

> Implantation of the porcine gut microbiota: dynamics and links with robustness at weaning Jordi Estellé UMR 1313 GABI, INRAE Jouy-en-Josas Jordi.Estelle@inrae.fr

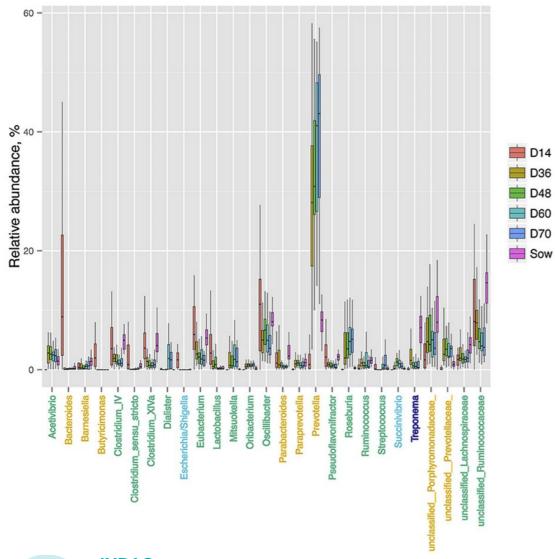
Weaning of piglets in intensive pig production

- Practiced at 3-4 weeks of age, while natural weaning occurs around 17 weeks after birth
- Sudden and stressful changes in diet, social, and environmental life conditions

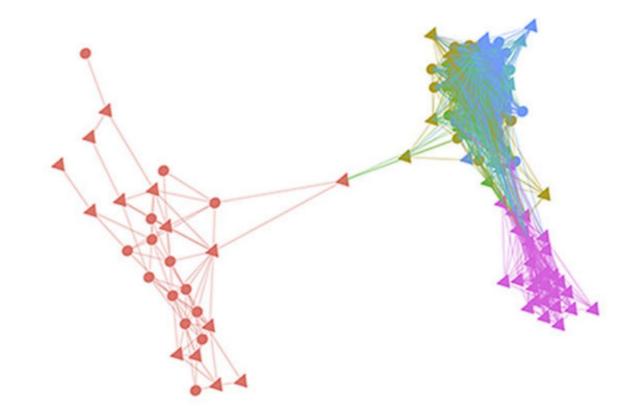




Weaning represents a big microbiota shift for piglets



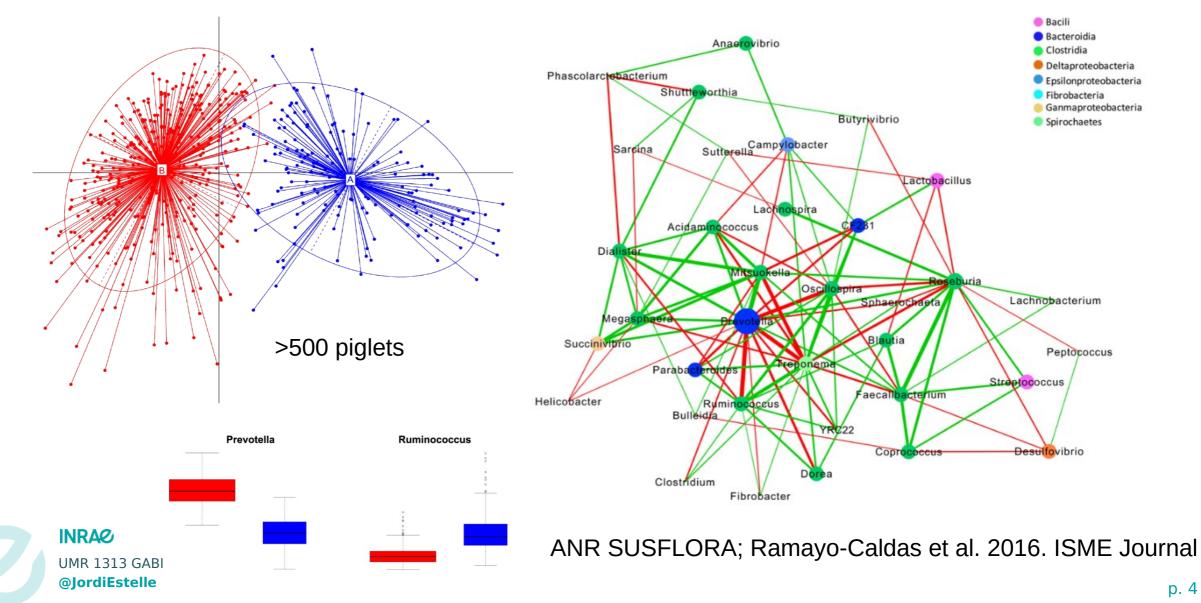
31 piglets weaned at 28 days-of-age



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ANR SUSFLORA; Mach et al. 2015. Environ Microbiol Rep

Microbiota tends to get more stable at 60 days of age, but still individual variability (e.g. enterotypes)



Weaning of piglets in intensive pig production

- Practiced at 3-4 weeks of age, while natural weaning occurs around 17 weeks after birth
- Sudden and stressful changes in diet, social, and environmental life conditions
- Undesired consequences: anorexia, growth check, intestinal inflammation, unbalanced gut microbiota & DIARRHEA
- A strong need of antimicrobial alternatives for diarrhea treatment and prevention!



Jambon de porcs sans antibiotiques**?





Jambon sans "antimicrobiens"? PIG PROGRESS

@JordiEstelle



Sows

Piglets

ANR PIGLETBIOTA Objective: find alternative to antimicrobials to promote robustness at weaning

Biorepository:

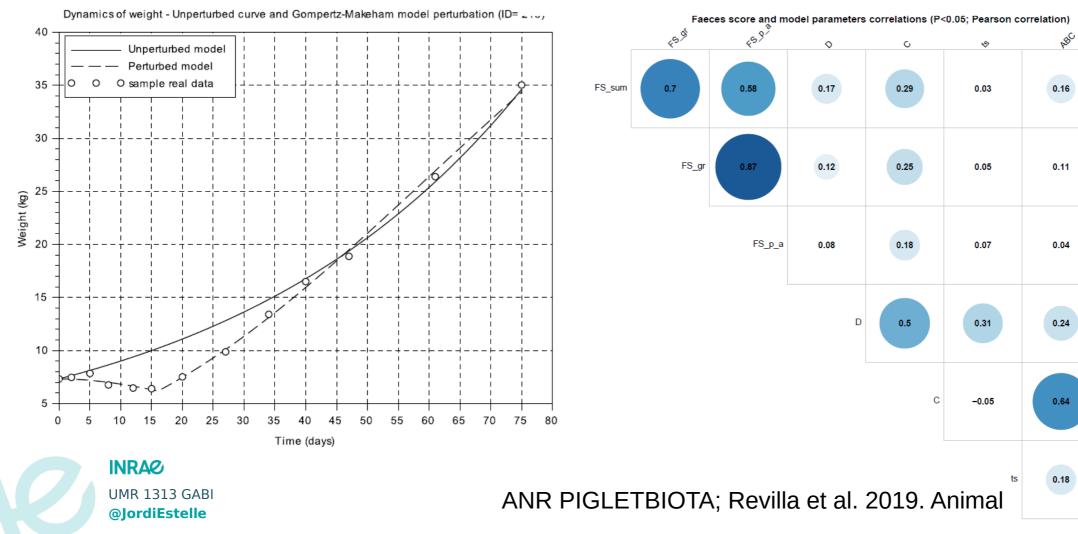
- >1600 TEMPUS tubes (blood RNA) ~1000 EDTA blood tubes (DNA)
- > 1600 plasma tubes
- Frozen PBMCs (>1600 samples)
- ~10 000 feces tubes (DNA and RNA)
- Growth and health phenotypes at weaning





Challenge: to model weaning robustness with growth

Expected vs. Observed growth: area between the curves (ABC)



ABC is significantly correlated with several health traits at weaning

0.8

0.6

0.4

0.2

0

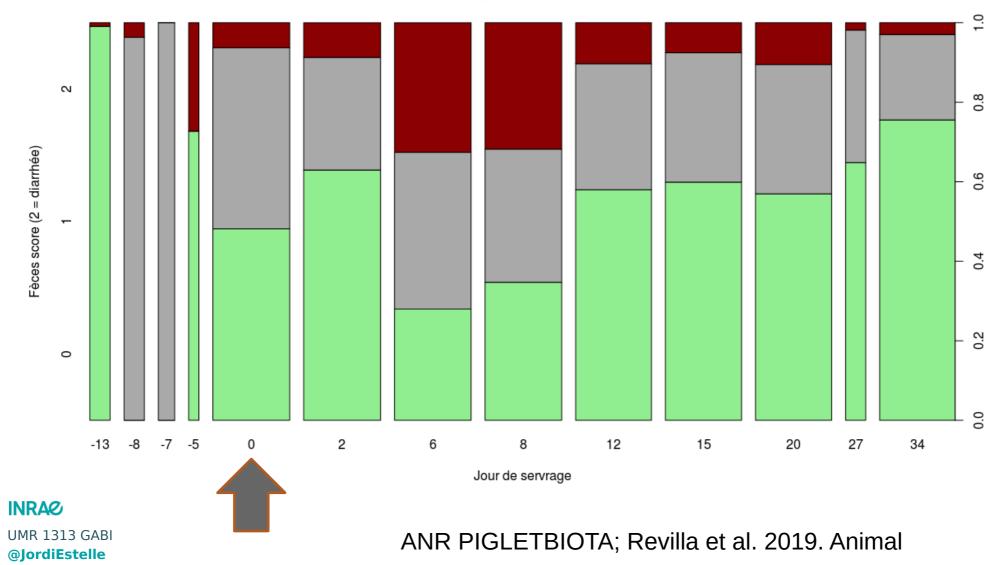
-0.2

-0.4

-0.6

-0.8

Diarrhea in piglets: ~1 week after weaning



Fèces porcelets GENESI

Challenge: adapt our structure and @BRIDGE to medium-throughput microbiota DNA extraction

~10 000 feces tubes (DNA and/or RNA)

 At sampling, anticipate the next steps by pre-alliquoting samples (~200mg per crytube) in order to save preprocessing time at the lab

 At the lab, adapt manual protocol to semi-automated microbiota DNA extraction using @BRIDGE facilities at GABI => increase repeatability and efficiency of extractions



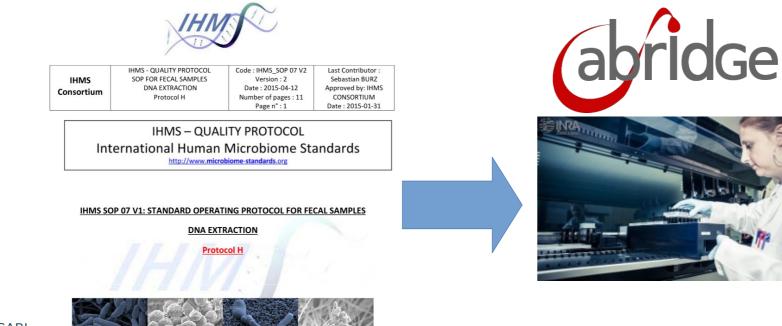
Challenge: adapt our structure and @BRIDGE to medium-throughput microbiota DNA extraction

International Human Microbiome

Standards (FP7, Coord. J.Doré)



 SOP "H" adapted to @BRIDGE's STAR nucleic acid workstation (Hamilton, Perkin Elmer)



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Massacci et al. 2020, Animal Microbiome p. 12

• PIGLETBIOTA ANR experiment at UE PAO (INRAE):

N. piglet s	Weaned at	Birth (d0)	d14	d21	d28	d35	d42	d49	d60
12	14 days	>	Faeces (12 pigs)	Faeces (12 pigs)					Faeces (6 pigs)
12	21 days			Faeces (12 pigs)	Faeces (12 pigs)				Faeces (6 pigs)
12	28 days				Faeces (12 pigs)	Faeces (12 pigs)			Faeces ► (6 pigs)
12	42 days						Faece S (12 pigs)	Faece S (12 pigs)	Faeces (6 pigs)



Massacci et al. 2020, Animal Microbiome p. 13

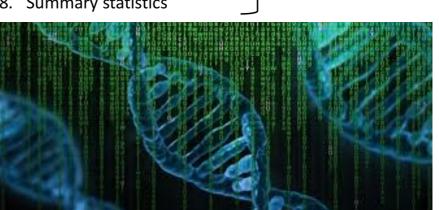
Dynamics of microbiota implantation by 16S seq.



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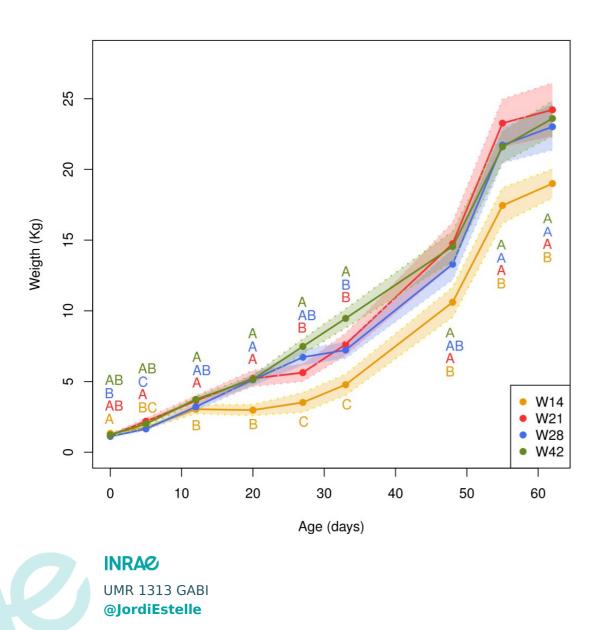
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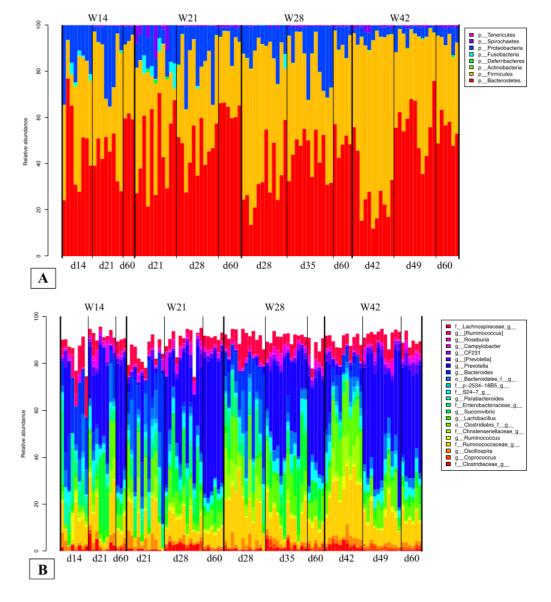
- 1. Inspect Illumina reads
- 2. Clean adapters / primers (depending on protocol)
- Join paired end reads 3.
- Remove bad quality reads 4.
- 5. Perform OTU calling
- Remove low abundance OTU 6
- 7. Remove chimera OTU
- Summary statistics 8.



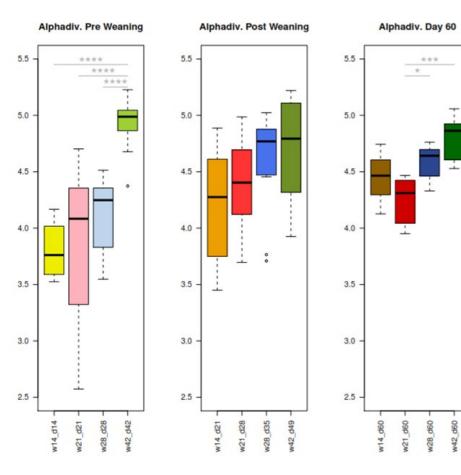
Massacci et al. 2020, Animal Microbiome p. 14

tive Insights Into Microbial Ecology





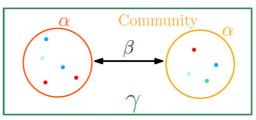
Massacci et al. 2020, Animal Microbiome p. 15



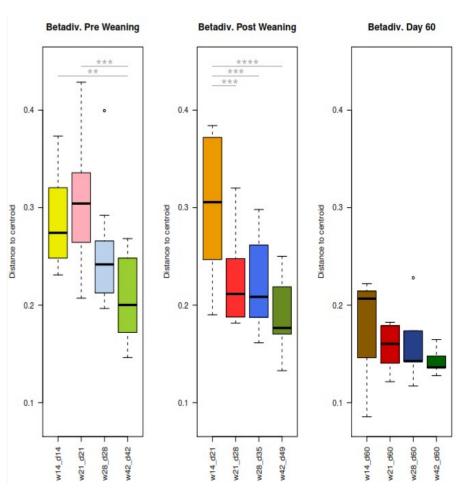
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UMR 1313 GABI @JordiEstelle The group weaned at 42 days old has a higher alpha-diversity during the pre-weaning, post-weaning and until the day 60. It has also lower beta-diversity (the composition is more homogeneous among the animals in this group)

=> RICHER IS BETTER!



Landscape



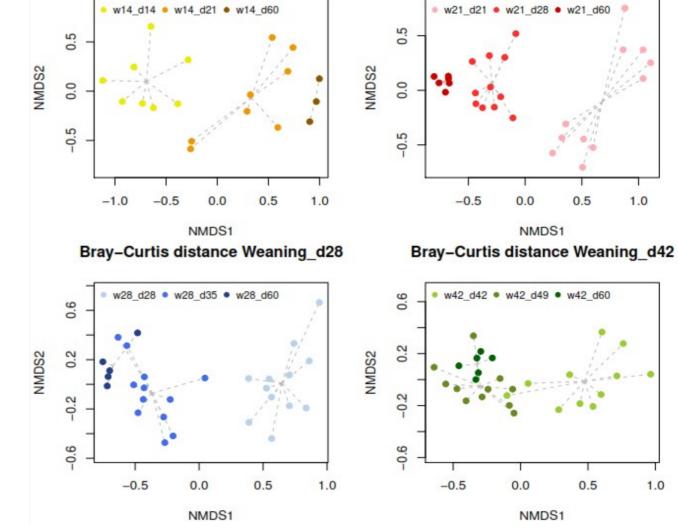
Massacci et al. 2020, Animal Microbiome p. 16

Bray-Curtis distance Weaning d14

- Each weaned group shows drastic changes between pre- and post-weaning gut microbiota composition
- Results in accordance with literature and our own previous results (Mach et al. 2015)

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Massacci et al. 2020, Animal Microbiome

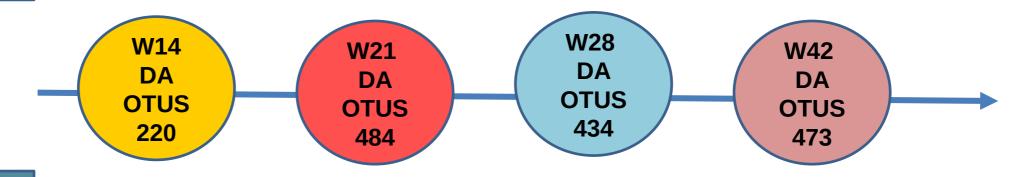
Bray-Curtis distance Weaning d21

p. 17

1.0

• Differential abundance analysis of OTUs:

More abundances of OTUs annotated as Bacteroides spp., Ruminococcus spp., Oscillospira spp., Clostridium spp., ...



Post-Weaning:

Pre-

Weaning:

More abundance of OTUs annotated as Succinivibrio spp , Prevotella spp., Campylobacter spp. Faecalibacterium prausnitzii,



Front Microbiol. 2017 Jun 30;8:1226. doi: 10.3389/fmicb.2017.01226. eCollection 2017.

Functional Characterization of Novel Faecalibacterium prausnitzii Strains Isolated from Healthy Volunteers: A Step Forward in the Use of F. prausnitzii as a Next-Generation Probiotic.

Martín R¹, Miquel S^{1,2}, Benevides L^{1,3}, Bridonneau C¹, Robert V¹, Hudault S¹, Chain F¹, Berteau O¹, Azevedo V³, Chatel JM¹, Sokol H^{1,4,5}, Bermúdez-Humarán LG¹, Thomas M¹, Langella P¹.



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

Harry Sokol*[†], Bénédicte Pigneur^{†‡}, Laurie Watterlot*, Omar Lakhdari*, Luis G. Bermúdez-Humarán*, Jean-Jacques Gratadoux*, Sébastien Blugeon*, Chantal Bridonneau*, Jean-Pierre Furet*, Gérard Corthier*, Corinne Grangette[§], Nadia Vasquez¹, Philippe Pochart¹, Germain Trugnan[‡], Ginette Thomas[‡], Hervé M. Blottière*, Joël Doré*, Philippe Marteau^{||}, Philippe Seksik^{‡**††}, and Philippe Langella*.**^{††}

Gastroenterol Res Pract. 2014;2014:872725. doi: 10.1155/2014/872725. Epub 2014 Mar 27.

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

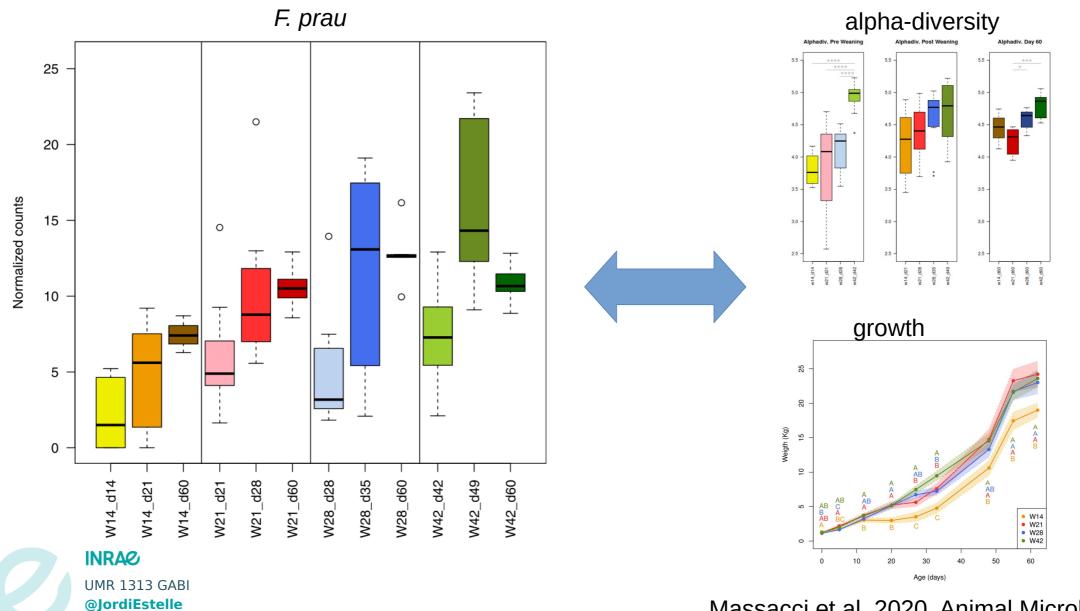
Cao Y¹, Shen J¹, Ran ZH¹.



Appl Environ Microbiol. 2015 Nov;81(21):7582-92. doi: 10.1128/AEM.02006-15. Epub 2015 Aug 21.

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

Lopez-Siles M¹, Martinez-Medina M¹, Abellà C¹, Busquets D², Sabat-Mir M³, Duncan SH⁴, Aldeguer X², Flint HJ⁴, Garcia-Gil LJ⁵.



Massacci et al. 2020, Animal Microbiome p. 20

F.prau as a useful pro-biotic in weanling piglets?

Massacci et al. Animal Microbiome (2020) 2:2 https://doi.org/10.1186/s42523-020-0020-4

RESEARCH ARTICLE

Late weaning is associated with increased microbial diversity and Faecalibacterium prausnitzii abundance in the fecal microbiota of piglets

Francesca Romana Massacci^{1,2,3}*, Mustapha Berri⁴, Gaetan Lemonnier¹, Elodie Guettier⁵, Fany Blanc¹, Deborah Jardet¹, Marie Noelle Rossignol¹, Marie-José Mercat⁶, Joël Doré^{7,8}, Patricia Lepage⁷, Claire Rogel-Gaillard¹ and Jordi Estellé¹

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Animal Microbiome

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- Late weaning at 42 days-of age would be a good compromise for enhancing gut health in piglets
- Coherent with general weaning practices performed in organic farming, but the implementation of late weaning in industrial conventional production would be challenging
- Possible perspective for probiotic candidates like F. prau to be used in preweaning piglets in order to limit the dysbiosis in the gut!



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