during the weaning period and for all their lifelong (Dou et al., 2017).
The lower beta diversity in the w42 group means that the population of the w42 is more homogeneous than the other weaned groups that are heterogeneous until day 60.

The adult microbiota is known to be more stable than younger microbiota (Edwards et al., 2017)
Each weaned group revealed significant differences between the samples point using the NMDS analysis.

The gut microbiota changes drastically before and after weaning, as already demonstrated in previous studies (Mach et al., 2015; Dou et al., 2017).

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Pre and post-weaned groups revealed significant differences between days but none statistical significance was revealed in the day 60 group.
RESULTS – Differential abundant analysis

Pre-Weaning:

Campylobacter spp., Clostridium spp., Lactobacillus spp., Lactobacillus mucosae, Streptococcus spp., Fusobacterium spp., Bacteroides spp.

Post-Weaning:


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➢ RESULTS – Differential abundant analysis

Pre-Weaning:

Campylobacter spp., Clostridium spp., Lactobacillus spp.,
Lactobacillus mucosae, Streptococcus spp., Fusobacterium spp., Bacteroides spp.

Post-Weaning:

Actinobacillus spp., Anaerotruncus spp., Dialister spp., Mucispirillum spp.,
Prevotella spp., Blautia spp., Faecalibacterium prausnitzii

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Martin R1, Miguel S1,2, Benedíquez L1,3, Bridonneau C1, Robert V1, Hudault S1, Chain F1, Bertheau O1, Azevedo V3, Chatel JM1, Sokol H1,4,5, Bermúdez-Humarín LG1, Thomas M1, Langella P1.

Faecalibacterium prausnitzii is an anti-inflammatory commensal bacterium identified by gut microbiota analysis of Crohn disease patients

Hary Sokol1*, Bénédicte Pigneux1, Laurie Watterlot1, Omar Lakhdari1, Luis G. Bermúdez-Humarín1, Jean-Jacques Gratadoux1, Sébastien Blugeon1, Chantal Bridonneau1, Jean-Pierre Furet1, Gérard Corthièr1, Corinne Grangette1, Nadia Vasquez1, Philippe Po chant1, Germain Trugnan1, Ginette Thomas1, Hervé M. Blottière1, Joël Dore1, Philippe Marteau1, Philippe Seksik1,*, and Philippe Langella1,*,**


Association between Faecalibacterium prausnitzii Reduction and Inflammatory Bowel Disease: A Meta-Analysis and Systematic Review of the Literature.

Cao Y1, Shen J1, Ran Zh1.


Mucosa-associated Faecalibacterium prausnitzii phylotype richness is reduced in patients with inflammatory bowel disease.

López-Siles M1, Martínez-Medina M1, Abella C1, Busquets O2, Sabat-Mir M3, Duncan SH4, Aldeguer X2, Flint HJ4, García-Gil LU5.
CONCLUSION

We show that late weaning leads to:

- higher diversity of potentially beneficial microbes prior to the crucial challenge of weaning
- might provide a competitive advantage to piglets

FUTURE STUDIES: What will be the impact of a late weaning in the long term life of pigs?
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THANKS FOR THE ATTENTION!!!!