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Microbiota intestinale e ruolo nella salute animale

Lorenzo Morelli & Maria Luisa Callegari

Piacenza, 31 gennaio 2020



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1. Due parole in generale

Piglets and microbiota: due parole chiave... di moda!



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☐ 2015	(46) >
☐ 2014	(40) >
☐ 2013	(35) >
☐ 2012	(24) >
☐ 2011	(26) >

...



1. Due parole in generale

- | | | | | | |
|---|--|--|------|---|---|
| ☐ 1 | Porcine epidemic diarrhea altered colonic microbiota communities in suckling piglets
Open Access | Tan, Z., Dong, W., Ding, Y., (...), Zhang, Q., Jiang, L. | 2020 | Genes
11(1),44 | 0 |
| View abstract Link to Full Text WebBridge Related documents | | | | | |
| ☐ 2 | Host genotype and amoxicillin administration affect the incidence of diarrhoea and faecal microbiota of weaned piglets during a natural multiresistant ETEC infection | Massacci, F.R., Tofani, S., Forte, C., (...), Trevisi, P., Magistrali, C.F. | 2020 | Journal of Animal Breeding and Genetics
137(1), pp. 60-72 | 0 |
| View abstract Link to Full Text WebBridge Related documents | | | | | |
| ☐ 3 | Short-chain fructo-oligosaccharides alleviates oxidized oil-induced intestinal dysfunction in piglets associated with the modulation of gut microbiota
Open Access | Yan, H., Zhou, P., Zhang, Y., (...), Liu, J., Zhang, H. | 2020 | Journal of Functional Foods
64,103661 | 0 |
| View abstract Link to Full Text WebBridge Related documents | | | | | |
| ☐ 4 | Post-natal co-development of the microbiota and gut barrier function follows different paths in the small and large intestine in piglets
Open Access | Arnaud, A.P., Rome, V., Richard, M., (...), David-Le Gall, S., Boudry, G. | 2020 | FASEB journal : official publication of the Federation of American Societies for Experimental Biology
34(1), pp. 1430-1446 | 0 |
| View abstract Link to Full Text WebBridge Related documents | | | | | |
| ☐ 5 | Early parenteral administration of ceftiofur has gender-specific short-and long-term effects on the fecal microbiota and growth in pigs from the suckling to growing phase
Open Access | Ruczicka, U., Metzler-Zebeli, B., Unterwiesing, C., (...), Knecht, C., Hennig-Pauka, I. | 2020 | Animals
10(1),17 | 0 |
| View abstract Link to Full Text WebBridge Related documents | | | | | |
| ☐ 6 | Maternal dietary fiber composition during gestation induces changes in offspring antioxidative capacity, inflammatory response, and gut microbiota in a sow model
Open Access | Li, Y., Liu, H., Zhang, L., (...), Li, J., Wu, D. | 2020 | International Journal of Molecular Sciences
21(1),31 | 0 |
| View abstract Link to Full Text WebBridge Related documents | | | | | |
| ☐ 7 | The extracellular proteins of Lactobacillus acidophilus DSM 20079 ^T display anti-inflammatory effect in both in piglets, healthy human donors and Crohn's Disease patients
Open Access | Hidalgo-Cantabrana, C., Moro-García, M.A., Blanco-Míguez, A., (...), Alonso-Arias, R., Sánchez, B. | 2020 | Journal of Functional Foods
64,103660 | 0 |
| View abstract Link to Full Text WebBridge Related documents | | | | | |



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1. Due parole in generale

Piglets and microbiota: non solo quantità ma anche qualità

Wang *et al. Microbiome* (2019) 7:109
<https://doi.org/10.1186/s40168-019-0721-7>

Microbiome

RESEARCH

Open Access

Longitudinal investigation of the swine gut microbiome from birth to market reveals stage and growth performance associated bacteria



Xiaofan Wang^{1†}, Tsungcheng Tsai^{1†}, Feilong Deng^{1,2}, Xiaoyuan Wei¹, Jianmin Chai¹, Joshua Knapp¹, Jason Apple¹, Charles V. Maxwell¹, Jung Ae Lee³, Ying Li^{2*} and Jiangchao Zhao^{1*}

Abstract

Background: Despite recent advances in the understanding of the swine gut microbiome at different growth stages, a comprehensive longitudinal study of the lifetime (birth to market) dynamics of the swine gut microbiome is lacking.

Results: To fill in this gap of knowledge, we repeatedly collected a total of 273 rectal swabs from 18 pigs during lactation (day (d) 0, 11, 20), nursery (d 27, 33, 41, 50, 61), growing (d 76, 90, 104, 116), and finishing (d 130, 146, 159, 174) stages. DNA was extracted and subjected to sequencing with an Illumina MiSeq sequencer targeting the V4 region of the 16S rRNA gene. Sequences were analyzed with the Deblur algorithm in the QIIME2 package. A total of 19 phyla were detected in the lifetime pig gut microbiome with *Firmicutes* and *Bacteroidetes* being the most abundant. Alpha diversity including community richness (e.g., number of observed features) and diversity (e.g., Shannon index) showed an overall increasing trend. Distinct shifts in microbiome structure along different growth stages were observed. LEfSe analysis revealed 91 bacterial features that are stage-specific. To validate these discoveries, we performed fecal microbiota transplantation (FMT) by inoculating weanling pigs with mature fecal microbiota from a growing stage pig. Similar stage-specific patterns in microbiome diversity and structures were also observed in both the FMT pigs and their littermates. Although FMT remarkably increased growth performance, it did not change the overall swine gut microbiome. Only a few taxa including those associated with *Streptococcus* and *Clostridiaceae* were enriched in the FMT pigs. These data, together with several other lines of evidence, indicate potential roles these taxa play in promoting animal growth performance. Diet, especially crude fiber from corn, was a major factor shaping the swine gut microbiome. The priority effect, i.e., the order and timing of species arrival, was more evident in the solid feed stages.

Conclusions: The distinct stage-associated swine gut microbiome may be determined by the differences in diet and/or gut physiology at different growth stages. Our study provides insight into mechanisms governing gut microbiome succession and also underscores the importance of optimizing stage-specific probiotics aimed at improving animal health and production.

Keywords: Swine gut microbiome, Dynamics, FMT, Growth stage and performance



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1. Due parole in generale

Piglets and microbiota: nuove osservazioni



JOURNALS
investing in science

FEMS Microbiology Letters, 362, 2015, fnv064

doi: 10.1093/femsle/fnv064

Advance Access Publication Date: 22 April 2015

Research Letter

RESEARCH LETTER – Environmental Microbiology

Archaeal microbiota population in piglet feces shifts in response to weaning: *Methanobrevibacter smithii* is replaced with *Methanobrevibacter boviskoreani*

Sara Federici^{1,†}, Francesco Miragoli^{1,†}, Vincenza Pisacane¹,
Annalisa Rebecchi¹, Lorenzo Morelli² and Maria Luisa Callegari^{1,*}

¹Centro Ricerche Biotecnologiche, Università Cattolica del Sacro Cuore, Via Milano 24, 26100 Cremona, Italy and ²Istituto di Microbiologia, Università Cattolica del Sacro Cuore, Via E. Parmense 84, 29122 Piacenza, Italy

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[†]These authors contributed equally to this work.

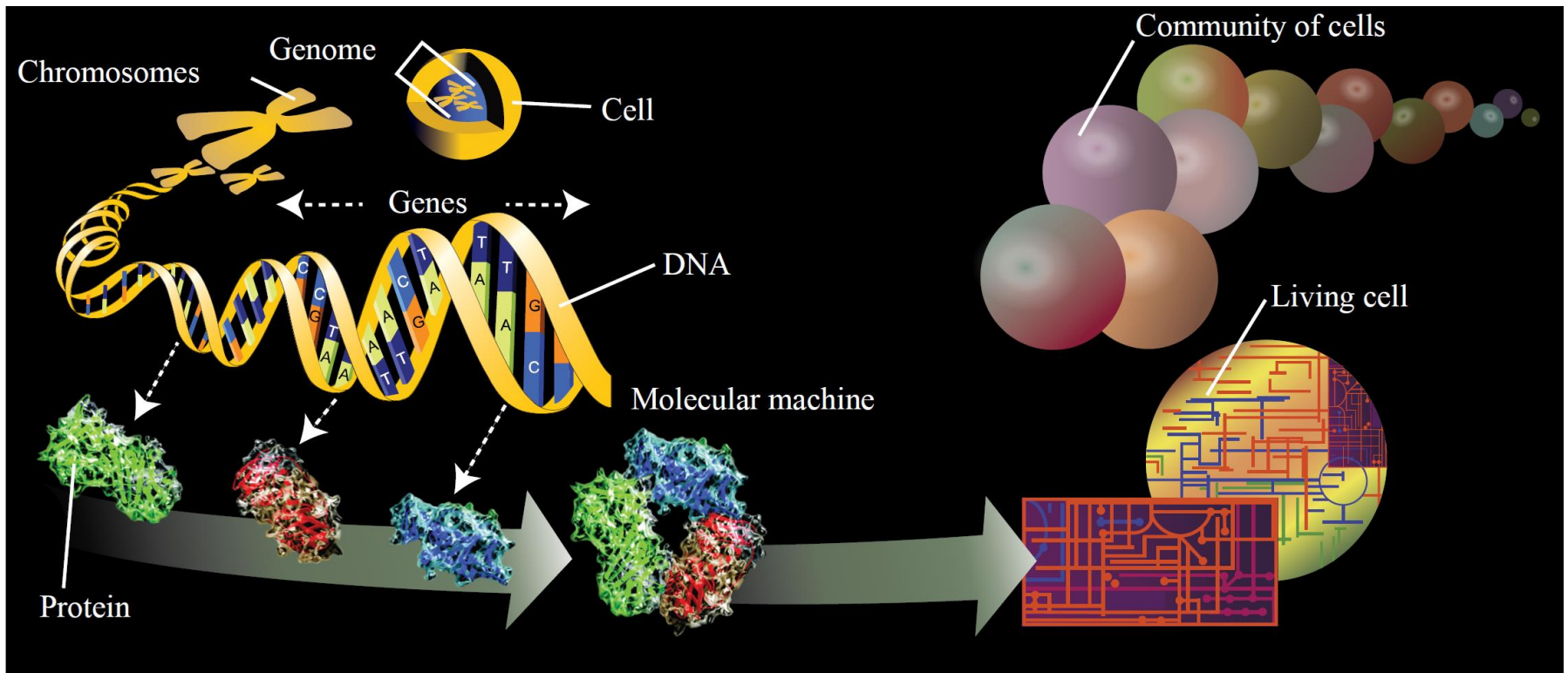
One sentence summary: New findings are presented on the ecology of methanogens in the intestine of monogastric animals, in which a rumen species, *Methanobrevibacter boviskoreani*, substituted *Methanobrevibacter smithii* during weaning.

Editor: Rustam Aminov



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Le omics !!!

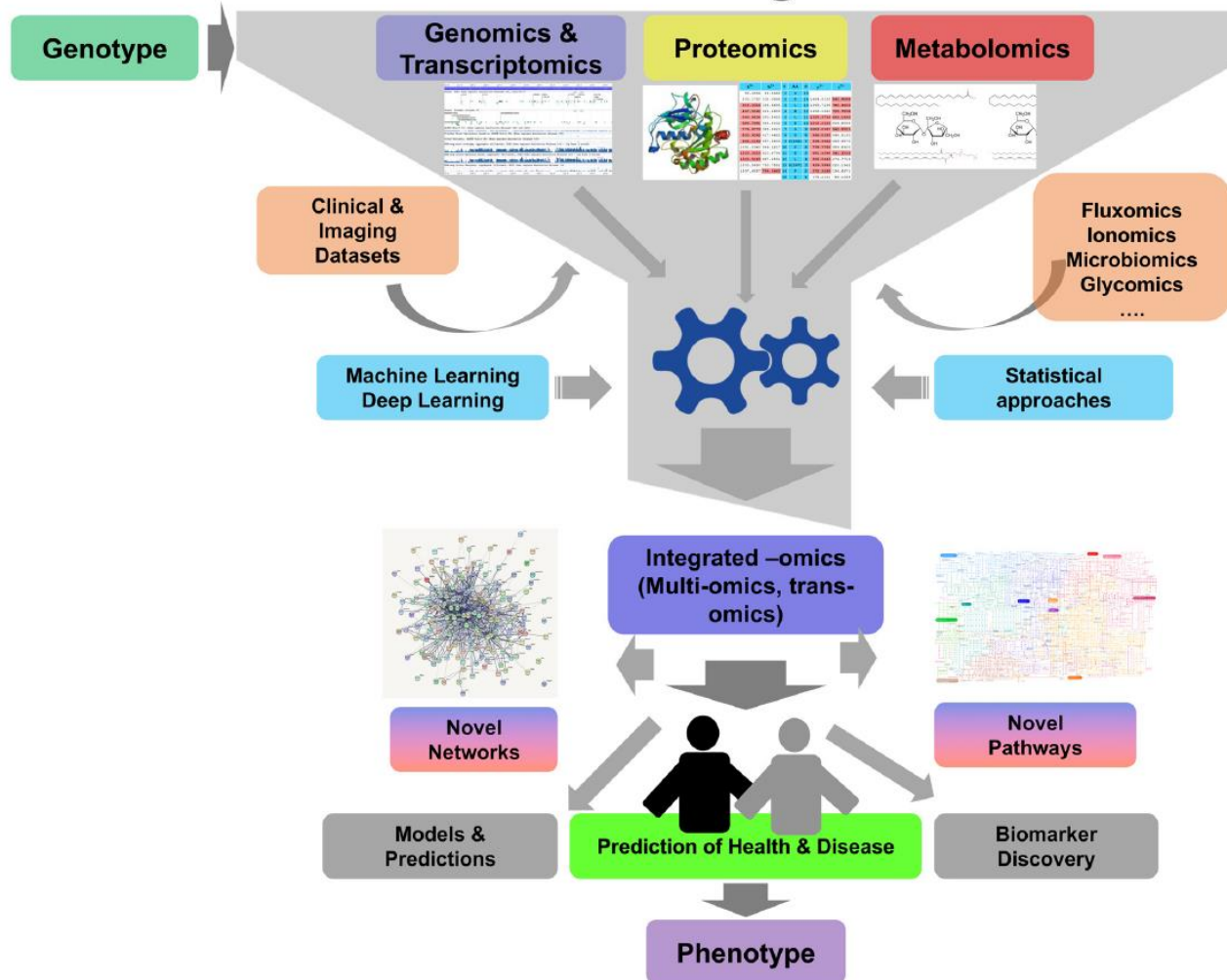




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Le omics in uno sguardo

Workflows in Integrated Omics





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1. Due parole in generale

Usando queste tecniche...

Pig gut metagenome consortium

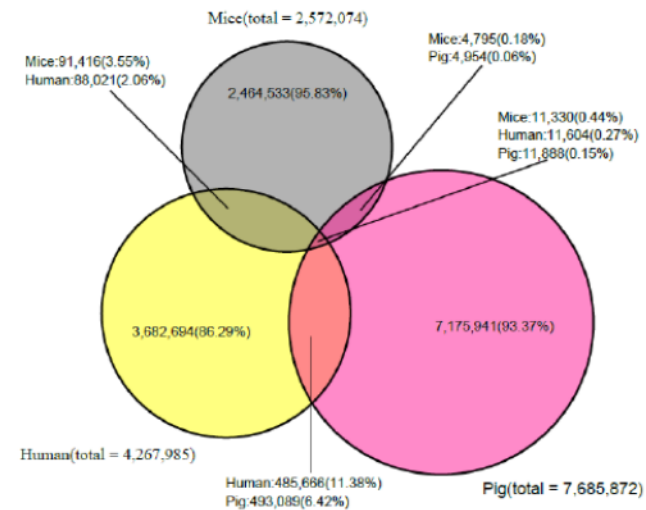
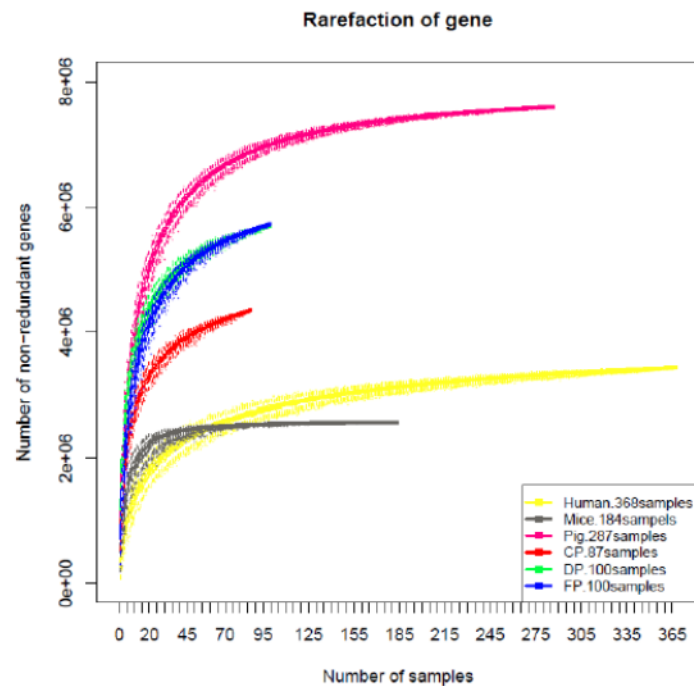
- **France**
 - **INRA GABI:** J Estellé, Y Ramayo-Caldas, G Lemonnier, C Denis, F Andreoletti, JJ Leplat, C Rogel-Gaillard
 - **MetaGenoPolis:** D. Ehrlich, N. Pons, E. Le Chatellier, S. Kennedy, F. Levenez and coll.
 - **INRA MICALIS:** J. Doré, E. Maguin
 - Experimental and commercial pig farms
- **China**
 - **Beijing Genome Institute-Shenzhen:** Wang Jun, Liang Xiao, Zhongkui Xia, Qiang Feng, and coll.
 - Pig farm
- **Denmark**
 - **Department of Biology, University of Copenhagen:** Pia Kiilerich, Karsten Kristiansen and coll.
 - **Danish Pig Research Centre, Nutrition and Reproduction:** A.Ø. Pedersen, N.J. Kjeldsen
 - Commercial pig farms





1. Due parole in generale

- A catalogue of 7.6M genes constructed with 287 pigs, with greater overlap with human than the mouse

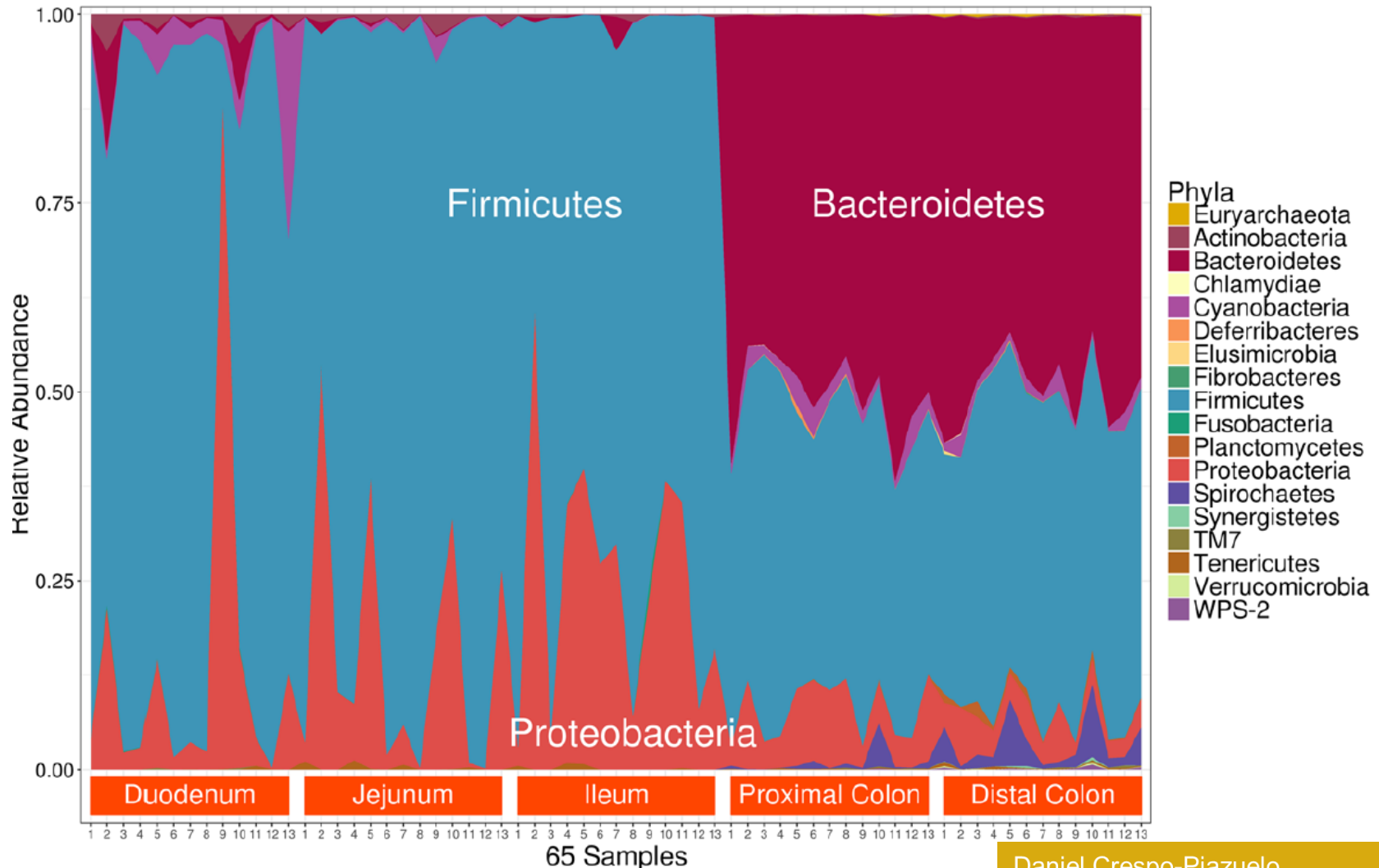


Xiao¹, Estellé¹, Kiillerich¹, et al., (accepted)



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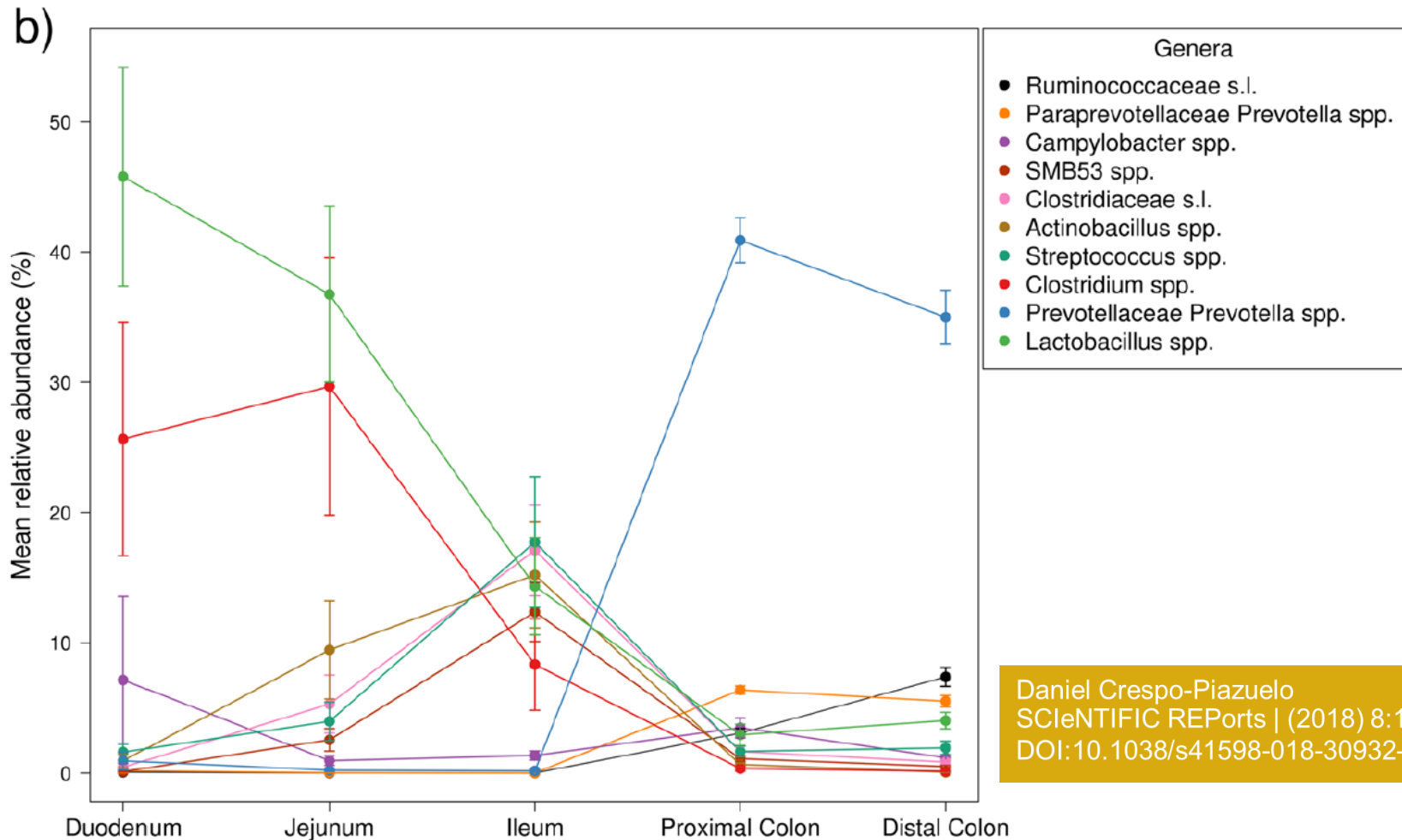
Microbiota intestinale del suino





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Microbiota intestinale del suino

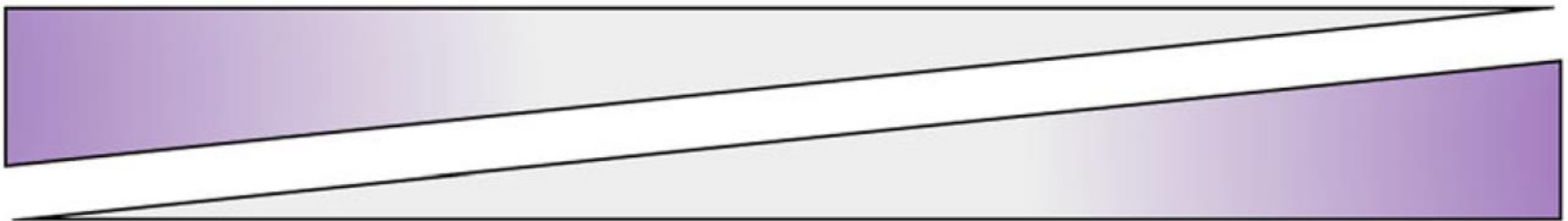




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Evoluzione del microbiota

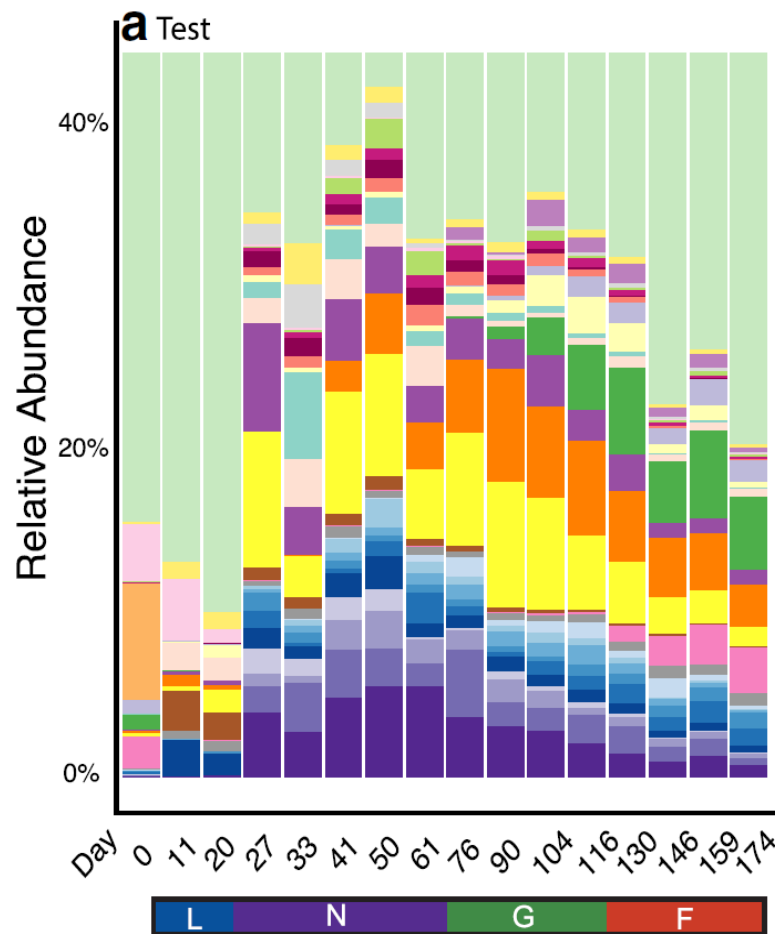
Variability among individual pigs



Gut microbial alpha diversity

Guevarra *et al.* *Journal of Animal Science and Biotechnology*
<https://doi.org/10.1186/s40104-018-0308-3>

Evoluzione del microbiota

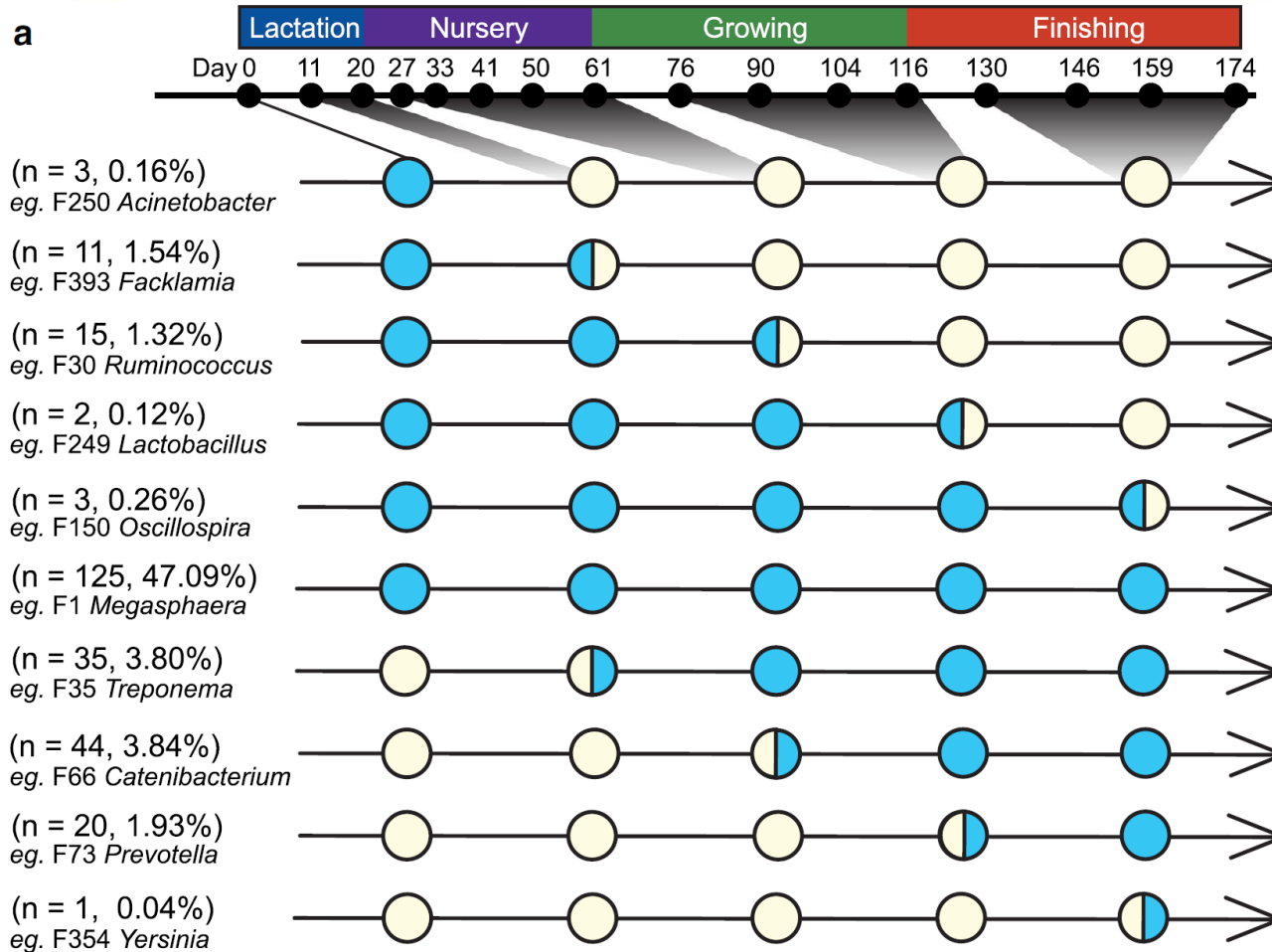


Wang *et al. Microbiome* (2019) 7:109
<https://doi.org/10.1186/s40168-019-0721-7>

- | | | |
|---|---|------------------------------------|
| Others | F13–Firmicutes–Anaerovibrio | F29–Bacteroidetes–Prevotella |
| F17–Actinobacteria–Collinsella aerofaciens | F16–Firmicutes–Blautia | F43–Bacteroidetes–Prevotella |
| F32–Proteobacteria–Succinivibrionaceae–unclassified | F8–Firmicutes–Phascolarctobacterium | F25–Bacteroidetes–Prevotella |
| F33–Proteobacteria–Succinivibrio | F4–Firmicutes–Clostridiaceae–unclassified | F21–Bacteroidetes–Prevotella |
| F7–Proteobacteria–Escherichia coli | F5–Firmicutes–Lactobacillus | F12–Bacteroidetes–Prevotella |
| F42–Firmicutes–Veillonellaceae–unclassified | F2–Firmicutes–Streptococcus luteciae | F9–Bacteroidetes–Prevotella |
| F37–Firmicutes–Faecalibacterium prausnitzii | F1–Firmicutes–Megasphaera | F36–Bacteroidetes–Prevotella copri |
| F40–Firmicutes–Faecalibacterium prausnitzii | F20–Bacteroidetes–Prevotella stercorea | F14–Bacteroidetes–Prevotella copri |
| F11–Firmicutes–Rummeliibacillus | F10–Bacteroidetes–YRC22 | F6–Bacteroidetes–Prevotella copri |
| F31–Firmicutes–Ruminococcaceae–unclassified | F23–Bacteroidetes–S24–7–unclassified | F3–Bacteroidetes–Prevotella copri |
| F18–Firmicutes–SMB53 | | |



Evoluzione del microbiota





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Evoluzione del microbiota

Nursing
(sow milk)



Enterobacteriaceae
Bacteroidaceae
Clostridiaceae
Enterococcaceae
Fusobacteriaceae
Porphyromonadaceae
Verrucomicrobiaceae
Rikenellaceae
Peptostreptococcaceae

Weaned
(feeds)



Prevotellaceae
Ruminococcaceae
Lactobacillaceae
Veillonellaceae
Paraprevotellaceae
Streptococcaceae
Succinivibrionaceae
Spirochaetaceae

1 7 14 21 28 35 42

Guevarra et al. *Journal of Animal Science and Biotechnology*
<https://doi.org/10.1186/s40104-018-0308-3>



Evoluzione del microbiota

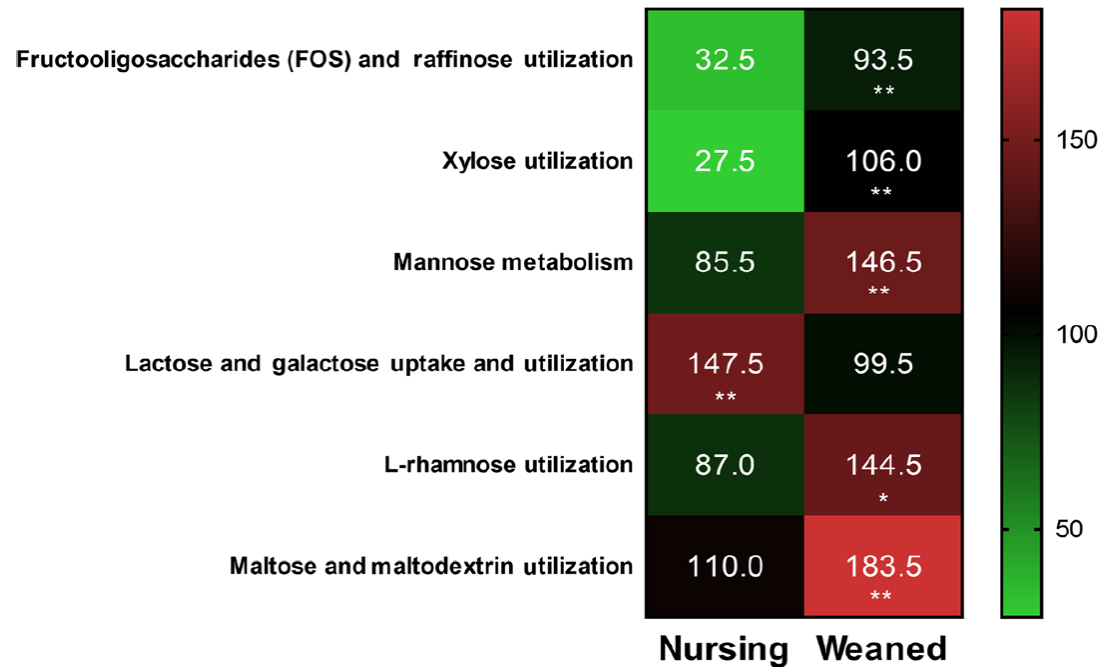
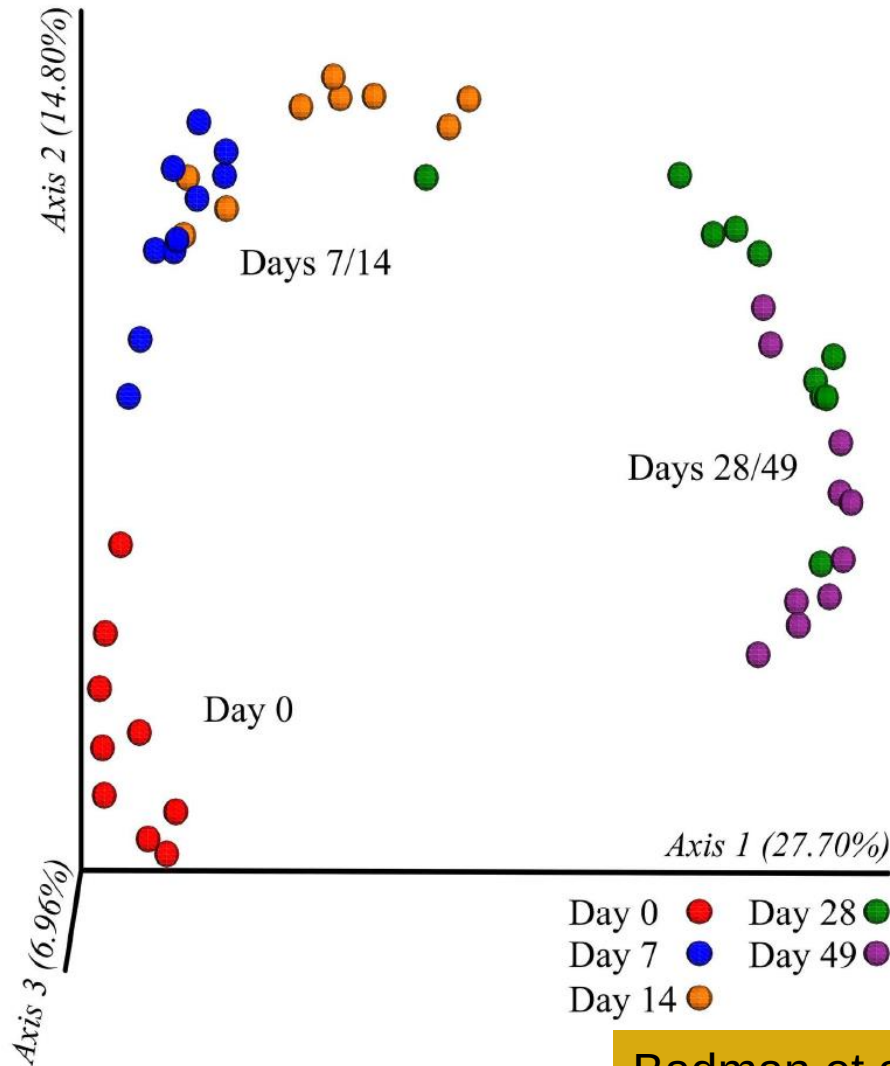


Fig. 3 The functional capacities of the microbiome between nursing and weaned piglets in association with carbohydrate metabolism as revealed by whole metagenome shotgun sequencing. The scale bar indicates normalized abundance of the level 3 SEED subsystem classified reads associated with carbohydrate metabolism. The $[P < 0.001]$, $[P < 0.01]$ and $[P < 0.05]$ were indicated as [***], [**] and [*], respectively



Evoluzione del microbiota nei vitelli



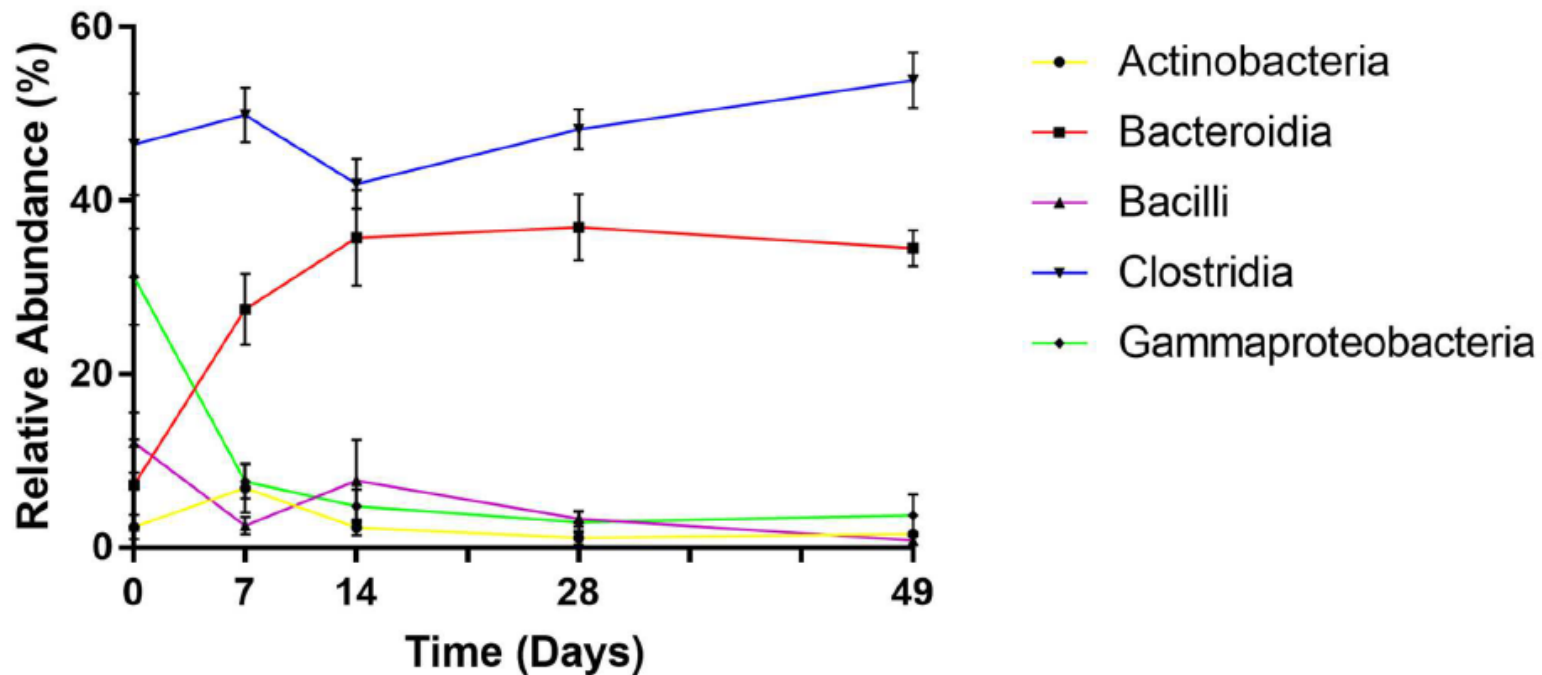
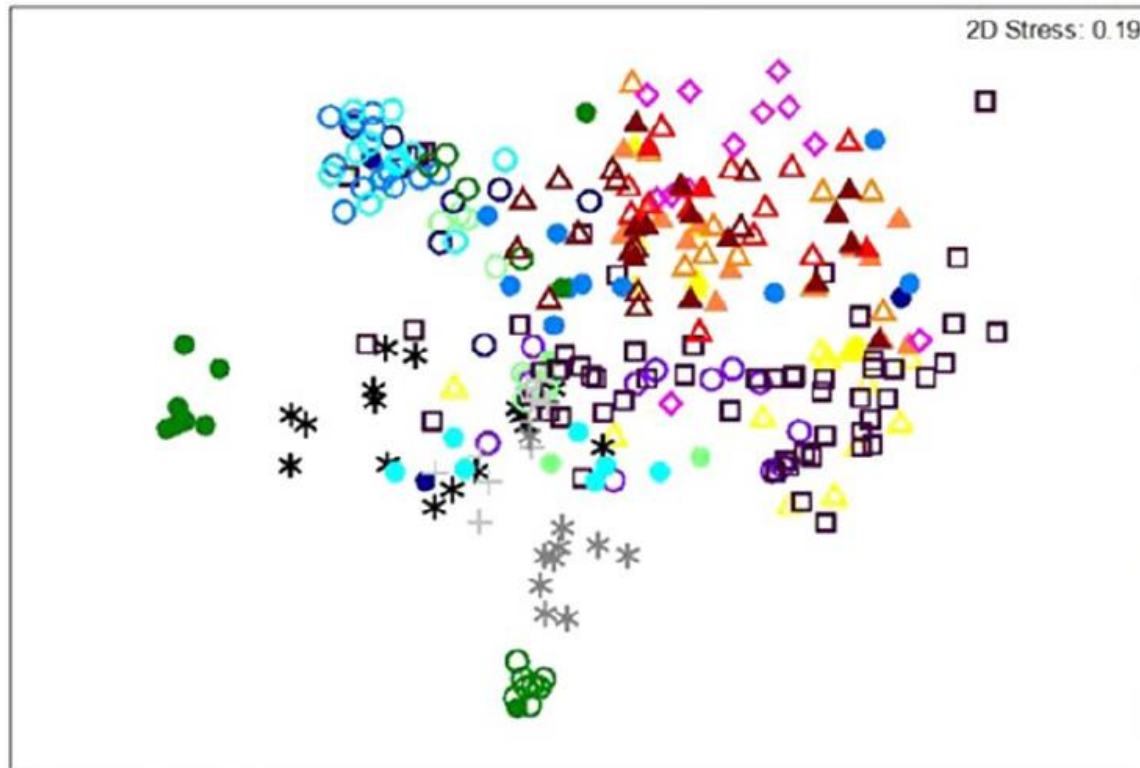


FIGURE 5 | Changes in relative abundance of dominant bacterial classes over time. Values are mean $\pm$ SEM.



Vagina come fonte
di contaminazione
di batteri e archaea
del rumine e del
reticolo

Maternal Microbiota

- * Colostrum
- + Udder
- * Vagina

Calf Microbiota

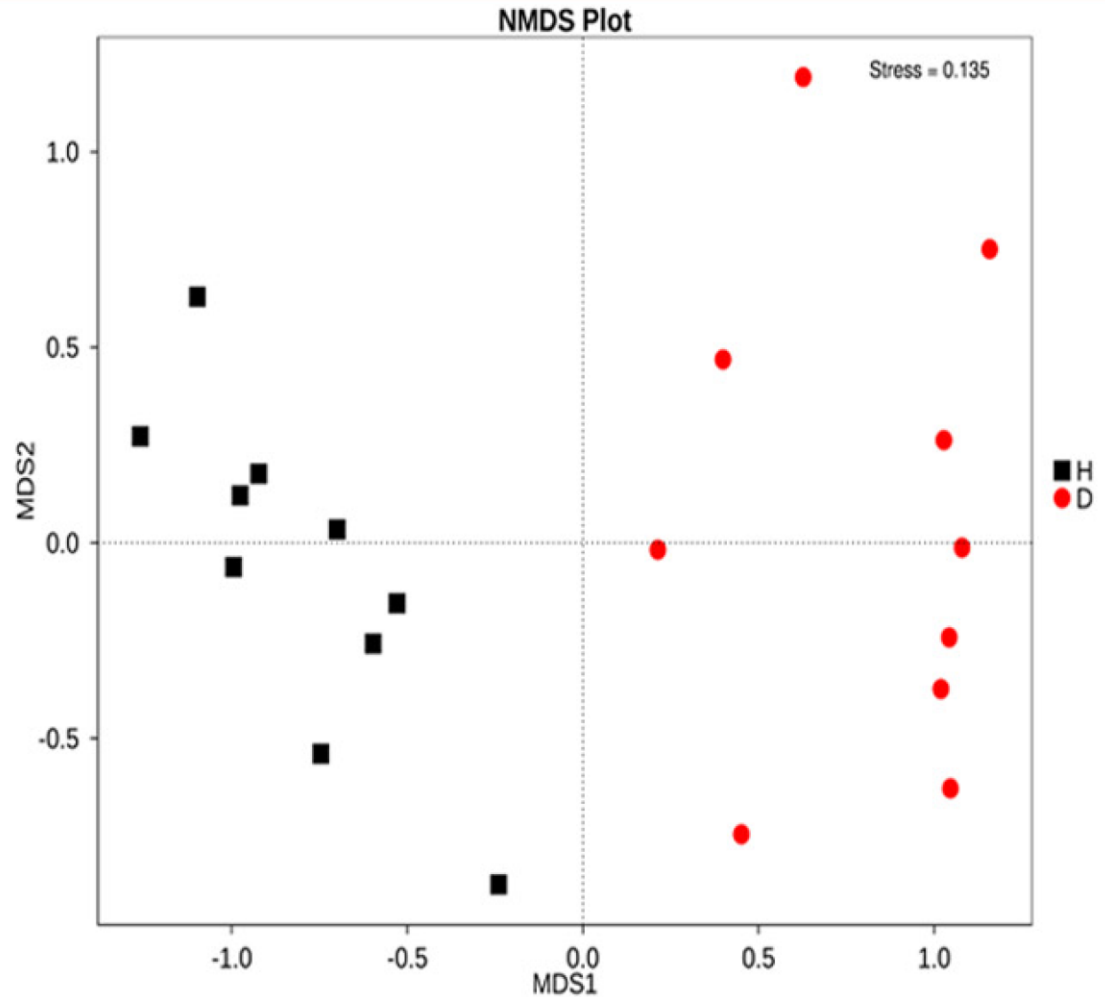
- | | | |
|-------------|--------------------|-----------|
| ▲ Reticulum | ● Duodenum | ● Ileum |
| ▲ Rumen | ● Proximal Jejunum | ○ Colon |
| ▲ Omasum | ● Medial Jejunum | □ Feces |
| ▲ Abomasum | ● Distal Jejunum | ◇ Pharynx |

- Mucosa
- Lumen



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Diarrea in fase di svezzamento



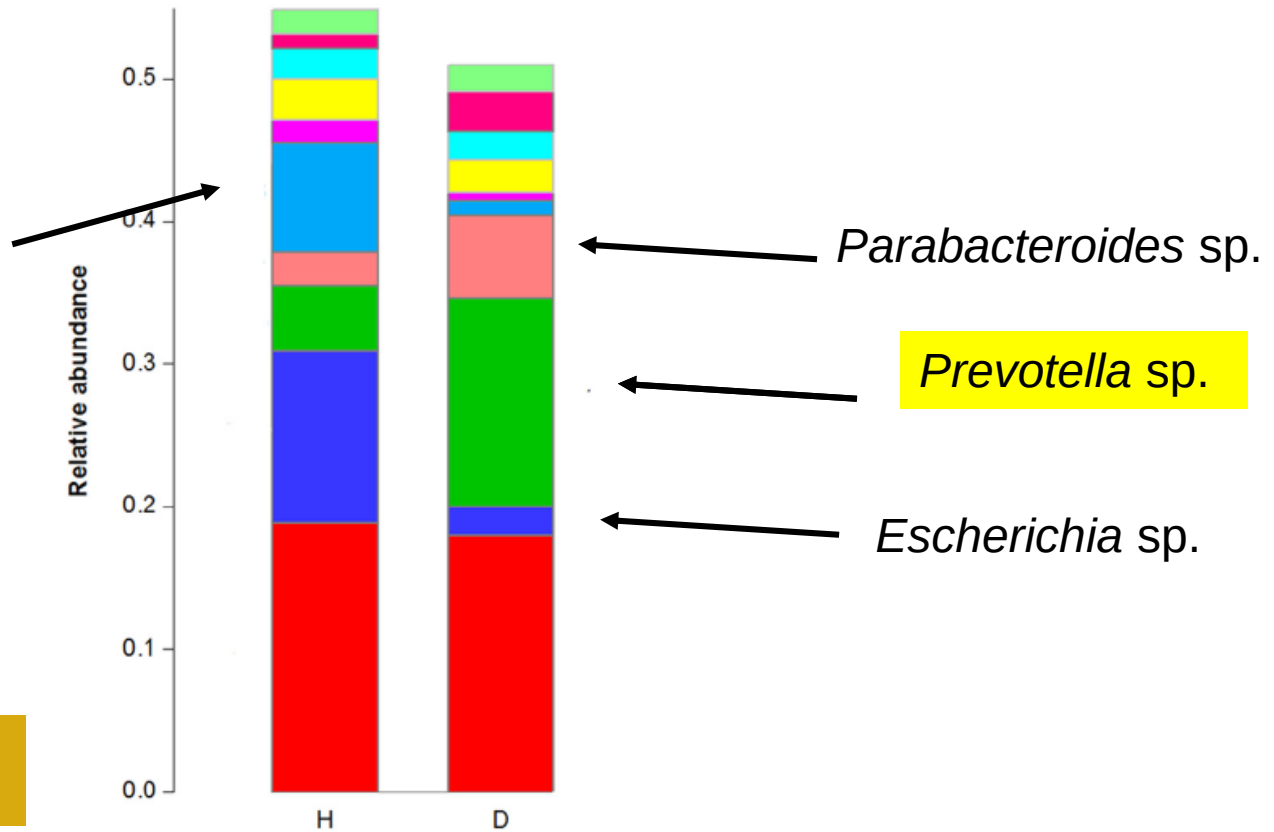
Yang et al. Front Microbiol.
2017; 8: 502.



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Diarrea in fase di svezzamento

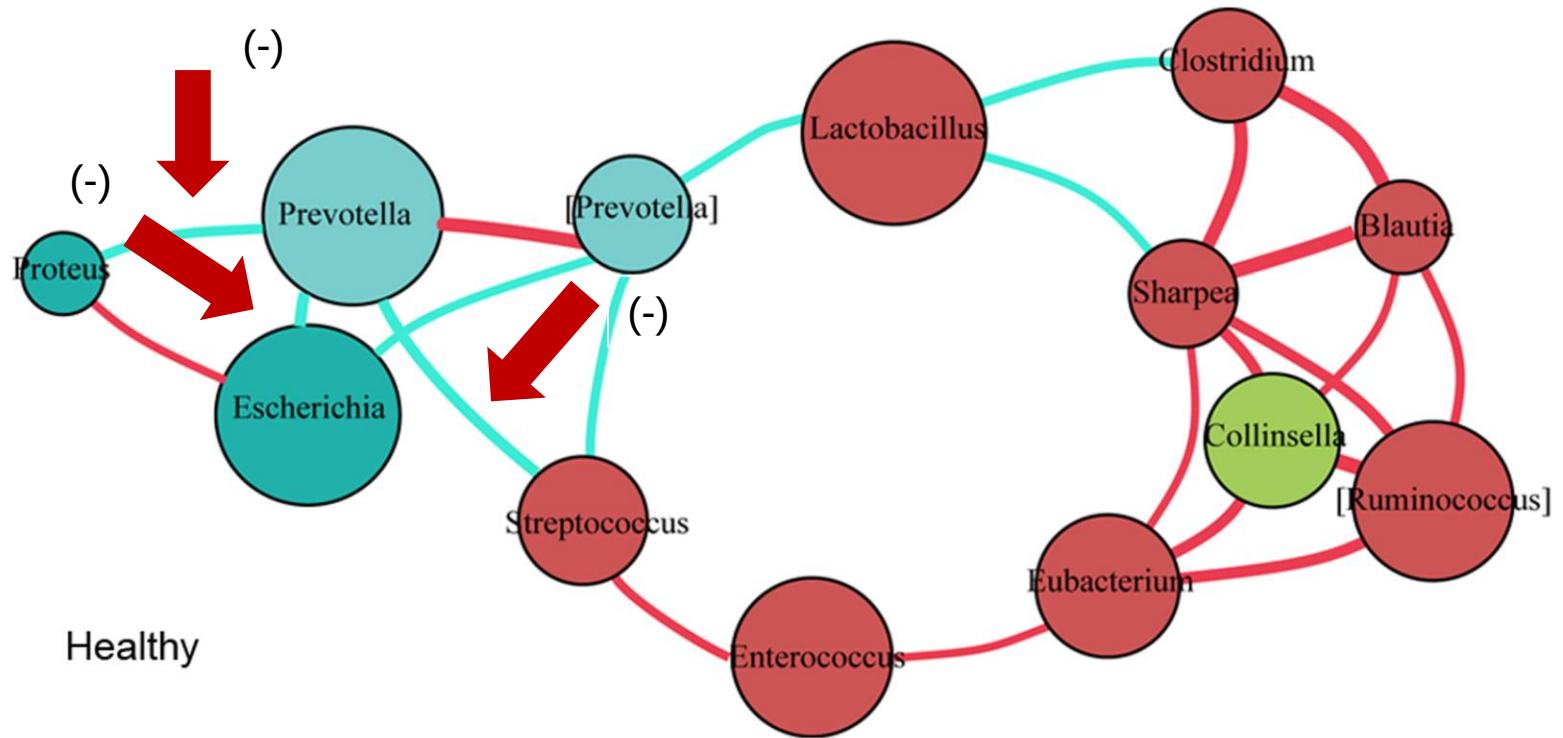
B



Yang et al. Front Microbiol.
2017; 8: 502.



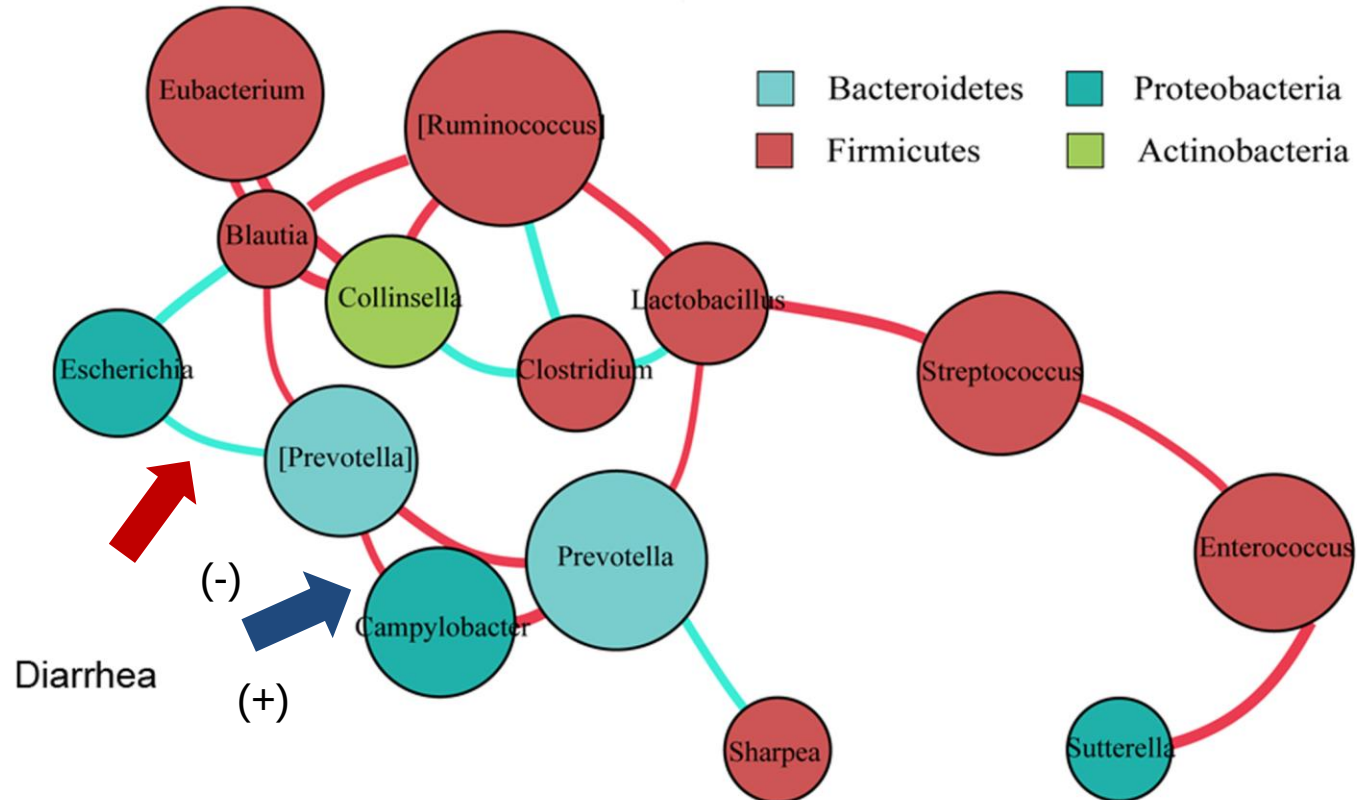
Diarrea in fase di svezzamento



Yang et al. Front Microbiol.
2017; 8: 502.



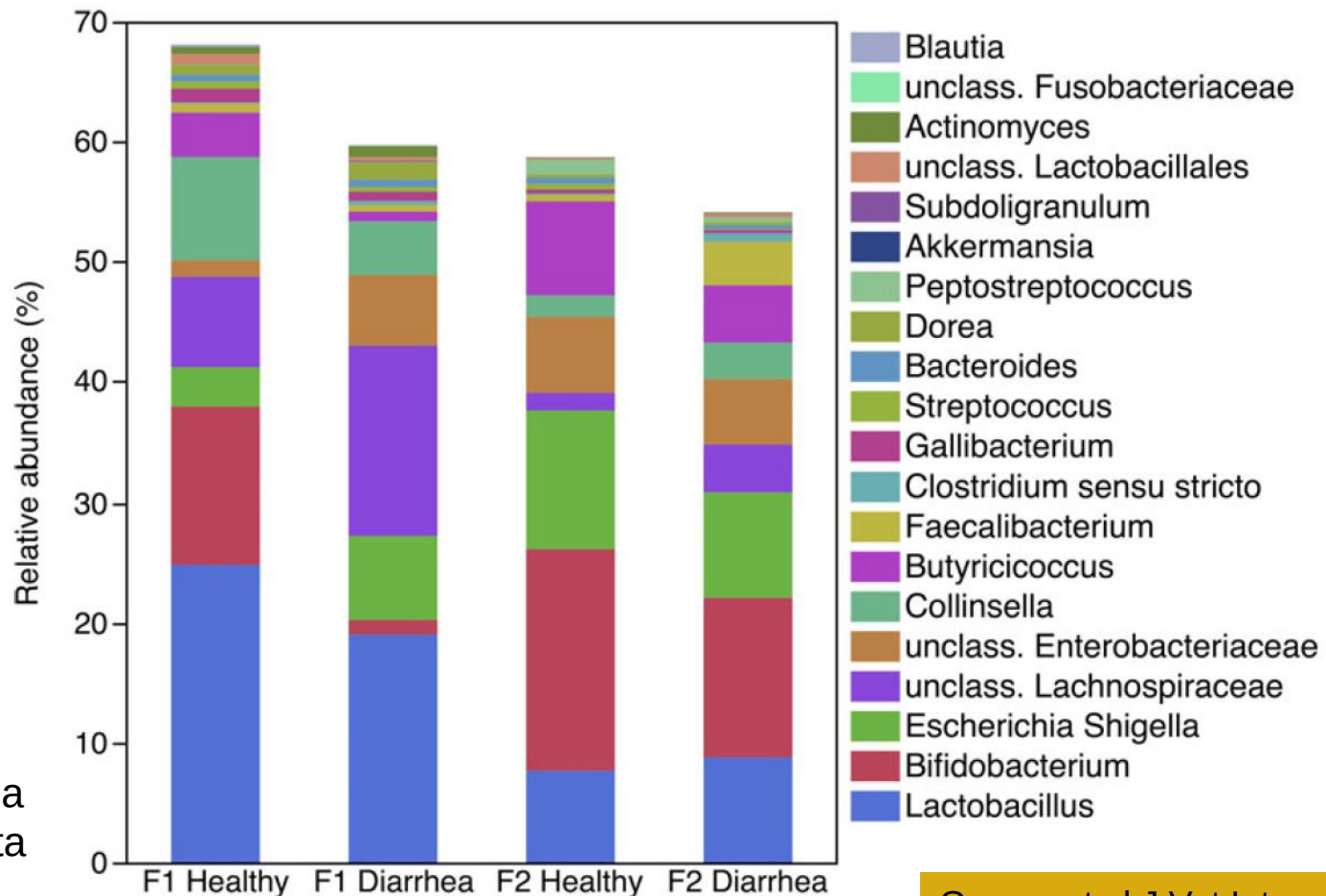
Diarrea in fase di svezzamento





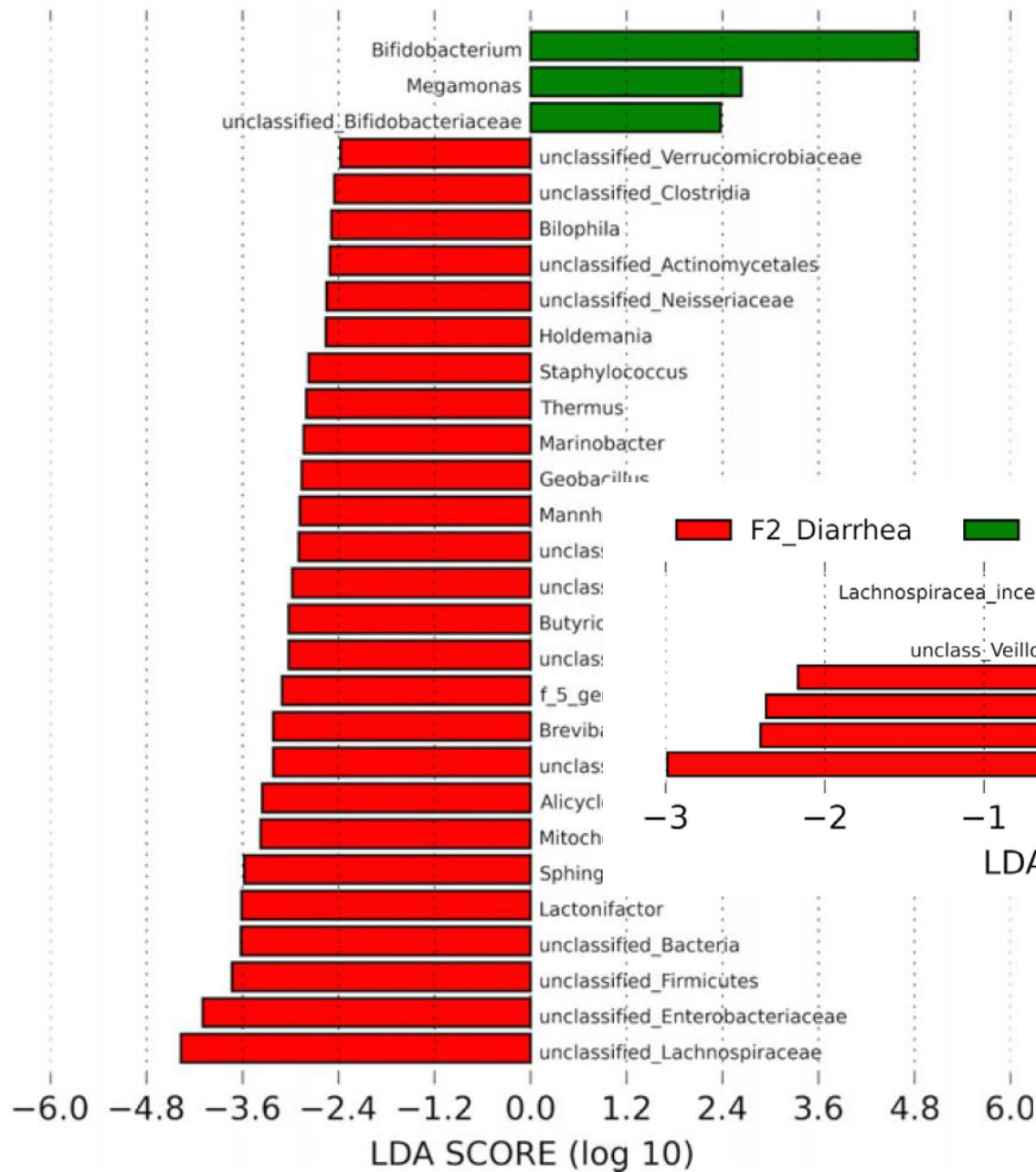
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Diarrea in fase di svezzamento in vitelli

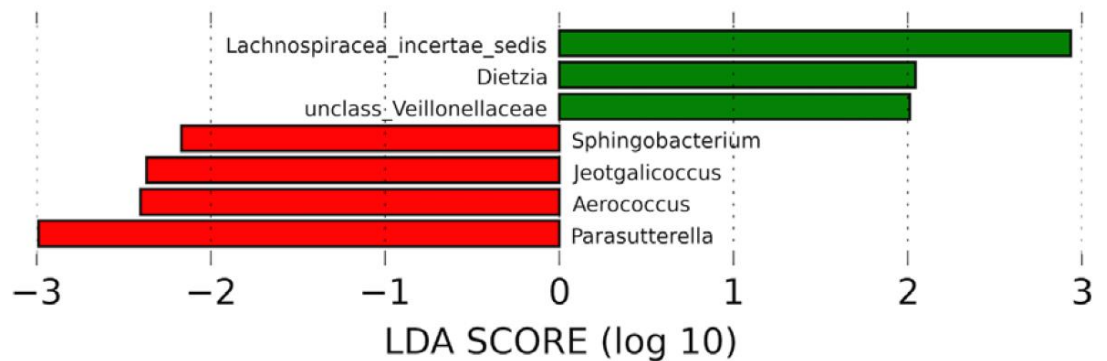


Gomez et al J Vet Intern Med
2017;31:928–939

■ F1_Diarrhea ■ F1_Healthy



■ F2_Diarrhea ■ F2_Healthy



Possibili interventi

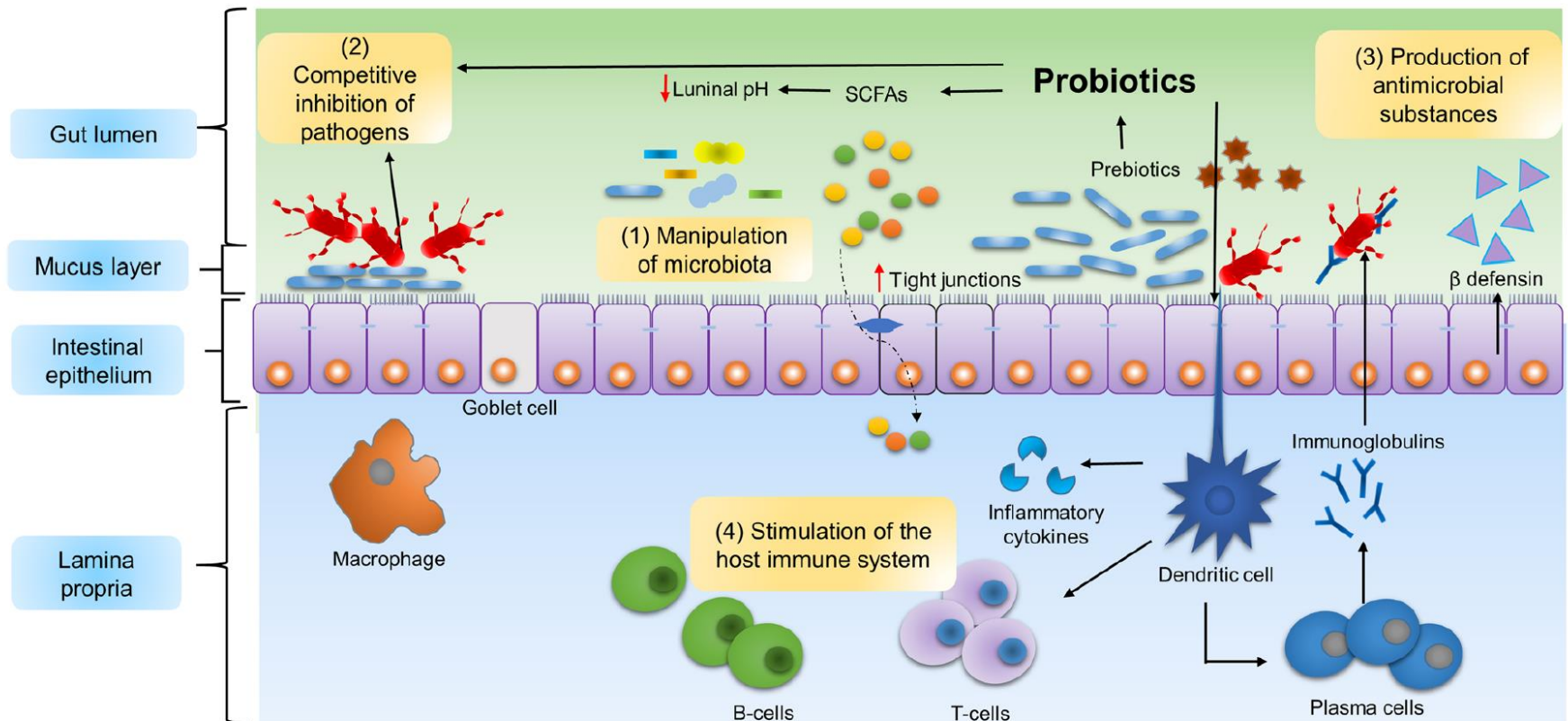


Fig. 2 The potential mechanisms by which probiotics affect intestinal microbial ecology. Probiotics may act through the following mechanisms: (1) manipulation of the microbiota by changing luminal pH, (2) competitive inhibition of pathogen, (3) production of antimicrobial substances and (4) stimulation of the pig's immune system

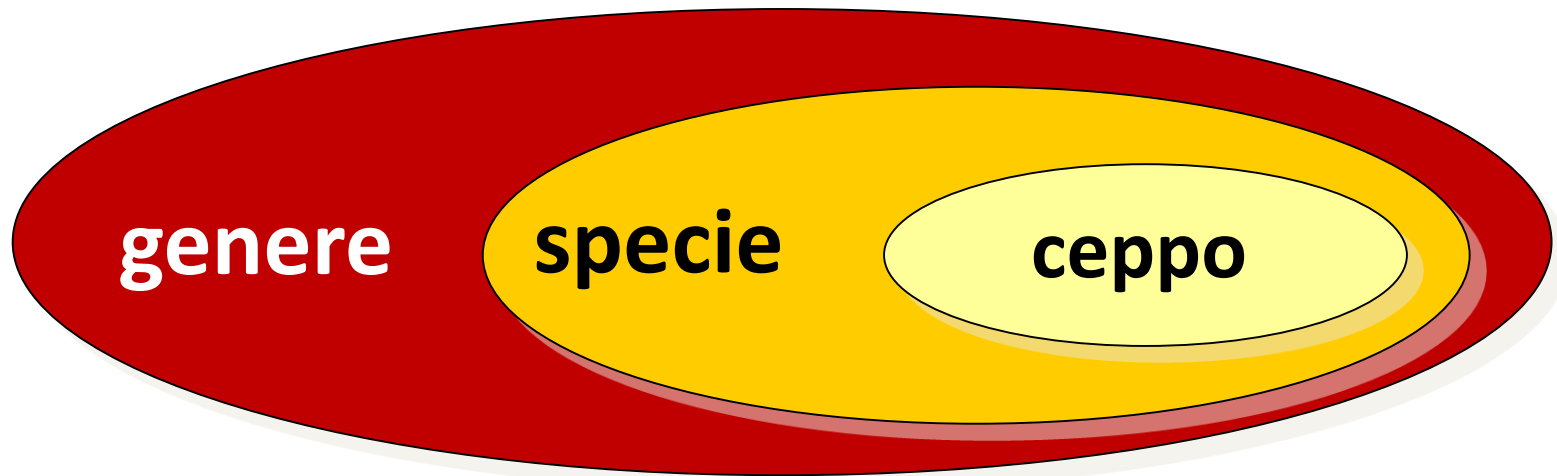


Che caratteristiche devono avere?

- ✓ Essere attivi e vitali
- ✓ Essere sicuri
- ✓ Sopravvivere nel tratto gastrointestinale
- ✓ Colonizzare l'intestino
- ✓ Possedere caratteristiche di probioticità (conferire un beneficio fisiologico dimostrato secondo criteri fissati)



Le caratteristiche di probioticità sono ceppo specifiche



Lactobacillus

casei

XYZ



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Dall'osservazione all'intervento: il progetto FOODTECH...



UNIONE EUROPEA
Fondo europeo di sviluppo regionale



Regione
Lombardia

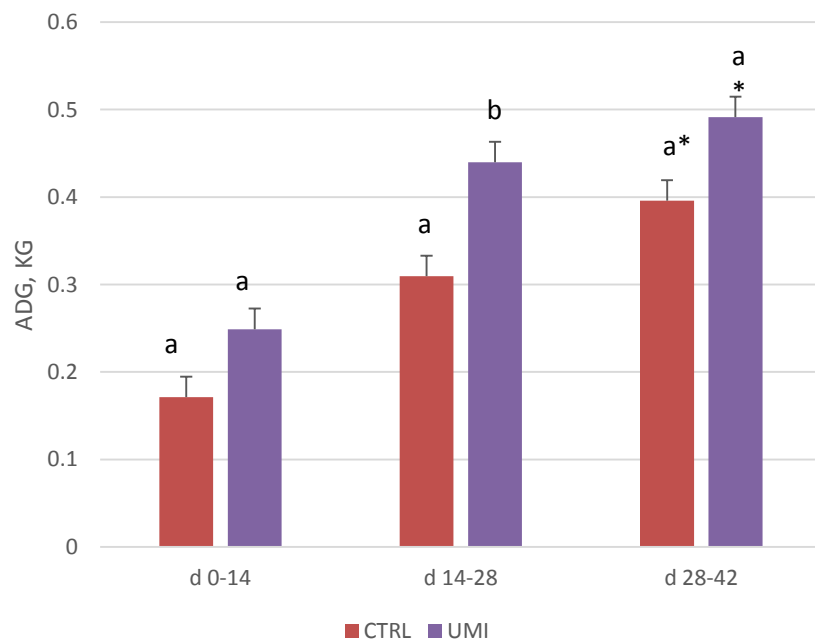


POR 2014-2020 FESR / INNOVAZIONE E COMPETITIVITÀ

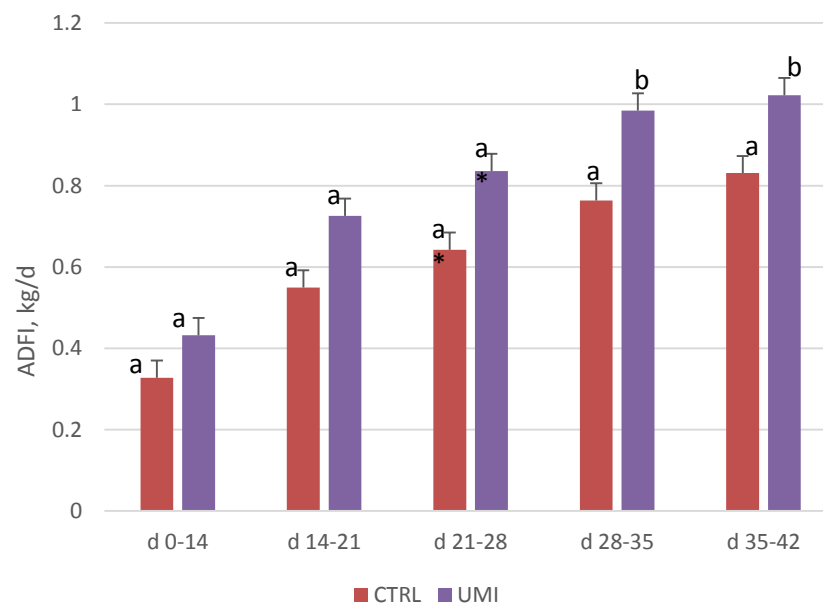


Acidi umici

Incremento ponderale giornaliero



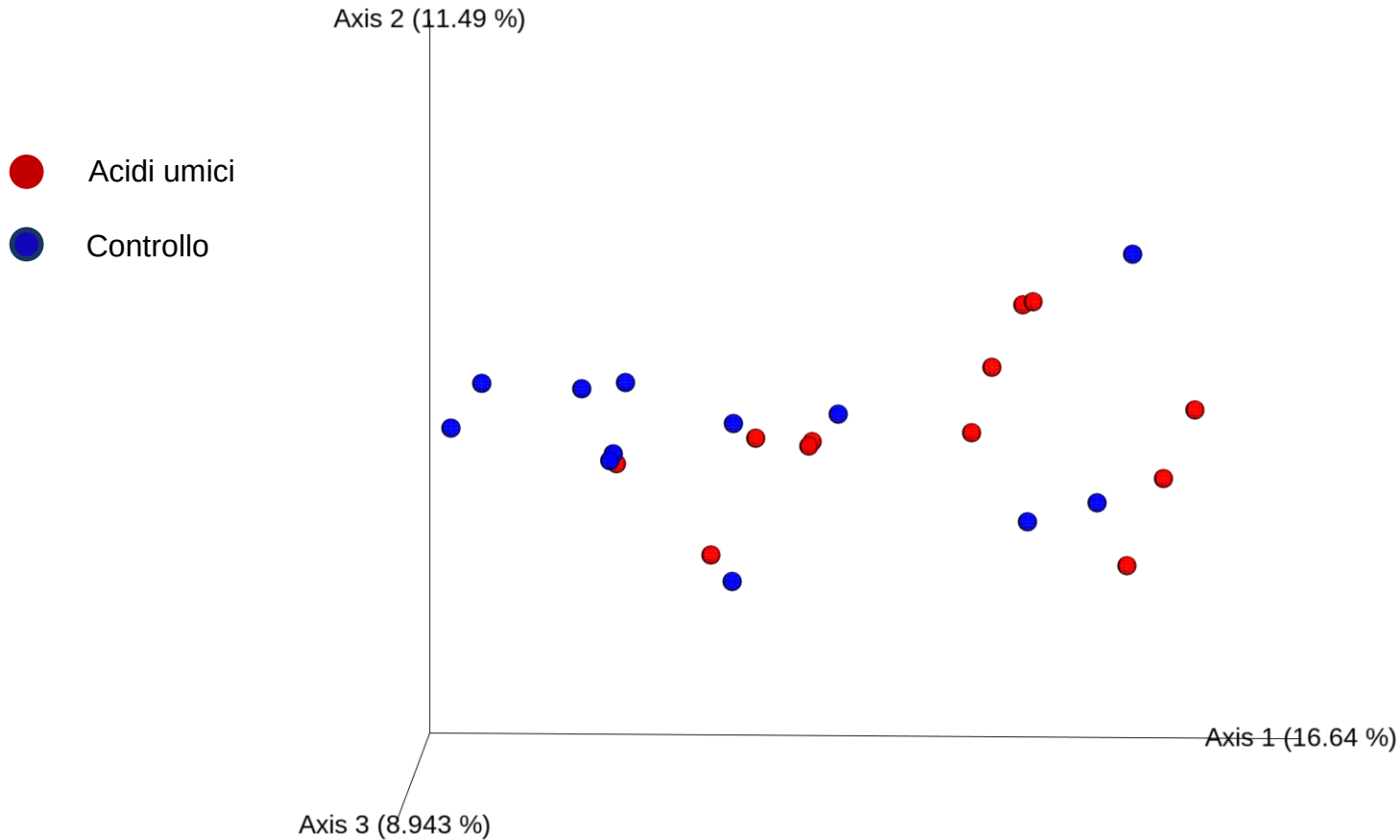
Assunzione giornaliera media





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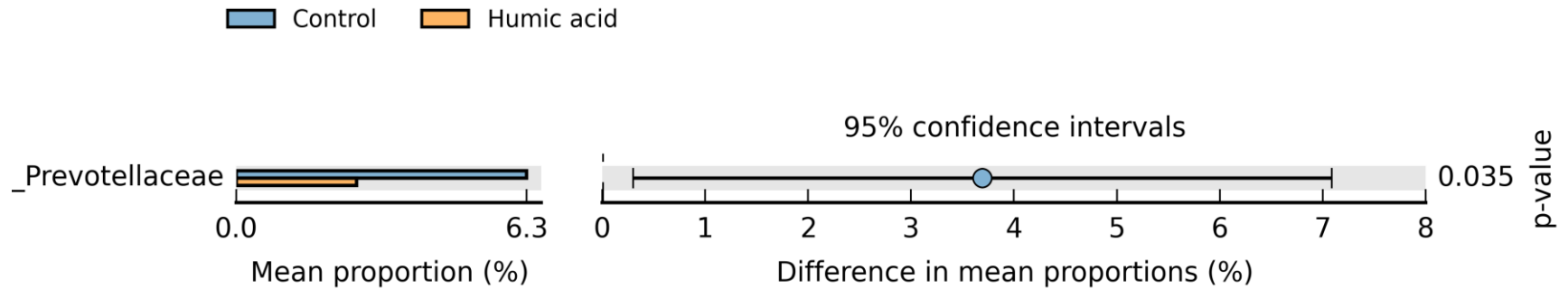
Microbiota intestinale e Acidi umici





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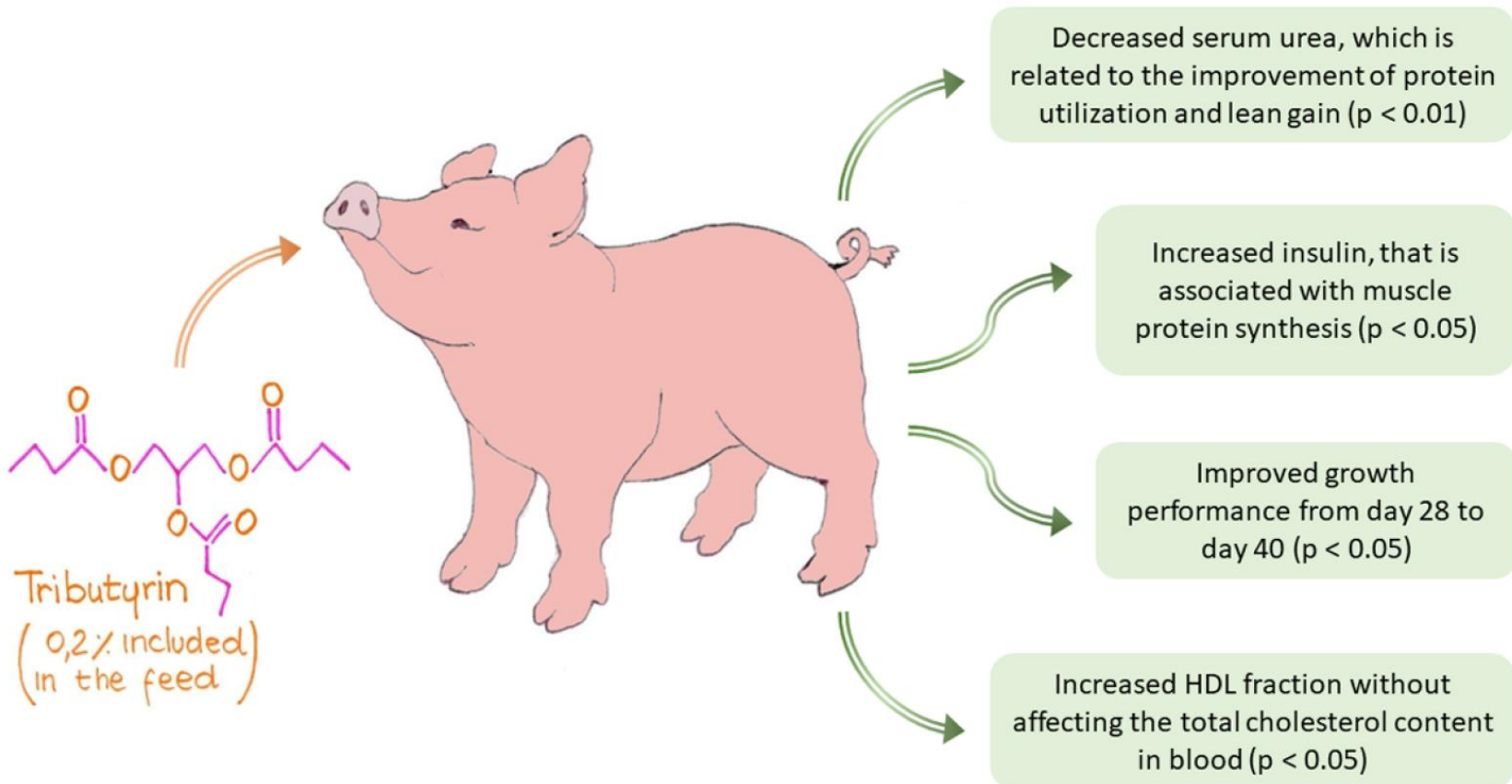
Microbiota intestinale e Acidi umici





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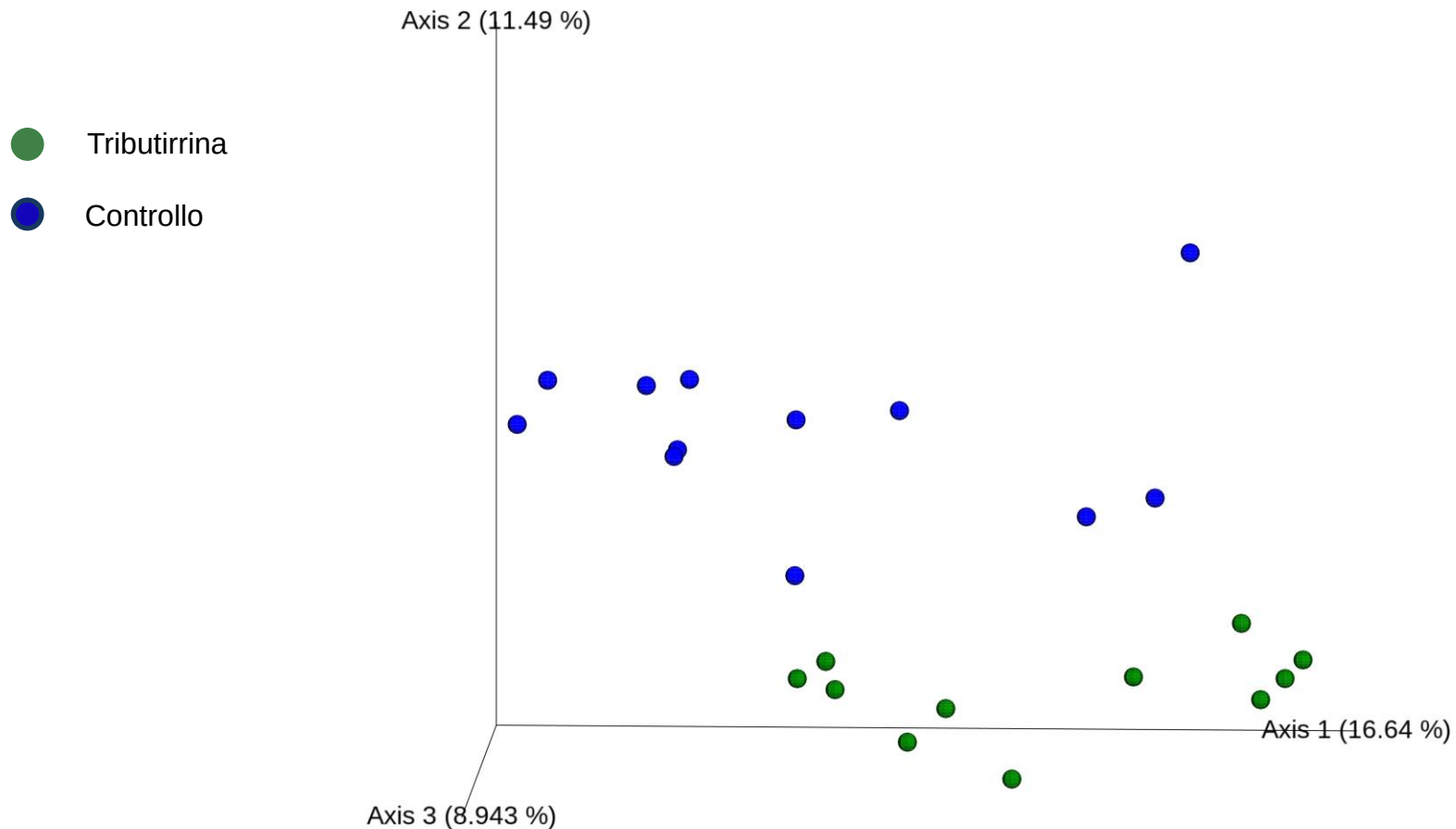
Microbiota intestinale e Tributirina

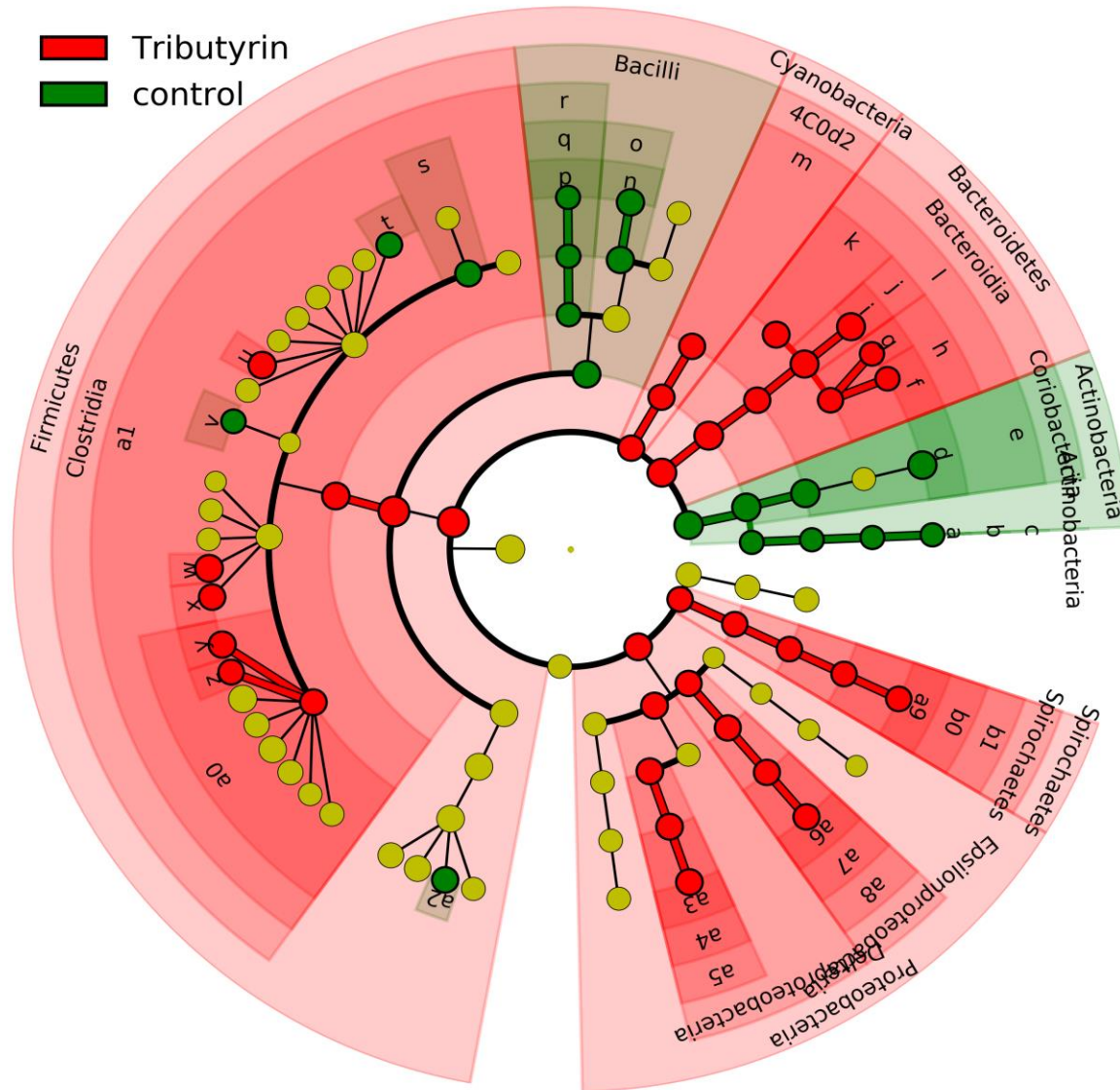




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Microbiota intestinale e Tributirina





- a: Bifidobacterium
- b: Bifidobacteriaceae
- c: Bifidobacteriales
- d: Olsenella
- e: Coriobacteriales
- f: CF231
- g: Prevotella
- h: Paraprevotellaceae
- i: Prevotella
- j: Prevotellaceae
- k: S247
- l: Bacteroidales
- m: YS2
- n: Streptococcus
- o: Streptococcaceae
- p: Turicibacter
- q: Turicibacteraceae
- r: Turicibacterales
- s: Clostridiaceae
- t: Blautia
- u: Roseburia
- v: Mogibacterium
- w: Oscillospira
- x: Ruminococcus
- y: Acidaminococcus
- z: Anaerovibrio
- a0: Veillonellaceae
- a1: Clostridiales
- a2: Eubacterium
- a3: Desulfovibrio
- a4: Desulfovibrionaceae
- a5: Desulfovibrionales
- a6: Campylobacter
- a7: Campylobacteraceae
- a8: Campylobacteriales
- a9: Treponema
- b0: Spirochaetaceae
- b1: Spirochaetales



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Un grazie a: Stefania Sotira, Matteo Dell'Anno, Valentina Caprarulo, Monika Hejna, Federica Pirrone, Telma Vieira Tucci, Luciana Rossi ecc...

Grazie per l'attenzione!!!!

