



Microbiota Intestinale



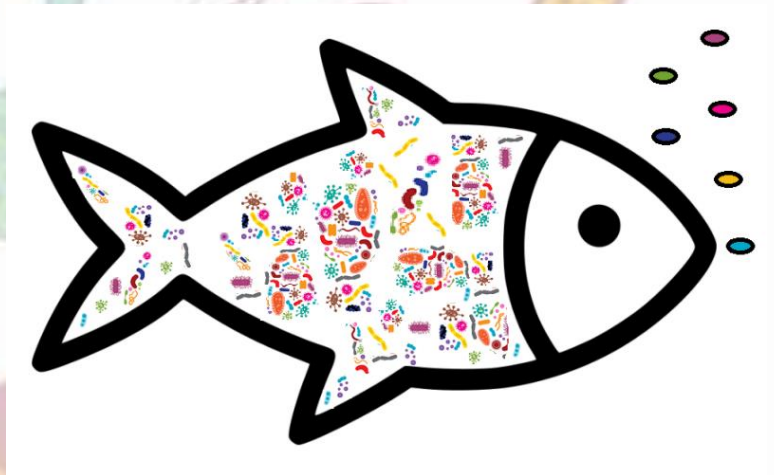
Francesca Fava, PhD

Fondazione Edmund Mach

Firenze, Accademia dei Georgofili, 7.12.2021

Ruolo del microbiota intestinale

- ☑ Mantenimento fisiologia intestinale
- ☑ Assorbimento dei nutrienti
- ☑ Adeguato funzionamento del sistema immunitario
- ☑ Protezione da patogeni
- ☑ Indice del benessere generale dell'organismo animale
- ☑ Performance zootecnica

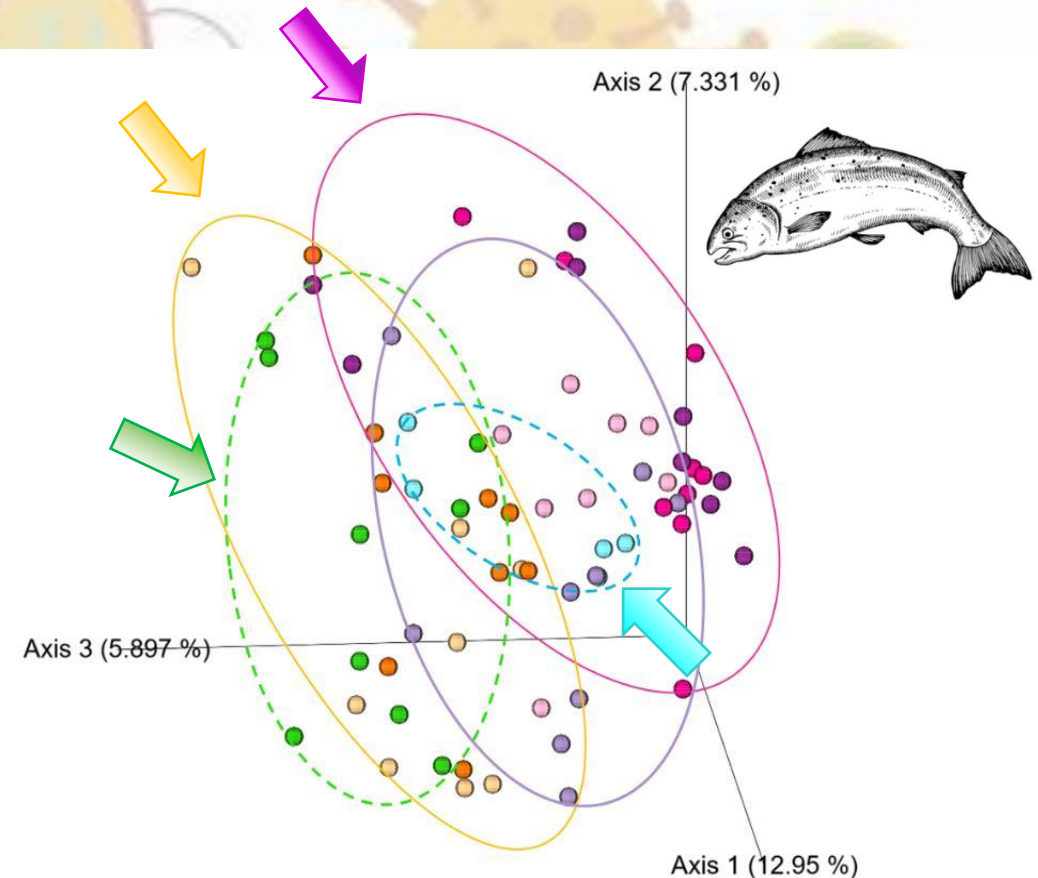


Il **microbiota** è l'**impronta digitale** dell'alimentazione

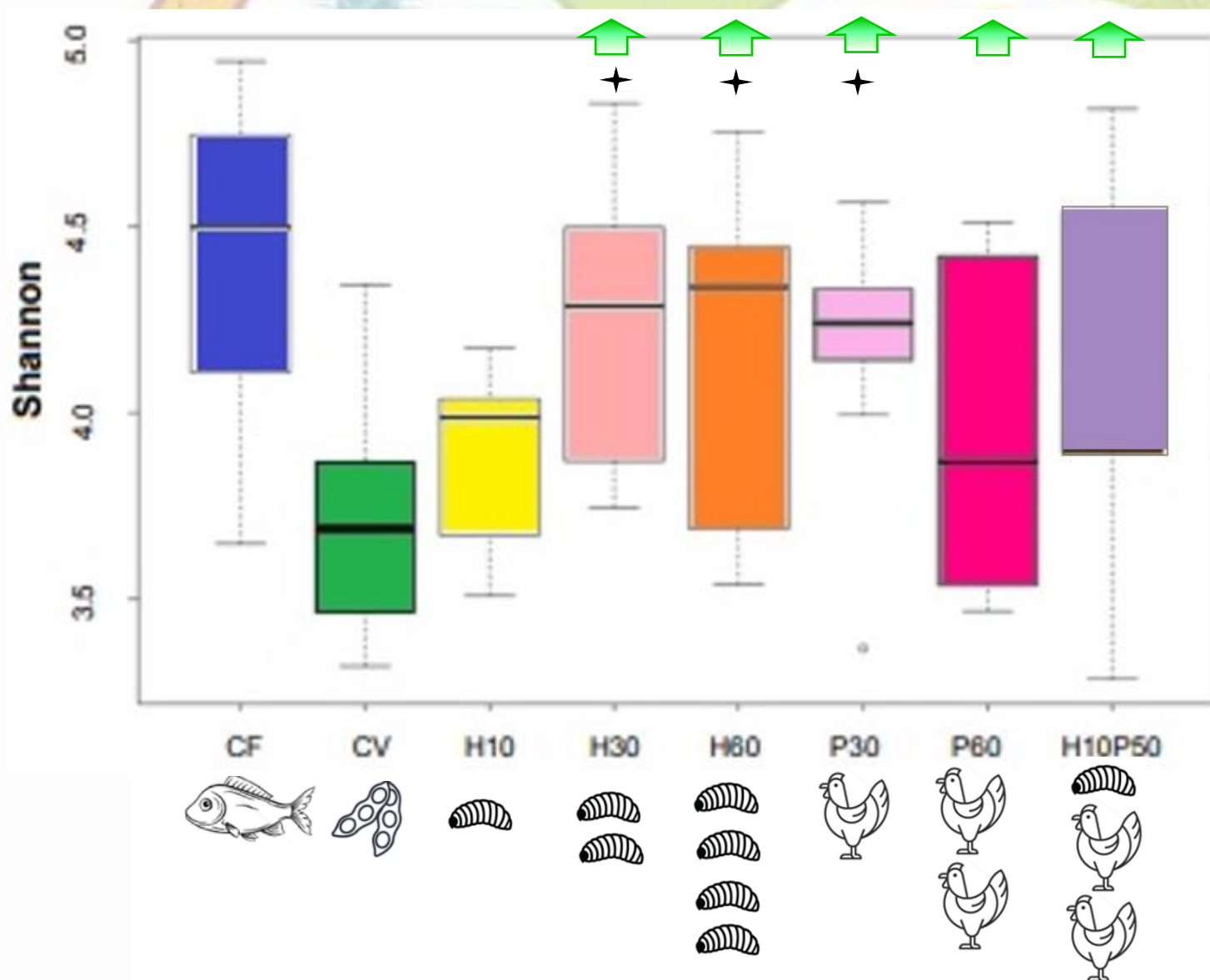
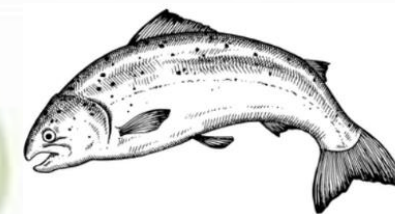




La composizione del **microbiota** distingue pesci alimentati con diverse formulazioni

- CF
- CV
- H10
- H10P50
- H30
- H60
- P30
- P60
- IM diets
- PBM diets
- PBM + IM
- CF
- CV

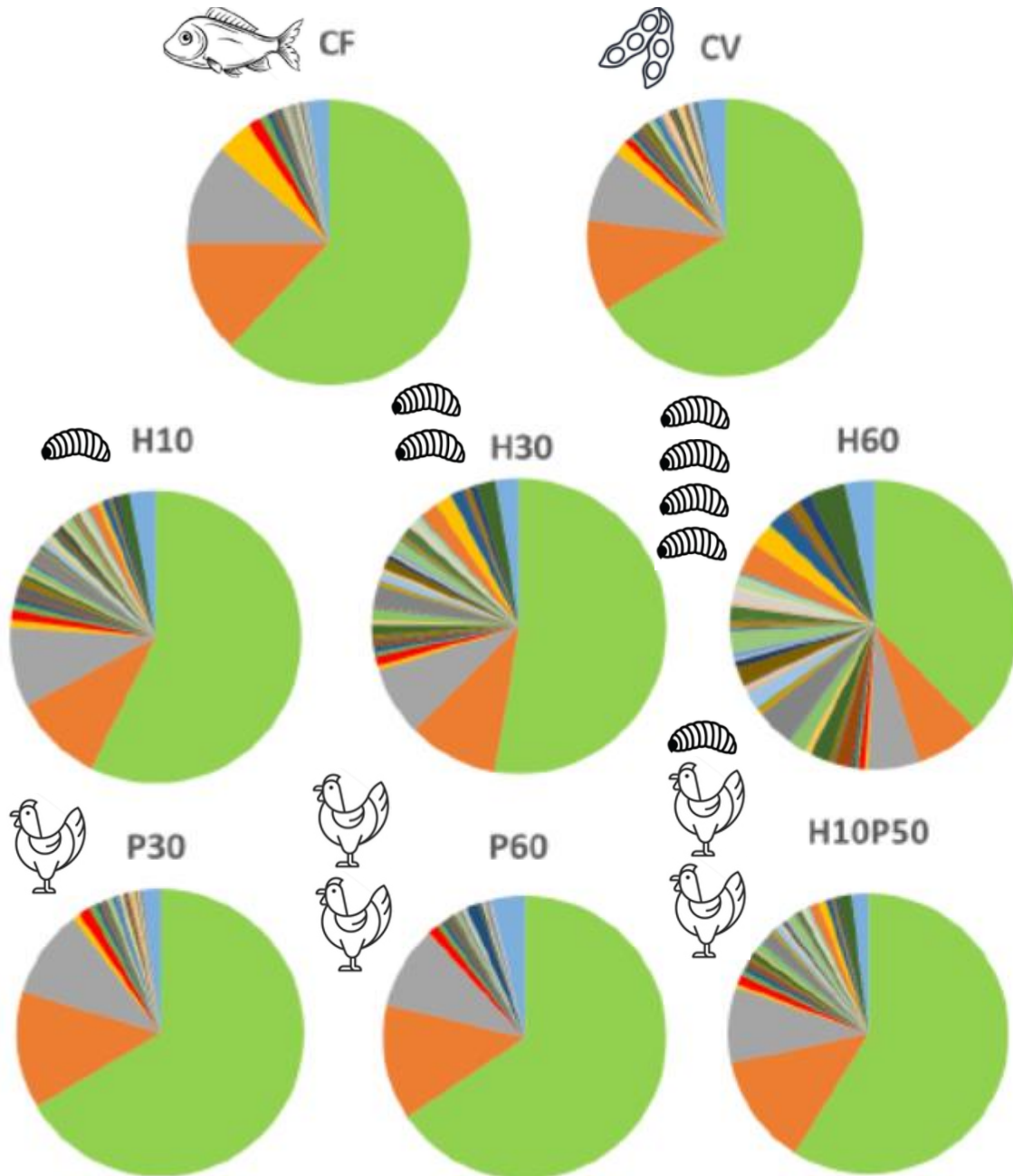


Farine di insetto e avicole

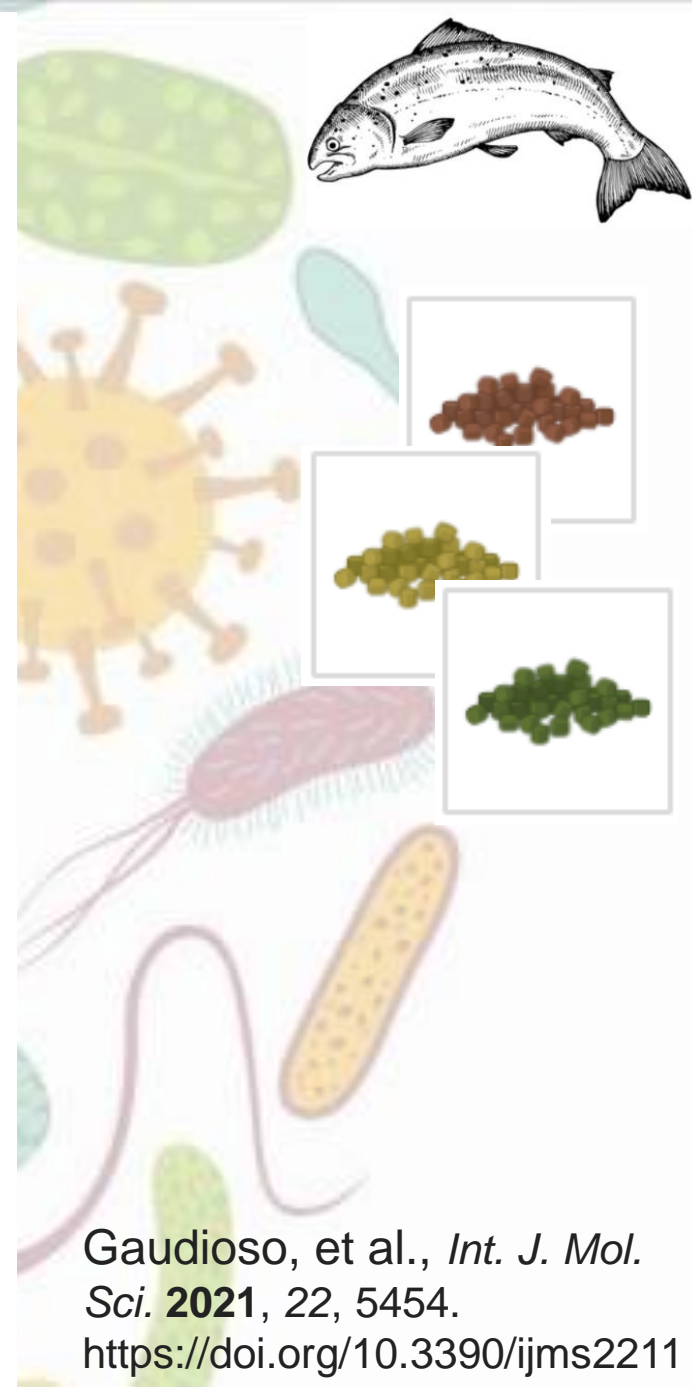


- 
 α -Diversità del microbiota migliora con farine di **INSETTO** e **AVICOLE**, singolarmente ed in combinazione
- 
 Maggiore diversità è un biomarcatore di **salute** e di aumentata **capacità metabolica**

✦ *Significativo a confronto con CF*

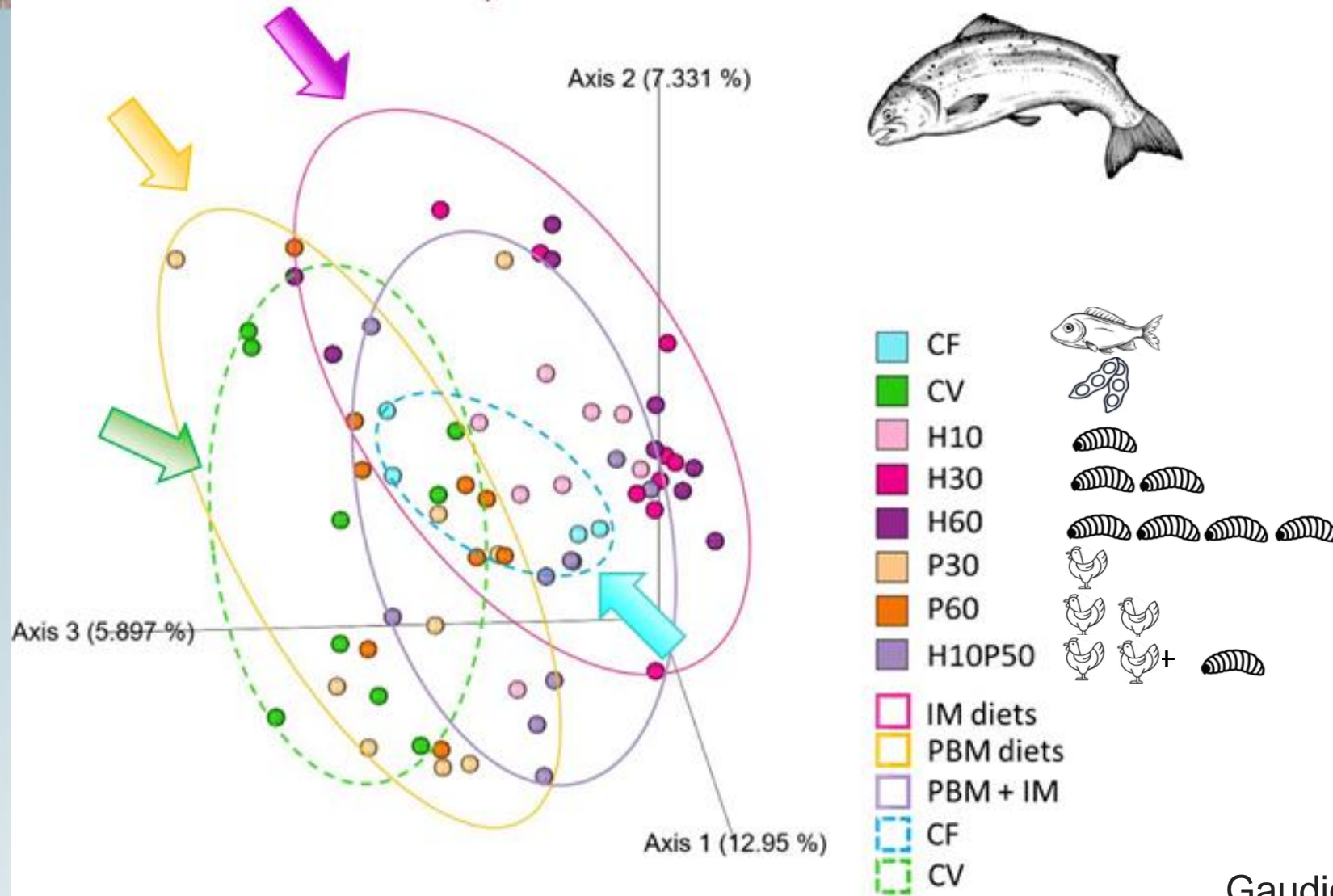


- o_Rickettsiales; f__mitochondria; Unidentified genus
- g_Weissella
- g_Lactobacillus
- g_Photorbacterium
- g_Streptococcus
- g_Leuzostoc
- g_Lactococcus
- f_Enterobacteriaceae; Unidentified genus 1
- g_Acinetobacter
- g_Pseudomonas
- g_Peptostreptococcus
- f_Enterobacteriaceae; Unidentified genus 2
- g_Erwinia
- g_Clostridium
- g_Fusobacterium
- f_Planococcaceae; Unidentified genus 1
- f_Verrucomicrobiales; Unidentified genus 1
- g_Bacillus
- f_Vibrionaceae; Unidentified genus
- g_Megaspheera
- g_Bacteroides
- g_Teplimicrobium
- f_Aeromonadaceae; Unidentified genus
- o_Vibrionales; Unidentified family
- g_Enterococcus
- g_Wautersiella
- g_Sporosarcina
- g_Kocuria
- g_Bifidobacterium
- f_Lactobacillaceae; Unidentified genus 1
- g_Pediacoccus
- g_Sphingomonas
- g_Aosspillum
- g_Camamonas
- f_Bacillaceae; Unidentified genus 1
- g_Chrysiobacterium
- f_Bacillaceae; Unidentified genus 2
- o_Lactobacillales; Unidentified family 1
- g_Aoxybacillus
- g_Ecthyobacter
- g_Corynebacterium
- f_Lachnospiraceae; Unidentified genus 1
- o_Bacillales; Unidentified family
- g_Halonorus
- g_Pseuobacillus
- f_Lachnospiraceae; Unidentified genus 2
- f_Alcaligenaceae; Unidentified genus
- g_Proteus
- f_Micrococcaceae; Unidentified genus
- g_Erythelothrix
- g_Provencia
- f_Erythelothricaceae; Unidentified genus 1
- g_Staphylococcus
- g_Morganella
- g_Phacolarectobacterium
- g_Actinomyces
- g_Dermacoccus
- g_Dysgenomonas
- g_Macroccoccus
- g_Pseudorambacter_Eubacterium
- f_Sphingobacteriaceae; Unidentified genus
- f_Enterococcaceae; Unidentified genus
- f_Erythelothricaceae; Unidentified genus 2
- f_Pseudomonadaceae; Unidentified genus
- o_Actinomycetales; Unidentified family
- o_Lactobacillales; Unidentified family 2
- Less abundant genera



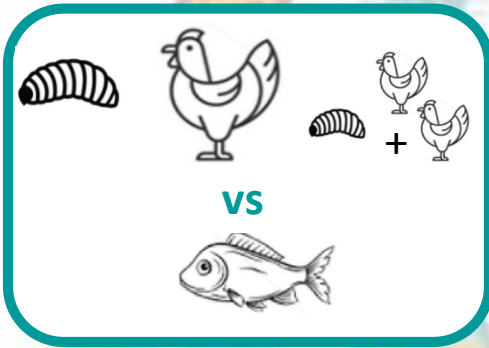
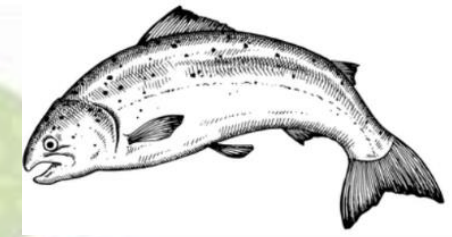
Gaudioso, et al., *Int. J. Mol. Sci.* **2021**, *22*, 5454.
<https://doi.org/10.3390/ijms22115454>


Farine di insetto e avicole

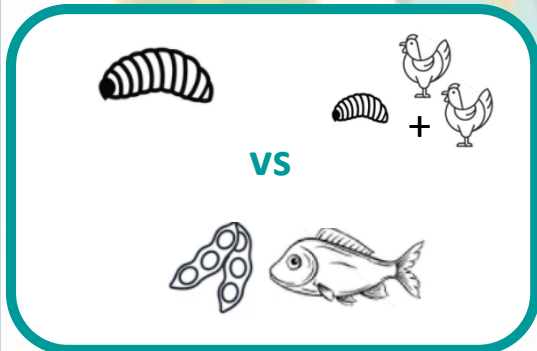



β -diversità distingue le diverse formulazioni

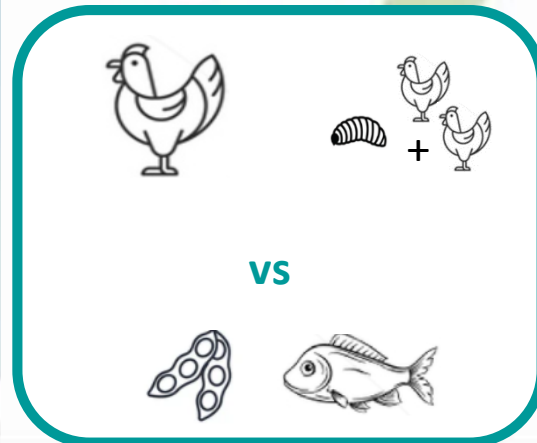
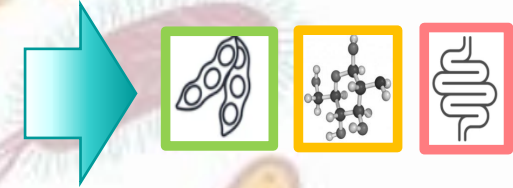
Farine di insetto e avicole



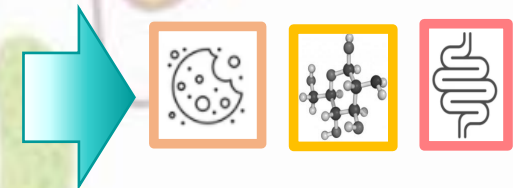
 ↓ Proteobacteria



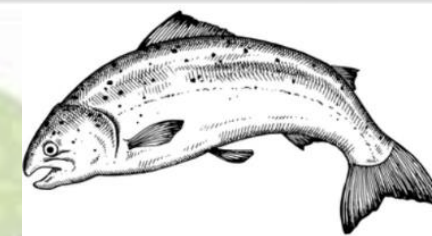
 ↑ Actinobacteria
↑ Lactobacillales



 ↑ Peptostreptococcaceae

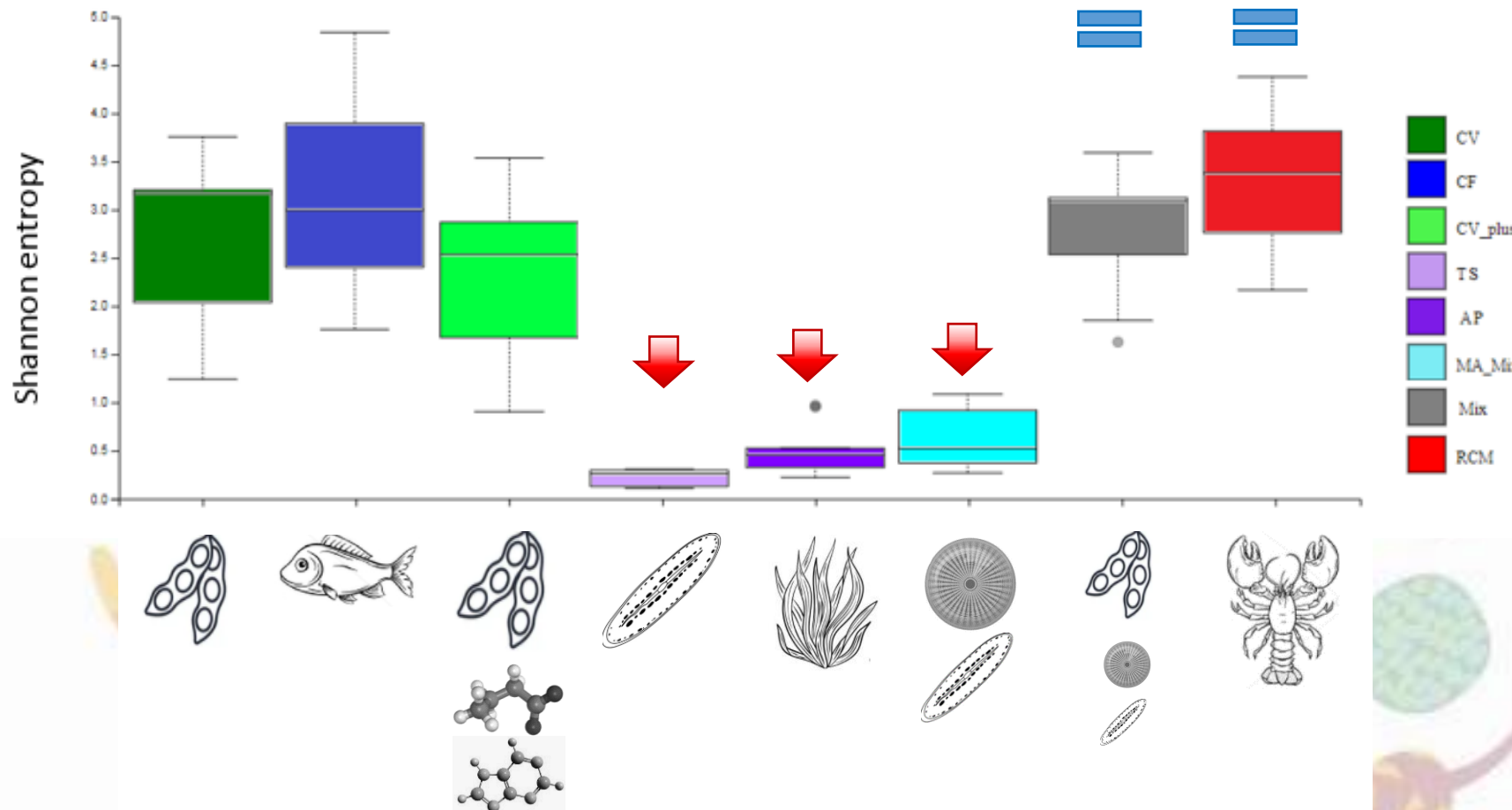


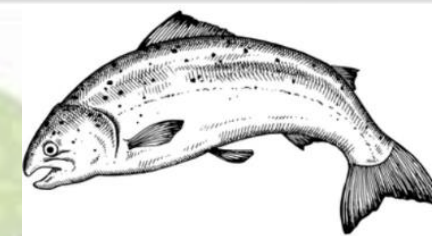
Spirulina, microalghe e gambero



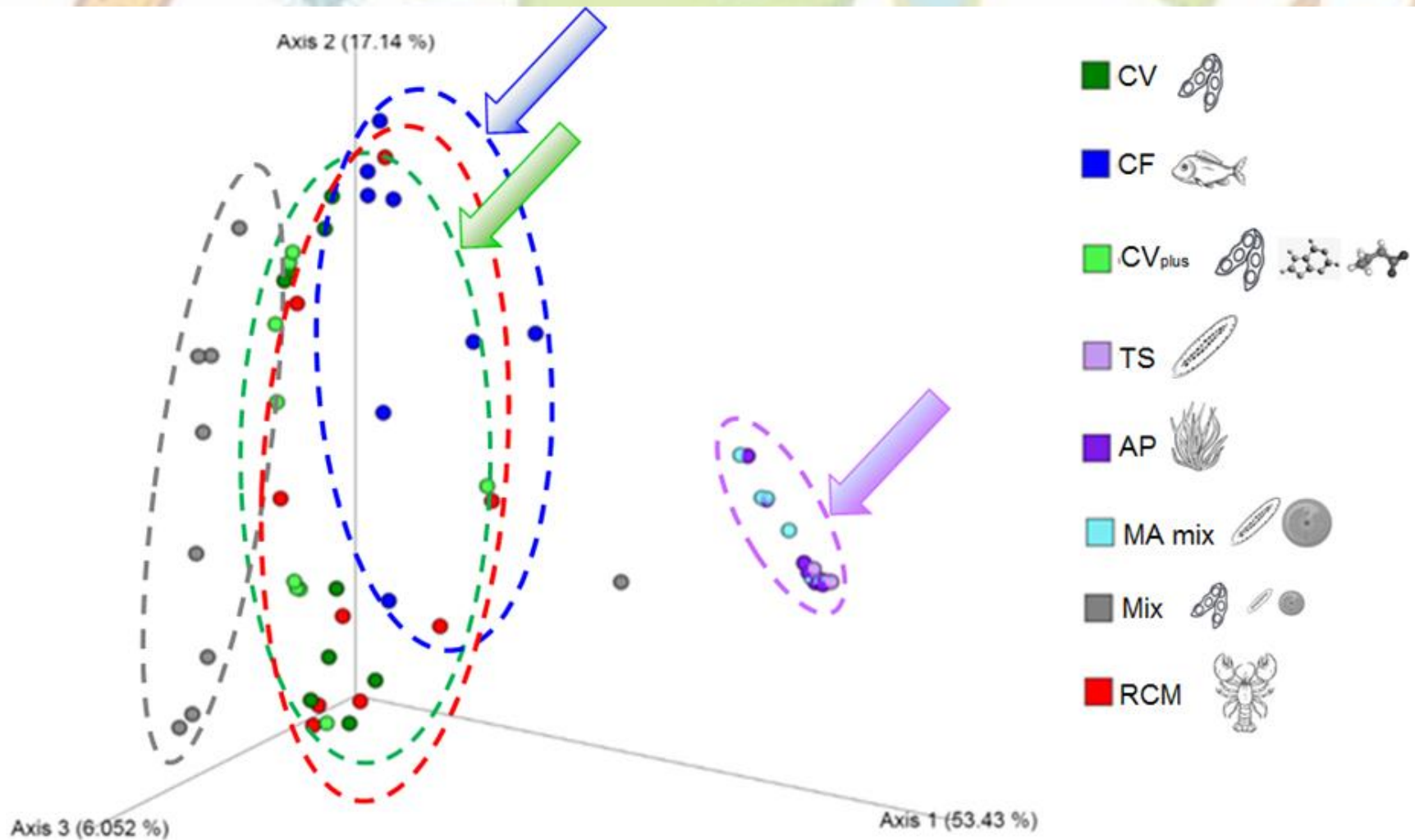
 **SPIRULINA e MICROALGHE** singole o in mix riducono significativamente α -diversità

 Farine di **GAMBERO** e **VEG+MICROALGHE** mantengono una α -diversità comparabile al controllo **FISH**



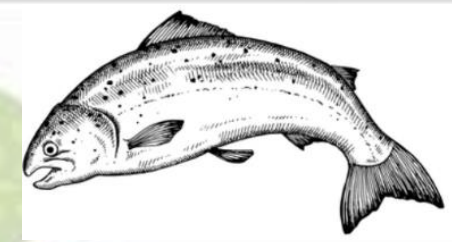


Spirulina, microalghe e gambero

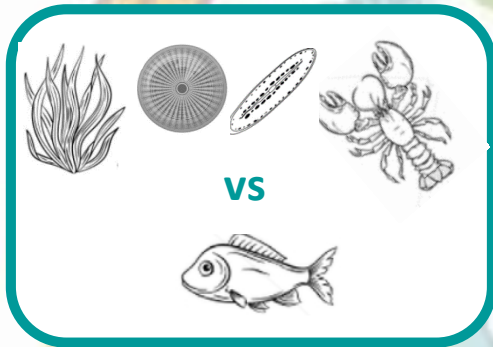



Formulazioni **VEG** simili tra loro e distinte da **Spirulina** e da **MA**, singole o in mix

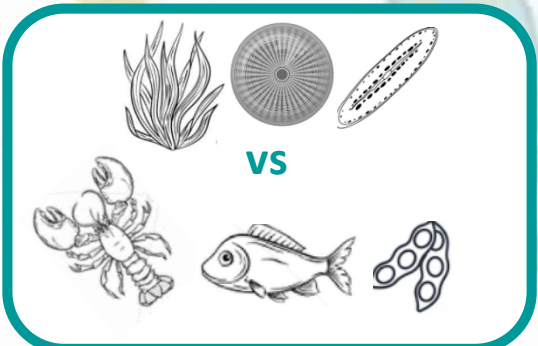
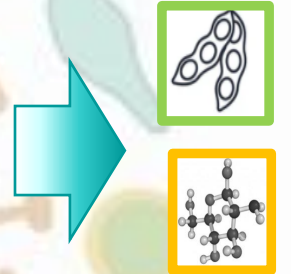
Formulazioni controllo **FISH** distinte da tutte le altre diete, ma più simili a farine di **GAMBERO**



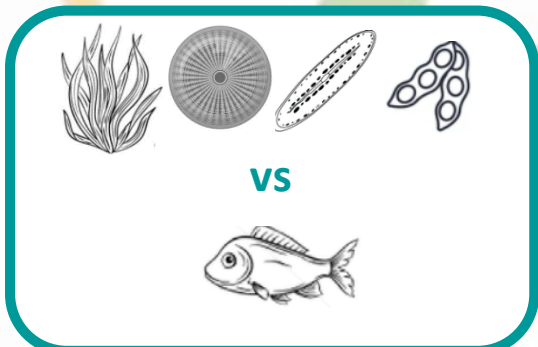
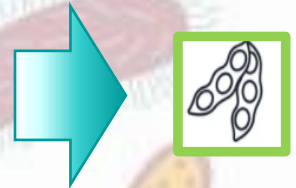
Spirulina, microalghe e gambero



 ↑ Firmicutes ↓ Proteobacteria

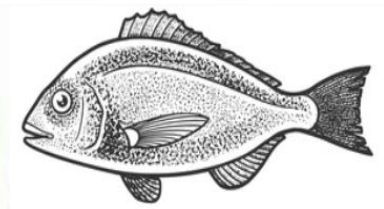


 ↑ Planctomycetes

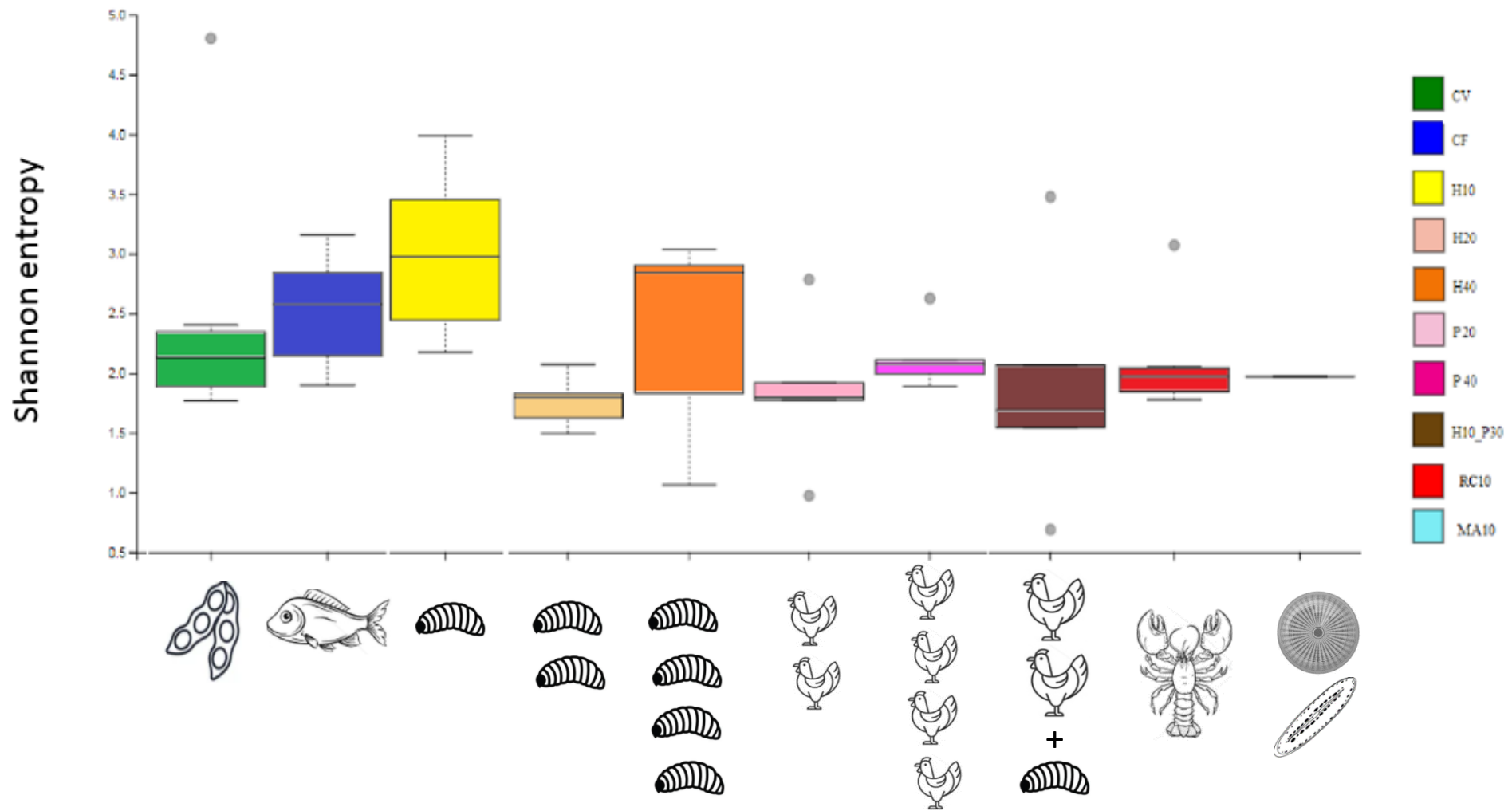


 ↑ *Lactobacillus* e *Streptococcus*
 ↓ *Weissella* ed *Enterococcus*



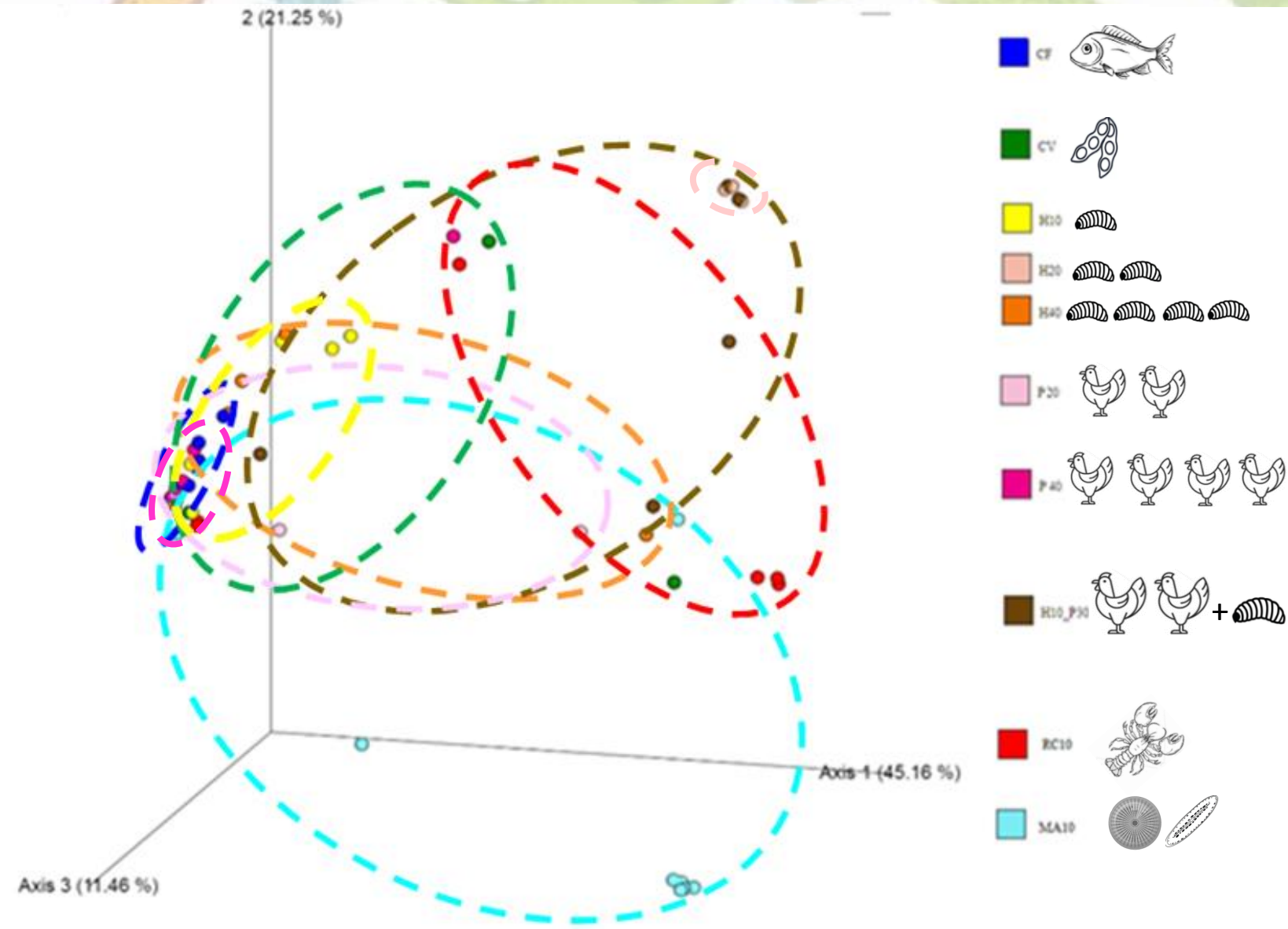
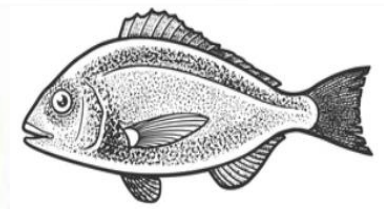


Farine di insetto, avicole, di gambero e con microalghe



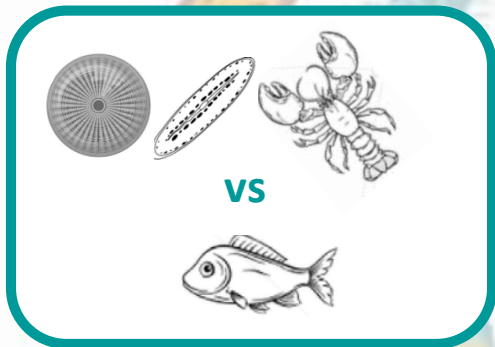
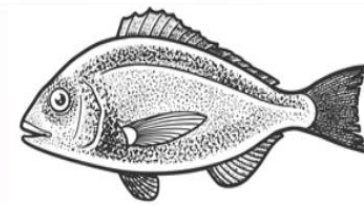
Ⓢ Nessuna differenza significativa in termini di α -diversità

Farine di insetto, avicole, di gambero e con microalghe

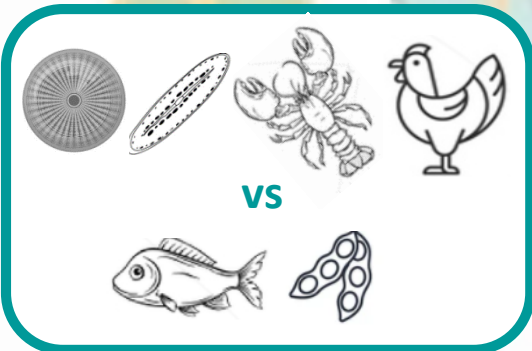


- S Elevata variabilità anche intra-gruppo, ad eccezione della dieta controllo **FISH**, con **β -diversità** più omogenea
- S Formulazioni total **VEG** sono significativamente distinte da **MA** per **β -diversità**

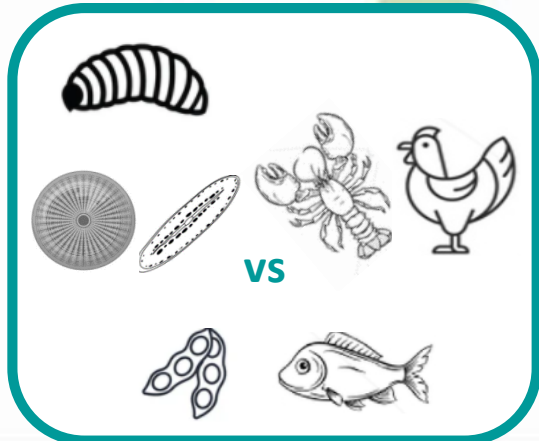
Farine di insetto, avicole, di gambero e con microalghe



 Phylum Firmicutes ↑



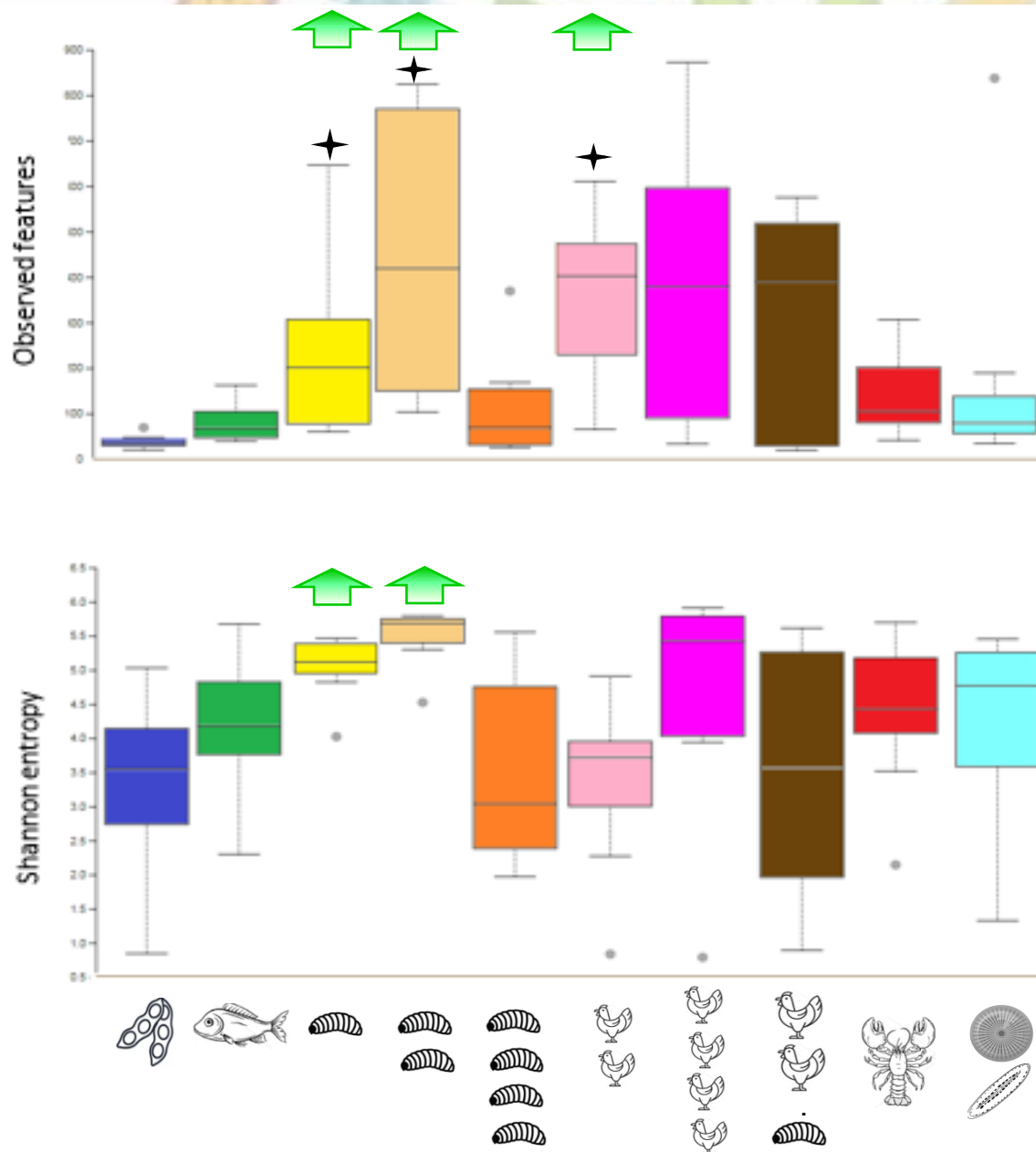
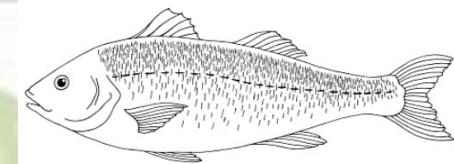
 Genere *Lactobacillus* ↑



 *Vibrio* ↑



Farine di insetto, avicole, di gambero e con microalghe

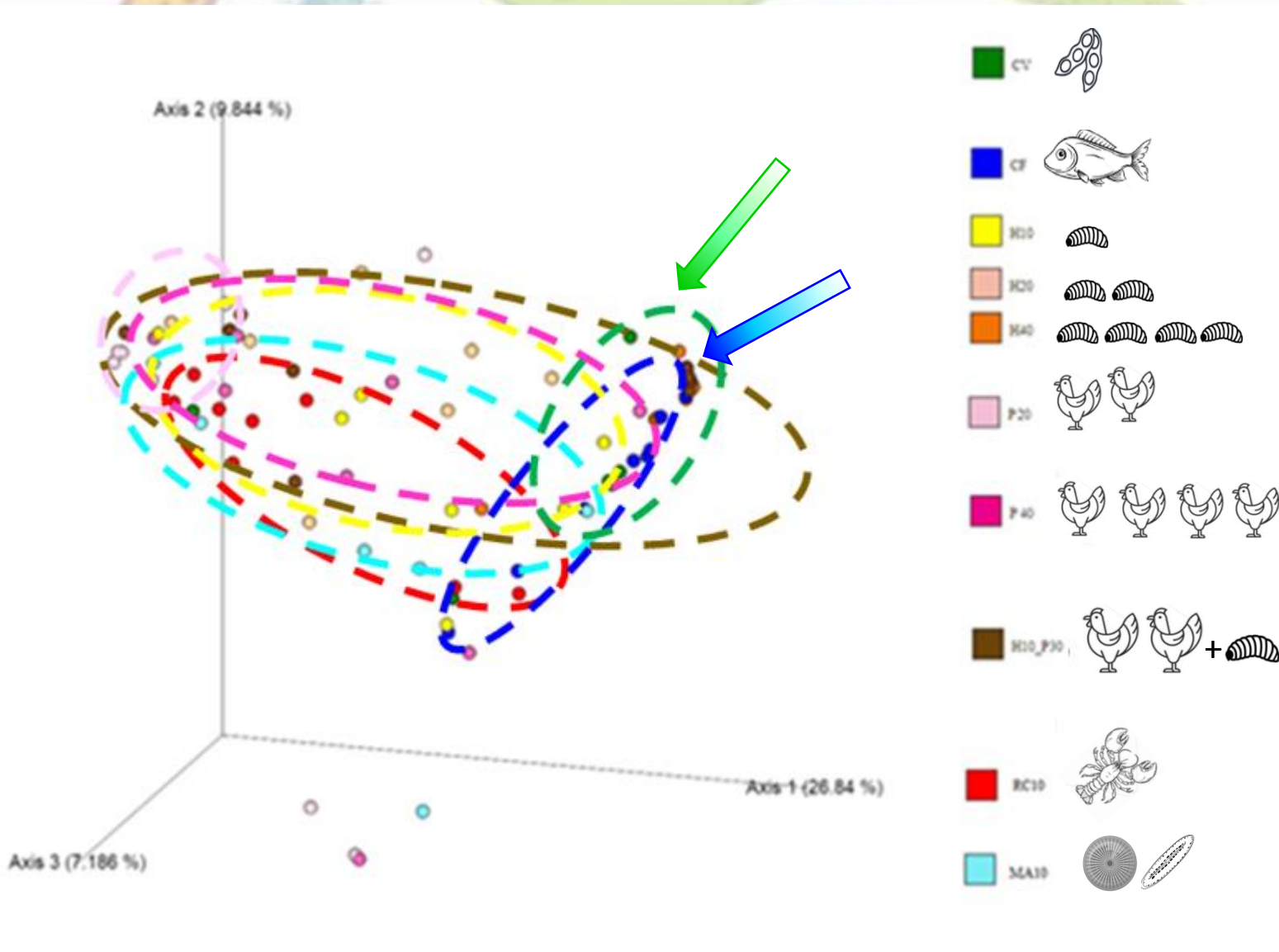
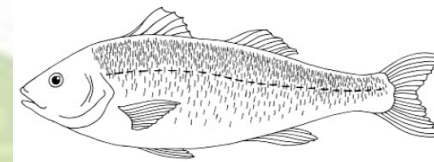


Farine di **INSETTO** e di **POLLO** a basse percentuali (H10, H20, P20) aumentano **α -diversità**, in termini di numero di specie ed omogeneità

A più alte percentuali di inclusione le farine di **INSETTO** (H40) esercitano pressione selettiva su alcuni microorganismi metabolizzatori, evidenziato da una ridotta **α -diversità**.

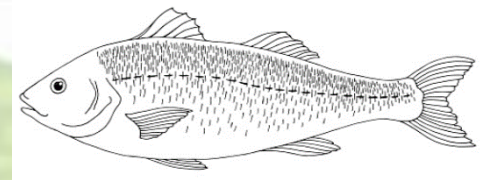
★ Significativo a confronto con CF

Farine di insetto, avicole, di gambero e con microalghe



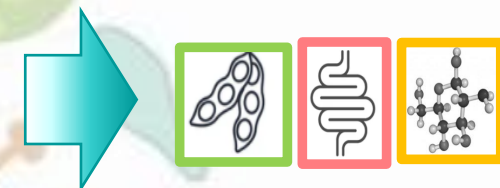
- Elevata **variabilità** anche intra-gruppo e intra-vasca
- Formulazioni **total VEG** non sono significativamente distinte dal **controllo FISH** per **β -diversità** e mostrano una maggior omogeneità

Farine di insetto, avicole, di gambero e con microalghe



basso
vs

↑ Bacillales e Corynebacteriales; *Lactobacillus*, *Oceanobacillus*, *Virgibacillus* e *Vagococcus*



vs

↑ Peptostreptococcaceae
 ↑ Mycoplasma



vs

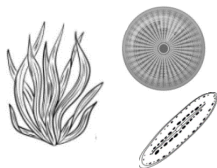
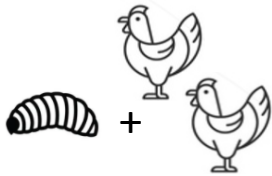
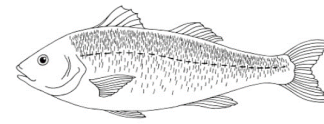
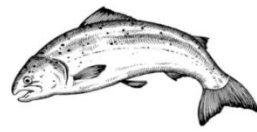
↑ *Lactobacillus*
 ↑ Bacillales (Thermoactinomycetaceae)



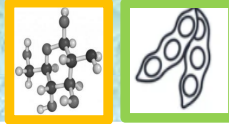
vs

↑ *Lactobacillus*





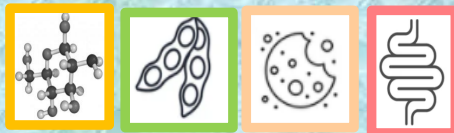
↑ Actinobacteria
↑ Lactobacillales



↑ *Paenicostridium* e
Bacteroidales, fam.
Peptostreptococcaceae



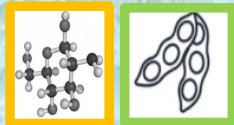
↑ Peptostreptococcaceae
↑ Lactobacillales



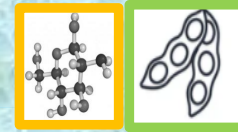
↑ Planctomycetes



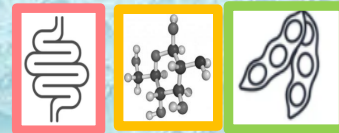
↑ *Deefgea*



↑ *Lactobacillus*



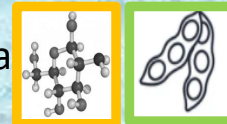
↑ *Photobacterium*
↑ *Lactobacillus* ↑ *Vibrio*



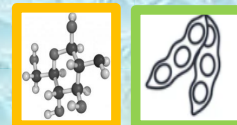
↑ *Lactobacillus*
↑ *Vibrio*



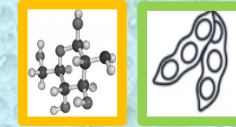
↑ *Lactobacillus*
↑ Actinobacteria



↑ *Lactobacillus*



↑ *Oceanobacillus*, fam.
Bacillaceae



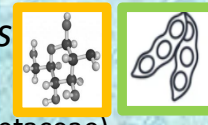
↑ Bacillales e
Corynebacteriales
↑ *Romboutsia*
(Peptostreptococcaceae)



↑ *Lactobacillus*
↑ *Mycoplasma*



↑ *Lactobacillus*
↑ Bacillales
(Thermoactinomycetaceae)



↑ *Paraclostridium*;
↑ Peptostreptococcaceae:



DEGRADAZIONE di
POLISACCARIDI
VEGETALI



DEGRADAZIONE di
CHITINA



DEGRADAZIONE
PROTEICA



SALUTE
INTESTINALE

Conclusioni

- ❑ Le diete sperimentali contenenti elevate percentuali di farine di **INSETTO** aumentano la diversità del microbiota intestinale, fornendo una più ampia capacità metabolica e maggior protezione da patogeni
- ❑ La combinazione di farine di **INSETTO** e farine **AVICOLE** promuove la crescita di microorganismi con diversificate capacità metaboliche, saccarolitici, chitinolitici e proteolitici, fornendo un vantaggio per la digeribilità sia di ingredienti vegetali, sia di fonti proteiche animali e promuovendo la salute intestinale
- ❑ **MICROALGHE** e **SPIRULINA** favoriscono l'aumento di generi batterici fermentativi soprattutto in **TROTA**, indicativi di aumentata capacità di metabolizzare matrici vegetali
- ❑ Farine di **GAMBERO** promuovono batteri chitinolitici e, particolarmente in **SPIGOLA**, batteri proteolitici

...Grazie!

