Sea-derived microalgae leads to healthier red meat and reduced methane emissions

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Ruminant Sector Challenges



Rumen Microbiome Central to the Challenges



 Bacteria
 Protozoa

 10⁹-10¹⁰/mL
 10⁴-10⁶/mL

Fungi 10³-10⁴/mL Archaea (methanogens) Approx. 10⁴/mL

Huws et al. 2018. Addressing Global Ruminant Agricultural Challenges Through Understanding the Rumen Microbiome: Past, Present, and Future. Frontiers in Microbiology. 9:2161. doi: 10.3389/fmicb.2018.02161.

The rumen microbiome in action



Rumen fermentation

- Cellulose/hemicellulose to Volatile fatty acids: Energy source but source of released H.
- Volatile fatty acids:

Acetate, lactate, butyrate, succinate, propionate

• Hydrogen sinks:

Pyruvate to lactate: utilizes 2H Lactate to propionate: utilizes 2H Acetyl-CoA to butyrate : utilizes 2H



Source: Ungerfeld EM. Metabolic Hydrogen Flows in Rumen Fermentation: Principles and Possibilities of Interventions. Frontiers in Microbiology.11:589. doi: 10.3389/fmicb.2020.00589.

Food Security



FAO predict meat and dairy production will have to increase by 76% and 63% respectively by 2050

Methane and Productivity

Data has shown that ruminants which release less methane are more productive.

Some dietary interventions to reduce methane may increase productivity.



Ruminants and Methane

- FAO state that livestock agriculture responsible for approx. 18% of GHG emissions, mainly in the form of methane.
- Paris agreement: Limit global warming to less than 2%. A 45% reduction in methane emissions could reduce global warming by 0.3°C.
- Recent US-EU climate pledge to reduce methane emissions by 30% by 2030.



Cross-Sectorial GHG emissions

- Fossil fuel industry are the greatest producers of CO₂ which remains in the atmosphere for over 100 years.
- Livestock mainly produce methane which has a half life of less than 10 years.
- Irrespective need to decrease environmental impact of livestock by 2050.



Lynch et al. Environ Res Lett. 15(4):044023.doi: 10.1088/1748-9326/ab6d7e.



<u>THE MASTER PLAN:</u> <u>Microbiome Applications for</u> <u>Sustainable food systems through</u> <u>Technologies and EnteRprise</u>

Project Co-ordinator: Prof Paul Cotter, Teagasc, Ireland





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ABInBev



Microbiome Applications for Sustainable Food Systems through Technologies and EnteRprise

MASTER takes a global approach to the development of microbiome products, foods/feeds, services or processes with high commercial potential.

This will benefit society through improving the quantity, quality and safety of food across multiple food chains. These include marine, plant, soil, rumen, meat, brewing, fruit and vegetable waste, and fermented foods.







Rumen microbiome

WP3: Rumen Microbiome – Improving animal production and reducing environmental impact through manipulation of the rumen microbiome Lead QUB (Huws), Co-Lead CSIC (Yanez-Ruiz), partners Teagasc, LUKE, INRA, Devenish, ICBF, AFBI, .

Objective:

- Utilise host genomics to alter the rumen microbiome and animal phenotype.
- Define the rumen microbiome (different life stages) to improve efficiency, reduce greenhouse gases emissions & improve the fatty acid content of meat and milk.
- Develop microbiome-based tools to predict animal phenotype.



Integrated microbiome technologies

WP5: Integrated Microbiome Technologies for the Food Chain Lead UNITN (Segata), Co-lead QUB (Creevey), partners WU, Teagasc, UCC, 4DC, ULE, ONT, FFOQSI, Novolyse, Qiagen, Baseclear, Danone in close interaction with WPs 1, 2, 3, 4 and 6

WP5 will provide the technological, computational, and analytical tools to (i) support the other WPs, (ii) establish standardized tools and procedures for companies in the food chain, (iii) meta-analyse the produced data, and (iv) build user- and company-friendly resources to support all the microbial tasks associated with the food chain.





WP5: Integrated Microbiome Technologies for for the Food Chain





WP3: Objectives

3.1: Utilise <u>host genomics</u> to beneficially alter the rumen microbiome and consequently animal phenotype.

3.2: Employ <u>novel feeding technologies</u> to define the rumen microbiome at different <u>stages of life</u> to improve efficiency, reduce greenhouse gas emissions and improve the fatty acid content of meat and milk.

3.3: Develop microbiome-based tools and mathematical models to predict animal phenotype.

This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 818368 🕳

3.2: Dietary manipulations of the rumen microbiome for improved animal phenotype.

3.2.1: Feed technologies in adult animals2) Microalgae (link to WP 2)

50:50 isoenergetic diet (grass silage:concentrate)

Microalgae supplementation

Medium

2.4% supplementary microalgae (6g DHA)

High

3.6% supplementary microalgae (9g DHA)

Low

1.2% supplementary microalgae (3g DHA)

Control

0% supplementary microalgae (0g DHA)

56/24 Finishing Texel X Scottish black face lambs

33 days



56 animals

- 24 Chambers trial
- 32 Feed trial

Before and after samples

- Methane
- Oral swab
- Blood
- Ruminal liquid
- Urine (digestibility)
- Faeces (digestibility/ microbiome)

Slaughter samples

- Ruminal liquid
- Small intestine
- Large intestine
- Cecum
- Meat (2 and 7 days): loins, shoulder, legs





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improved animal phenotype.

3.2: Dietary manipulations of the rumen microbiome for











Animal Performance, digestibility and methane emission

- The DMI tended to decrease (P=0.078) in High treatment compared to the other diets (n=24).
- Digestibility of DM, OM, NDF, ADF and Energy were greater (P≤0.030) in Low and High treatment than in Control and Medium treatment, while N digestibility and retention were similar (P≥0.325) between treatments (n=24).









Animal Performance, digestibility and methane emission

- No differences (P≥0.453) between <u>Control</u> and <u>Microalgae-fed lambs</u> were observed for initial body weight (BW) (n=56). Differences in BW were seen at different time points (see arrows below)
- The average daily gain (ADG) was greater (P=0.020), and the relative growth tended (P=0.068) to be greater in Low than in Medium treatment (n=56).





Animal Performance, digestibility and methane emission

Indirect open-circuit respiration calorimeter chambers



- Ruminal pH was lower (P=0.024) in <u>Medium</u> and <u>High treatment</u> than in Low treatment.
- Total VFA concentration was greater (P=0.012) in <u>High</u> than in <u>Control</u> and <u>Low treatment</u>.
- Methane emissions and methane/DMI were similar (P≥0.143) between treatments, however an approx. 8% reduction was seen with <u>High</u> <u>treatment</u>.





Animal Performance, digestibility and methane emission

Indirect open-circuit respiration calorimeter chambers



- <u>Tendency for acetate to be lower in lambs fed medium and high</u> levels of microalgae.
- Whilst not significant <u>modest increases in propionate</u> were also seen in lambs fed medium and high levels of microalgae.







 DHA concentration increased in the loins as the microalgae content on the lamb's diet increased (P<0.05).







Meat quality and consumption

Microbiology testing (food standards):

ALS: Presumptive Coliforms; Escherichia coli; Thermotolerant *Campylobacter*; Aerobic colony count; ß-Glucuronidase + *E. coli*; Salmonella; Listeria spp.

Fatty acid concentration increased during the cooking (water loss of 37.8%)



Home-sensorial trial in course



Raw and cooked fatty acid of legs and shoulder patties (50:50%)















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*P < 0.05



Animal microbiome and ruminal fermentation

Shotgun metagenomic sequencing





Illumina Nova seq 6000 S4 300 flow cell (150bp PEat ~>6.2GB/ sample).

- The average number of reads per sample after quality control was 23,553,087
- A total of 4712 metagenome associated genomes (MAGs) were extracted and characterized, functionally and taxonomically with an average number of 1,955 ORFs and average N50 metric was 23,937.

Abundance percentages across samples of the most abundant genera





Animal microbiome and ruminal fermentation



No differences seen in Archaea







Animal microbiome and ruminal fermentation



No differences seen in Archaea







CAZyme abundances



Higher abundances of many of these enzymes families when lambs fed medium levels of microalgae







Higher abundances of some of these enzymes families when lambs fed high levels of microalgae



3.2.1: Feed technologies in adult animals2) Microalgae oil (link to WP 2)





Conclusion



- Feeding freeze-dried microalgae at low, medium and high levels had no detrimental affect of animal health.
- Feeding freeze-dried microalgae at low, medium and high levels **significantly increased DHA content of meat and burgers** (pre and post cooking) with a small reduction in methane emissions (8%) seen following feeding on 4.5g/day of the microalgae (High)- **human health benefits**.
- **Modest reductions seen in methane emissions** (8%) likely due to changes in the bacterial fraction leading to the tendencies towards beneficial volatile fatty acid changes.
- No major effects on animal productivity.
- Gastrointestinal tract microbiome analysis ongoing with initial interesting data.
- Microalgae oil experiments ongoing.

Ruminant Sector Challenges

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The MASTER Consortium







Thank you



