The holoruminant concept applied to greenhouse gas mitigation

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The hologenome concept

"Host genome and microbiome are one evolutionary unit"
Roughgarden et al. 2018

Host genome



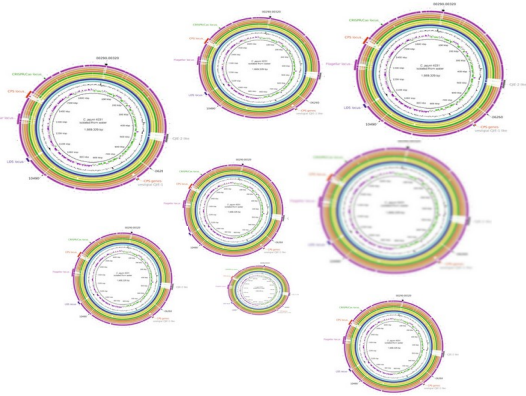
Metabolites

ncRNAs

Proteins

miRNAs

Microbiome

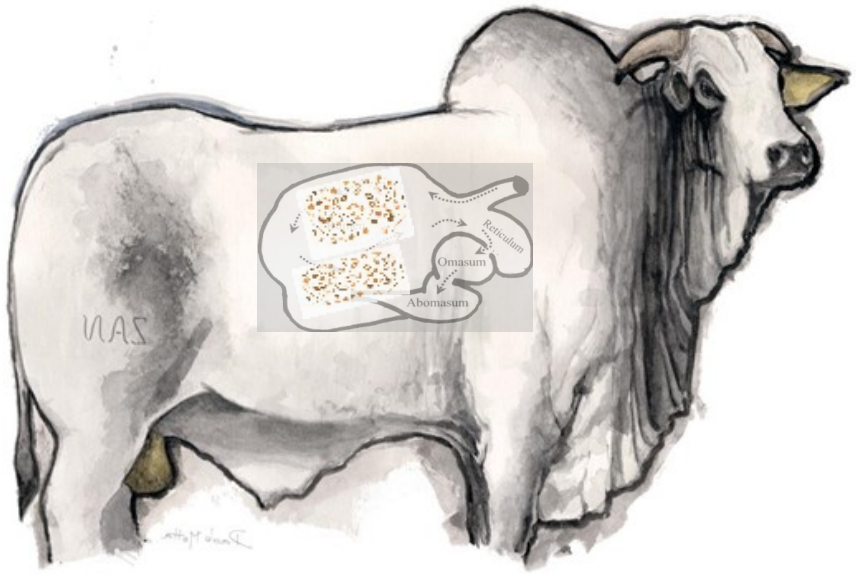


Mutual regulation

The Hologenome Concept - Ruminants

Digestion of complex polysaccharides (celulose, hemi-celulose…)

M.O. fermentation



Fatty acids

70% of metabolized energy

Feed efficiency

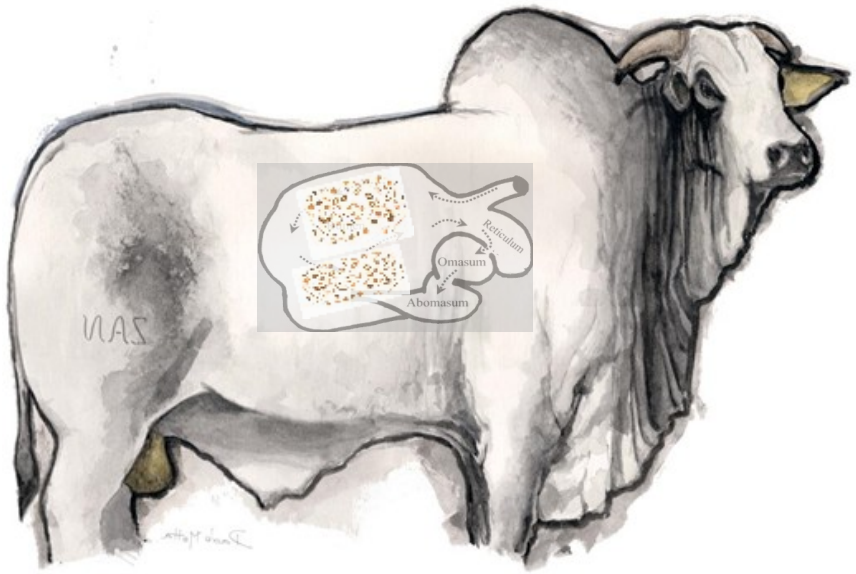
The Hologenome Concept - Ruminants

Digestion of complex polysaccharides (celulose, hemi-celulose…)

M.O. fermentation

Fatty acids

70% of metabolized energy



Feed efficiency

Methane

Digestion of complex polysaccharides (celulose, hemi-celulose…)

M.O. fermentation

$2H + CO_2 = CH_4$

2-12% feed energy loss

CH_4 traps ~ 120 times as much heat as CO_2[1]

[1] https://climate.mit.edu/ask-mit/what-makes-methane-more-potent-greenhouse-gas-carbon-dioxide



“Water footprint” Project

Julio Palhares



Regular Diet
N=26



By-products
N=26

Growth

Beef production

Feed efficiency

Methane emission

Water footprint

The Nelore Hologenome Project

Ruminal content

Feces

Ruminal wall

Liver

Muscle

Metagenome

Metatranscriptome

Metabolites

RNAseq/miRNAseq

Proteomics

FAPESPWeek NETHERLANDS
OCT 27-29, 2026



Liliane Conteville

Microbial abundance *vs* Sustainability traits

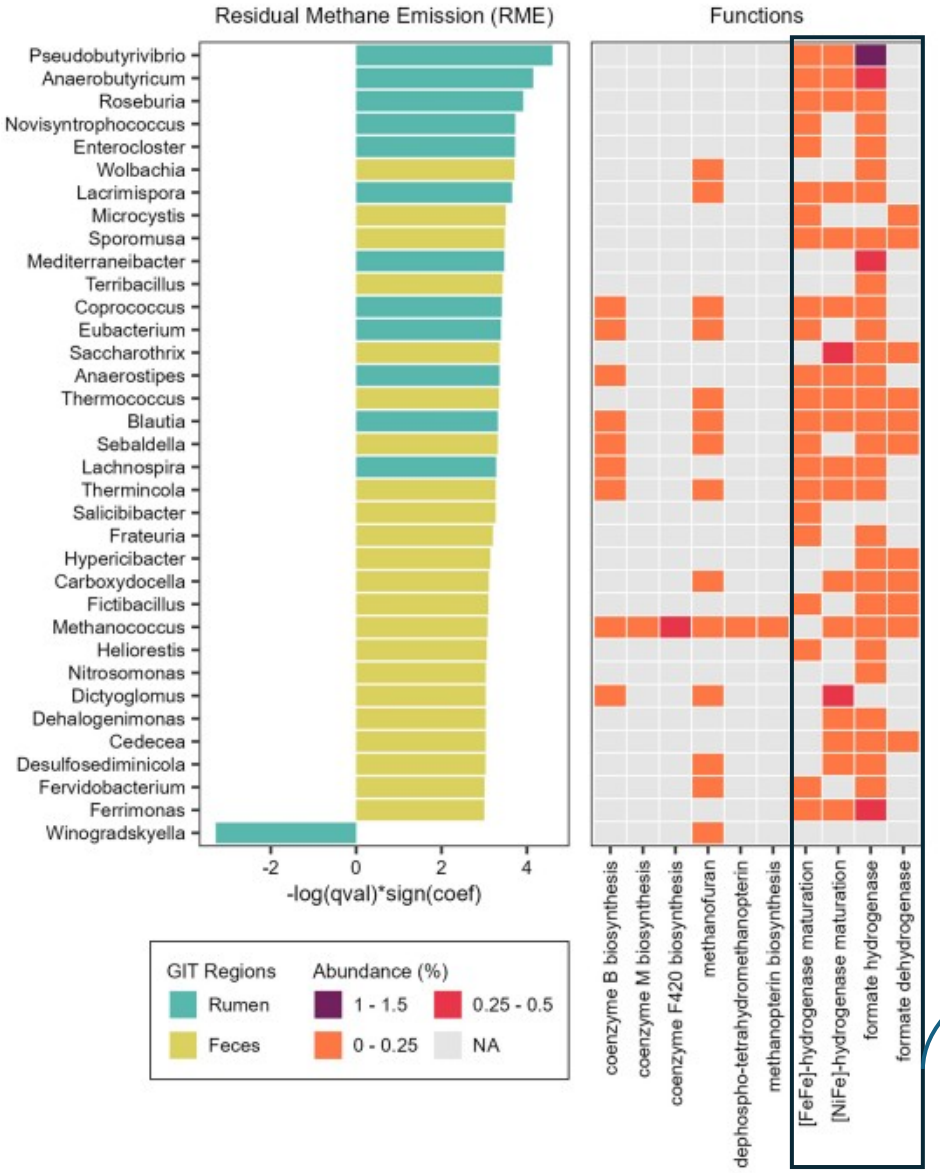
ORIGINAL RESEARCH article

Front. Microbiol., 14 December 2023

Sec. Systems Microbiology

Volume 14 - 2023 | https://doi.org/10.3389/fmicb.2023.1282851

Rumen and fecal microbiomes are related to diet and production traits in *Bos indicus* beef cattle



$2H + CO_2 = CH_4$

CO_2 H_2

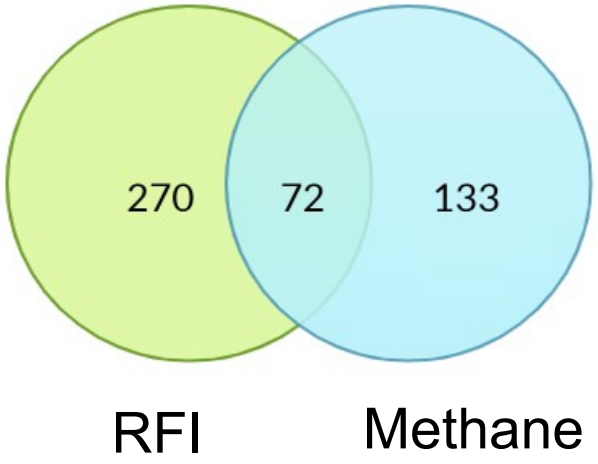
Formate

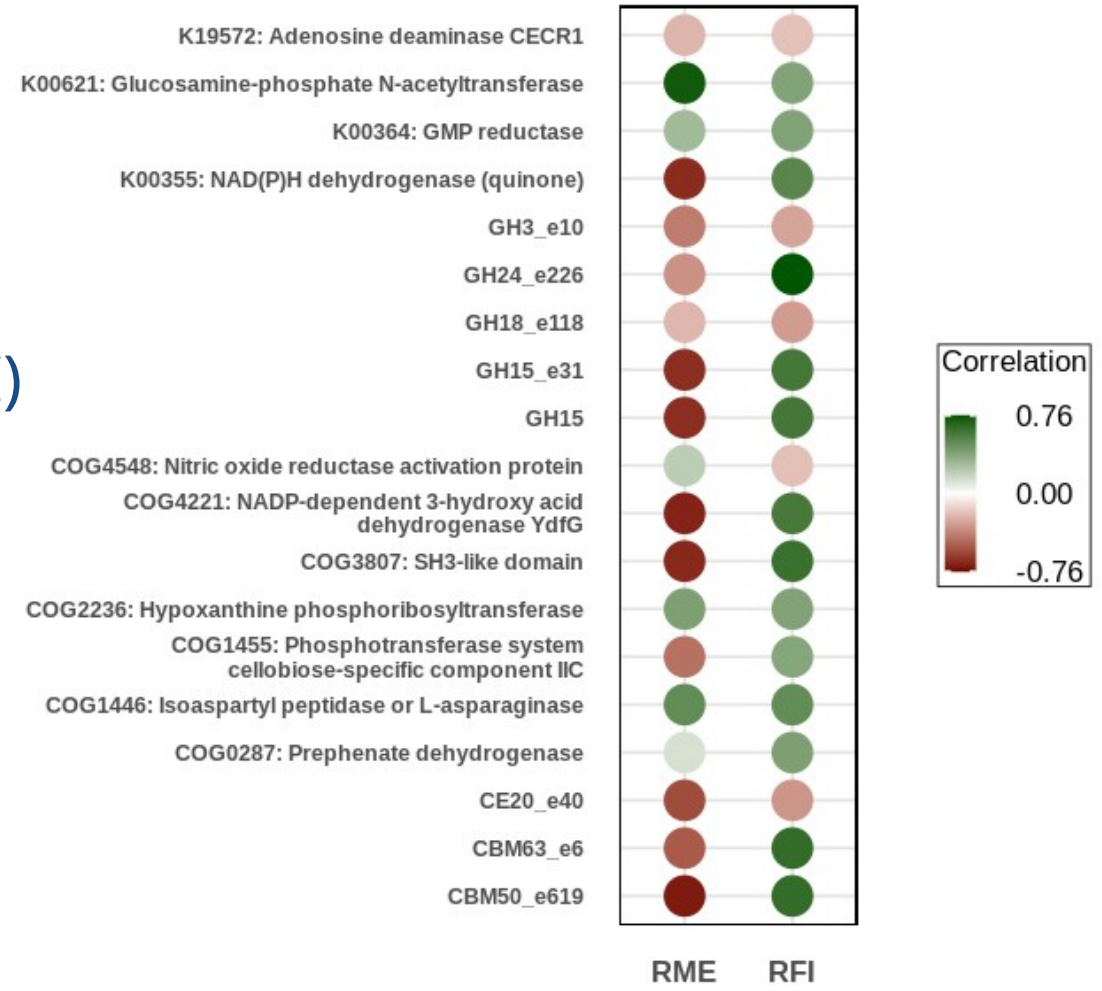
doi: 10.3389/fmicb.2023.1282851

Catalog of active genes in the Nelore ruminal microbiome: Association with phenotypes

624,925 Active genes

475 Methane or Feed Efficiency (RFI)







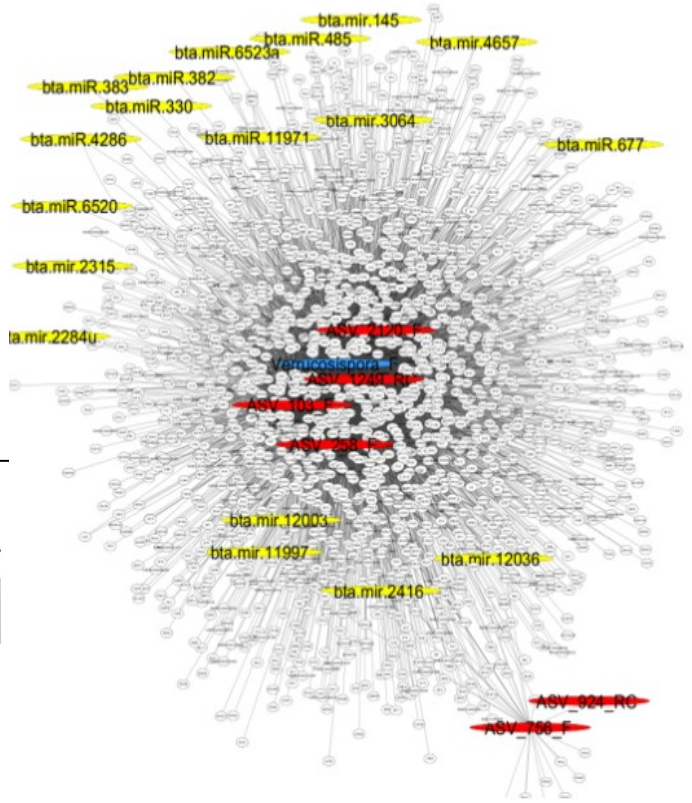
Juliana Virginio

Submitted to Sci. Reports



Tainã F. Cardoso

Multiomics integration





Mammalian Genome (2025) 36:1153–1172
https://doi.org/10.1007/s00335-025-10160-w

Exploring genome, transcriptome, and microbiome interactions related to feed efficiency and methane emissions in *Bos indicus* through multi-omics network analysis

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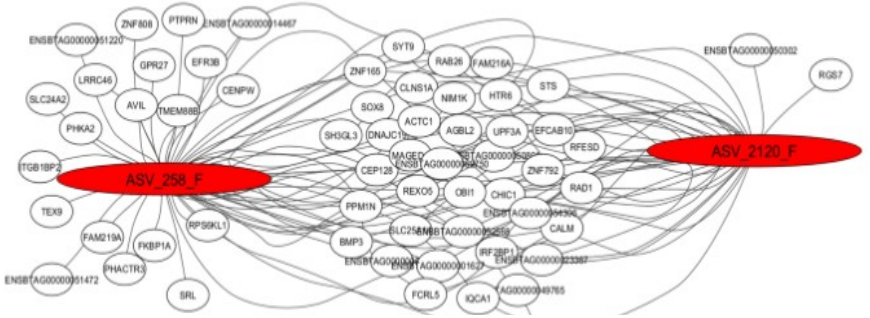
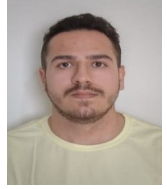


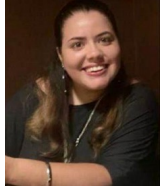
ASVs

miRNA

mRNA

Network relationships between the different omics within the top epistatic SNP-SNP modules associated with RFI


Wanderson Anjos


Bárbara Padilha

Would the microbiome of young grazing animals be related to RFI measured later in the feedlot?

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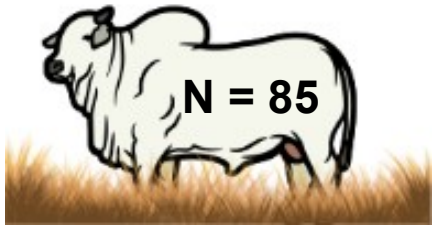
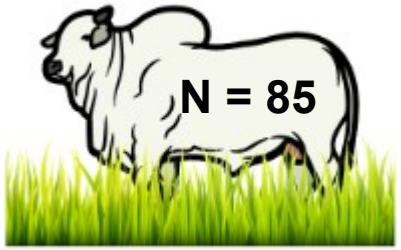
Age at sampling

320 days



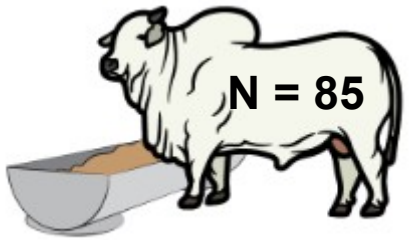
Post-weaning
Dry season

460 days



Growth
Rainy season

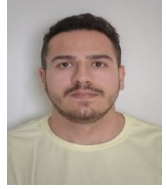
580 days



High grain feedlot

ABCZ

CNPq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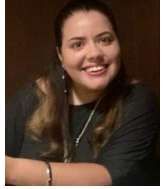
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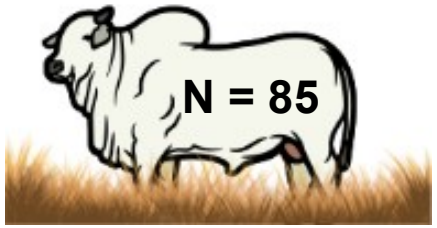
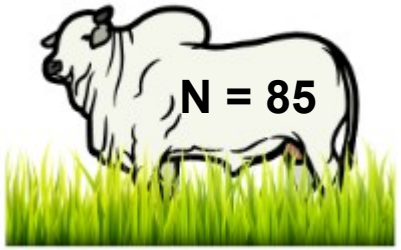


Post-weaning
Dry season

30 MOs

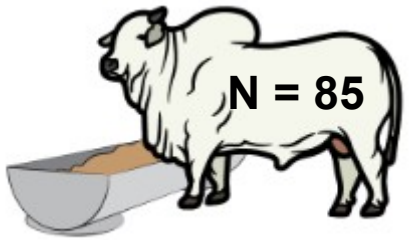
460 days



Growth
Rainy season

18 MOs

580 days



High grain feedlot

14 MOs

62 MOs associated with Feed Efficiency measured in feedlot

ABCZ

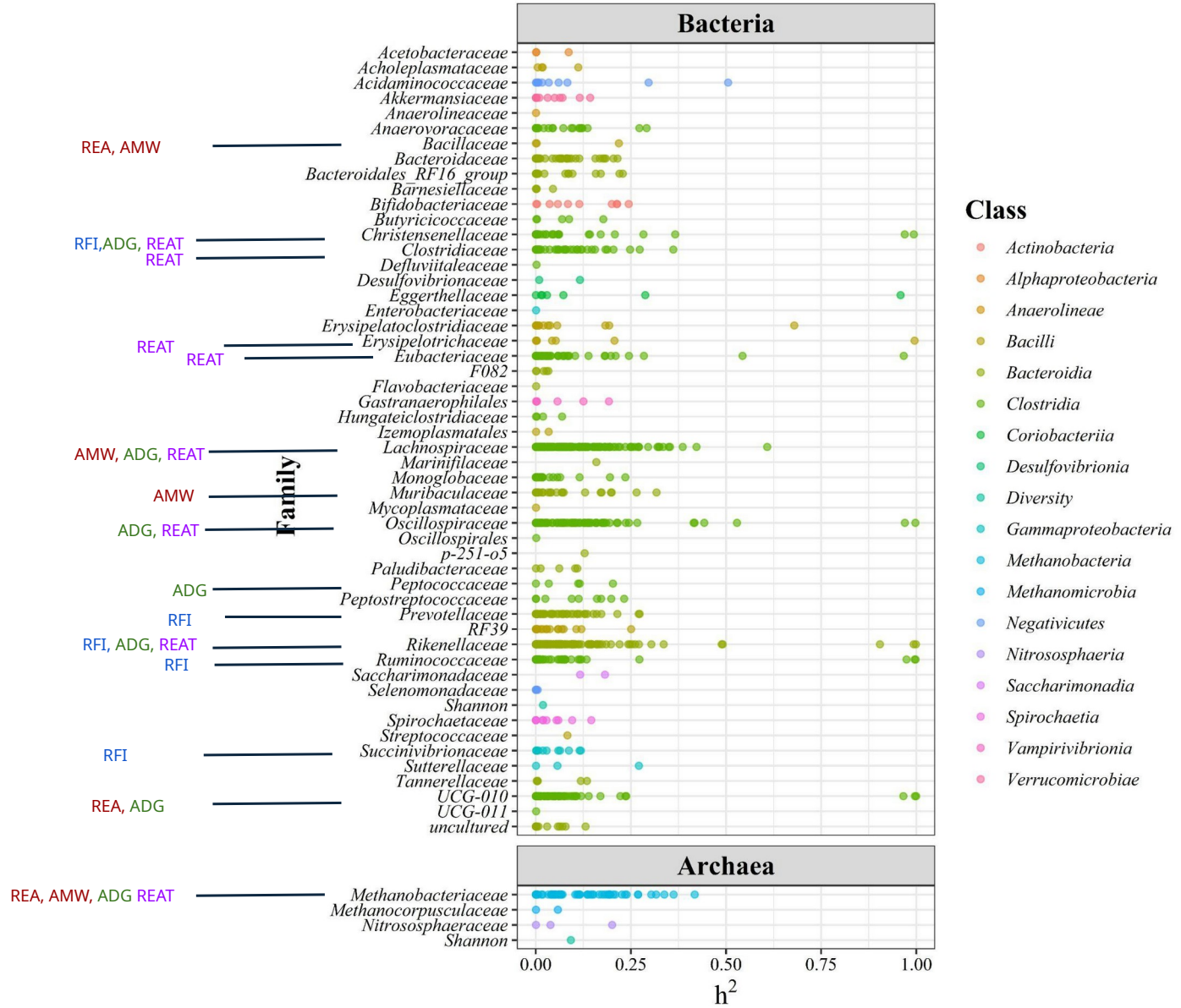
CNPq

Trait-associated MOs are inheritable



430 Fecal samples

Phenotypes:
REA: Rib Eye Area
AMW: Average Metabolic Weight
RFI: Residual Feed Intake
ADG: Average Daily Gain
REAT: Reactivity



Submitted to J. Integrative Biology

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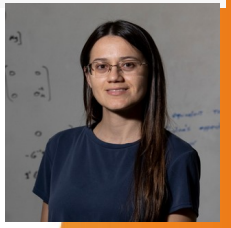
UNIVERSITY OF GEORGIA


Daniela Lourenco

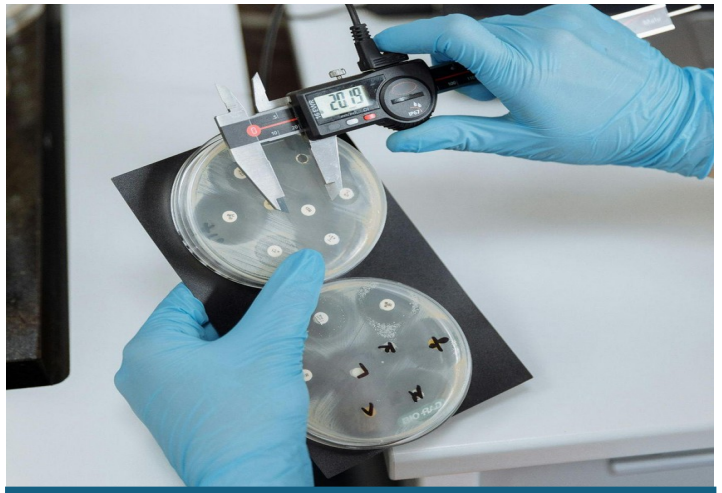

Fernando Bussiman

Future perspectives



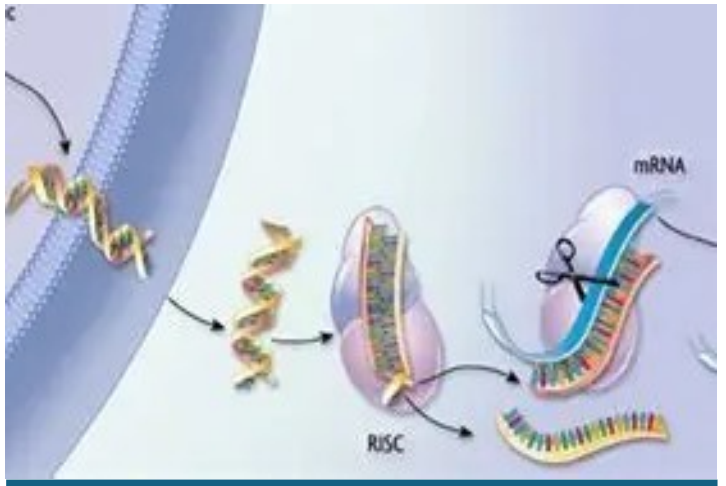
Inclusion of microbiota in animal breeding

- Population- and environmental-level sampling
- Reliable parameters estimates



Bioproducts development

- Microorganism isolation
- Enzymes production *in vitro*



Biotechniques for hologenome regulation

- Target-driven EVs
- RNAi

Research team

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Bedankt! **Obrigada!**

Thank you!

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