

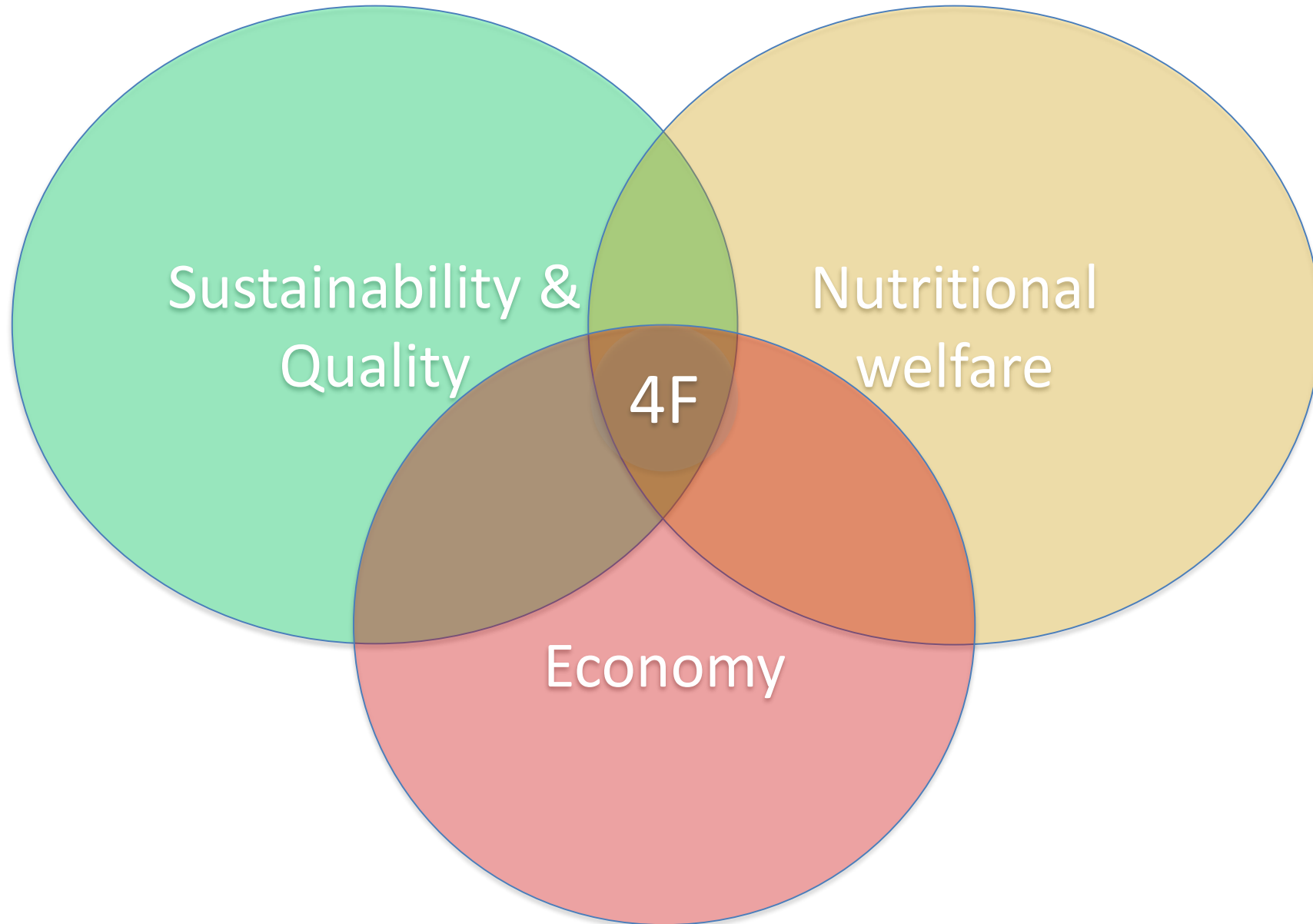


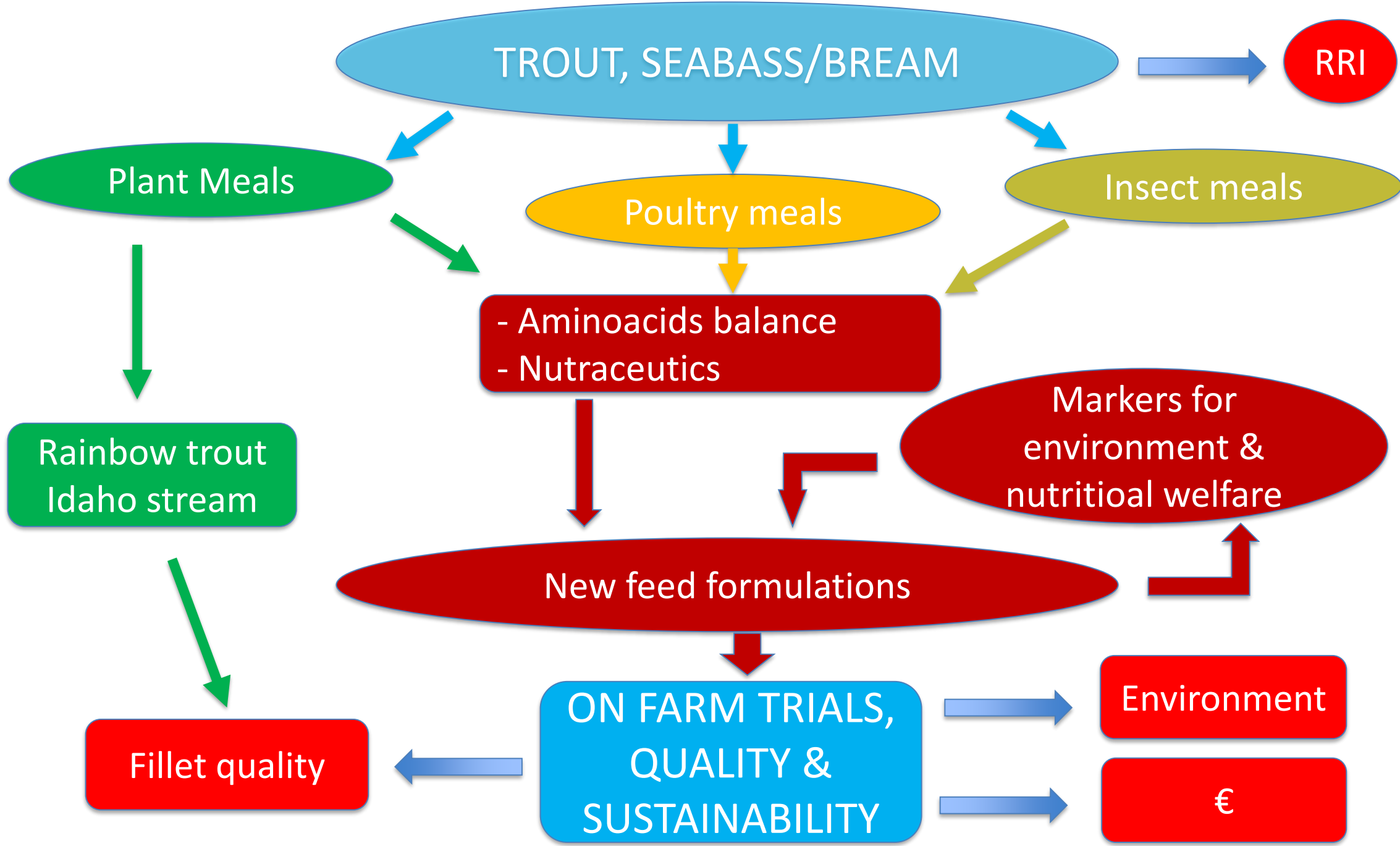
# AGER 4F: Balancement of the carnivorous fish diet, for the minimization of FM inclusion

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# Fish meal substitution

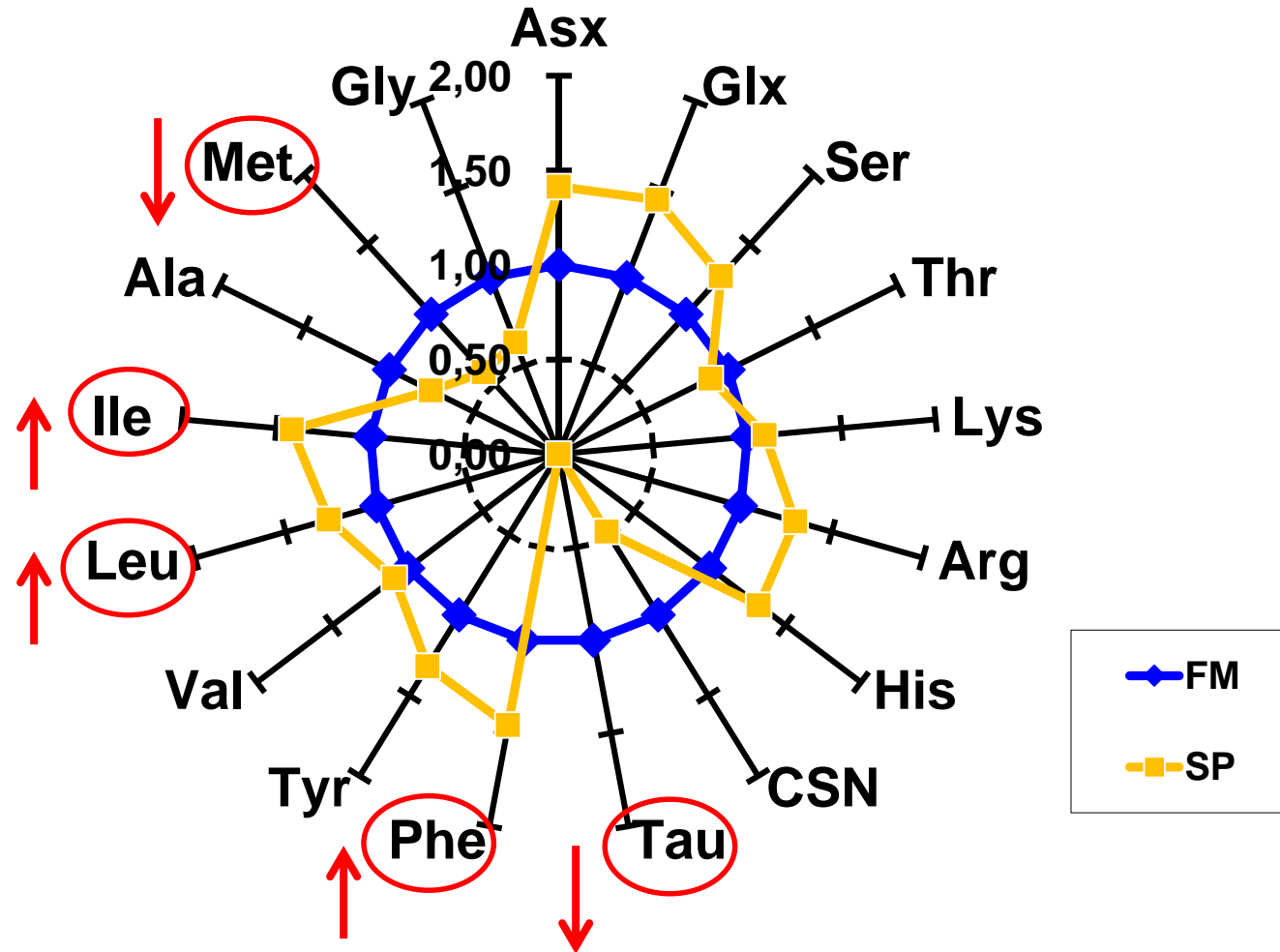




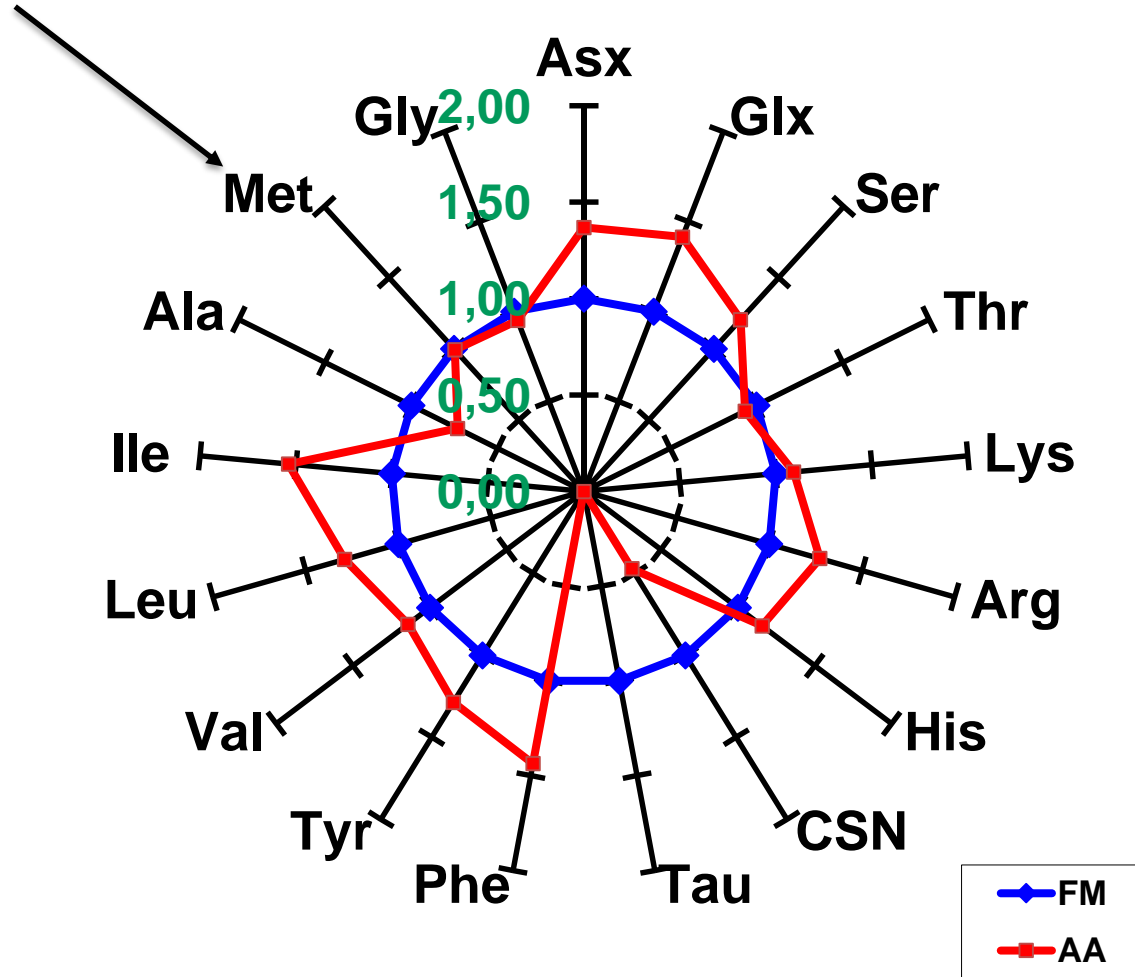
A red oval with a thin blue border, centered on a white background. Inside the oval, the text "AMINOACIDS BALANCE: THE EXAMPLES OF METHIONINE AND TAURINE" is written in white, uppercase, sans-serif font, centered horizontally and vertically.

AMINOACIDS BALANCE: THE  
EXAMPLES OF METHIONINE  
AND TAURINE

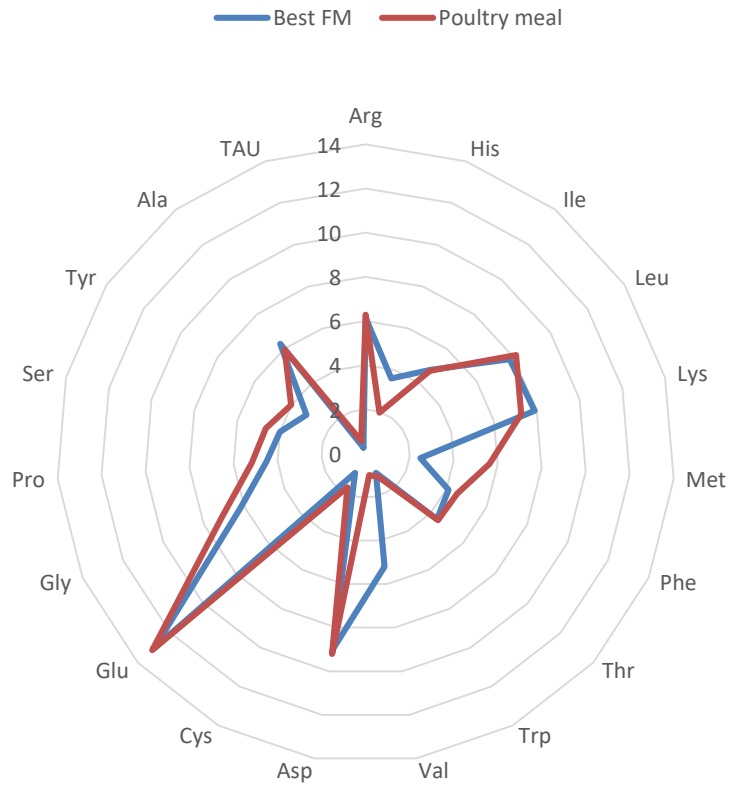
# Amino acid profile soy protein and fishmeal



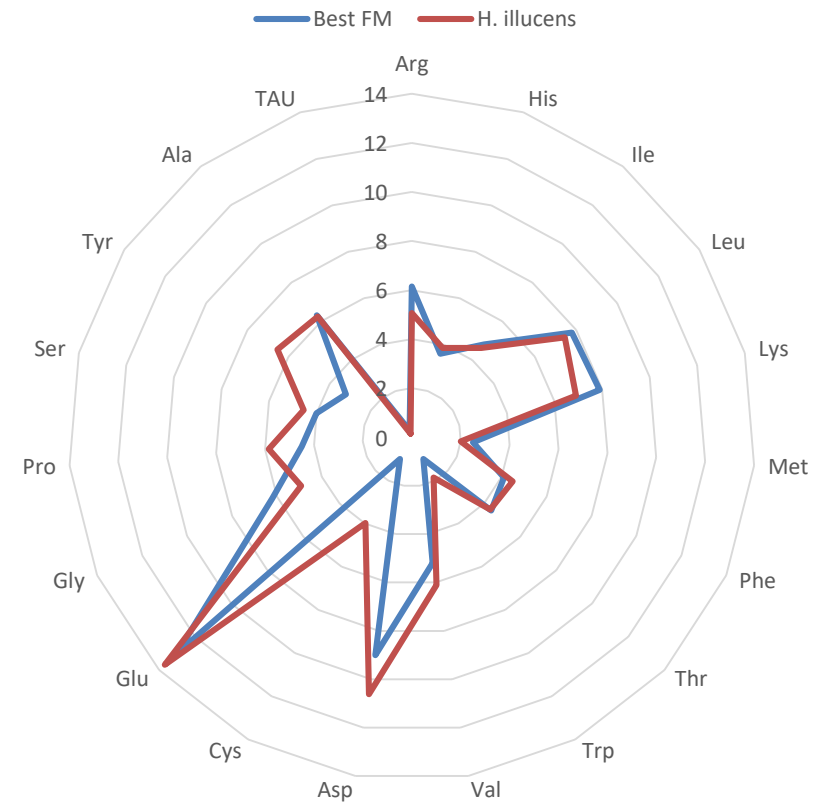
# Supplement with Methionine



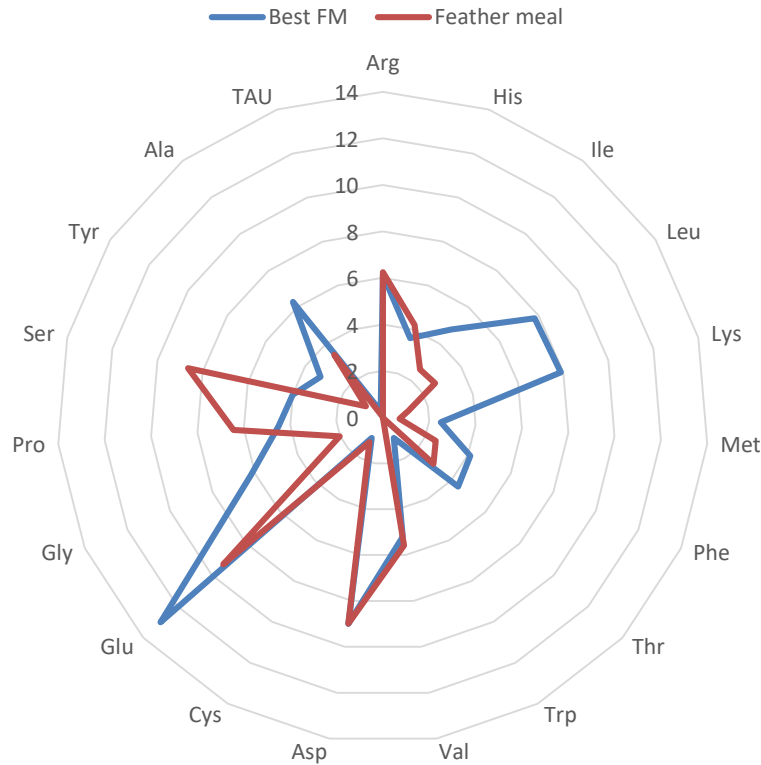
Comparison between aminoacids profile



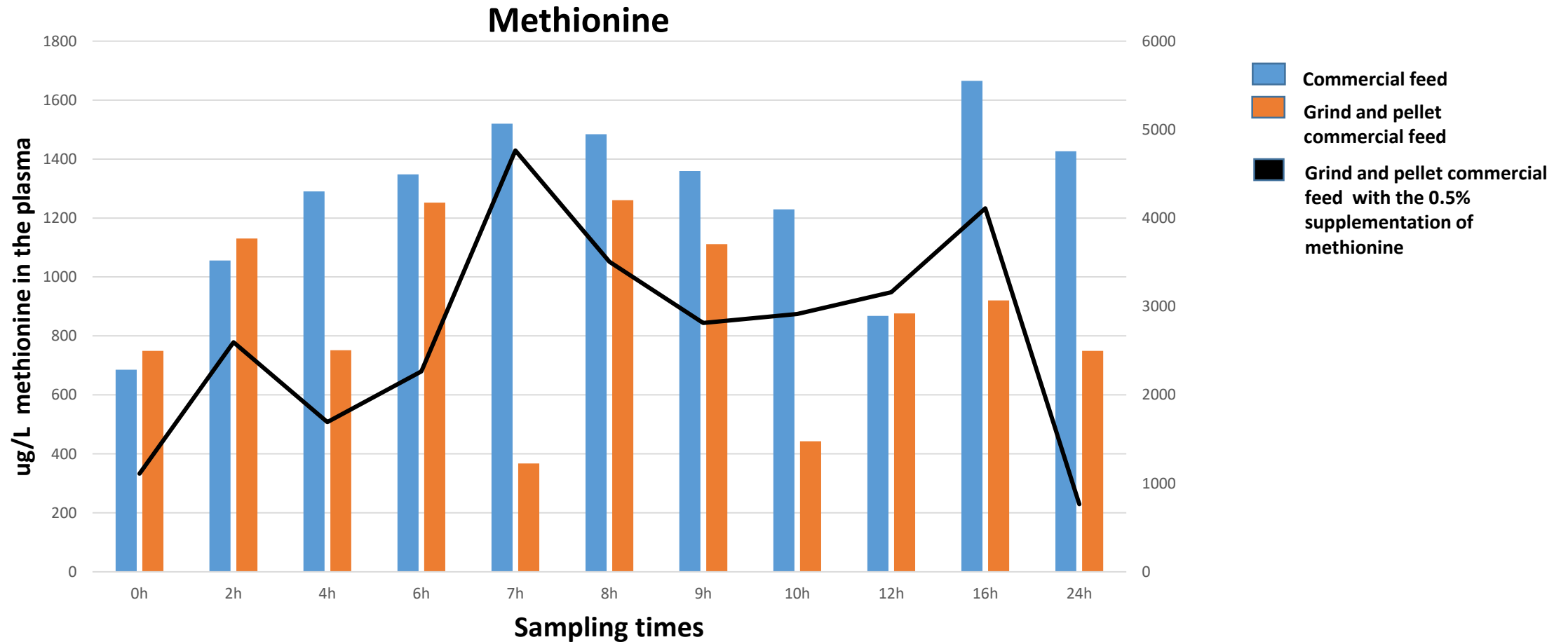
Comparison between aminoacids profile



Comparison between aminoacids profile



**Trial with 3 kind of feeds:**  
commercial feed, grind and pellet commercial feed, grind and pellet commercial feed with the 0.5%  
supplementation of methionine.



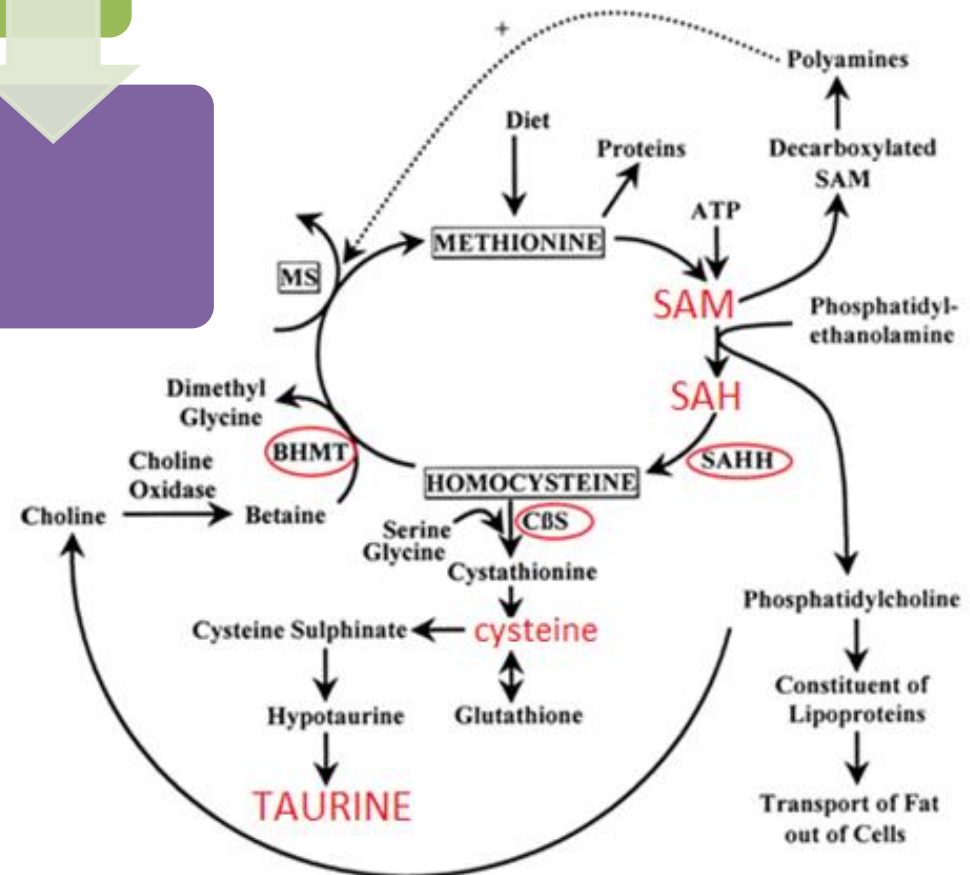


# Background

Methionine: a source of sulphur required for the synthesis of cysteine and taurine as well as an essential methyl-donor in cellular metabolism. A total of 48% of dietary Met metabolism takes place in the liver.

Changes in the metabolism of Met can influence the production of nutrients essential for proper functioning of the skeletal, cardiovascular, and nervous systems.

Homocysteine: a sulphur amino acid metabolite derived from Met. The maintenance of methyl groups and homocysteine homeostasis in the hepatic tissue is dependent on the balance between S-adenosylhomocysteine (SAH) and its precursor, a powerful inhibitor of transmethylation reactions, S-adenosylmethionine (SAM).



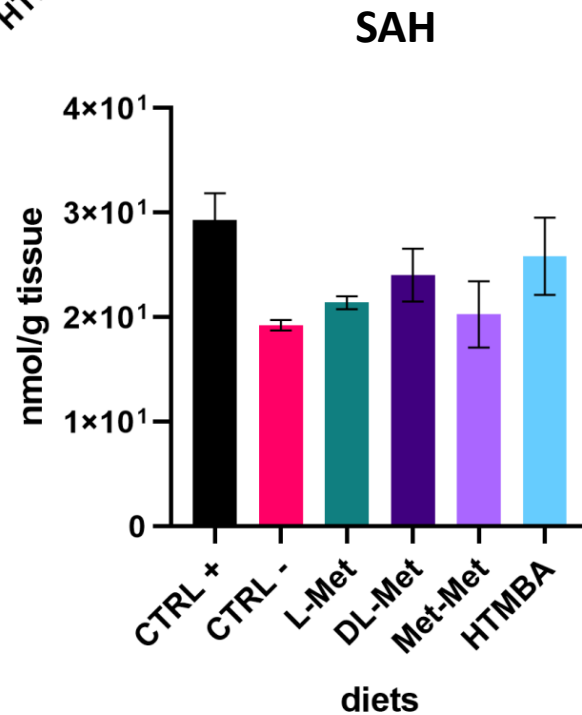
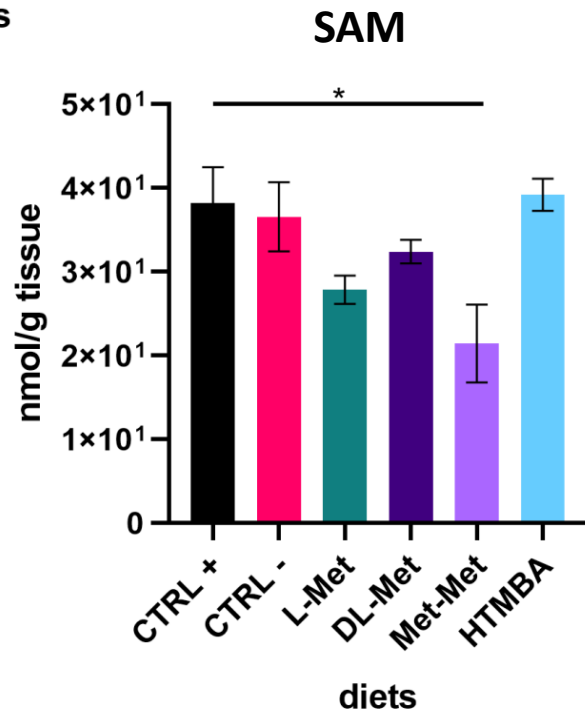
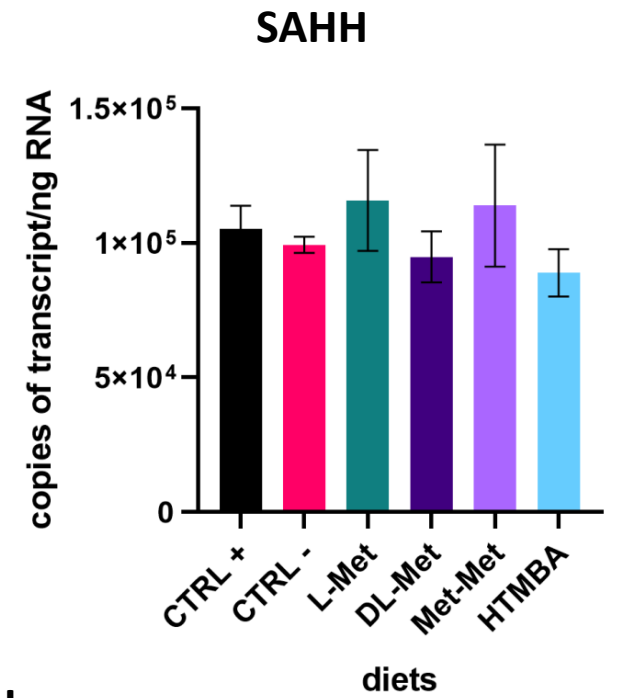
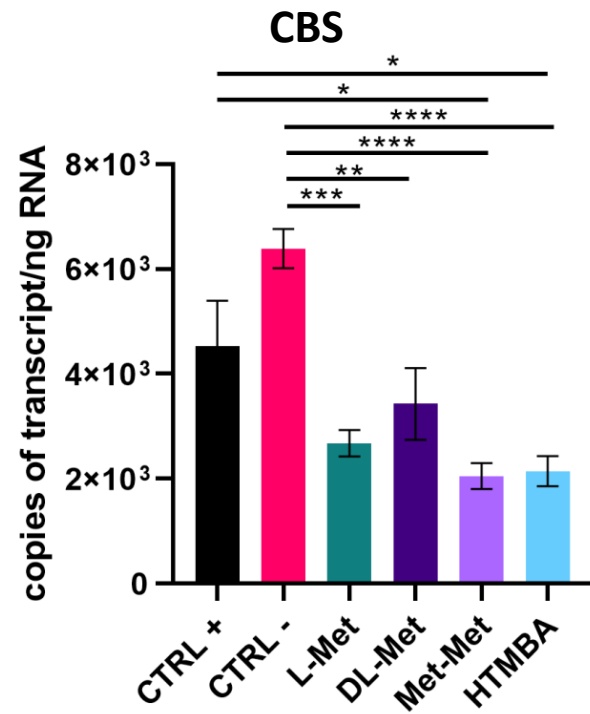
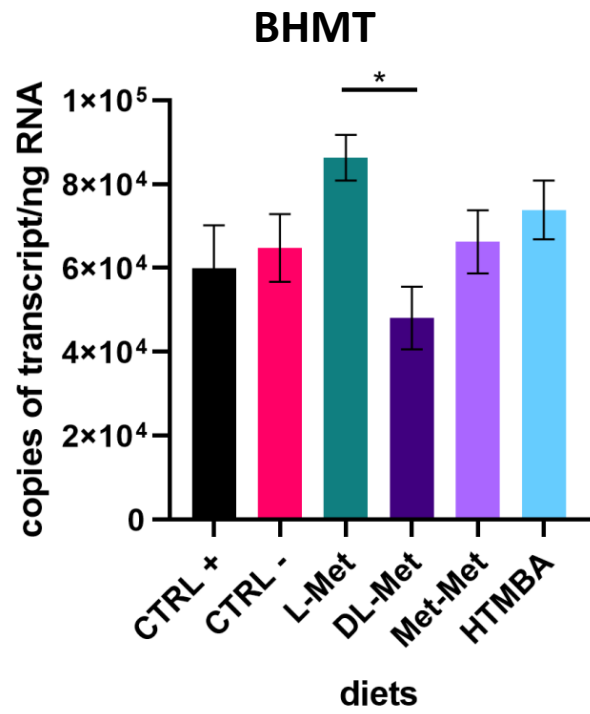
**BHMT: Betaine-Homocist. S-Methyltransferase**

**CBS: Cystathionine-β-Synthase**

**SAHH: S-Adenosylhomocysteine Hydrolase**

**SAM: S-Adenosyl-Methionine**

**SAH : S-Adenosyl-L-Homocysteine**



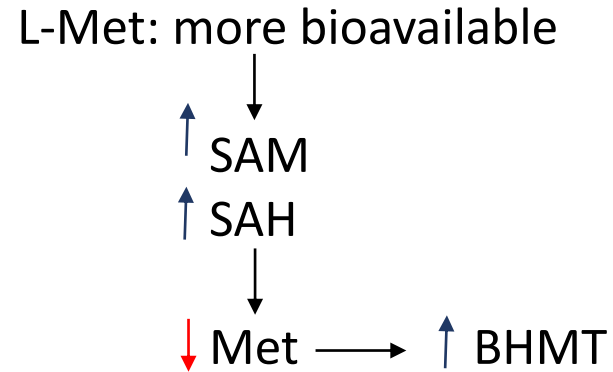
\* p<0,05  
 \*\* p<0,01  
 \*\*\* p<0,001  
 \*\*\*\* p<0,0001

	CTRL +	CTRL -	L-Met	DL-Met	Met-Met	HTMBA
<b>FCR BIO</b>	1.33 ± 0.04	1.42 ± 0.06	1.35 ± 0.01	1.32 ± 0.01	1.32 ± 0.03	1.35 ± 0.05
<b>FCR ECO</b>	1.34 ± 0.04	1.43 ± 0.06	1.36 ± 0.01	1.33 ± 0.01	1.33 ± 0.03	1.36 ± 0.04
<b>SGR</b>	0.83 ± 0.02	0.79 ± 0.02	0.83 ± 0.01	0.82 ± 0.01	0.82 ± 0.01	0.81 ± 0.04
<b>Pm iniz. (g)</b>	46.38 ± 0.69	46.25 ± 0.47	46.26 ± 0.47	46.74 ± 0.41	47.67 ± 0.68	46.77 ± 1.21
<b>Pm fin. (g)</b>	103.32 ± 1.19	99.38 ± 2.09	103.21 ± 0.34	103.62 ± 1.54	105.69 ± 0.57	102.26 ± 1.22
<b>Accr. (%)</b>	122.82 ± 5.05	114.88 ± 4.48	123.11 ± 1.51	121.69 ± 1.76	121.76 ± 2.22	118.77 ± 8.02
<b>Mortalità (%)</b>	0.62 ± 0.54	0.94 ± 0.01	0.62 ± 0.54	0.94 ± 0.94	0.61 ± 0.52	0.92 ± 0.92
<b>Feed Intake</b>	75.83 ± 1.52	67.23 ± 13.26	68.88 ± 13.88	67.17 ± 14.60	68.35 ± 12.90	67.03 ± 14.21

**FCR BIO:**  
CTRL- vs HTMBA p<0.05

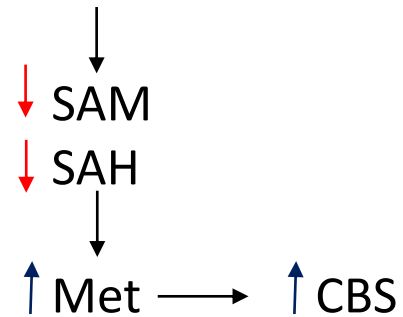
**FCR ECO:**  
CTRL- vs DL-Met p<0.05  
CTRL- vs HTMBA p<0.05

## Hypothesis:



L-met can be directly used to synthesize SAM or can be degraded through pathways such as transamination. SAM can undergo the transmethylation pathway to synthesize homocysteine or the transsulfuration pathway, with the products cysteine, glutathione, taurine.

HTMB, DL-Met protect, Met-Met, DL-Met: slow assimilation

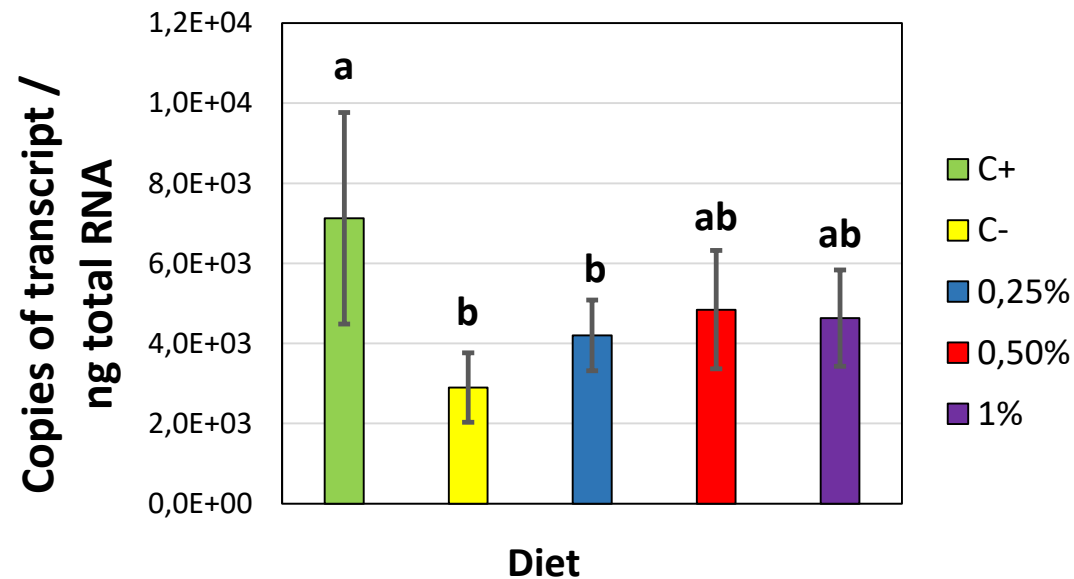


**It is a temporal issue**

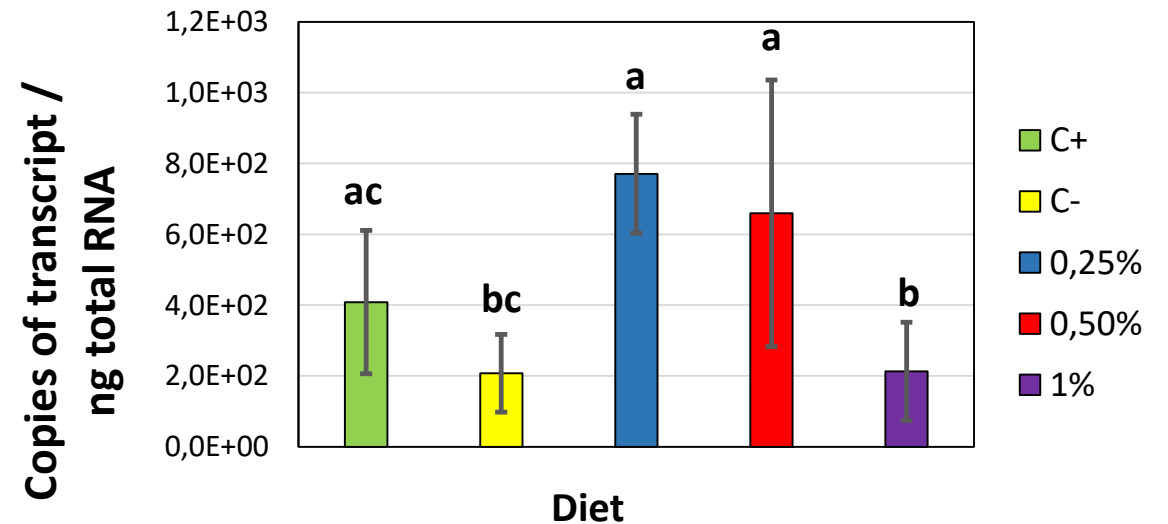
# Taurine need in the diet for Rainbow trout

- **Positive control** : (fish meal diet base)
- **Negative control**: (vegetable meal diet poor in Tau)
- **0,25%** = (negative control + 0,25% Tau)
- **0,50%** = (negative control + 0,50% Tau)
- **1,0%** = (negative control + 1,0% Tau)

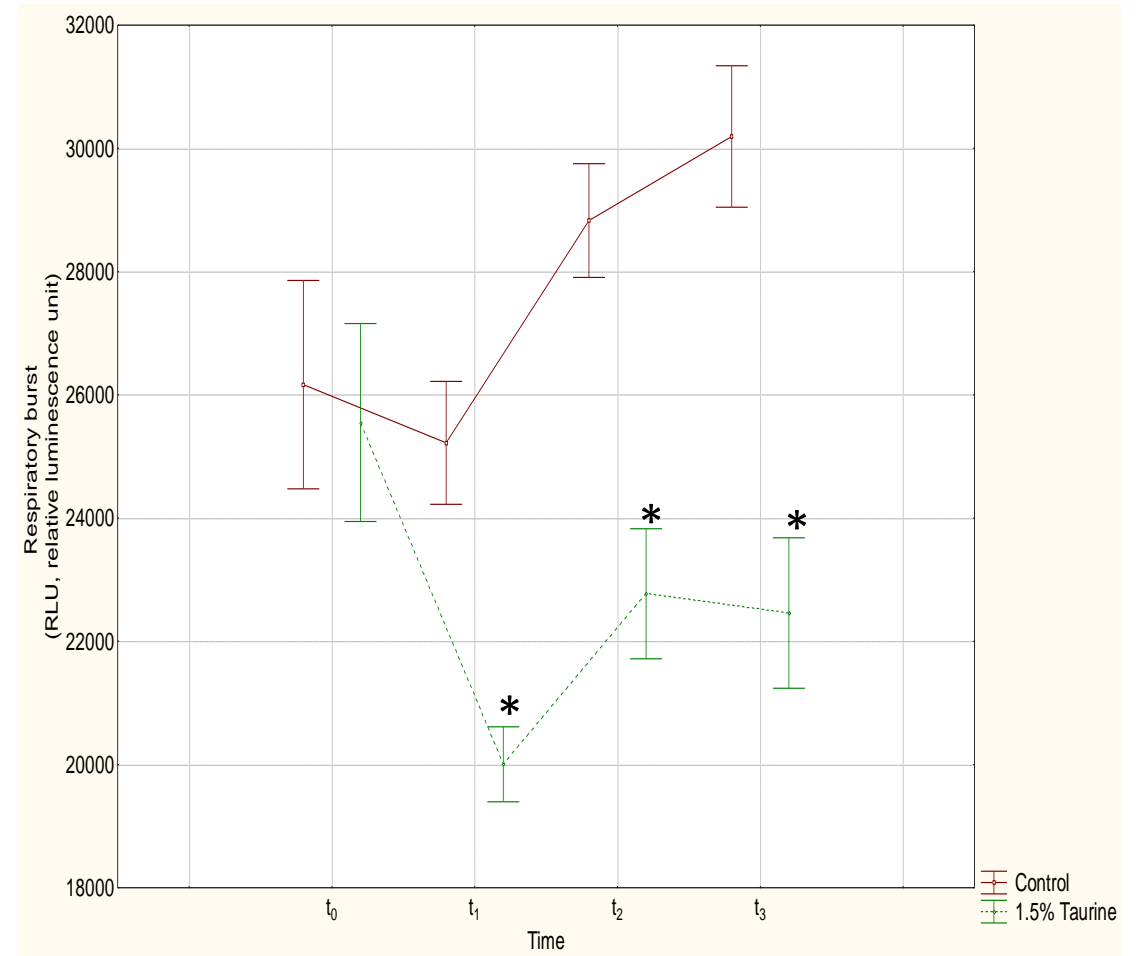
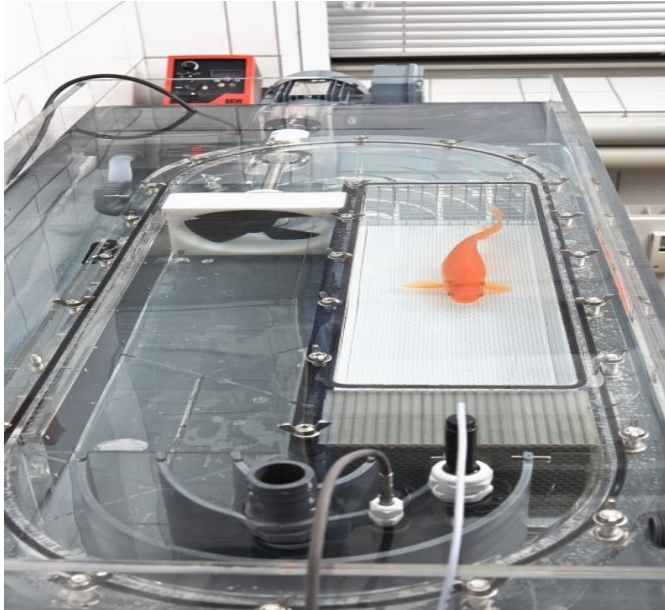
## TauT expression in kidney



## TauT expression in liver



# Taurine

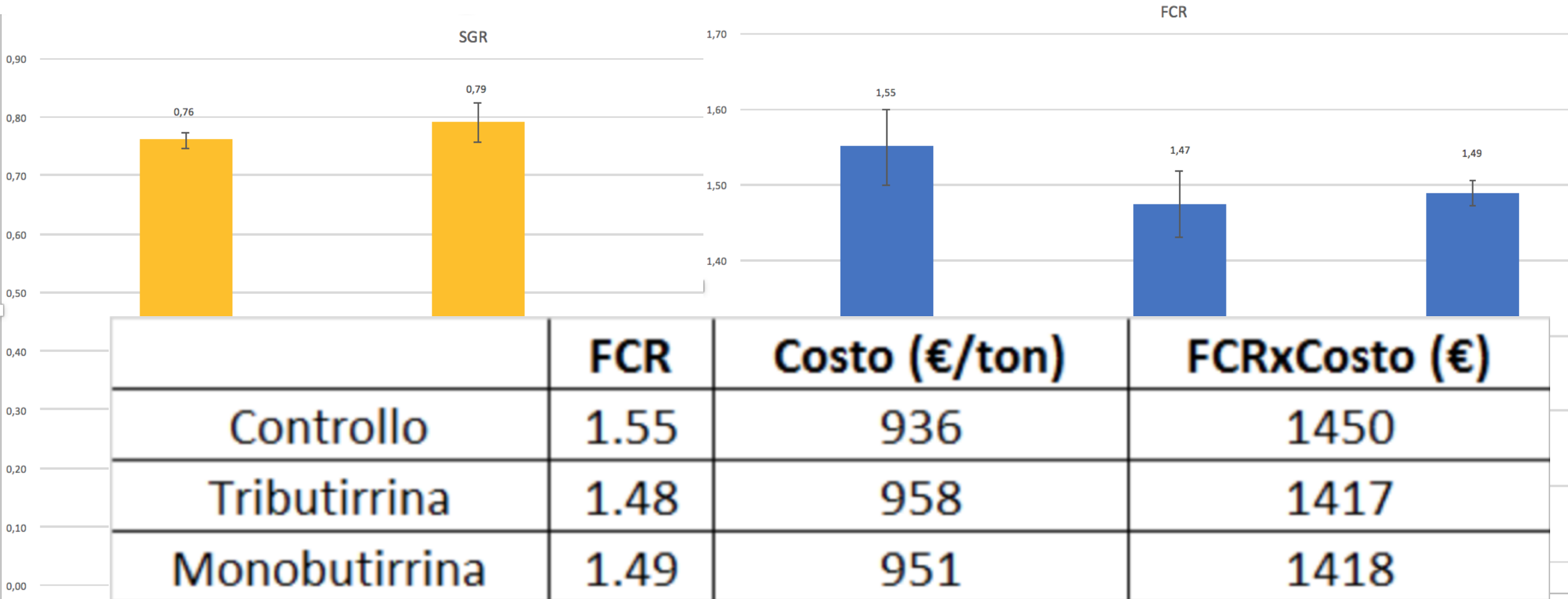


**Table 3.** The RBA values after PMA stimulation in Ctrl and 1.5% Tau group. (\*) means significant differences between groups for the same t ( $p < 0.05$ ).



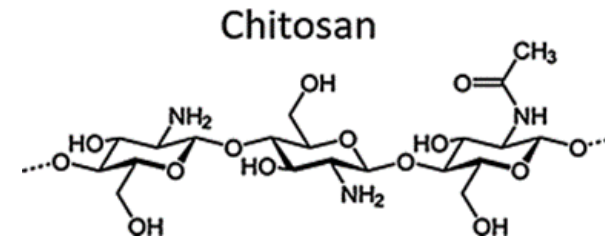
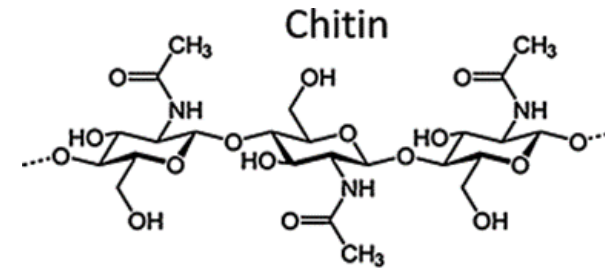
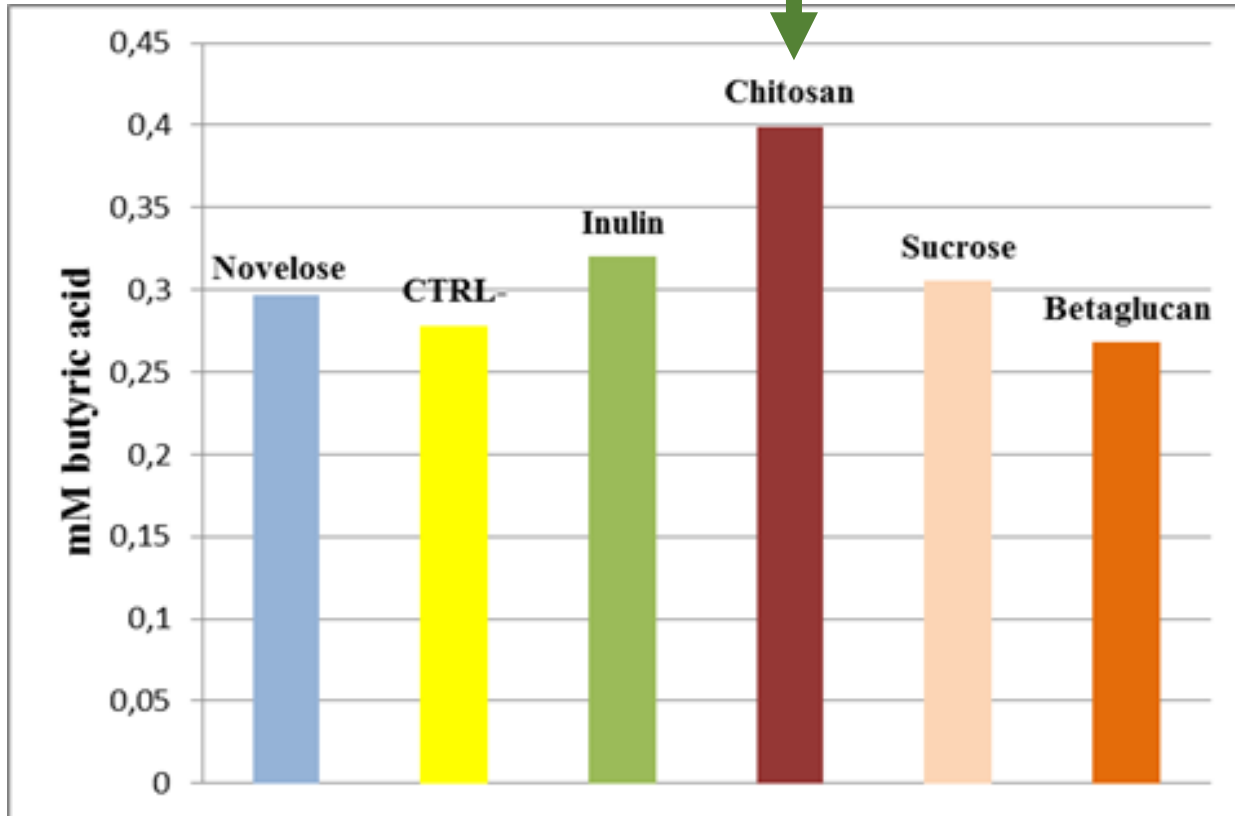
SCFAs

# Effects of Butyrate on SGR and FCR





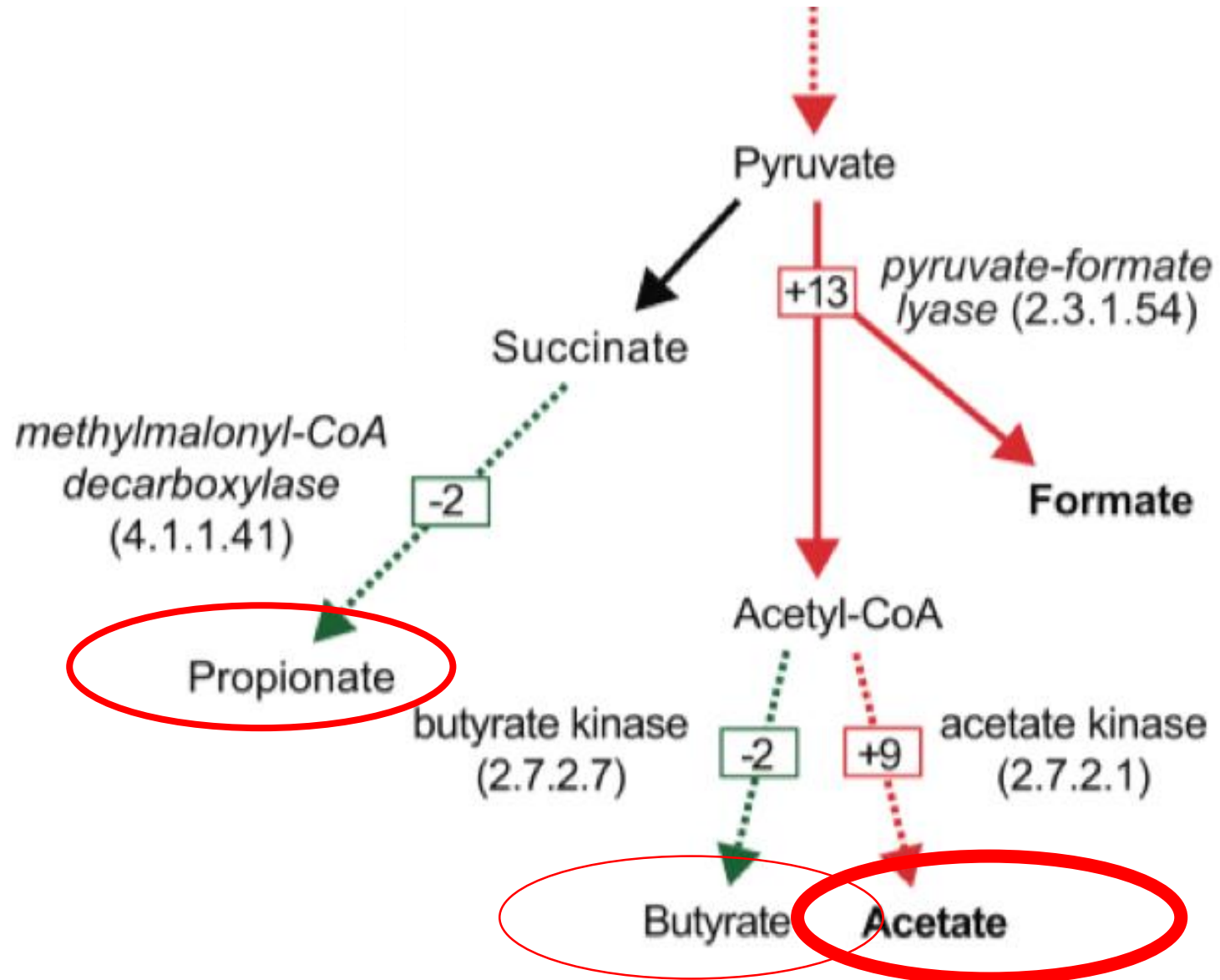
# Preliminary *in vitro* test for butyric acid quantification



- Collecting feces from seabass fed with a control diet (Bulk collection);
- Anaerobic growth of feces in medium with prebiotics addition;
- Extraction of butyric acid following De Baere *et al.* (2013) protocol;
- Quantification by HPLC-UV;
- Among all prebiotics, chitosan resulted the substrate giving the highest level of butyric acid.

# Rainbow trout fecal content

	Acetate (mM/l)	Propionate (mM/l)	Butyrate (mM/l)
Time T <sub>0</sub>	7.05	Traces	Traces
Control	6.38	Traces	0.51
Mono-Butyrate	12.88	1.97	1.48
Insect-chitin	12.26	1.22	2.06
Shrimp meal	13.74	0.74	0.30

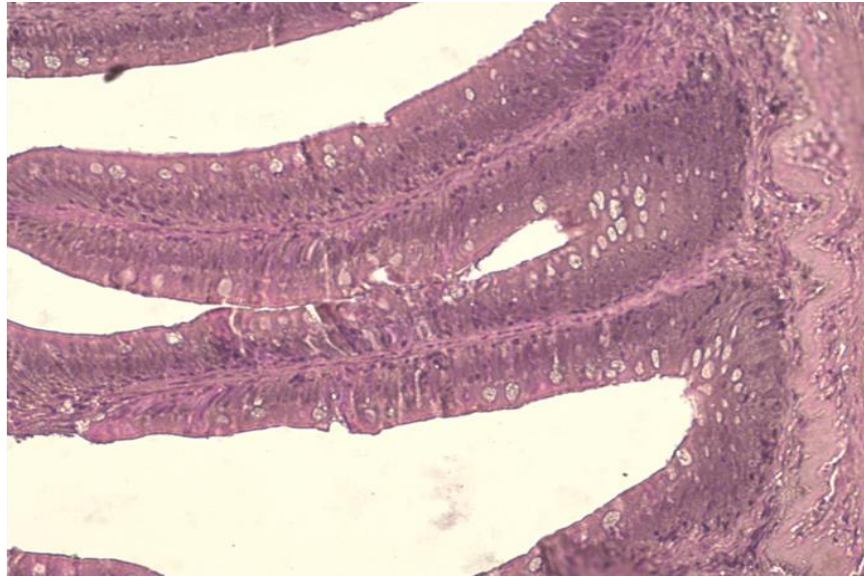


Samuel & Gordon, 2006, modif.

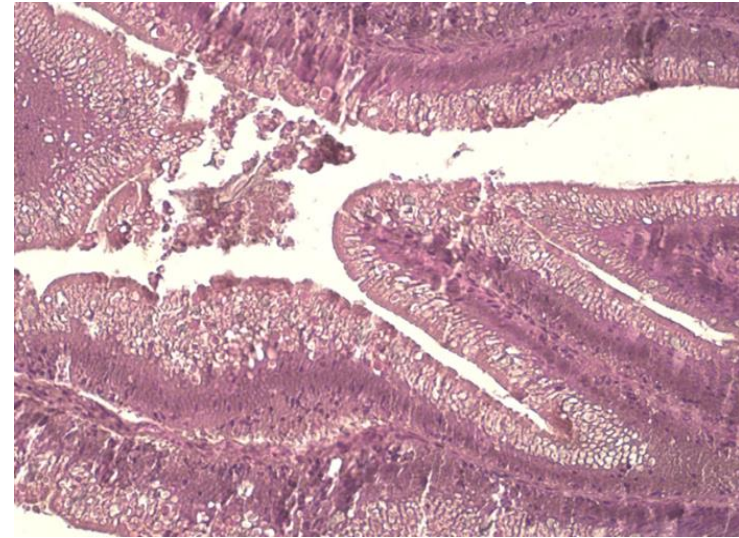
CTRL

PROXIMAL INTESTINE

DISTAL INTESTINE



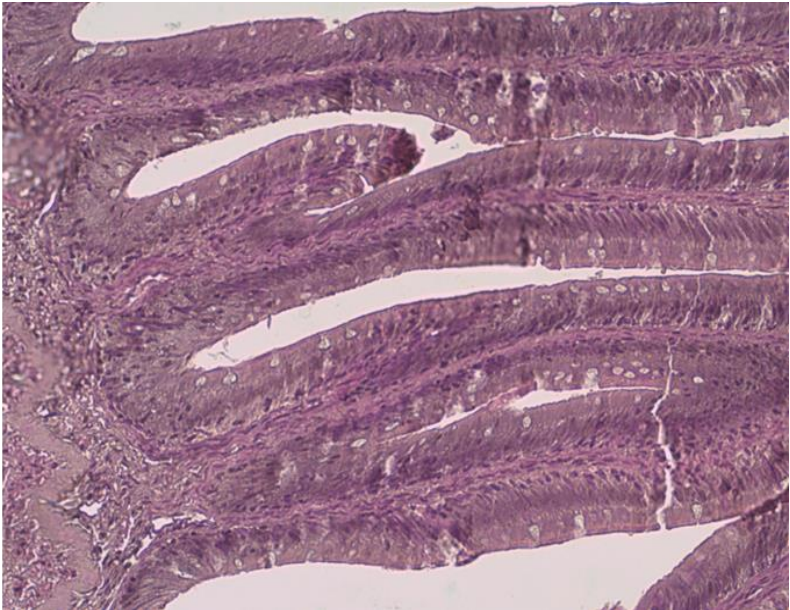
10 X



10 X

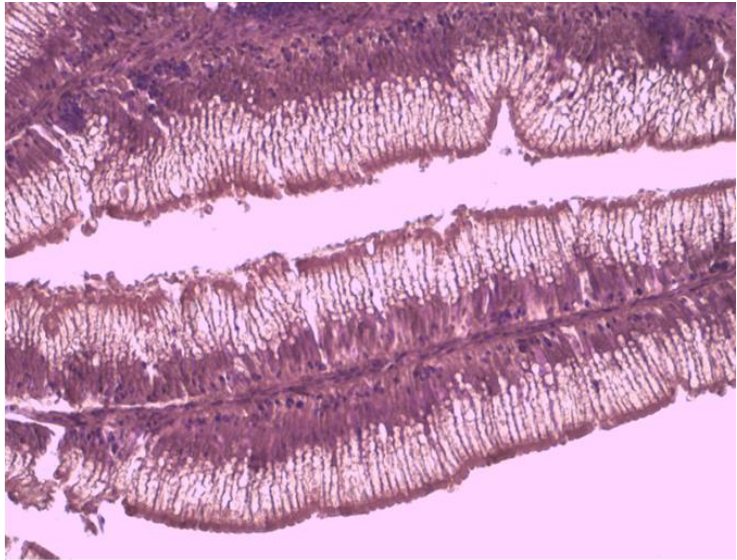
CTRL + CHITIN

PROXIMAL INTESTINE



10 X

DISTAL INTESTINE



10 X

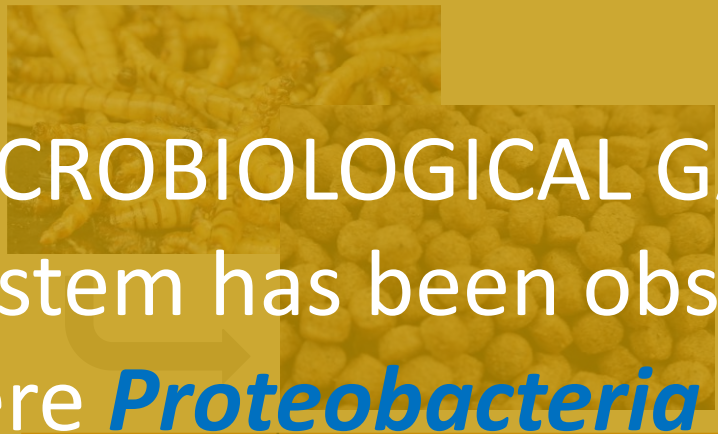
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WATER AND GUT MICROBIOTA  
AS MARKER OF  
ENVIRONMENTAL CONDITIONS  
AND NUTRITIONAL WELFARE

# - WATER MICROBIOLOGICAL GARDEN

A peculiar microbial ecosystem has been observed characterizing the farming systems, where *Proteobacteria* and *Bacteroidetes* were the main colonizing phyla, indicating different risks for bacterial diseases;

- No significant differences were observed among water samples collected within different formulation tests, but among samples collected at different time, indicating a continuous evolution of the water microbiota.



Tank Name	Feed Formulation
INS A	Substitution of fish meal with insect 0%
INS B	Substitution of fish meal with insect 50%
INS C	Substitution of fish meal with insect 75%
INS D	Substitution of fish meal with insect 100%
INS E	Substitution plant oil with insect oil 33%
INS F	Substitution plant oil with insect oil 66%

## Growth performances

	Hi 0	Hi 10	Hi 20	Hi 30
$BW_i$ (g)	67.01 ± 1.71	66.38 ± 2.51	65.63 ± 0.42	66.95 ± 2.31
$BW_f$ (g)	223.20 ± 23.67	220.34 ± 29.60	216.97 ± 26.16	221.74 ± 22.25
WG (g)	156.86 ± 4.33	154.20 ± 6.04	146.89 ± 8.03	152.30 ± 10.18
SGR	1.42 ± 0.01	1.40 ± 0.06	1.38 ± 0.04	1.38 ± 0.04
FCR	0.90 ± 0.02	0.93 ± 0.04	0.95 ± 0.03	0.93 ± 0.04

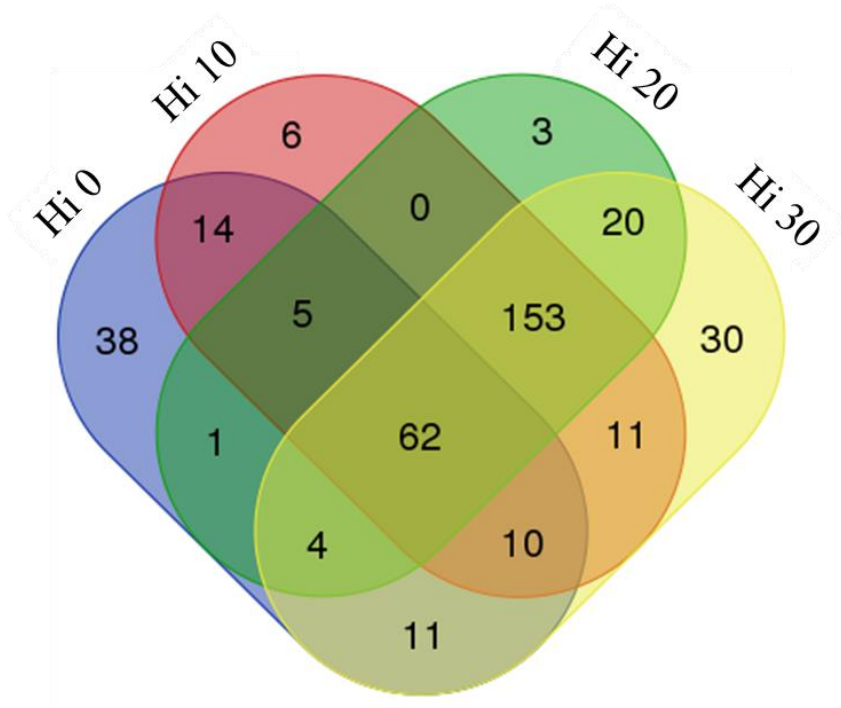
*BW<sub>i</sub>* initial body weight, *BW<sub>f</sub>* final body weight, *WG* weight gain, *SGR* specific growth rate, *FCR* feed conversion ratio

All fish had tripled their initial body weight, and growth performance parameters (WG and SGR) likewise FCR were not negatively affected by the diet composition.



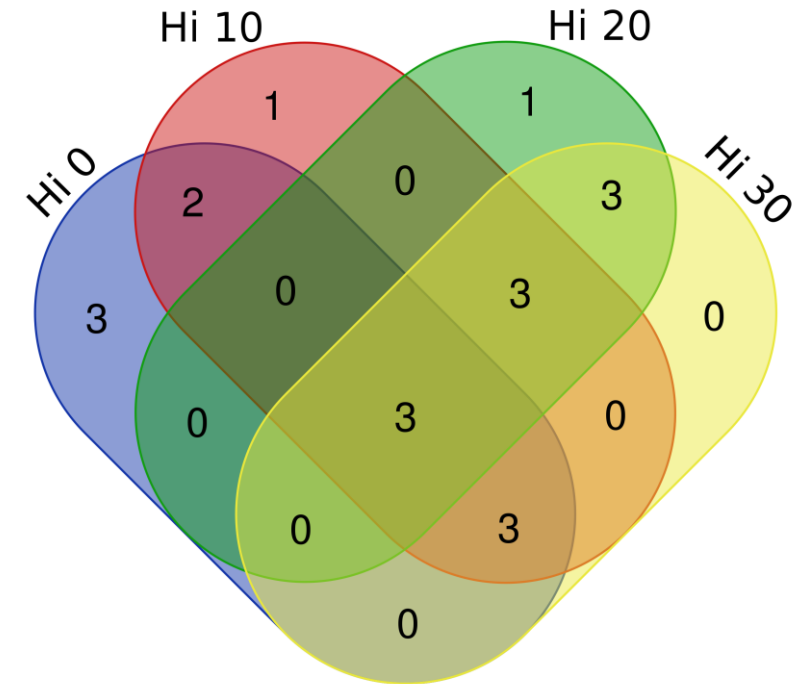
# Analysis of gut microbiota structure

## FECES



The “core microbiota” was constituted by 62 OTUs (shared by 80% of samples), **23 OTUs** were common to 100% of samples with a dominance of bacteria assigned to *Firmicutes* phylum.

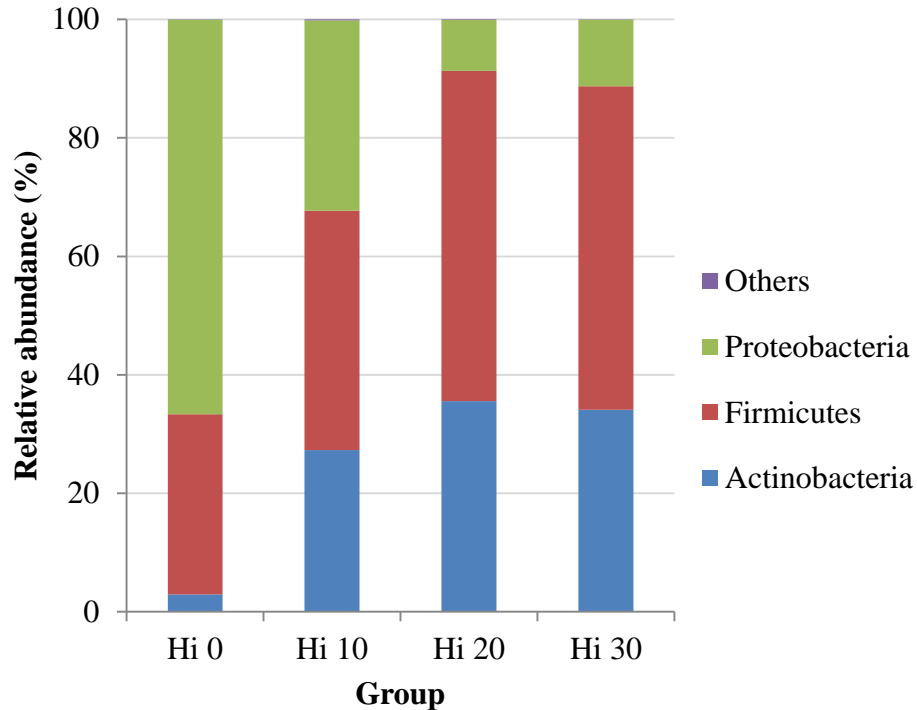
## MUCOSA



The “core microbiota” was constituted by only **3 OTUs** assigned to *Propiobacterinae*, *Shewanella*, and *Mycoplasma* genera.

# Effects of *H. illucens* supplemented diets on intestinal microbial communities

The whole microbial community profile of fecal samples was mainly comprised of 7 phyla, 12 classes, 26 orders, 68 families, 98 genera, and 55 species

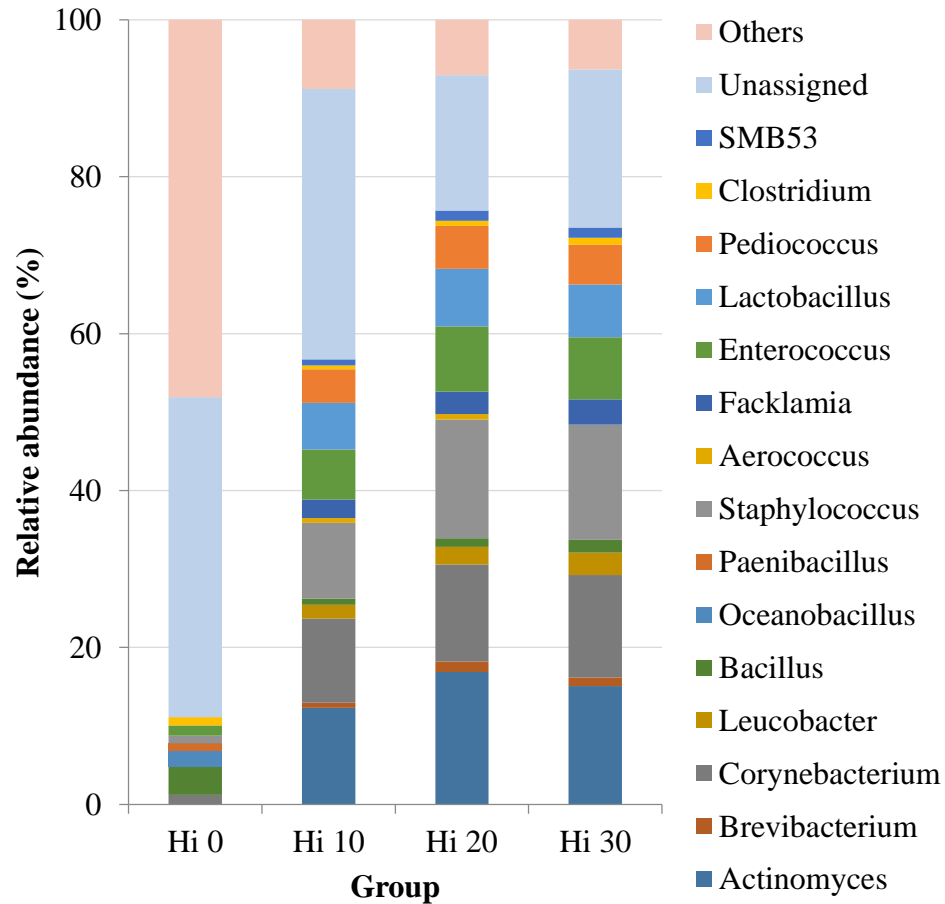


## At phylum level

The amounts of *Actinobacteria* and *Proteobacteria* were significantly influenced ( $p < 0.05$ ) by including insect meal in the diet



	Hi 0	Hi 10	Hi 20	Hi 30
<b>Phylum</b>				
<i>Actinobacteria</i>	2.94 ± 1.16 <sup>b</sup>	27.30 ± 3.31 <sup>a</sup>	35.56 ± 1.37 <sup>a</sup>	34.08 ± 3.58 <sup>a</sup>
<i>Firmicutes</i>	30.39 ± 9.76	40.38 ± 4.79	55.77 ± 1.55	54.66 ± 4.32
<i>Proteobacteria</i>	66.62 ± 9.43 <sup>a</sup>	32.16 ± 7.59 <sup>a</sup>	8.59 ± 2.13 <sup>b</sup>	11.21 ± 7.77 <sup>b</sup>



## At genus level

Genus	Hi 0	Hi 10	Hi 20	Hi 30
<i>Actinomyces</i>	0.25 ± 0.07 <sup>b</sup>	12.29 ± 1.30 <sup>a</sup>	16.86 ± 0.44 <sup>a</sup>	15.08 ± 1.51 <sup>a</sup>
<i>Brevibacterium</i>	0.10 ± 0.03 <sup>b</sup>	0.65 ± 0.04 <sup>ab</sup>	1.38 ± 0.16 <sup>a</sup>	1.12 ± 0.32 <sup>a</sup>
<i>Corynebacterium</i>	1.23 ± 0.42 <sup>b</sup>	10.74 ± 1.78 <sup>a</sup>	12.33 ± 0.94 <sup>a</sup>	13.04 ± 1.40 <sup>a</sup>
<i>Leucobacter</i>	0.14 ± 0.08 <sup>b</sup>	1.76 ± 0.16 <sup>a</sup>	2.27 ± 0.25 <sup>a</sup>	2.83 ± 0.48 <sup>a</sup>
<i>Bacillus</i>	3.60 ± 2.00	0.76 ± 0.07	1.10 ± 0.18	1.66 ± 0.75
<i>Oceanobacillus</i>	1.96 ± 0.75 <sup>a</sup>	0.24 ± 0.04 <sup>ab</sup>	0.19 ± 0.03 <sup>ab</sup>	0.10 ± 0.01 <sup>b</sup>
<i>Paenibacillus</i>	0.99 ± 0.52	0.12 ± 0.03	0.23 ± 0.05	0.27 ± 0.06
<i>Staphylococcus</i>	0.97 ± 0.34 <sup>b</sup>	9.69 ± 1.54 <sup>a</sup>	15.13 ± 1.11 <sup>a</sup>	14.66 ± 1.89 <sup>a</sup>
<i>Aerococcus</i>	n. d. <sup>b</sup>	0.61 ± 0.13 <sup>a</sup>	0.68 ± 0.04 <sup>a</sup>	0.42 ± 0.07 <sup>a</sup>
<i>Facklamia</i>	0.07 ± 0.02 <sup>b</sup>	2.34 ± 0.46 <sup>a</sup>	2.84 ± 0.20 <sup>a</sup>	3.22 ± 0.57 <sup>a</sup>
<i>Enterococcus</i>	1.32 ± 0.48 <sup>b</sup>	6.36 ± 0.77 <sup>a</sup>	8.35 ± 0.27 <sup>a</sup>	7.93 ± 0.87 <sup>a</sup>
<i>Lactobacillus</i>	0.32 ± 0.08 <sup>b</sup>	5.98 ± 1.00 <sup>a</sup>	7.33 ± 0.59 <sup>a</sup>	6.75 ± 0.43 <sup>a</sup>
<i>Pediococcus</i>	0.23 ± 0.14 <sup>b</sup>	4.28 ± 0.68 <sup>a</sup>	5.45 ± 0.29 <sup>a</sup>	5.03 ± 0.53 <sup>a</sup>
<i>Clostridium</i>	1.05 ± 0.43	0.49 ± 0.18	0.66 ± 0.18	0.89 ± 0.49
<i>SMB53</i>	0.04 ± 0.02 <sup>b</sup>	0.77 ± 0.12 <sup>ab</sup>	1.30 ± 0.23 <sup>a</sup>	1.32 ± 0.11 <sup>a</sup>

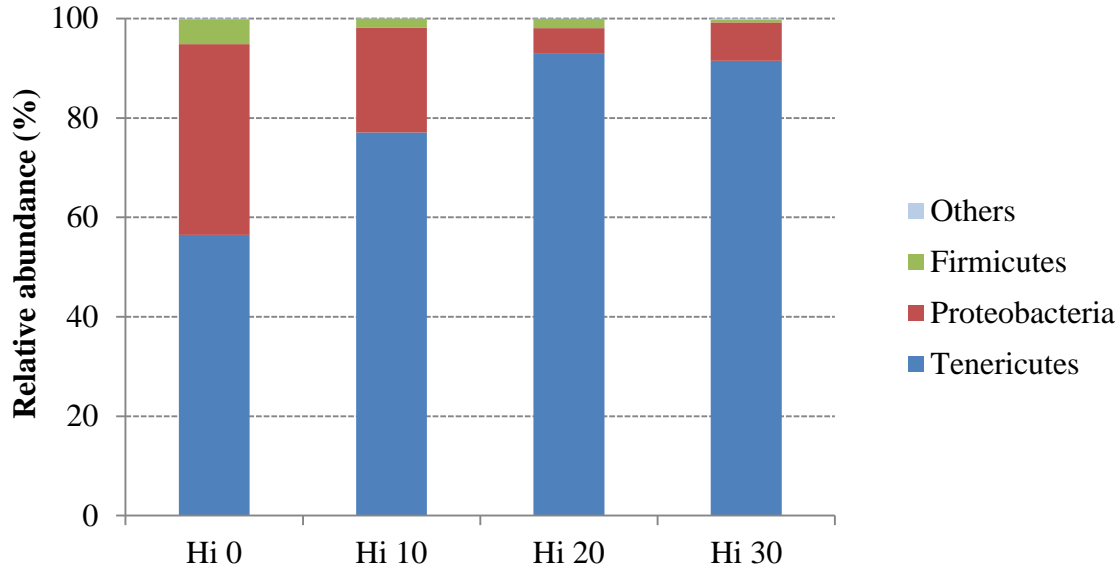


*Actinomyces*, *Brevibacterium*, *Corynebacterium*,  
*Leucobacter*, and *Staphylococcus*  
**LAB: *Aerococcus*, *Facklamia*, *Enterococcus*,  
*Lactobacillus*, and *Pediococcus***

Beneficial bacterial species positively correlated to insect-meal diets:  
*Corynebacterium variabile*, *Lactobacillus paraplantarum*, *Lactobacillus zae*,  
*Weisella cibaria*, *Clostridium butyricum*, and *Clostridium fimentarium*

# Dietary modulation of autochthonous intestinal microbiota

The bacterial OTUs found in fish mucosa samples were mainly comprised of 6 phyla, 7 classes, 10 orders, 15 families, and 22 genera



## At phylum level

*Tenericutes* and *Proteobacteria* were significantly influenced by insect meal inclusion (20% and 30%) in the diet.



Phylum	Hi 0	Hi 10	Hi 20	Hi 30
<i>Tenericutes</i>	56.48 ± 21.74 <sup>b</sup>	77.06 ± 17.44 <sup>ab</sup>	93.03 ± 10.12 <sup>a</sup>	91.52 ± 12.68 <sup>a</sup>
<i>Proteobacteria</i>	38.36 ± 18.26 <sup>a</sup>	21.07 ± 16.85 <sup>ab</sup>	5.03 ± 7.51 <sup>b</sup>	7.69 ± 12.82 <sup>b</sup>
<i>Firmicutes</i>	5.05 ± 8.37	1.84 ± 4.00	1.86 ± 4.34	0.49 ± 0.96

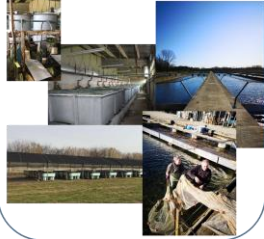
# Insect meal: not only growth but beneficial effects on the microbiota garden

- ✓ Insect meal was well accepted by fish up to 30% inclusion.
- ✓ Our results confirmed that bacterial communities adhering to mucosa differ from transient microflora in fish intestine: *Proteobacteria* and *Firmicutes* dominated the allochthonous gut microbiota while *Tenericutes* and *Proteobacteria* phyla harboured trout intestinal mucosa.
- ✓ Dietary Hi meal positively modulated gut microbiota (autochthonous and allochthonous) increasing its richness and diversity: effect of chitin and lauric acid (C12:0) contained in Hi prepupae.
- ✓ OTUs attributable to LAB (beneficial genera) were only found in high amount in the gut content samples of trout fed insect meal, but were practically absent in gut mucosa of the same fish. *The increasing number of LAB could be promoted by chitin, which acts as a prebiotic.*
- ✓ An increased number of bacteria belonging to *Mycoplasma* genus was found in the mucosa of trout fed Hi 20 and Hi 30 diets. They are obligate commensal microorganisms of the gut ecosystem that produce lactic acid and acetic acid as their major metabolites. *Mycoplasma could have a beneficial action on host health.*
- ✓ Hi meal caused a significant reduction of *Proteobacteria* (*Gammaproteobacteria*) both in the gut digesta and mucosa. *Interestingly all genera adversely affected by insect-meal diets were Gram-negative bacteria that include potential pathogen species.*

### Alternatives to Fish meal

Insect meal + poultry by products

- digestibility of protein meals
- performance: pilot scale
- large-scale trial **on going**



# Rainbow trout on-farm trial feeding "AGER 4F Feeds"

3 diets (4 replicates)

- 1) Contr Commercial feed (Plant based)
- 2) PBP (Poultry meal based feed)
- 3) HI (Insect meal based feed)

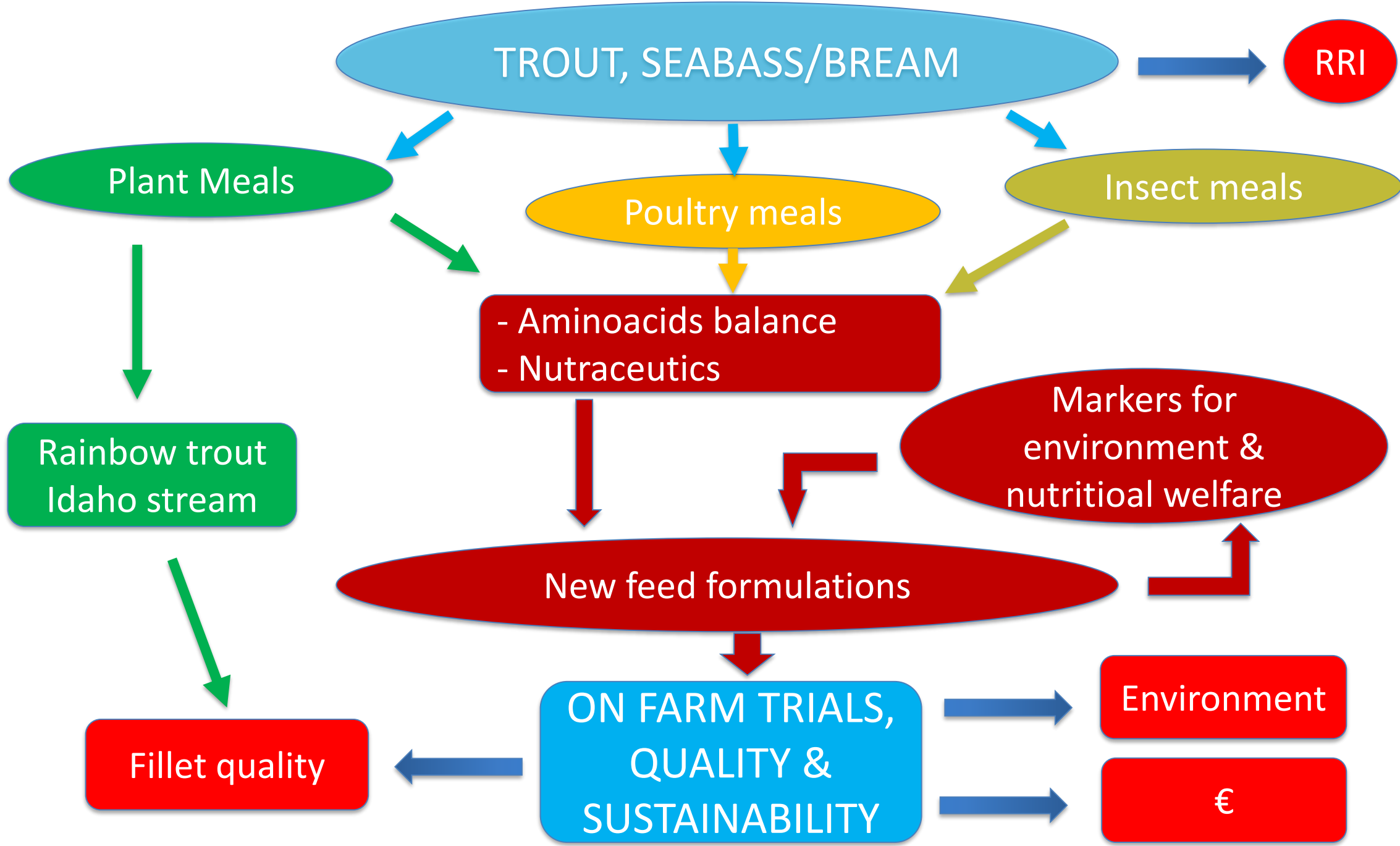


	CTRL	PBP	HI
PI (kg)	50,20	50,25	50,13
Peso al 3/02/2020 (kg)	77,05	77,01	76,27





A challenging on-farm trial,  
feeding Sea bream with  
Zero FM, will start next  
month





A large, horizontally-oriented red oval with a thin white border, centered on a white background. Inside the oval, the text "DISSEMINATION AND RESPONSIBLE RESEARCH & INNOVATION (RRI)" is written in white, uppercase, sans-serif font, centered both horizontally and vertically.

DISSEMINATION AND  
RESPONSIBLE RESEARCH &  
INNOVATION (RRI)

# Acquacoltura & Sostenibilità

Comunicazione e disseminazione dei risultati a cura di Consorzio Italbiotec



L'attività di comunicazione condotta dal progetto 4F – FineFeedForFish mira alla diffusione di nuove buone pratiche e soluzioni ecosostenibili al comparto ittico e ad incrementare la consapevolezza dei cittadini circa il contributo dell'acquacoltura nell'affrontare la sfida al cambiamento climatico. Fin dall'avvio del progetto, 4F si è impegnato nella progettazione e sviluppo di prodotti di comunicazione in grado di coinvolgere gli stakeholder, qui di seguito si riportano i più significativi:

- 35 articoli di divulgazione pubblicati sul sito AGER e condivisi su testate online **+ 16.000 lettori raggiunti**
- 14 articoli scientifici pubblicati su riviste peer review
- 1 servizio televisivo su rete nazionale
- 28 presentazioni orali dei risultati scientifici presso congressi nazionali ed internazionali
- 12 video divulgativi dedicati alla valorizzazione degli obiettivi e delle strategie **+500 visualizzazioni**
- 1 Corso e-learning (8 video lezioni) dedicato all'acquacoltura sostenibile e al benessere animale
- 1 Summer School «Acquacoltura & Sostenibilità» con **30 studenti, ricercatori e professionisti**
- 1 pubblicazione «ACQUACOLTURA E COMUNICAZIONE: strumenti e metodi di debunking»
- Poster, roll-ups, leaflets prodotti e distribuiti in forma digitale e cartacea **+ 2500 lettori raggiunti**
- 1 Community online «Acquacoltura& Sostenibilità» **+ 250 utenti attivi**



ACQUACOLTURA E COMUNICAZIONE:  
strumenti e metodi di debunking

Acquacoltura Summer School 2019 – Alghero





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<sup>1</sup>University of Bologna, <sup>2</sup>University of S

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ALMA MATER STUD  
IL PRESENTE MATERIALE È RISERVATO AL PERSONALE DELL'UNIVERSITÀ DI BOLOGNA E NON PUÒ ESSERE UTILIZZATO AI TERMI

Peer

# Effect of a specific composition of short- and medium-chain fatty acid 1-

Rev Fish Biol Fisheries  
<https://doi.org/10.1007/s11160-019-09558-y>



ORIGINAL RESEARCH

Rainbow  
modulate  
in the die

Genciana Terova  
Chiara Ceccotti

Received: 5 Octob  
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animals



Article

## The Effects of *Illucens* Prebiotics on the Growth and Health of Rainbow Trout (*Oncorhynchus mykiss*)

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Article

## A First Attempt to Produce Proteins from Insects by Means of a Circular Economy

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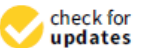
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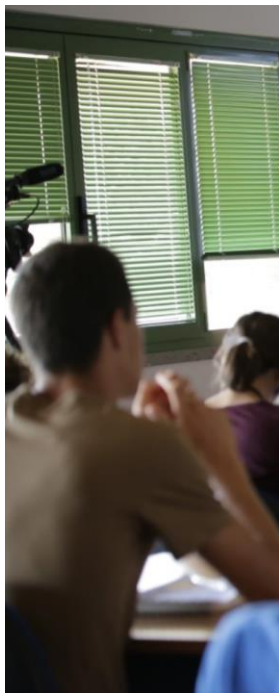
## Protective Effect of Dietary Taurine from ROS Production in European Seabass under Conditions of Forced Swimming

Chiara Ceccotti <sup>1</sup>, Basim S.A. Al-Sulaivany <sup>2</sup>, Omar A.M. Al-Habbib <sup>3</sup>, Marco Saroglia <sup>1</sup>, Simona Rimoldi <sup>1</sup> and Genciana Terova <sup>1,\*</sup>

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