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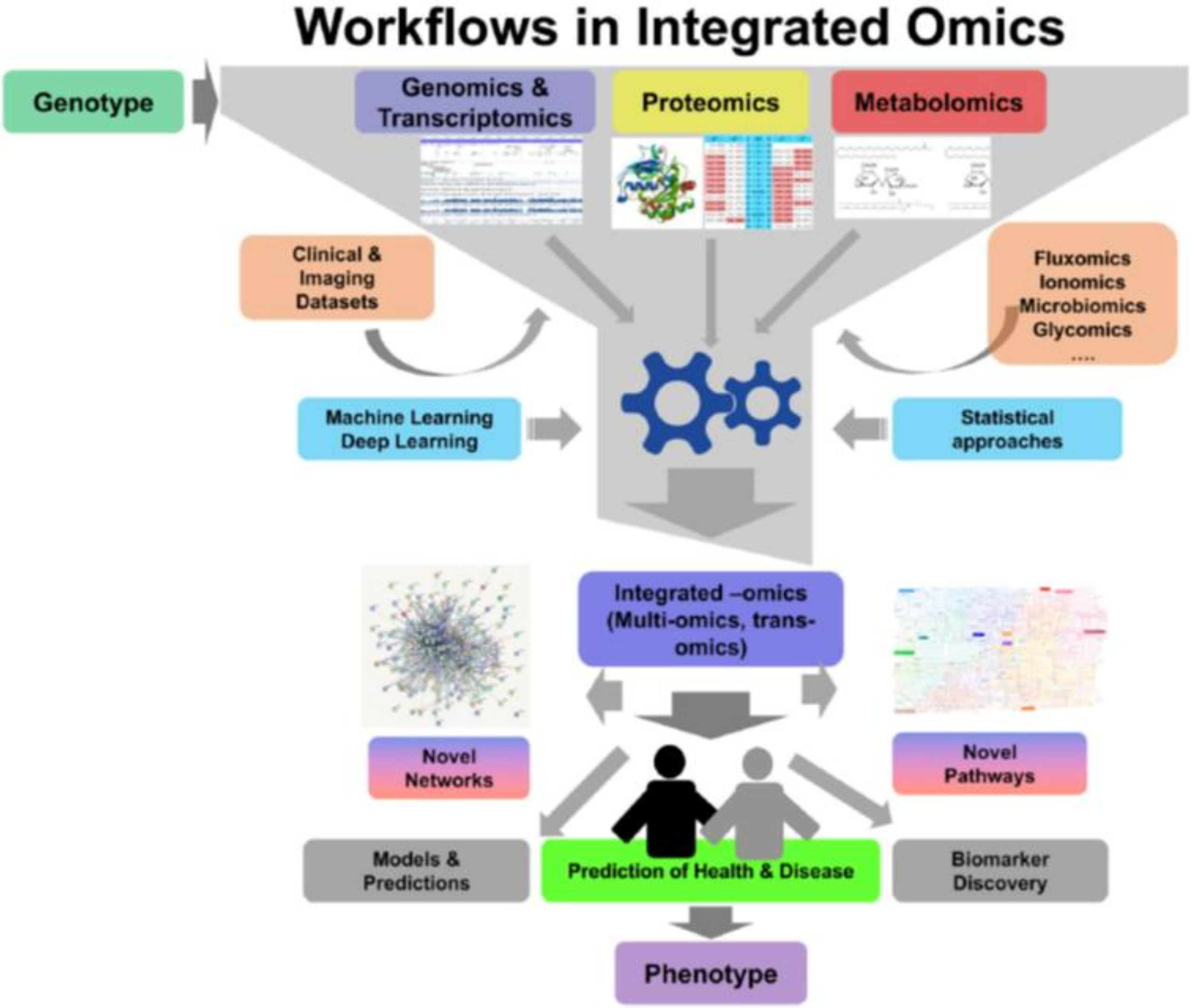
Modulazione del microbiota intestinale attraverso strategie mirate alla riduzione degli antibiotici negli allevamenti

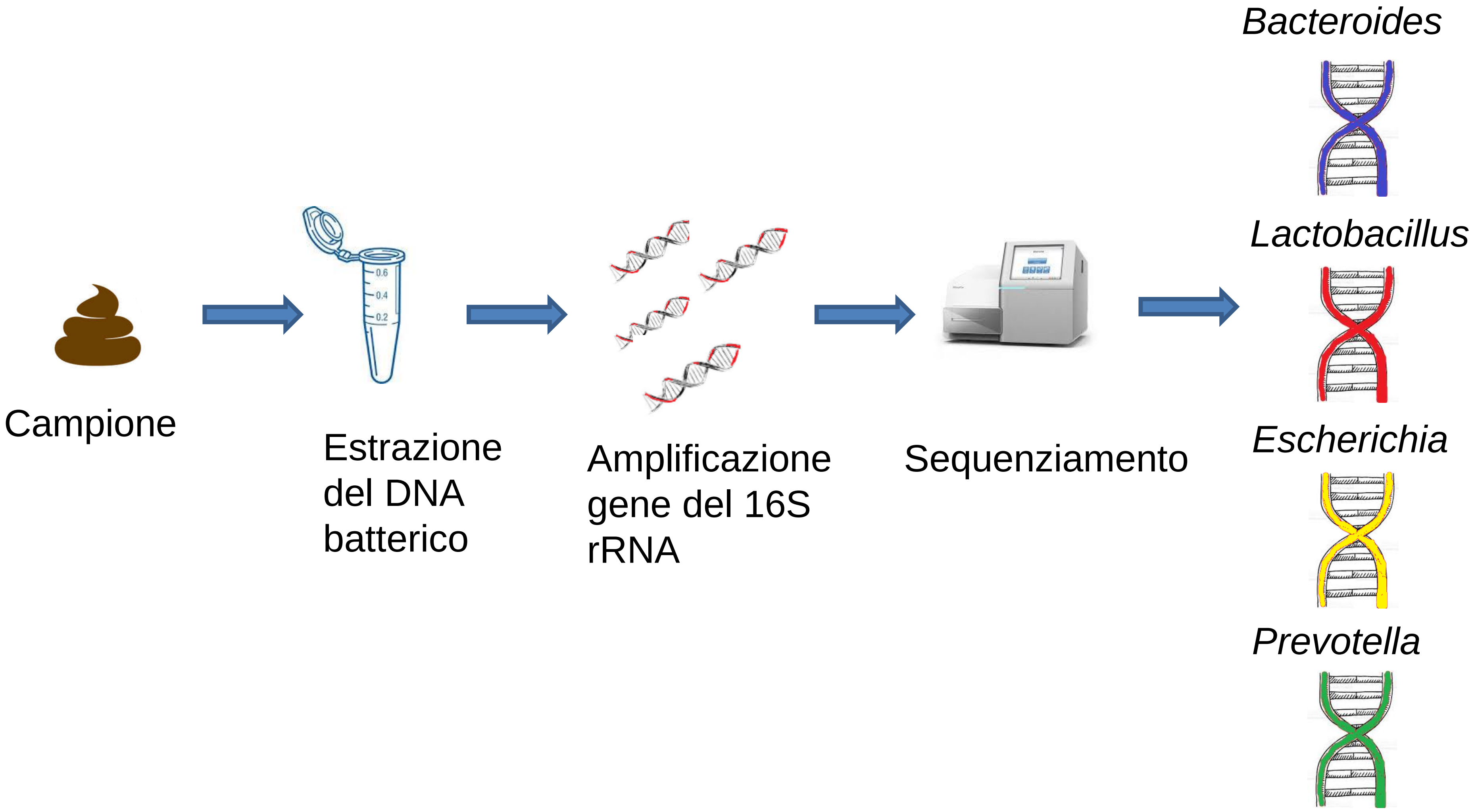
Maria Luisa Callegari

Cremona, 11 Novembre 2020

Le omics in uno sguardo



Metabarcoding



Campione

Estrazione del DNA batterico

Amplificazione gene del 16S rRNA

Sequenziamento

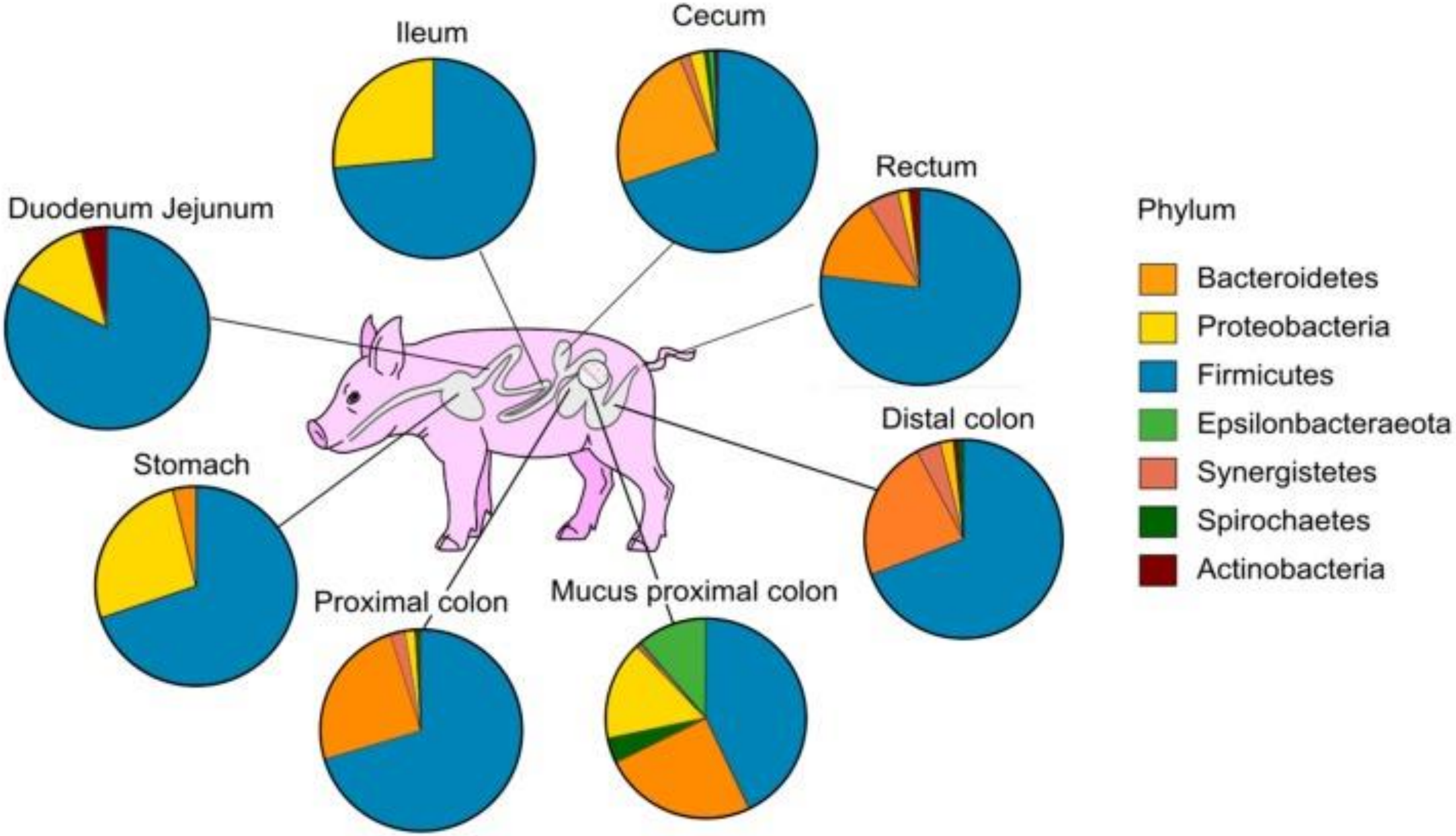
Bacteroides

Lactobacillus

Escherichia

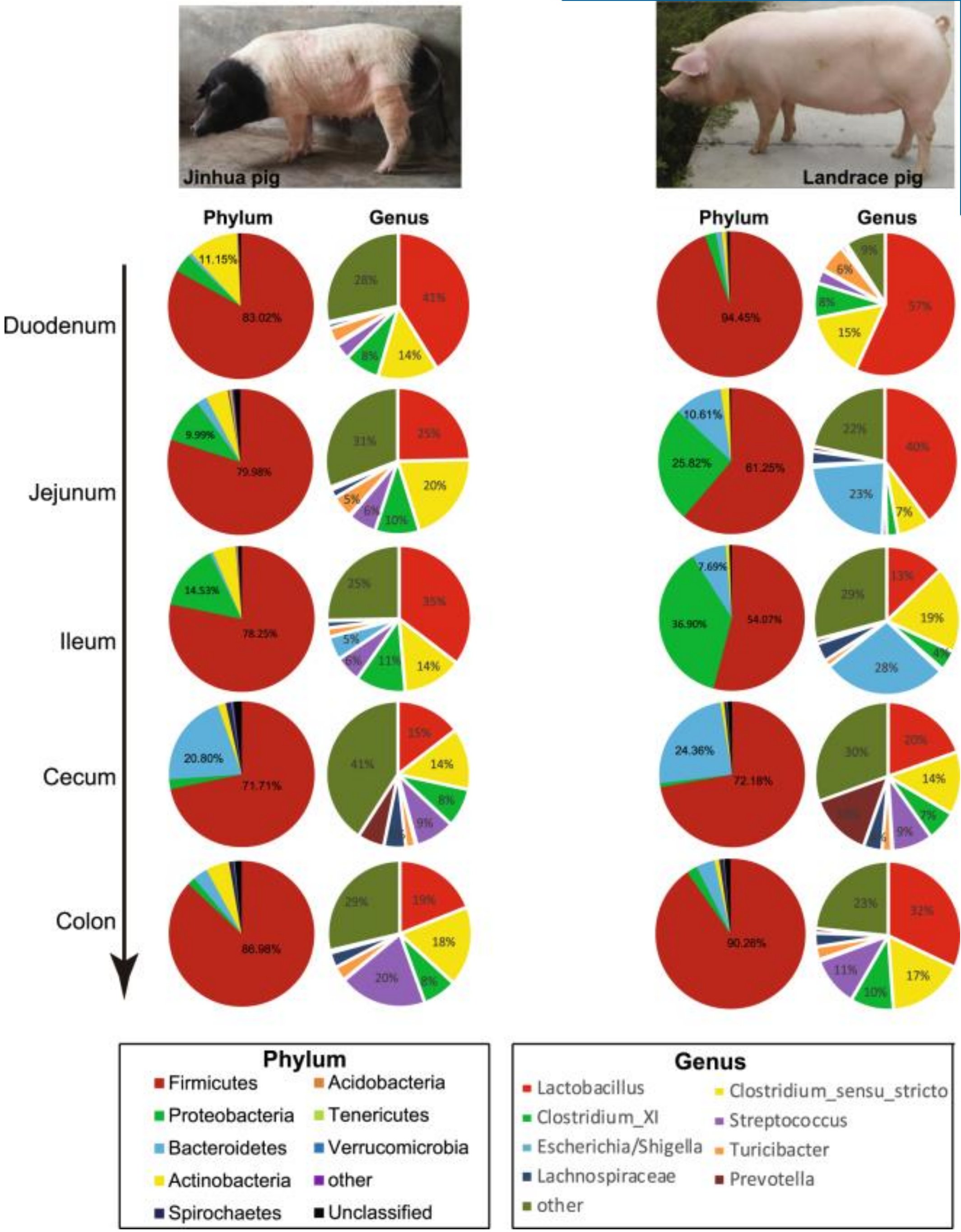
Prevotella

Microbiota intestinale del suinetto



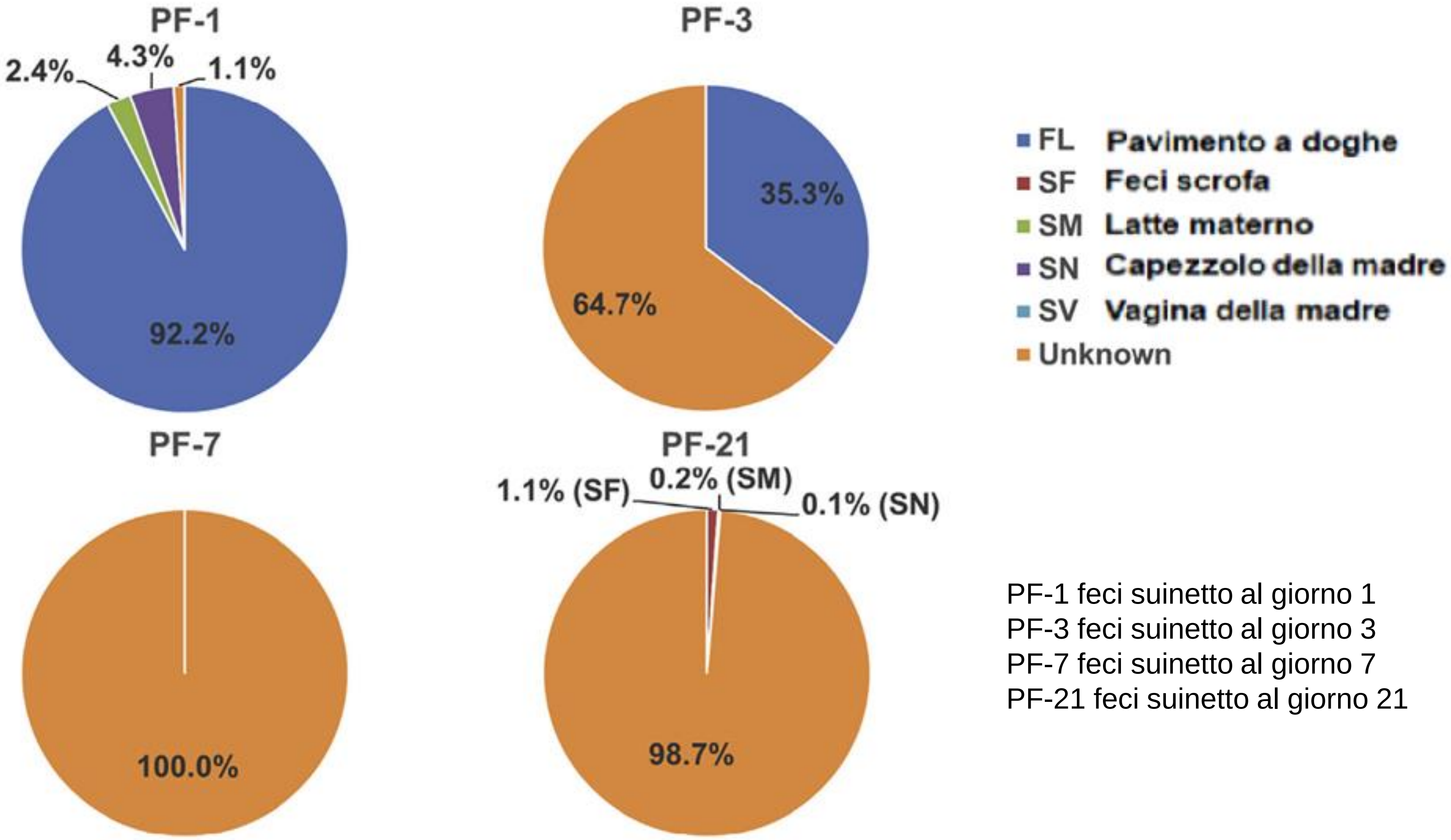
Microbiota Composition and Functional Profiling Throughout the Gastrointestinal Tract of Commercial Weaning Piglets. Gresse et al 2019; Microorganisms. 2019 Sep; 7: 343.

Microbiota e razza



Xiao et al. Sci Rep. 2018; 8: 5985.

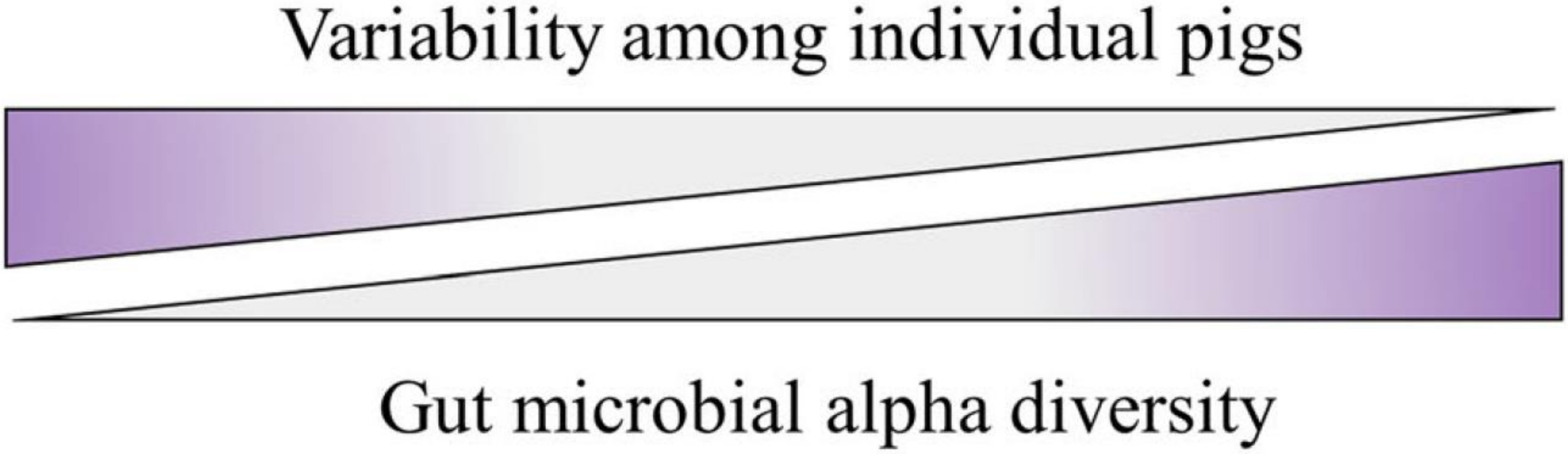
Prima colonizzazione



PF-1 feci suinetto al giorno 1
PF-3 feci suinetto al giorno 3
PF-7 feci suinetto al giorno 7
PF-21 feci suinetto al giorno 21

Chen et al 2017. Anaerobe 49 (2018) 30-40

Evoluzione del microbiota

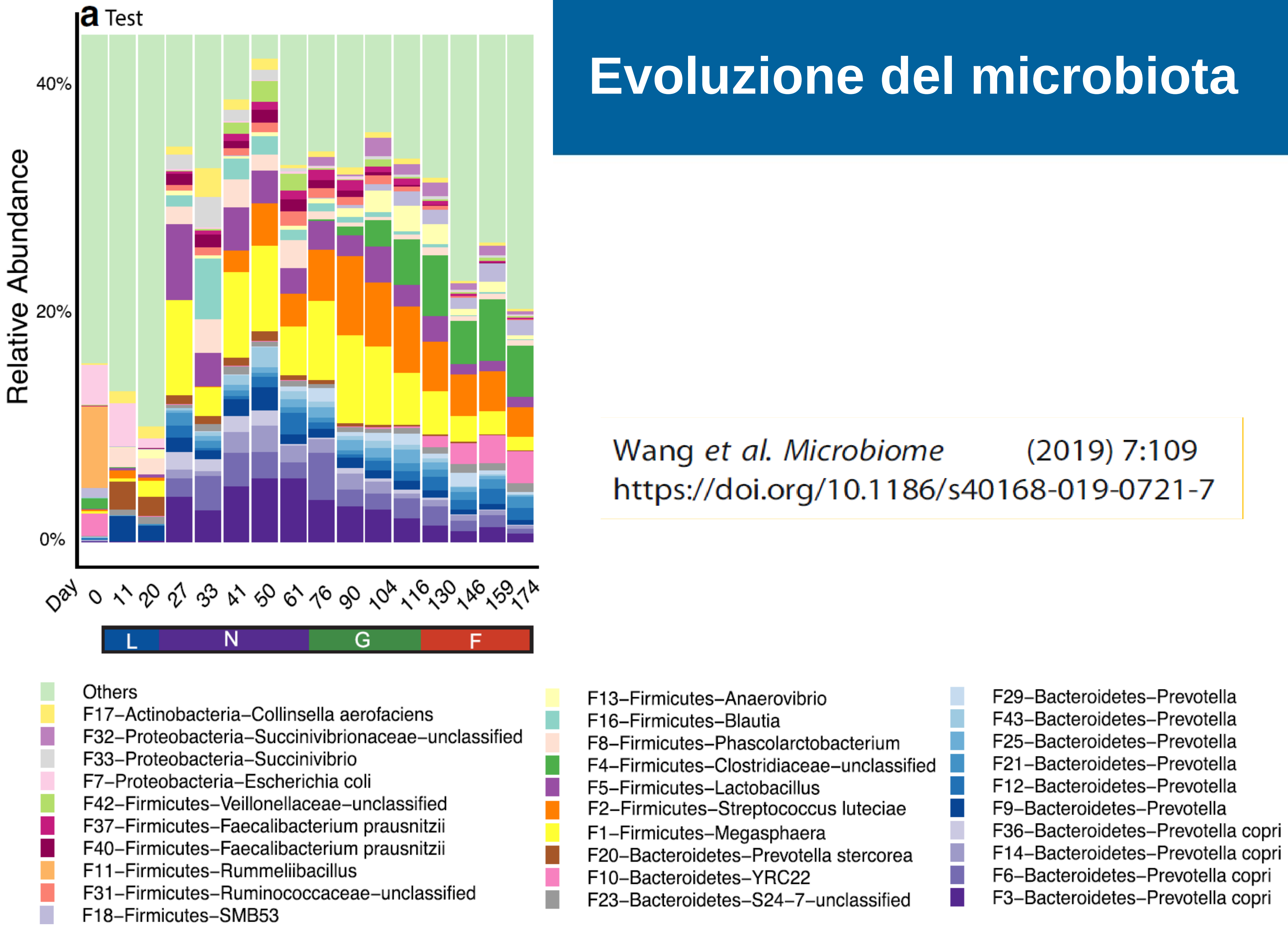


Variability among individual pigs

Gut microbial alpha diversity

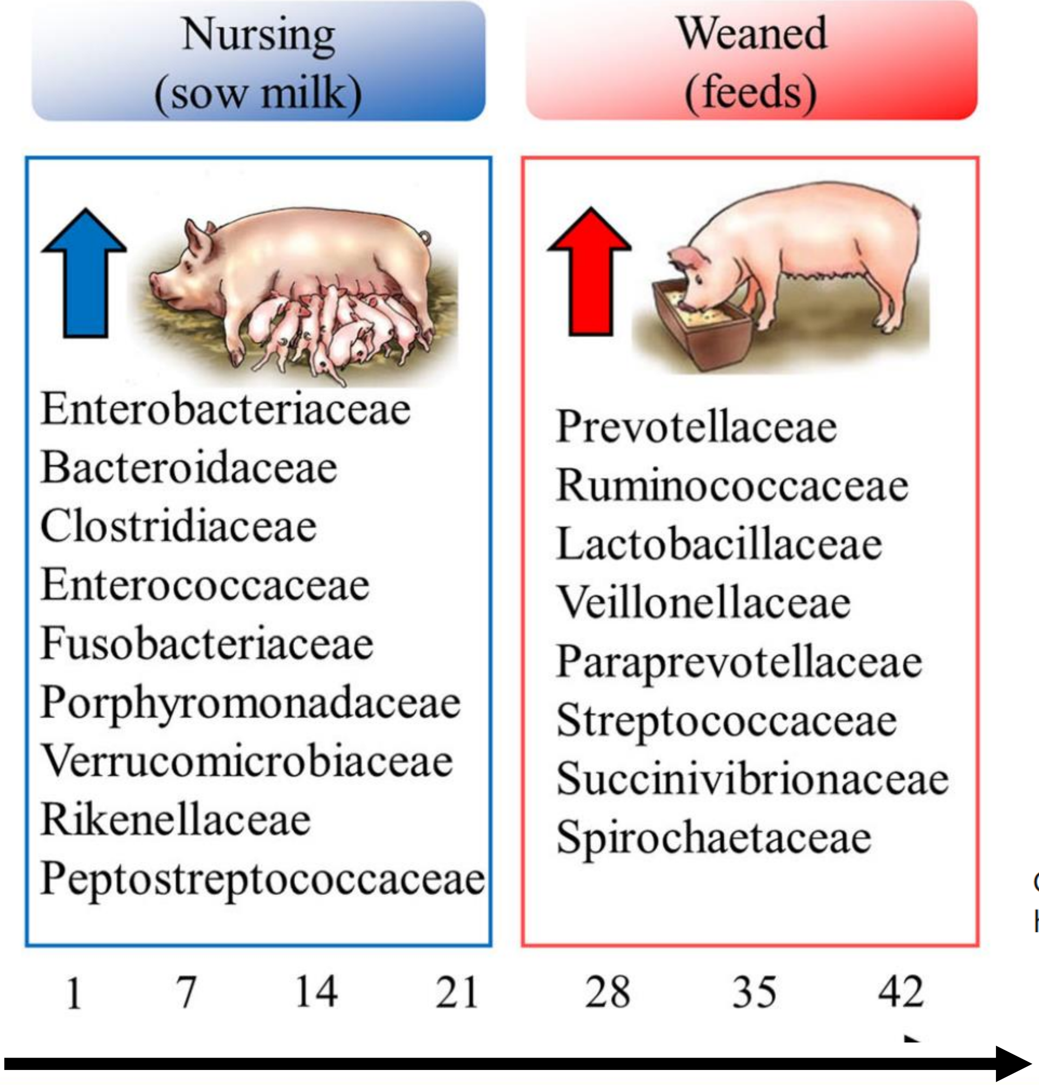
Guevarra *et al. Journal of Animal Science and Biotechnology*
https://doi.org/10.1186/s40104-018-0308-3

Evoluzione del microbiota



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

Evoluzione del microbiota



Nursing
(sow milk)

Enterobacteriaceae
Bacteroidaceae
Clostridiaceae
Enterococcaceae
Fusobacteriaceae
Porphyromonadaceae
Verrucomicrobiaceae
Rikenellaceae
Peptostreptococcaceae

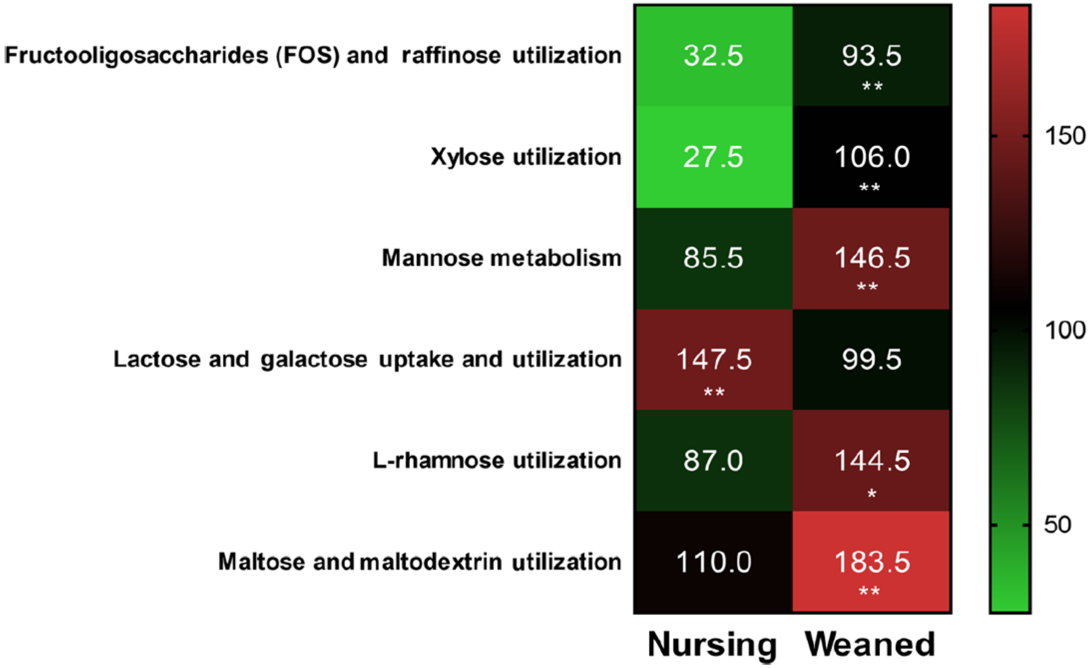
Weaned
(feeds)

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

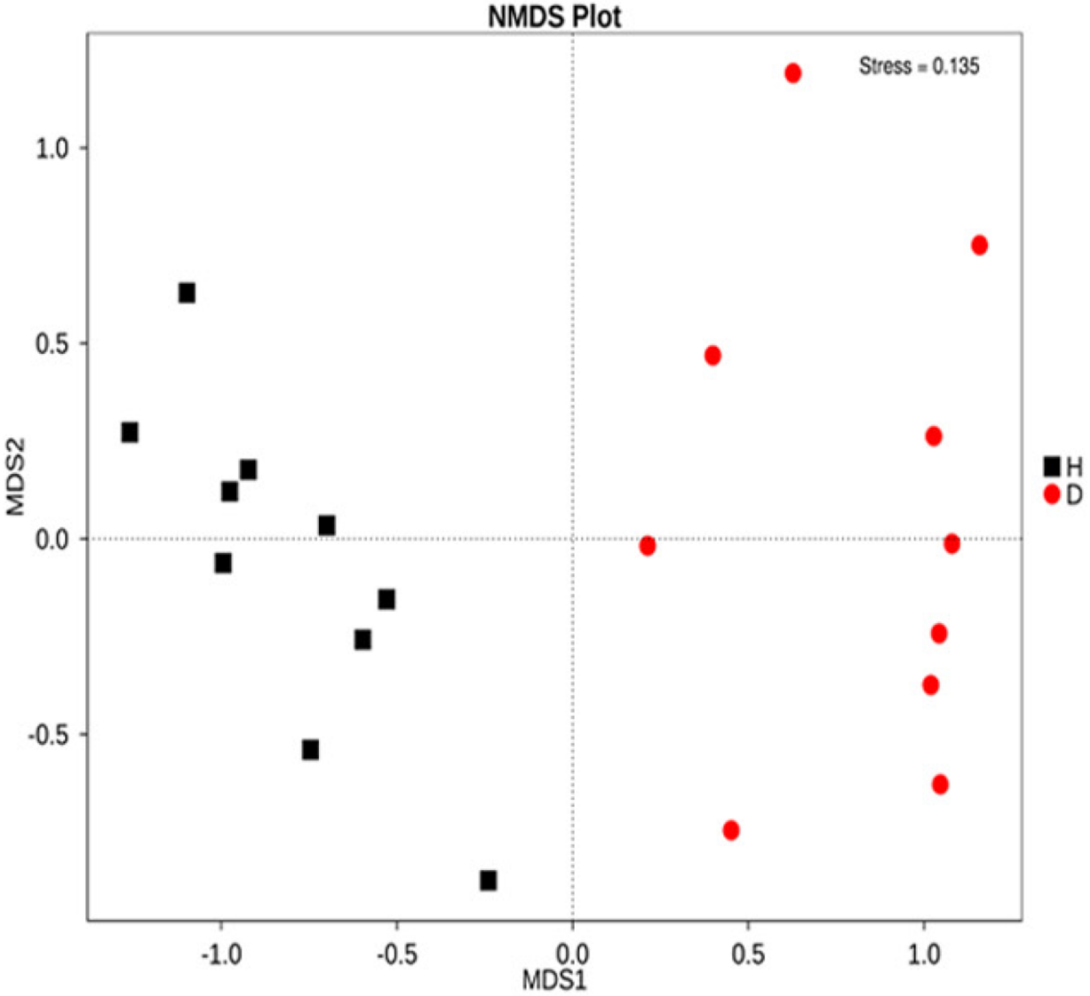


	Nursing	Weaned
Fructooligosaccharides (FOS) and raffinose utilization	32.5	93.5 **
Xylose utilization	27.5	106.0 **
Mannose metabolism	85.5	146.5 **
Lactose and galactose uptake and utilization	147.5 **	99.5
L-rhamnose utilization	87.0	144.5 *
Maltose and maltodextrin utilization	110.0	183.5 **

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

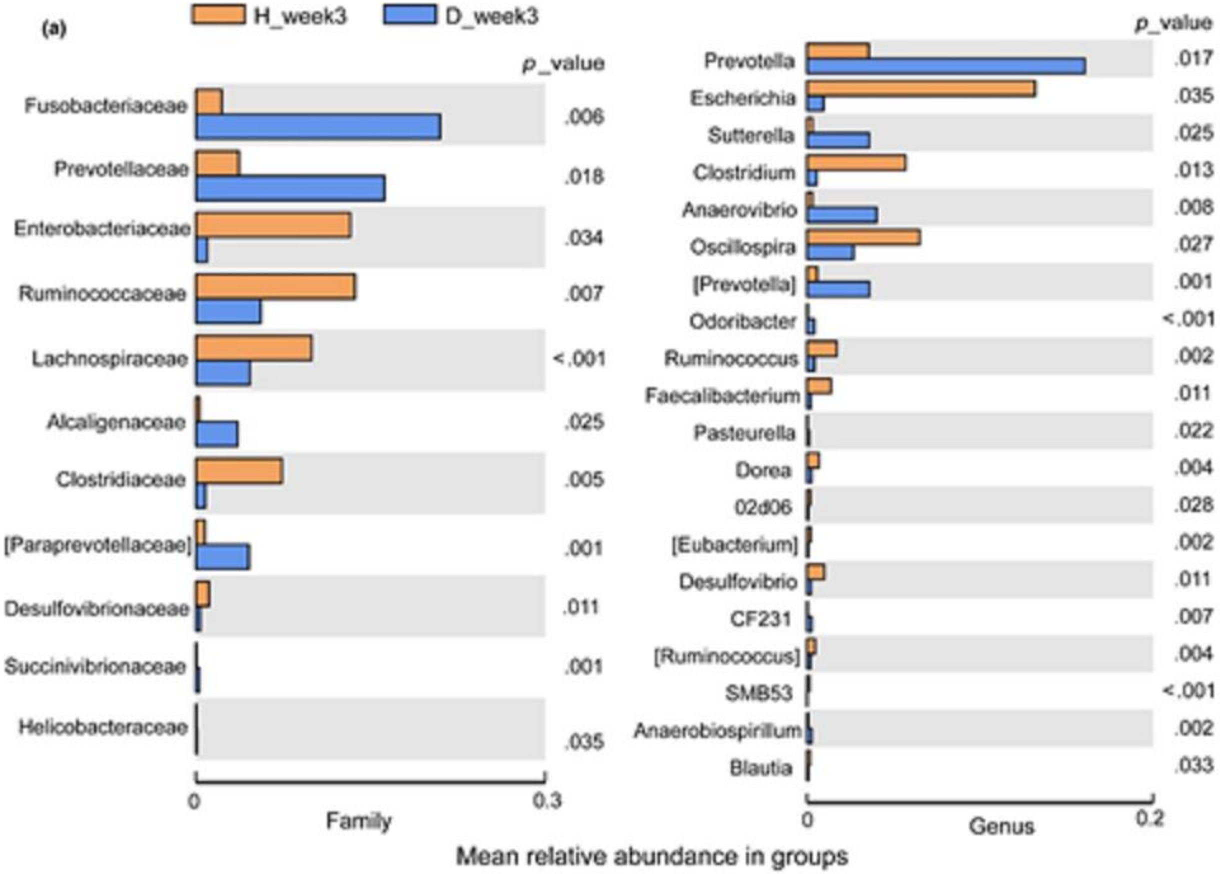
Guevarra *et al. Journal of Animal Science and Biotechnology*
https://doi.org/10.1186/s40104-018-0308-3

Diarrea in fase di svezzamento



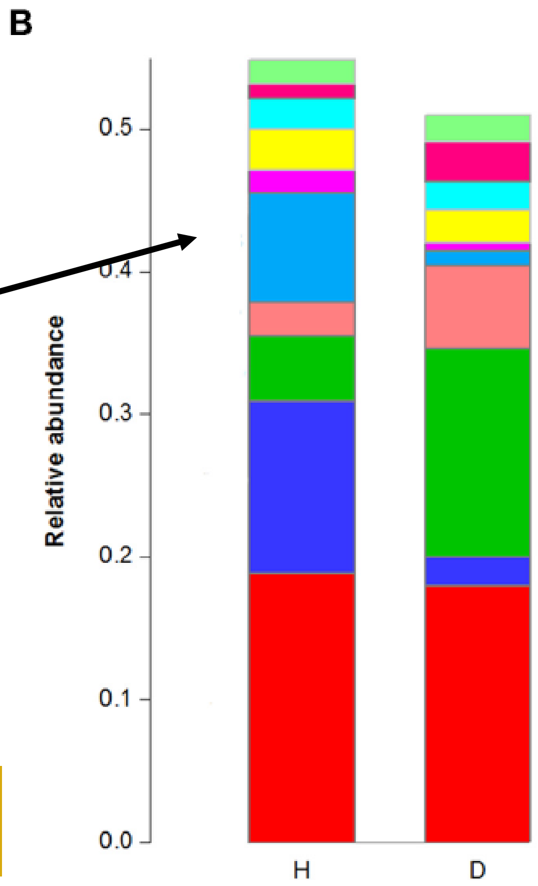
Yang et al. Front Microbiol. 2017; 8: 502.

Microbiota intestinale e diarrea



Longitudinal development of the gut microbiota in healthy and diarrheic piglets induced by age-related dietary changes. MicrobiologyOpen, Volume: 8, Issue: 12, First published: 09 September 2019, DOI: (10.1002/mbo3.923

Diarrea in fase di svezzamento



Lactobacillus sp.

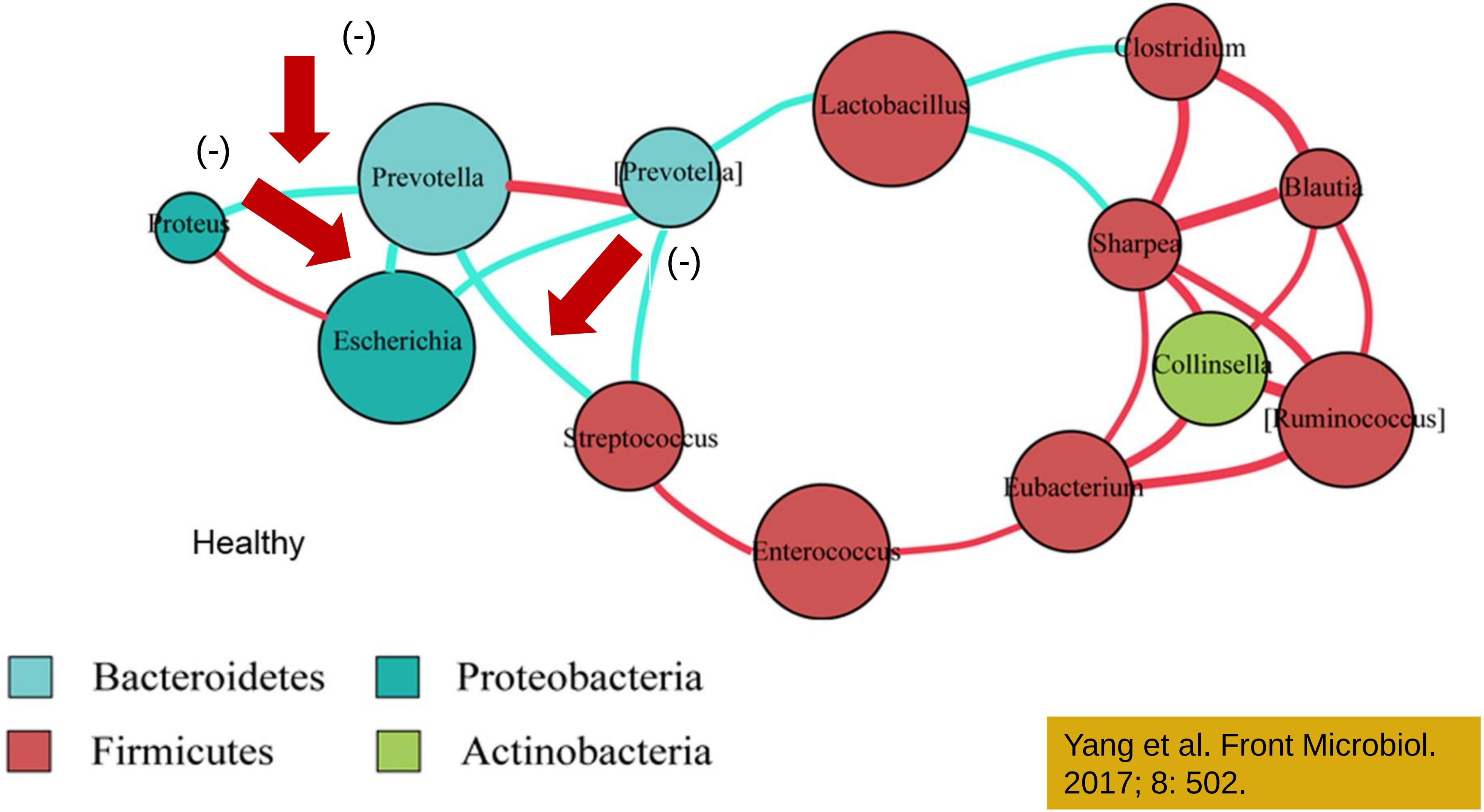
Parabacteroides sp.

Prevotella sp.

Escherichia sp.

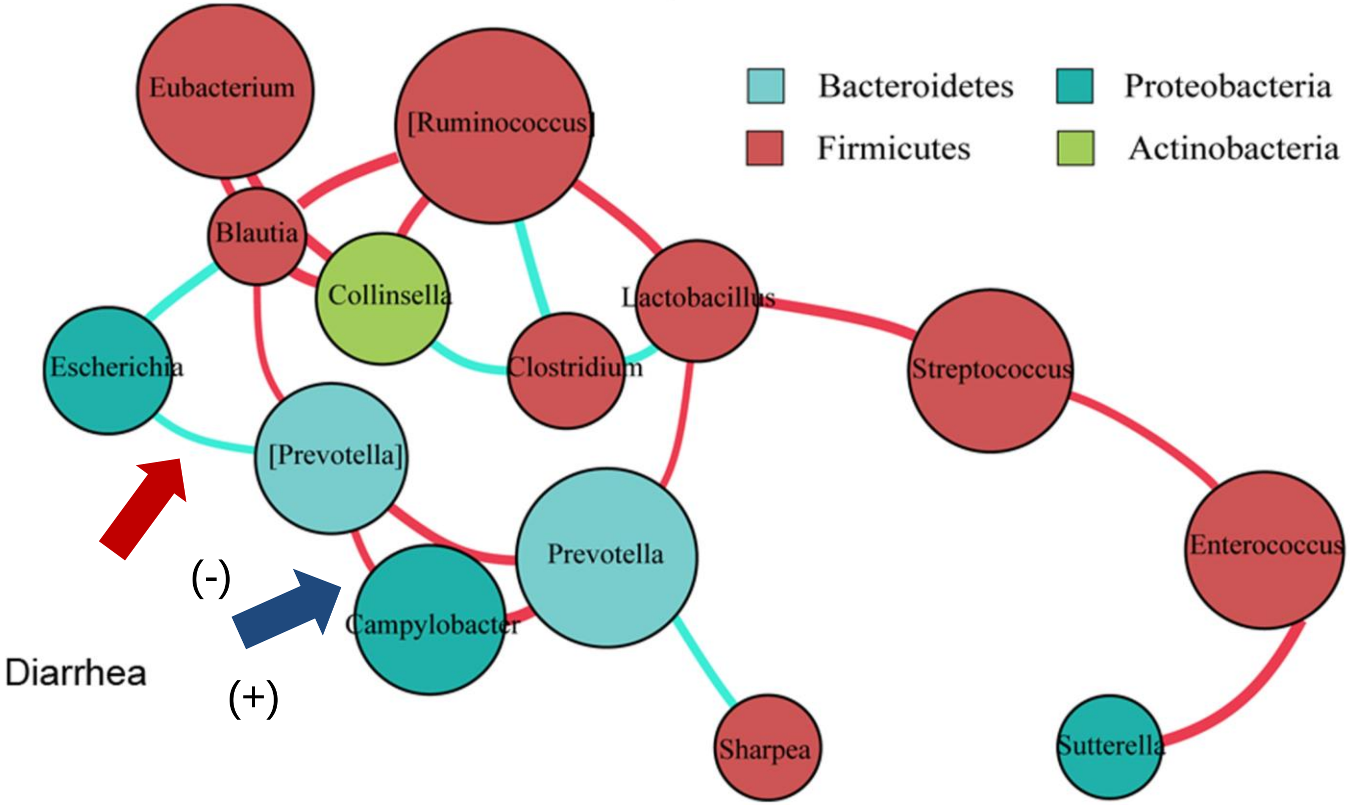
Yang et al. Front Microbiol. 2017; 8: 502.

Diarrea in fase di svezzamento



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

Diarrea in fase di svezzamento



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

Possibili interventi

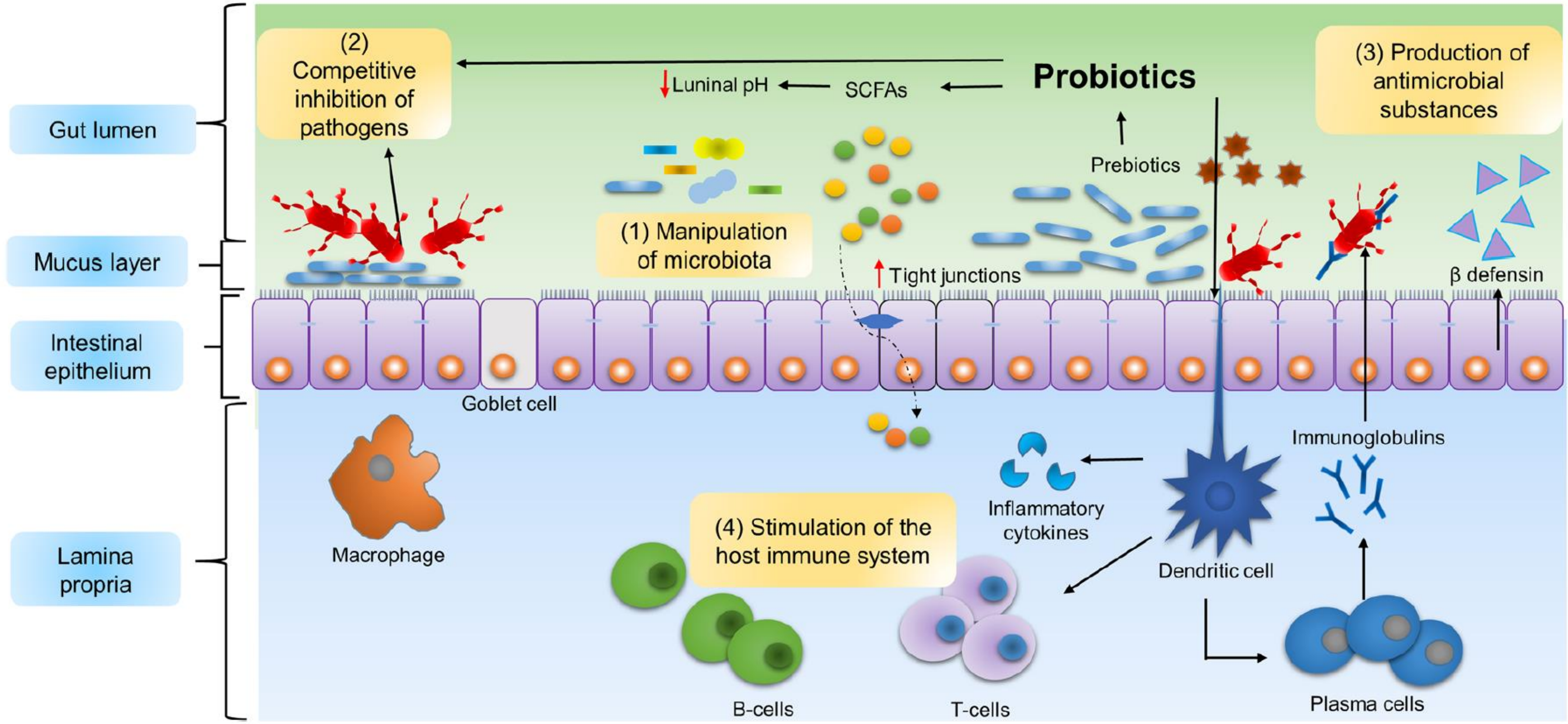


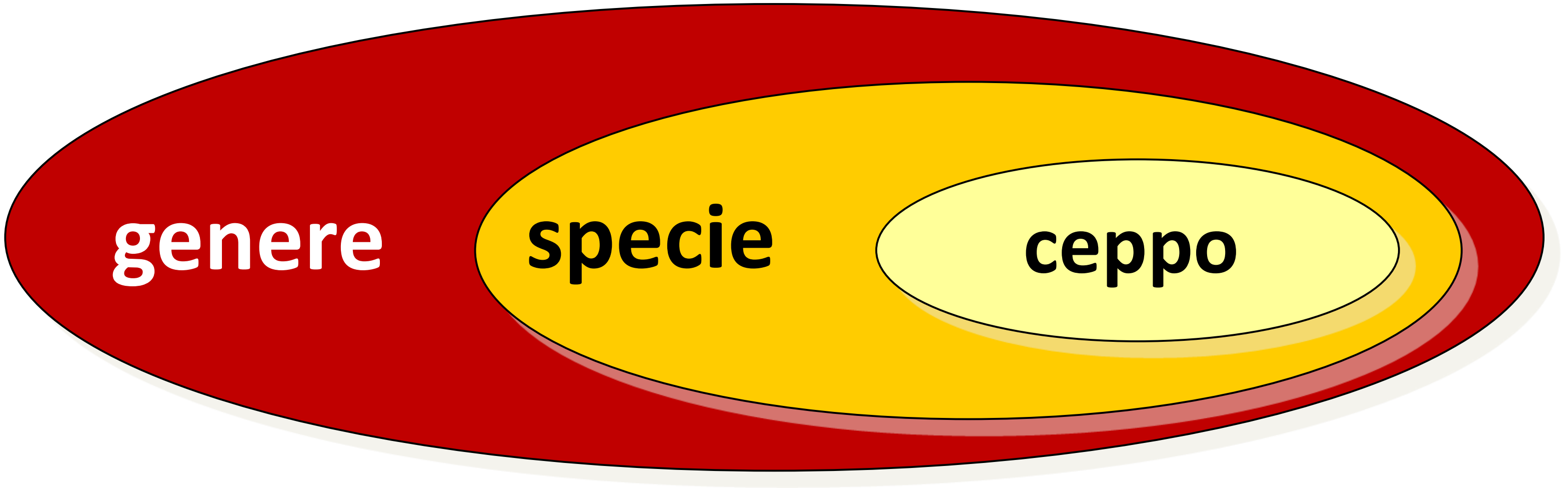
Fig. 2 The potential mechanisms by which probiotics affect intestinal microbial ecology. Probiotics may act through the following mechanisms: (1) manipulation of the microbiota by changing luminal pH, (2) competitive inhibition of pathogen, (3) production of antimicrobial substances and (4) stimulation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

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

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



genere

specie

ceppo

Lactobacillus *reuteri* XYZ

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Dall’osservazione all’intervento: il progetto FOODTECH…

UNIONE EUROPEA
Fondo europeo di sviluppo regionale

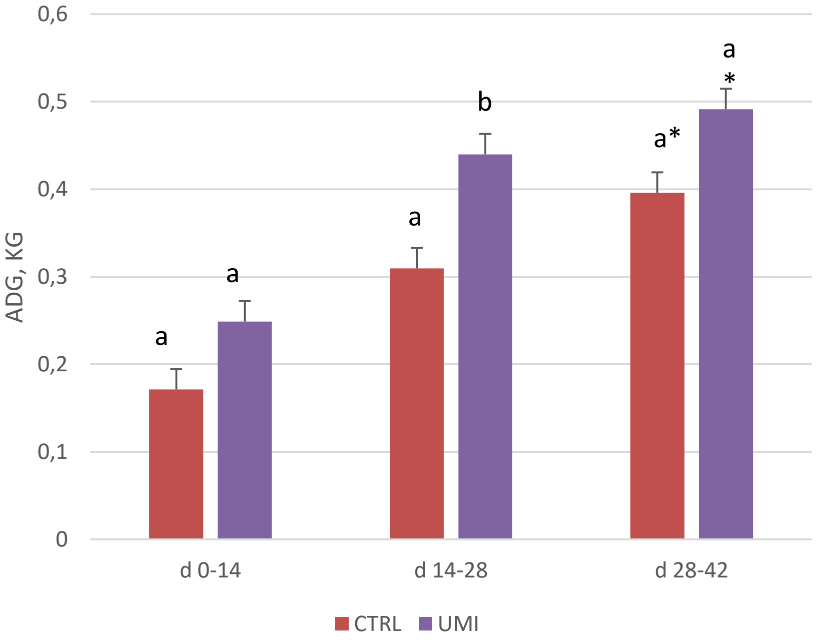
Regione
Lombardia

fesr

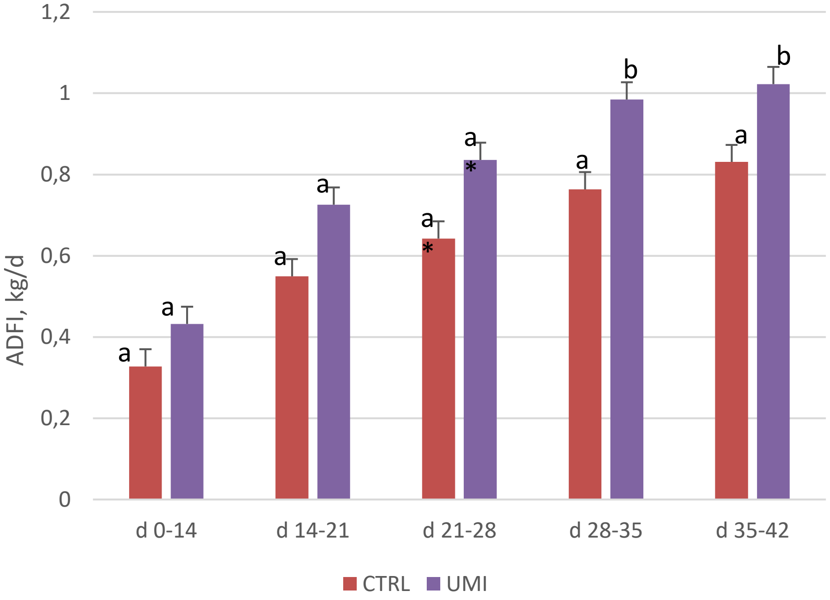
POR 2014-2020 FESR / INNOVAZIONE E COMPETITIVITÀ

Acidi umici o leonardite

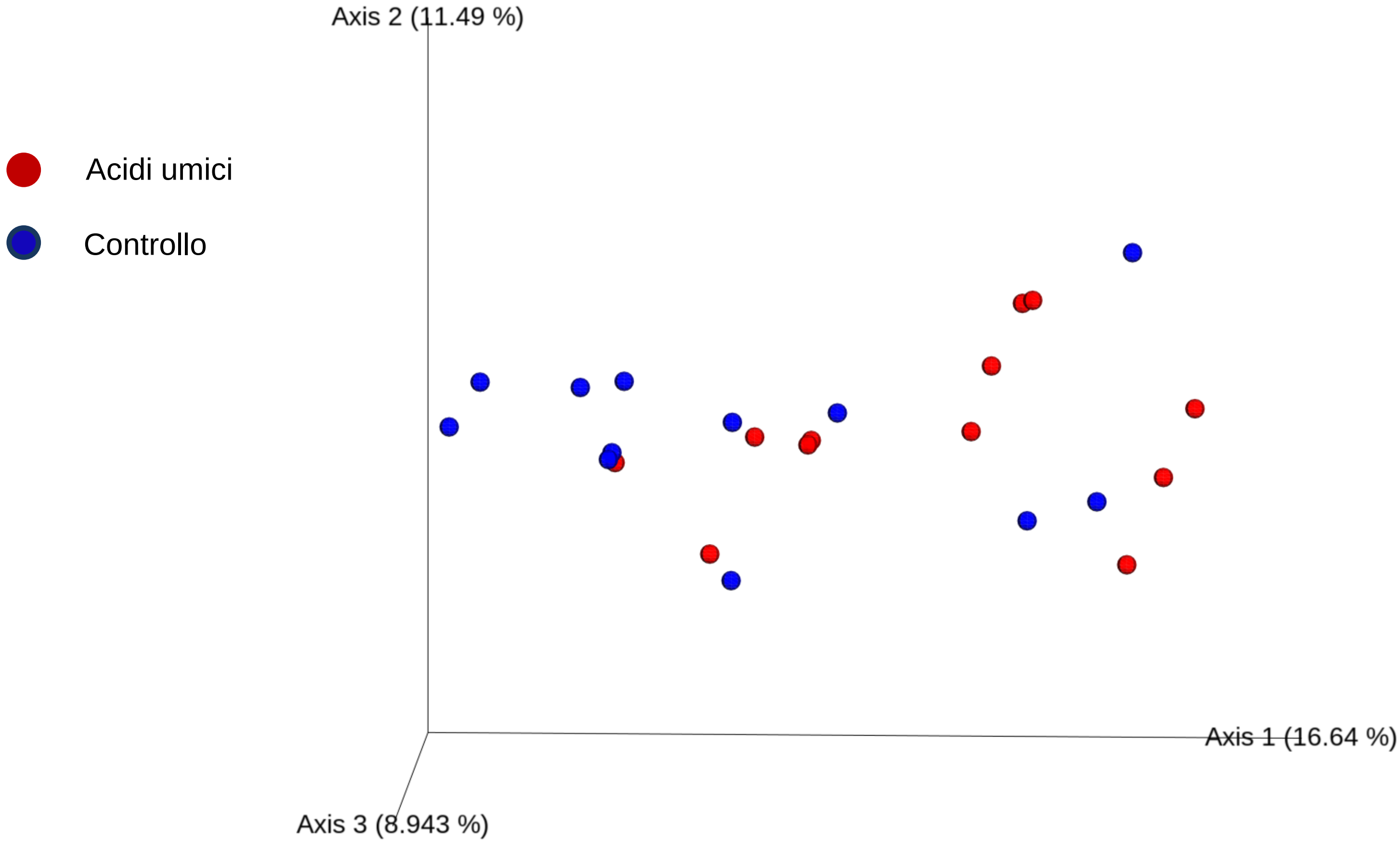
Incremento ponderale giornaliero



Assunzione giornaliera media



Microbiota intestinale e Acidi umici



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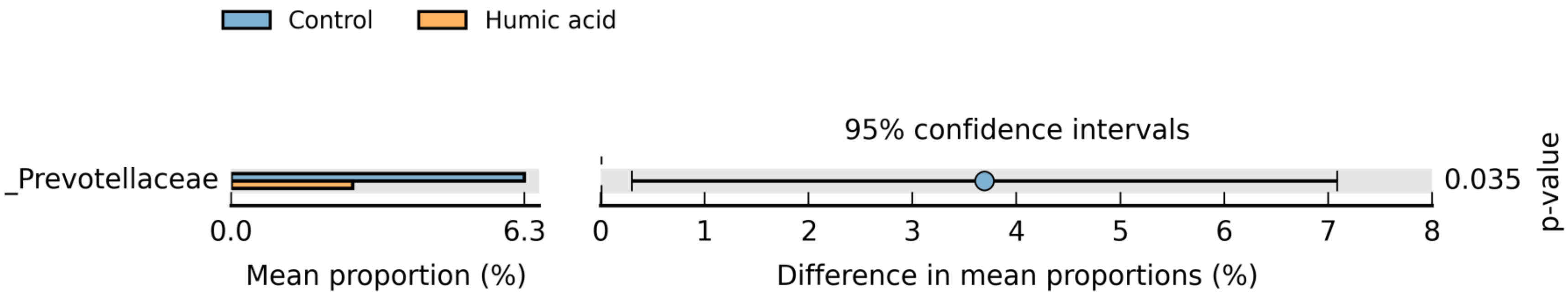
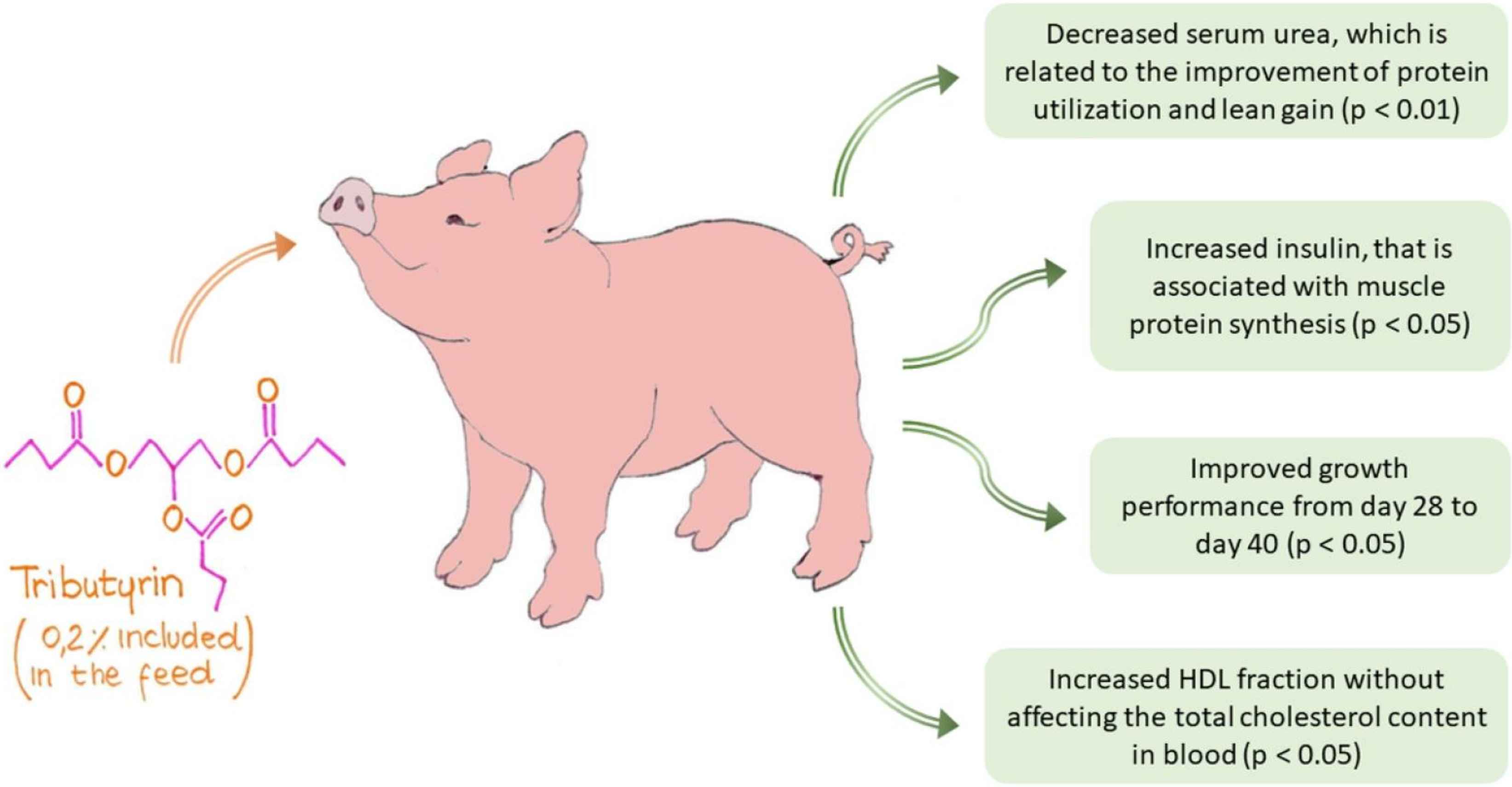
Microbiota intestinale e Acidi umici



Microbiota intestinale e Tributirrina



Decreased serum urea, which is related to the improvement of protein utilization and lean gain ($p < 0.01$)

Increased insulin, that is associated with muscle protein synthesis ($p < 0.05$)

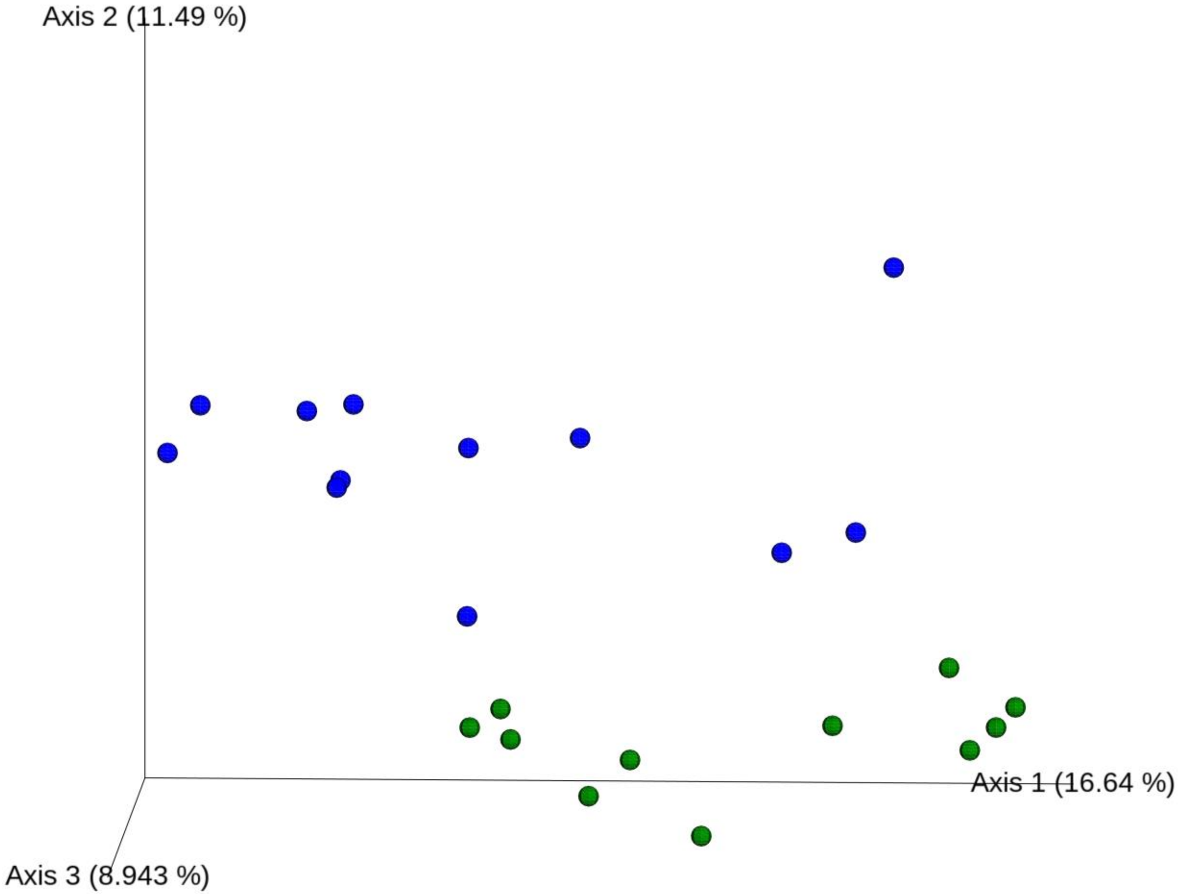
Improved growth performance from day 28 to day 40 ($p < 0.05$)

Increased HDL fraction without affecting the total cholesterol content in blood ($p < 0.05$)

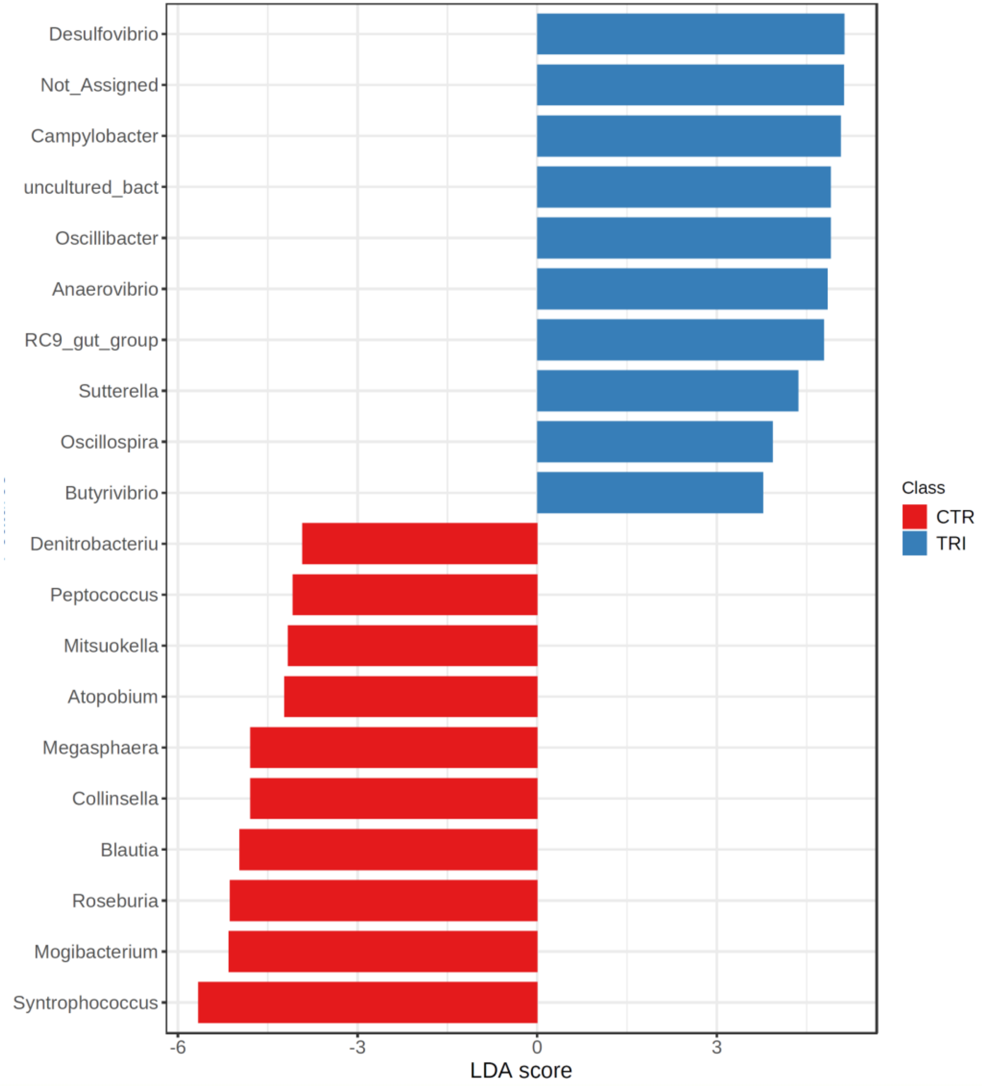
Microbiota intestinale e Tributirrina

● Tributirrina

● Controllo

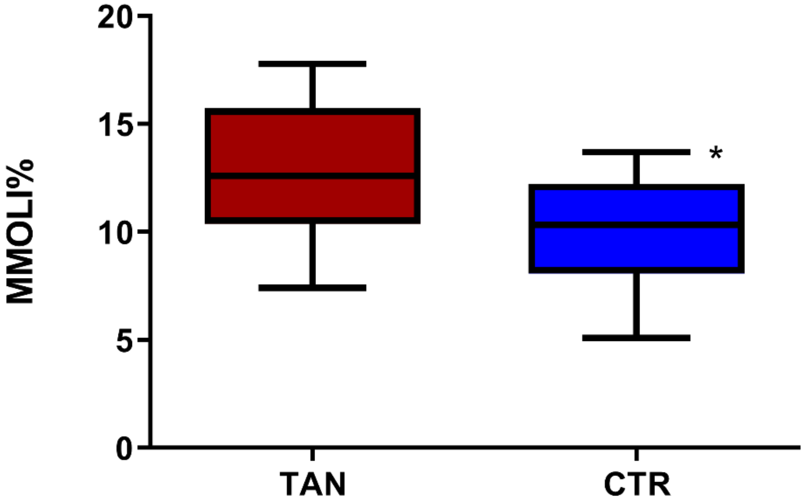


Microbiota intestinale e tributirrina

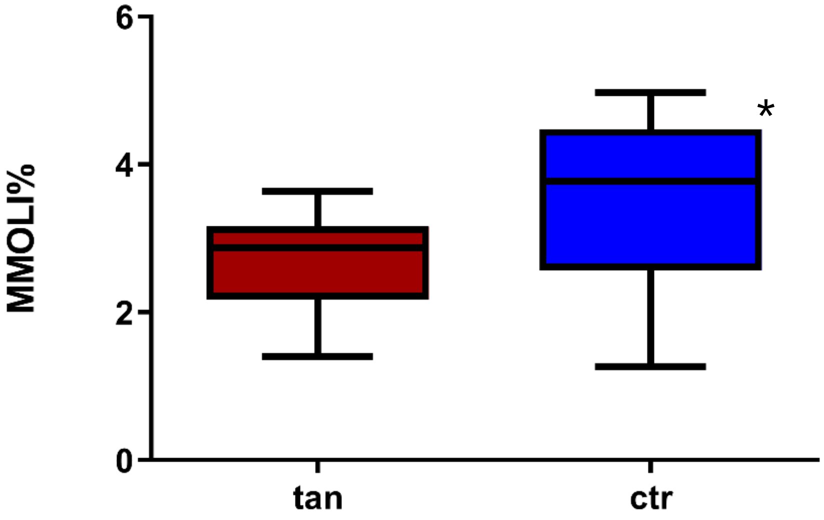


La composizione del microbiota intestinale modulata dalla tributirina aumenta l'abbondanza relativa di un numero di generi batterici come *Oscillospira*, *Oscillibacter*, *Mucispirillum* e *Butyrivibrio*. Questi generi erano positivamente correlati al ADG e / o al peso corporeo (BW).

Microbiota intestinale e tannini



Acido butirrico



Acido valerianico

Tannini di quebracho e castagno

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Microbiota intestinale e Tannini

	log 2FC	FDR
Shuttleworthia	4,4402	4,18E-06
Syntrophococcus	-4,7316	4,18E-06
Atopobium	-4,0962	6,30E-06
Pseudobutyrivibrio	2,8196	6,30E-06
Peptococcus	2,0023	7,57E-06
Mitsuokella	-3,2245	1,05E-05
Sharpea	-4,8289	1,05E-05
Prevotella	-2,2012	1,23E-05
Anaerostipes	3,0896	7,15E-05
Solobacterium	2,7762	7,54E-05
Acidaminococcus	-3,8175	0,000115
Megamonas	-3,7222	0,000122
Megasphaera	-2,1381	0,000186
Pseudoramibacter	-4,7715	0,000407
Faecalibacterium	1,8584	0,000681
Clostridium	2,776	0,000695
Oscillibacter	1,7001	0,000978
Butyrivibrio	3,199	0,002217
Dialister	-1,513	0,006128
Roseburia	-1,9688	0,009045
Oscillospira	1,481	0,013524
Howardella	-1,3444	0,020488
Desulfovibrio	-1,0091	0,032081
RC9_gut_group	-1,4789	0,038221
Mucispirillum	-1,1901	0,038912

Grazie per l’attenzione!!!