A Forgotten Organ – The Gut Microbiome of Dogs and Cats

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Taste, Texture & Health

PETFOOD FORUM ASIA

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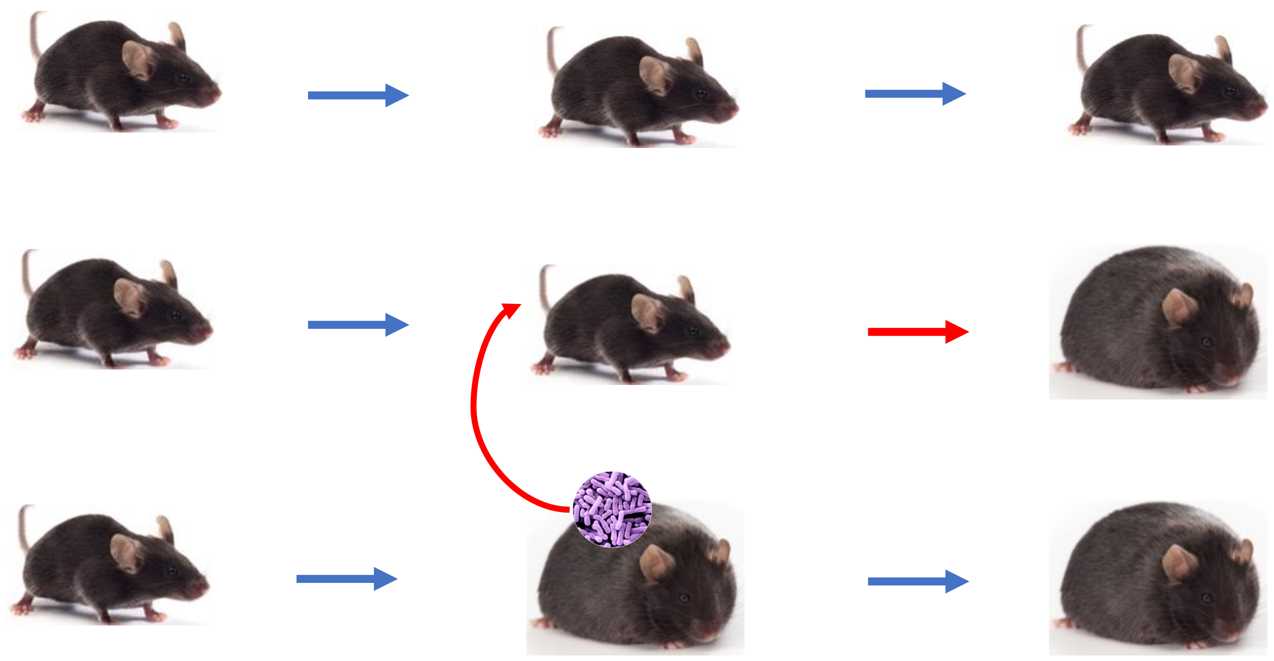
dsm-firmenich

Gut microbiota increases the body fat in germ free mice

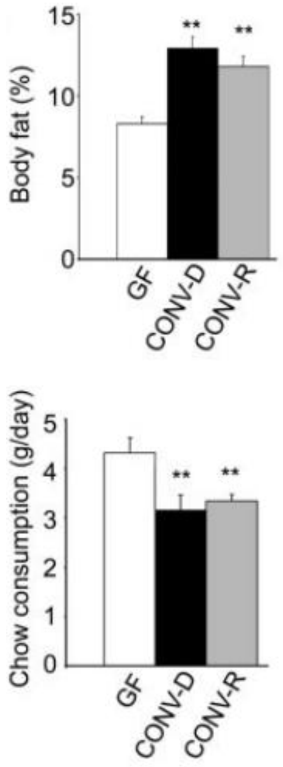


GF

GF/CONV-D

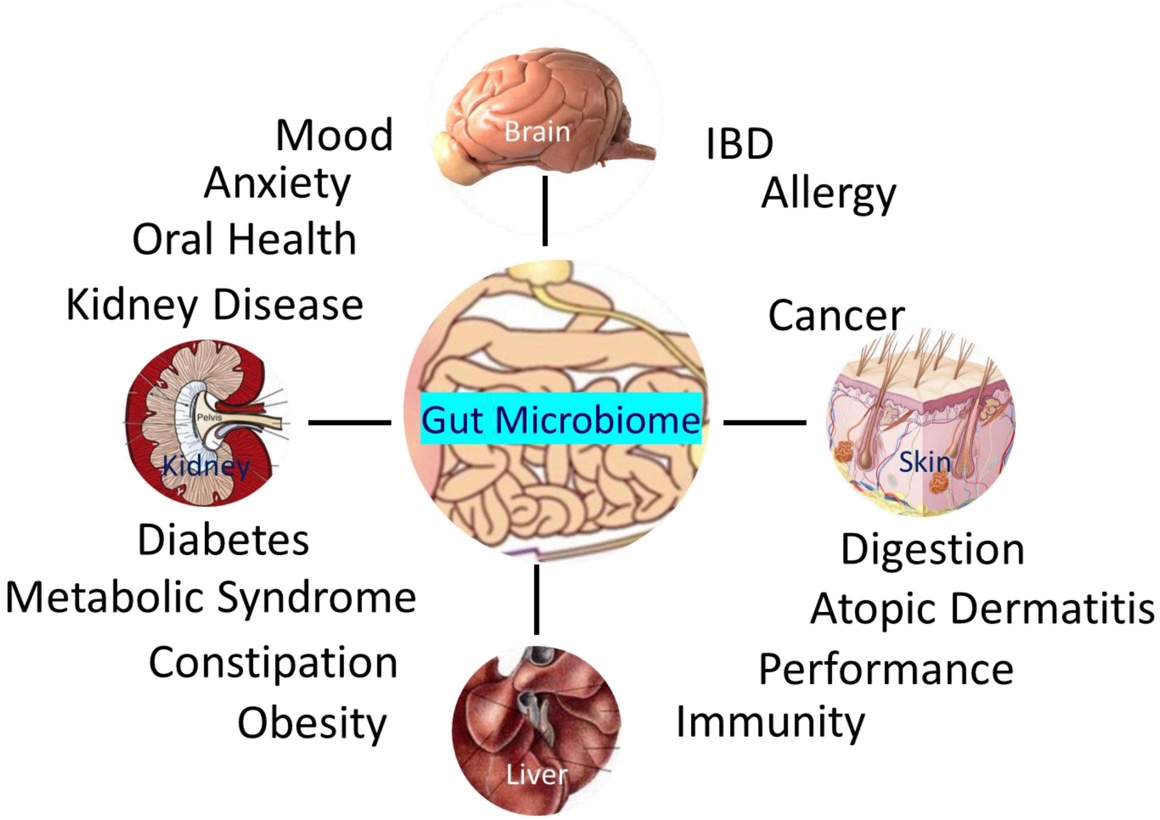
CONV-R

BF 57%↑

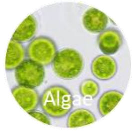


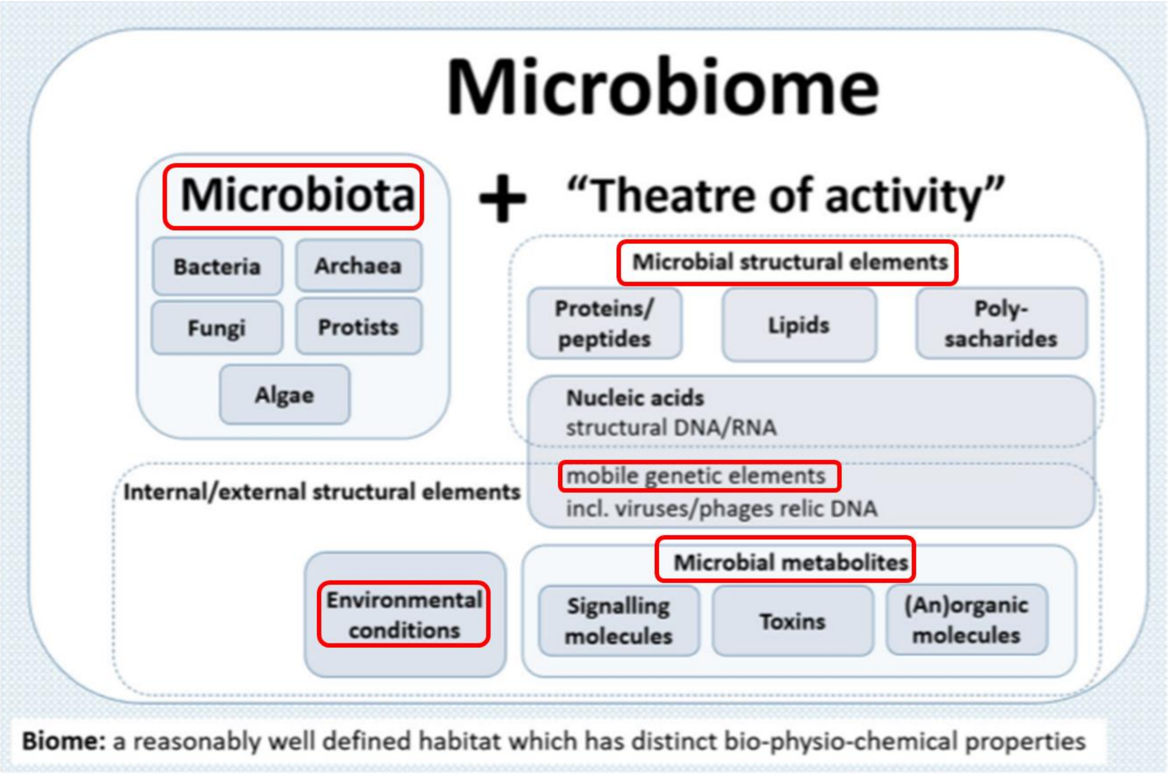
Backhel et al., 2004

Gut microbiome organ axis



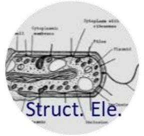
Microbiome





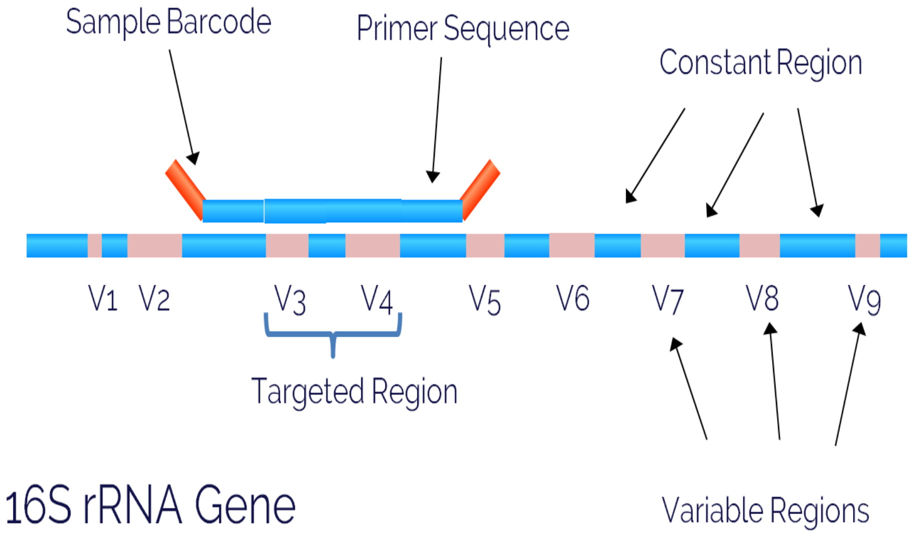
Biome: a reasonably well defined habitat which has distinct bio-physio-chemical properties

Berg et al. 2020



Microbiome assessment

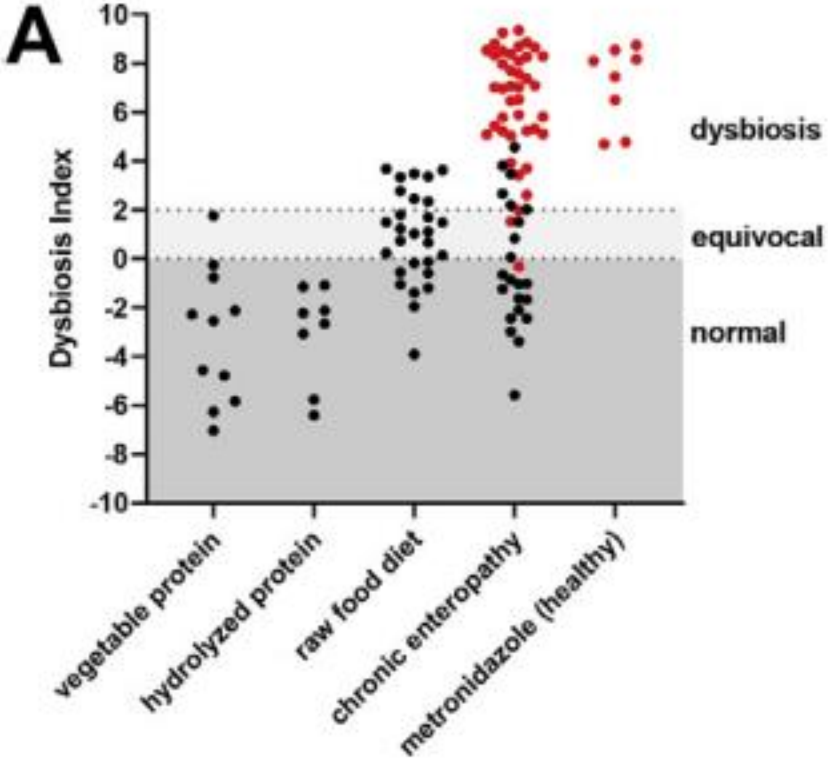
- **16S rRNA gene sequencing**
- Metagenomics (shotgun sequencing)
- Metatranscriptomics
- Metabolomics
- Quantitative real-time PCR
- Fluorescence in situ hybridization (FISH)
- Bacterial culture



https://www.lcsciences.com

What is a healthy microbiome?

- α-diversity: within a sample
- β-diversity: between samples
- Observed OTU
- Loss of beneficial bacteria
- Overgrowth of pathogenic bacteria
- Dysbiosis: imbalance of microorganisms
  - Canine Dysbiosis Index (< 2)
    - Faecalibacterium
    - Fusobacterium
    - C. hiranonis
    - Blautia
    - uricbacter,
    - Streptococcus
    - E. coli



Pilla & Suchodolski, 2021

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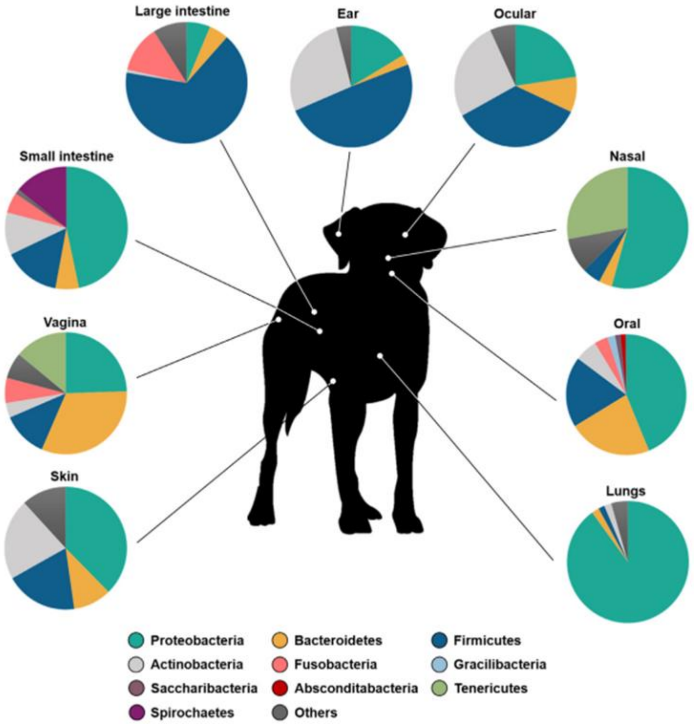
Various microbiomes

Microbiome

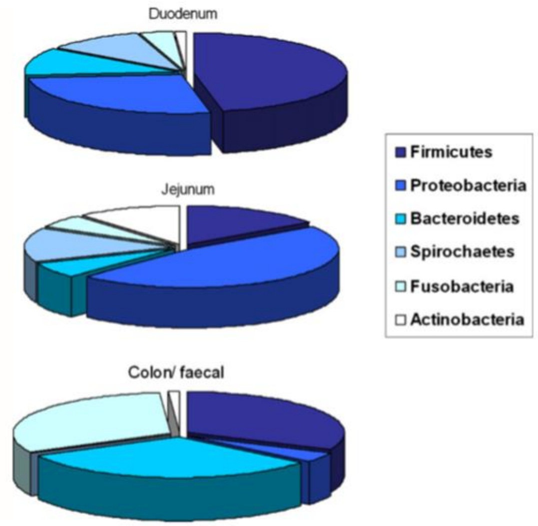
- Gut
- Skin
- Lung
- Urogenital
- Mouth
- Nose
- Ear
- Blood
- …

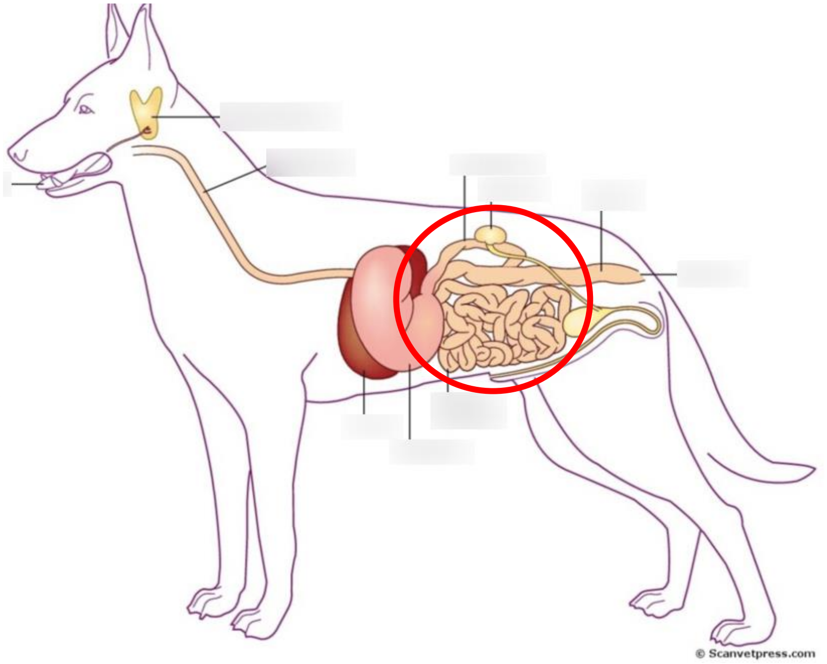


Pereira & Clemente, 2021

Gut microbiome

- Different compartments
- Large intestine
- Fecal sample
- Bacteria

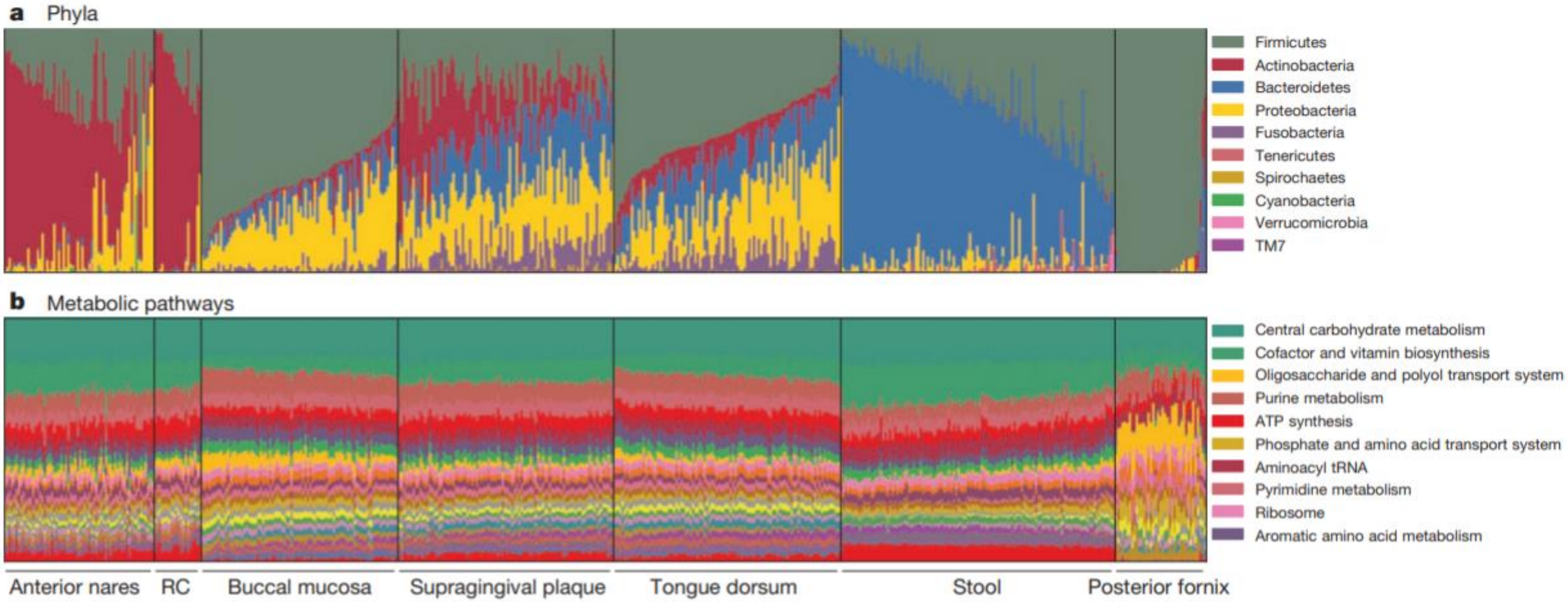




Schmitz & Suchodolski 2016

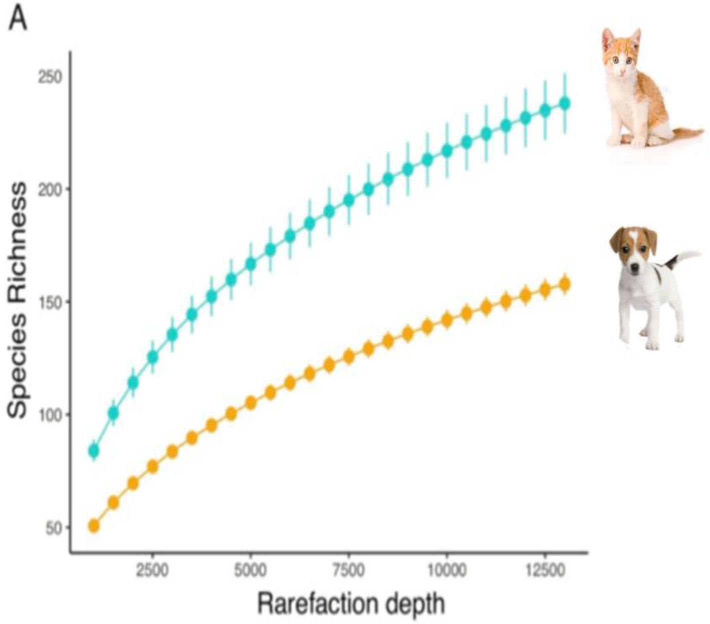
https://quizlet.com/252065925/dog-digestive-system-diagram/

Gut microbiome: composition vs. function



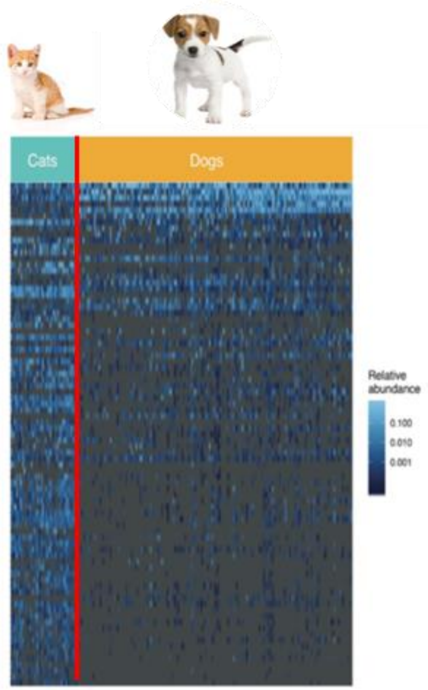
Huttenhower et al. 2012

Gut microbiome: dog vs. cat



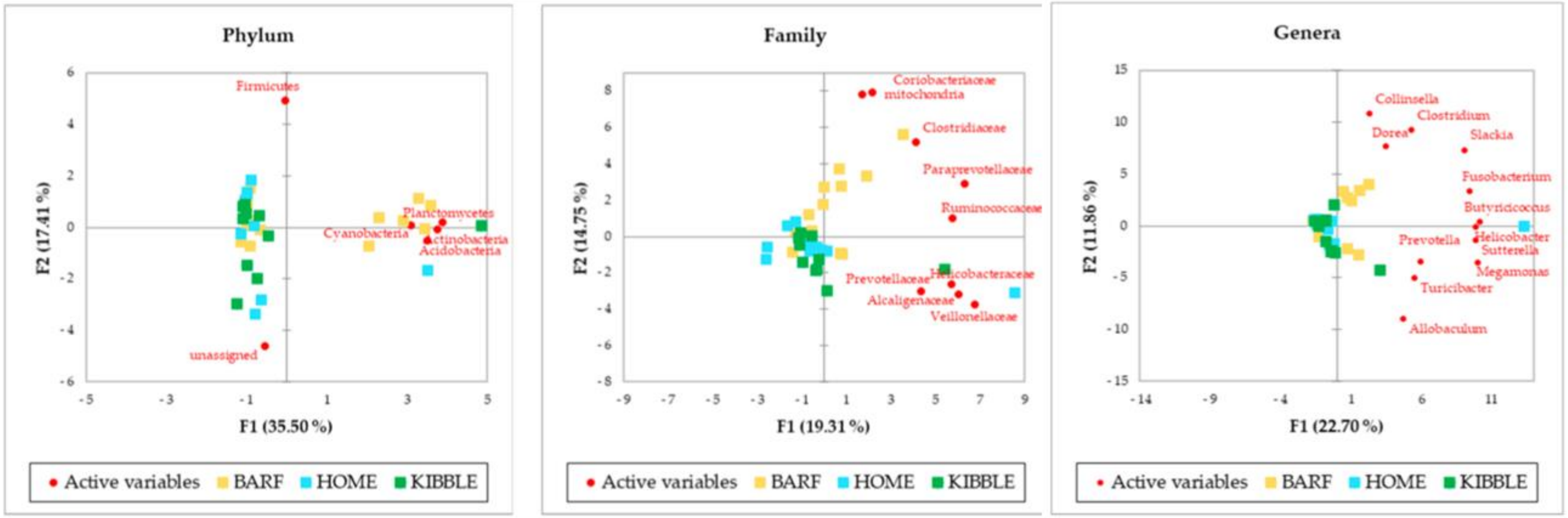
Main phyla

- Firmicutes
- Bacteroidetes
- Proteobacteria
- Fusobacteria
- Actinobacteria



Jha et al., 2020

Gut microbiome: diet effect

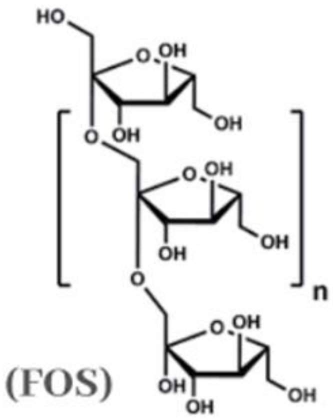


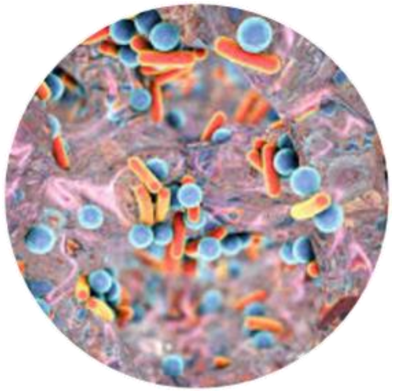
(a) (b) (c)

Figure 2. Principal Component Analysis (PCA) of bacteria Absolute Abundancies (AA) regarding (a) phylum level, (b) family level and (c) genus level on fecal samples of dogs fed with a raw-meat-based diet (BARF), a homemade based diet (HOME) and a commercial complete extruded diet (KIBBLE).

Scarsella et al. 2020

Dietary modulation of gut microbiome: -biotics





Prebiotics

Probiotics

Postbiotics

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Scarsella et al. 2020

ISAPP definitions

Probiotics

Live microorganisms that, when administered in adequate amounts, confer a health benefits on the host (2014)

Prebiotics

A substrate that is selectively utilized by host microorganisms conferring a health benefit (2017)

Synbiotics

A mixture comprising live microorganisms and substrate(s) selectively utilized by host microorganisms that confers a health benefit on the host (2020)

Postbiotics

A preparation of inanimate microorganisms and/or their components that confers a health benefit on the host; It must contain inactivated microbial cells or cell components, with or without metabolites, that contribute to observed health benefits. (2021)

The International Scientific Association for Probiotics and Prebiotics (ISAPP)

Gut microbiome modulation: Prebiotics

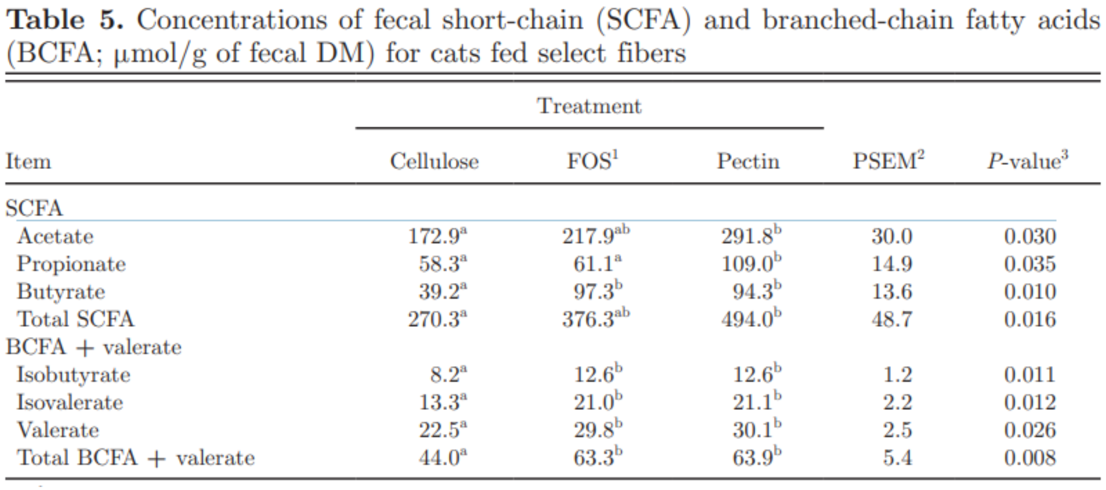
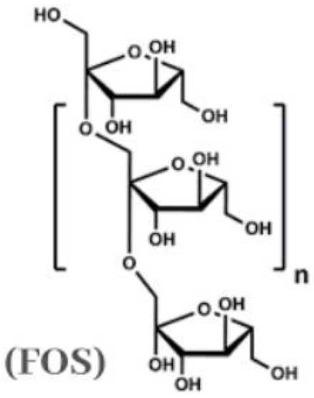


Table 5. Concentrations of fecal short-chain (SCFA) and branched-chain fatty acids (BCFA; µmol/g of fecal DM) for cats fed select fibers

	Treatment				
Item	Cellulose	FOS^{1}	Pectin	PSEM^{2}	*P*-value^{3}
SCFA					
Acetate	172.9^{a}	217.9^{ab}	291.8^{b}	30.0	0.030
Propionate	58.3^{a}	61.1^{a}	109.0^{b}	14.9	0.035
Butyrate	39.2^{a}	97.3^{b}	94.3^{b}	13.6	0.010
Total SCFA	270.3^{a}	376.3^{ab}	494.0^{b}	48.7	0.016
BCFA + valerate					
Isobutyrate	8.2^{a}	12.6^{b}	12.6^{b}	1.2	0.011
Isovalerate	13.3^{a}	21.0^{b}	21.1^{b}	2.2	0.012
Valerate	22.5^{a}	29.8^{b}	30.1^{b}	2.5	0.026
Total BCFA + valerate	44.0^{a}	63.3^{b}	63.9^{b}	5.4	0.008



(FOS)

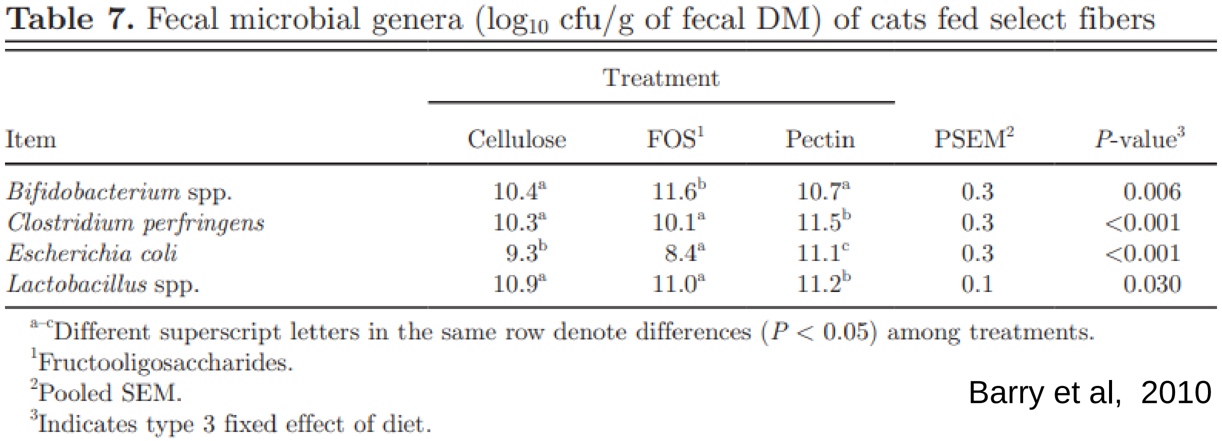


Table 7. Fecal microbial genera ($\log_{10}$ cfu/g of fecal DM) of cats fed select fibers

	Treatment				
Item	Cellulose	FOS^{1}	Pectin	PSEM^{2}	*P*-value^{3}
Bifidobacterium spp.	10.4^{a}	11.6^{b}	10.7^{a}	0.3	0.006
Clostridium perfringens	10.3^{a}	10.1^{a}	11.5^{b}	0.3	<0.001
Escherichia coli	9.3^{b}	8.4^{a}	11.1^{c}	0.3	<0.001
Lactobacillus spp.	10.9^{a}	11.0^{a}	11.2^{b}	0.1	0.030

[a–c] Different superscript letters in the same row denote differences ($P < 0.05$) among treatments.

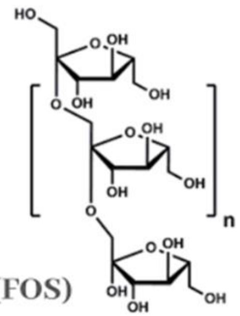
[1] Fructooligosaccharides.

[2] Pooled SEM.

[3] Indicates type 3 fixed effect of diet.

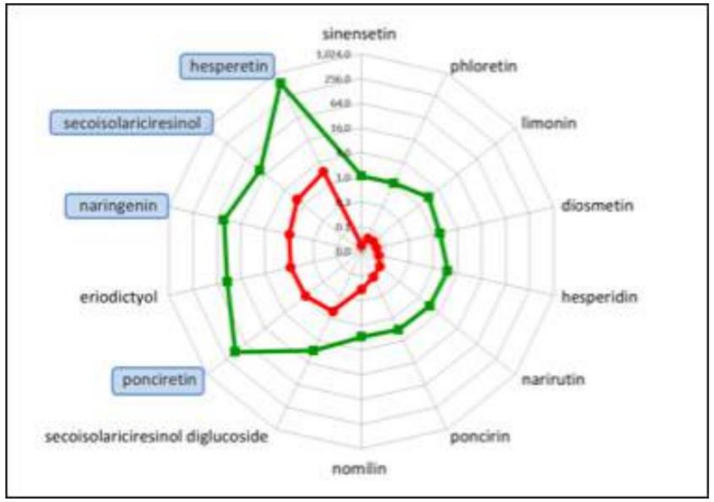
Barry et al, 2010

Gut microbiome modulation: Prebiotics

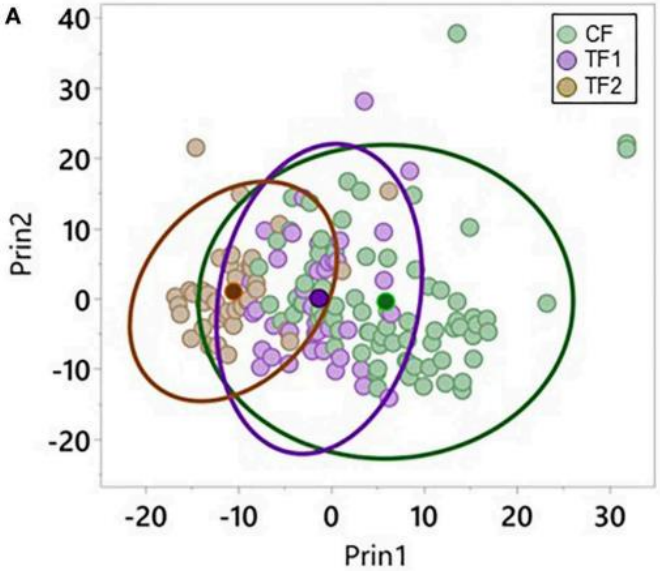


(FOS)

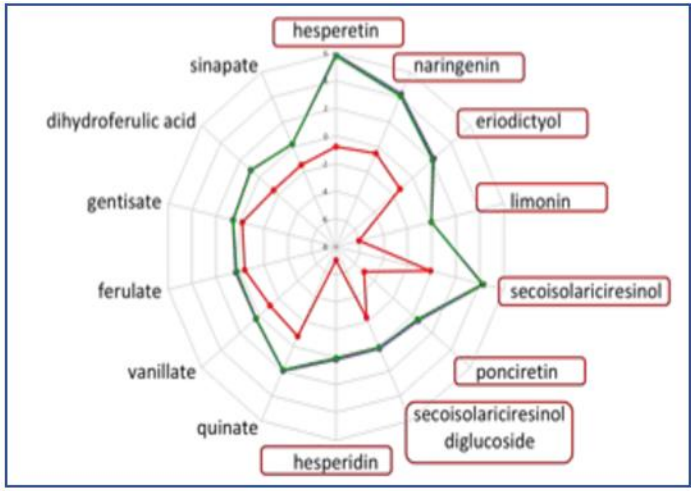
TF1: Ground pecan shells, Flaxseed, Dried beet pulp, Dried citrus pulp, Pressed cranberries and Psyllium seed husk
TF2: Powdered cellulose, Rice hulls, Dried beet pulp, Psyllium seed husk and Fructooligosaccharides



Plot shows log-transformed data. Red: Control food; Green: Test food



Fritsch et al, 2023

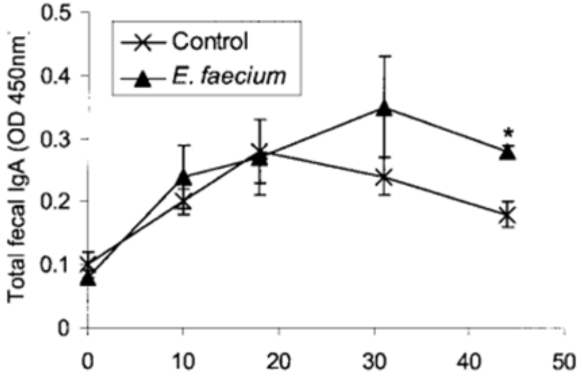


Plot shows log-transformed data. Red: Control food; Purple: Test food 4 weeks; Green: Test food 8 weeks.

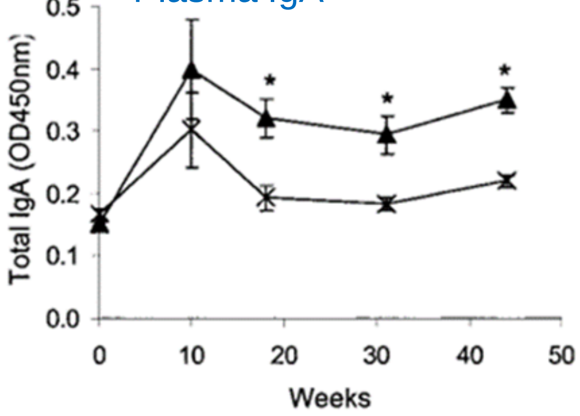
Wernimont et al, 2019

Gut microbiome modulation: Probiotics

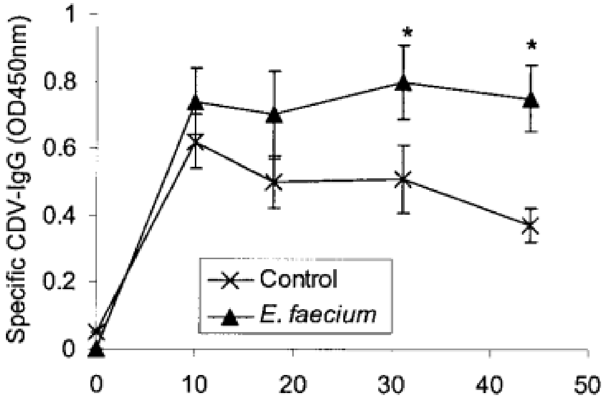
Fecal IgA



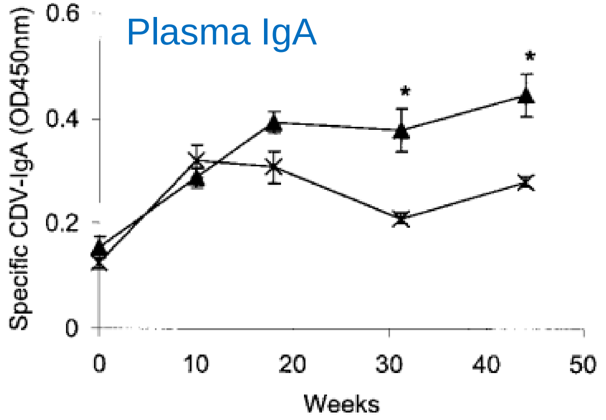
Plasma IgA



Plasma IgG



Plasma IgA



Benyacoub et al, 2003

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Gut microbiome modulation: Probiotics

Medians (1st;3rd quartiles) of fecal score, ammonia, and fecal odor of dogs fed the control or *B. subtilis* C-3102diet.

Item	Control	*B. subtilis* C-3102	P value
Score	3 (3;4)	4 (3;4)	<0.001
Ammonia (g/kg)	0.705 (0.601;0.776)	0.602 (0.589;0.625)	0.037
Odor	2 (2;2)	1 (1;2)	<0.001

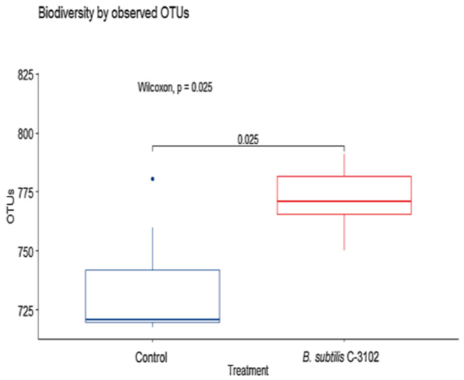


Fig. 2. Richness of bacterial communities (number of OTUs per 12,804 reads) of feces of dogs fed the control or *Bacillus subtilis* C-3102 diet ($P = 0.025$).

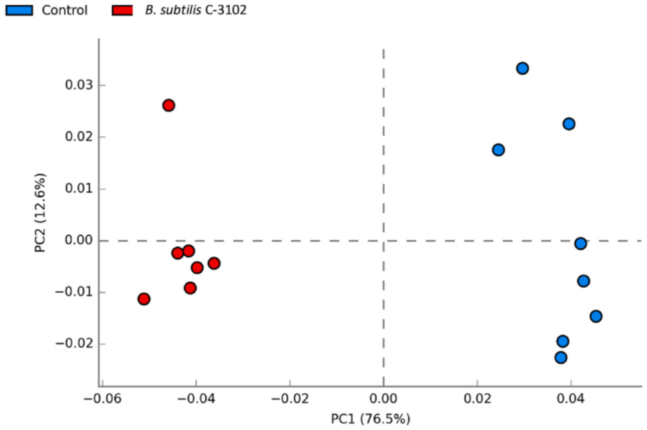
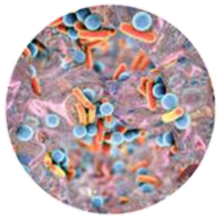


Fig. 1. Principal component analysis (PCA) of the bacterial community in feces of dogs fed the control or *Bacillus subtilis* C-3102 diet.

De Lima et al., 2020

Gut microbiome modulation: Postbiotics

Heat killed *Lactobacillus delbrueckii* & *Lactobacillus fermentum*



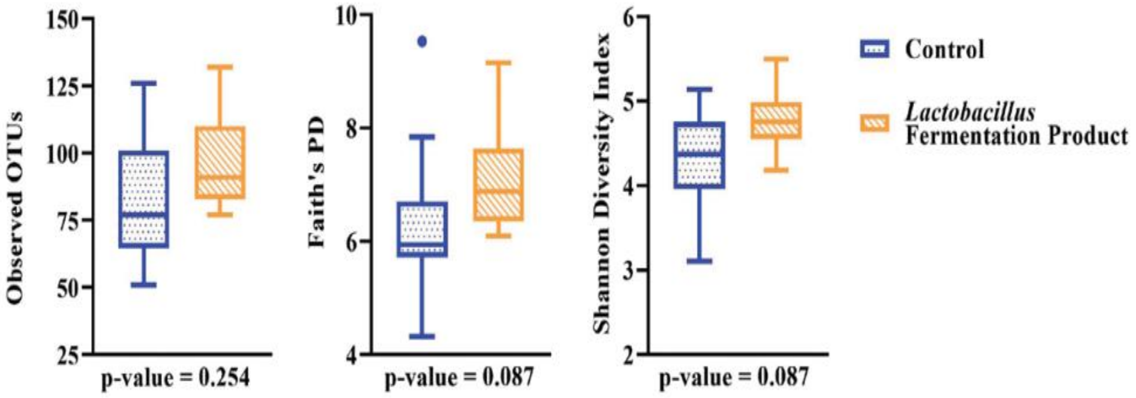


Figure 2. Alpha diversity measures of fecal samples collected from dogs supplemented with *Lactobacillus* fermentation product or placebo (dextrose) control. Alpha-diversity is represented by observed OTU, Faith's phylogenetic diversity (PD), and Shannon diversity index. Faith's PD and Shannon diversity index suggest that species richness tended to be higher in dogs supplemented with *Lactobacillus* fermentation product than those fed the control. The observed OTU comparison, however, did not reach statistical significance.

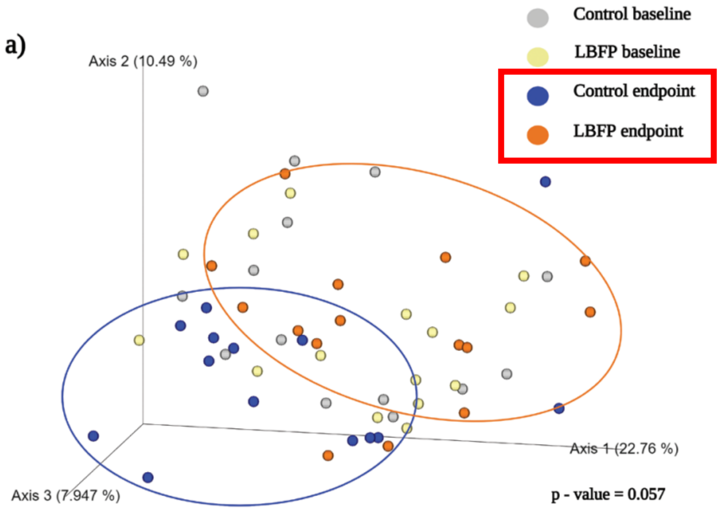
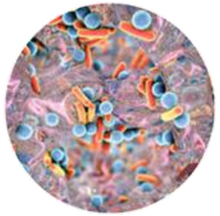


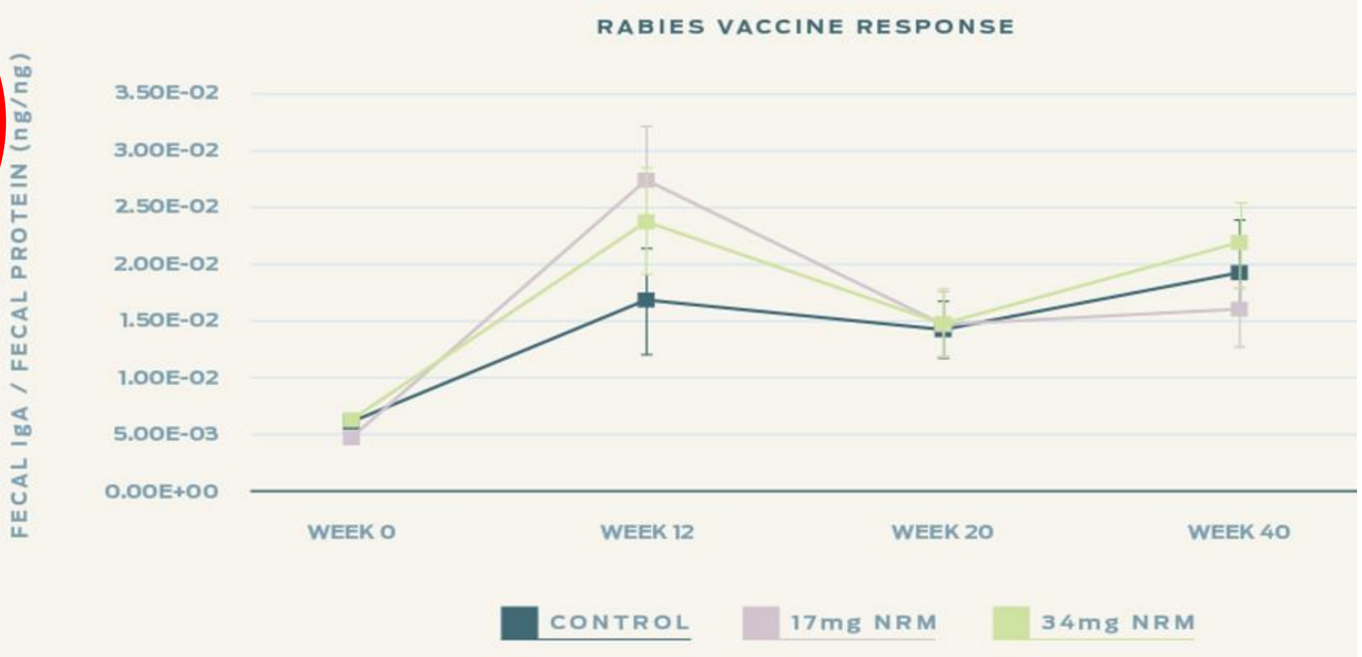
Figure 3. Beta diversity measures of fecal samples collected from dogs supplemented with *Lactobacillus* fermentation product or placebo (dextrose) control. Principal coordinates analysis (PCoA) plots of unweighted (a) and weighted (b) UniFrac distances of fecal microbial communities were performed on the 97% OTU abundance matrix using QIIME2. Unweighted UniFrac distances suggest a trend of bacterial population separation between treatment groups.

Koziol et al, 2023

Gut microbiome modulation: Postbiotics



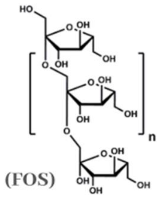
Heat killed *Lactobacillus delbrueckii* & *Lactobacillus fermentum*

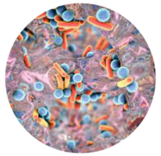


https://www.purinainstitute.com/science-of-nutrition/promoting-gastrointestinal-health/non-replicating-microorganism

NRM: Non-replicating Microorganisms (Heat killed *Lactobacillus delbrueckii* & *Lactobacillus fermentum*)

Comparison of Pre-, Pro- & Postbiotics





	Prebiotics	Probiotics	Postbiotics
Characteristics	Mostly polysaccharides	Live microorganisms	Dead microorganisms
Health benefits	Yes	Yes	Yes
Heat resistance	Yes	No	Yes/No
Applications	Dry, Wet, Treat, Supp.	Dry, Treat, Supp.	Dry, Wet, Treat, Supp.
Availability	Many	Limited (EU)	Limited/Increasing
Storage stability	Stable	Unstable	Stable/Unstable
Awareness of pet owners	Good	Good	Poor/Improving
Market penetration	Excellent	Good (US)	Poor/Increasing

Thank You!

https://www.istockphoto.com/photo/cats-and-dogs-over-thanksgiving-pumpkins-gm877205556-244802876