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SRUC

Metagenomic analysis indicates an association of rumen microbial genes with appetite in beef cattle

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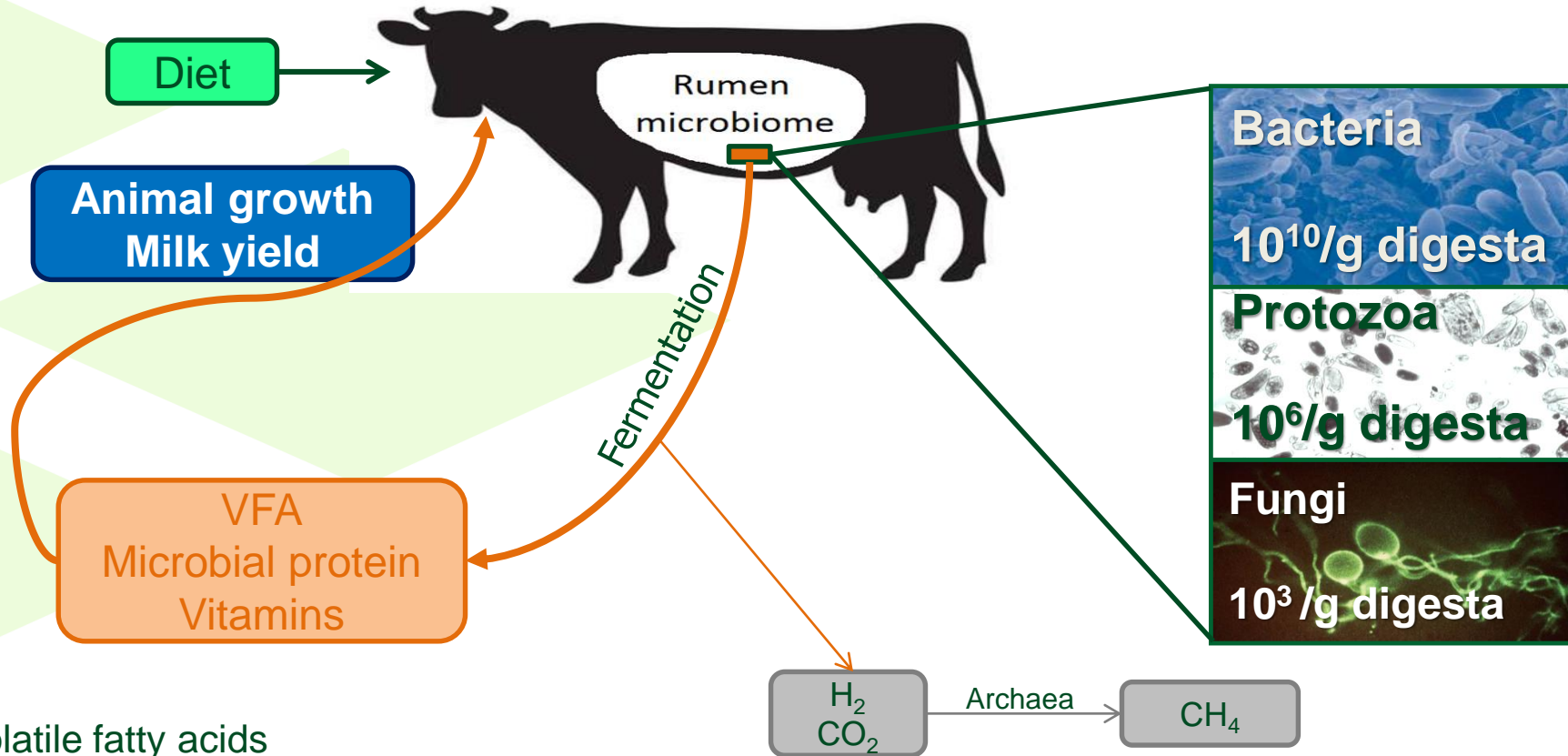


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The rumen microbiome

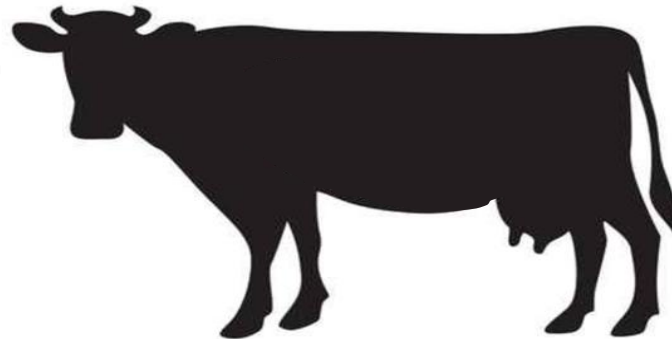
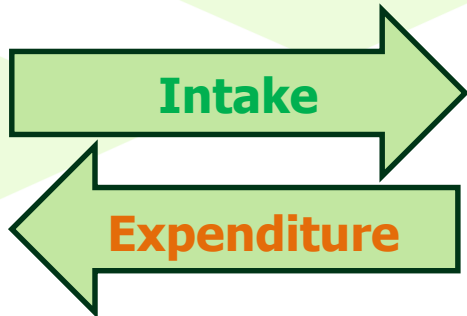


VFA – Volatile fatty acids

Appetite & the rumen microbiome

Appetite was assessed through Daily Feed Intake (DFI)

- Host energy homeostasis
- Host-microbiome communication



Main objectives

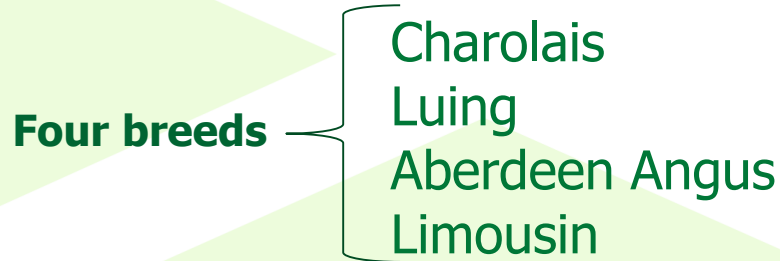


- Investigation of the association between **rumen microbial genes** and **appetite** of the host animal (assessed by daily feed intake)
- Identification of rumen microbial genes that could be used as **biomarkers** for appetite in beef cattle

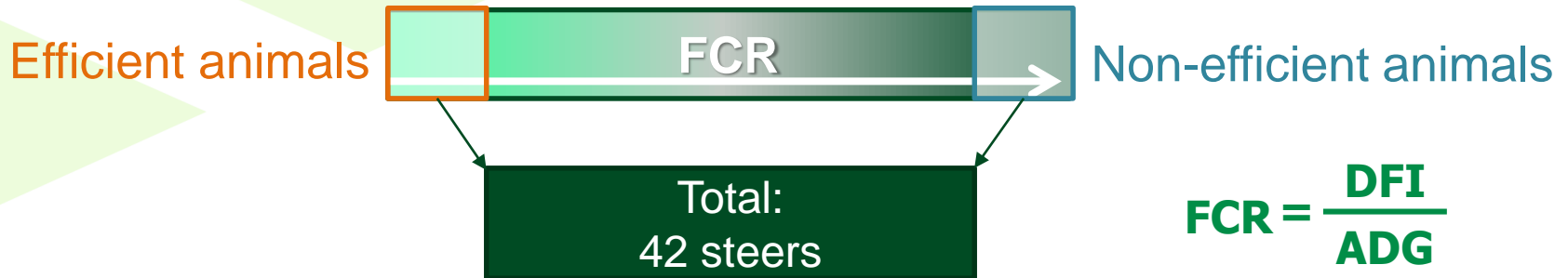
Material & Methods



The database



The animal selection



FCR – Feed Conversion Ratio; DFI – Daily Feed Intake; ADG – Average Daily Gain

Identification of microbial genes for prediction of appetite



Rumen Digesta Sampling

DNA extraction

Metagenomics

KEGG

Linear Models

Partial Least Squares (PLS)

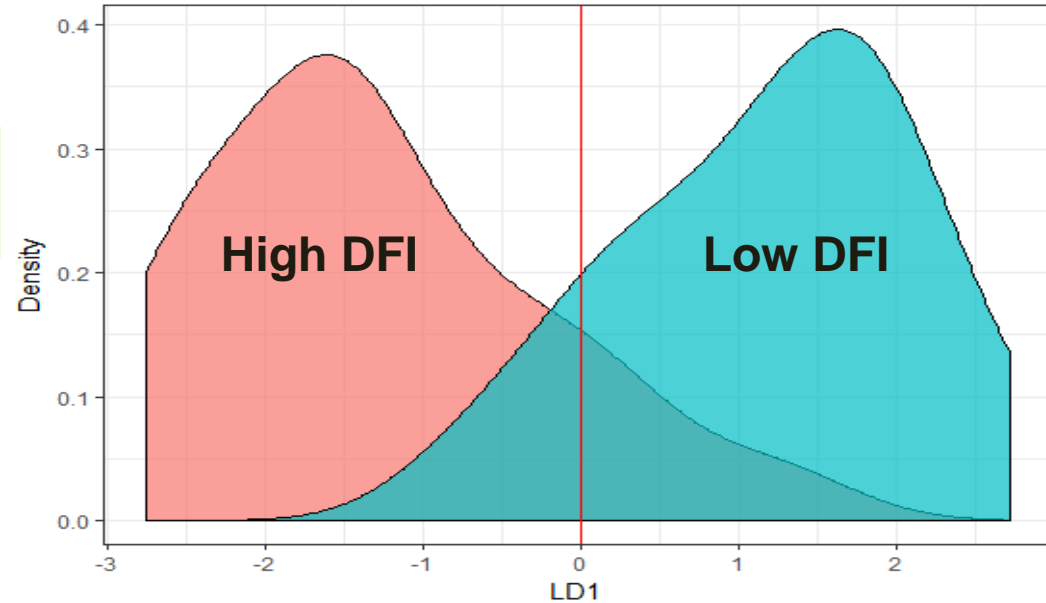
Identification of the most informative microbial genes

18 microbial genes explained 73% of the variation of DFI

Identified microbial genes distinguish between high and low DFI animals

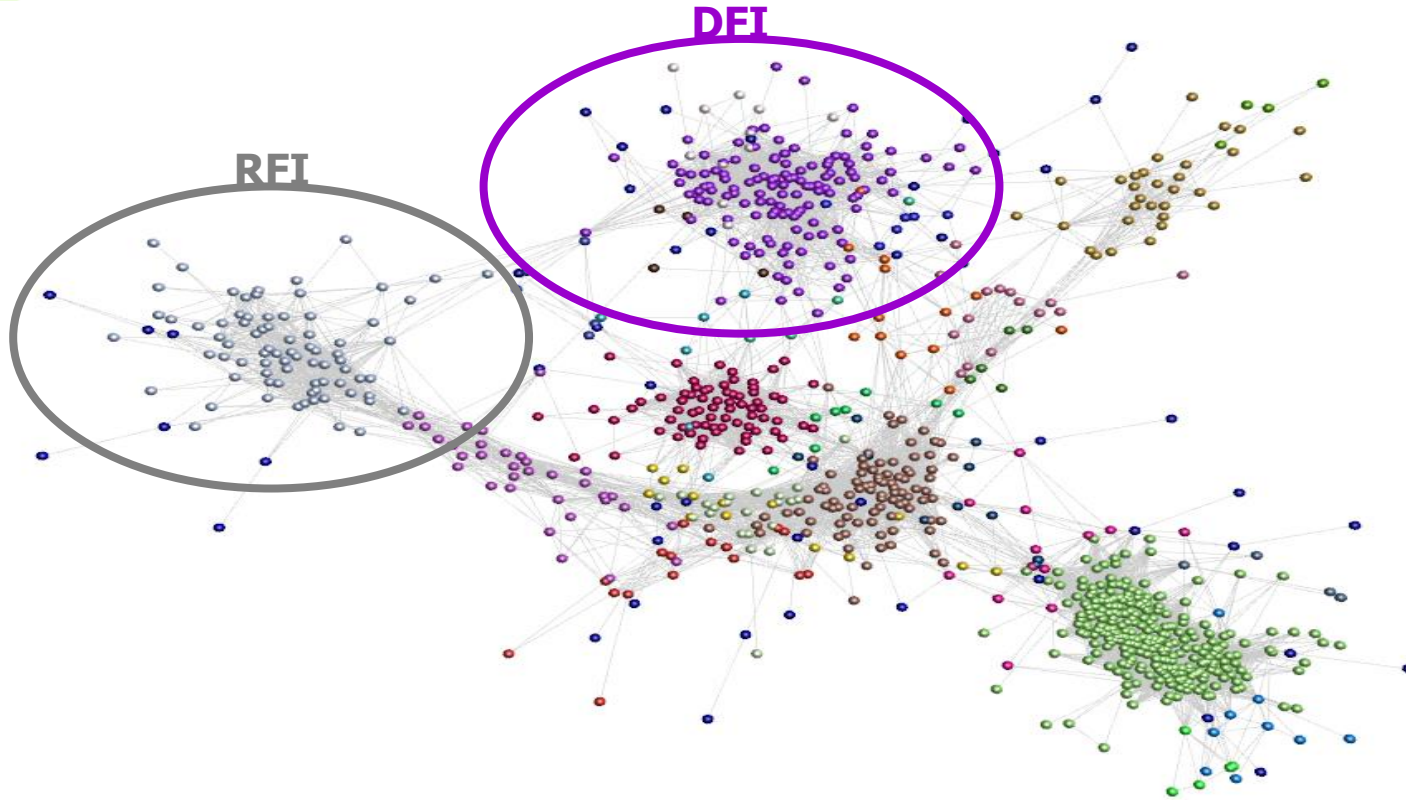


Confusion Matrix LDA		Predicted Group	
		High	Low
Observed Group	High	17	3
	Low	3	19
Accuracy		85.71%	



Animals classified as High and Low DFI based on their DFI in comparison to the group median; LD1 – Linear Discriminant 1.

Co-abundance network of microbial genes



Co-abundance network. minimum correlation threshold = 0.80. Enrichment analyses p-value = 0.05.

Microbial genes for DFI prediction



Function: Housekeeping

- ⊕ *nusB* (N utilization protein B)
 - Transcription termination and anti-termination processes
 - Bacterial growth
- ⊕ *ehbD* (energy-converting hydrogenase B subunit D)
 - Autotrophic CO₂ assimilation, microbial growth

RFI

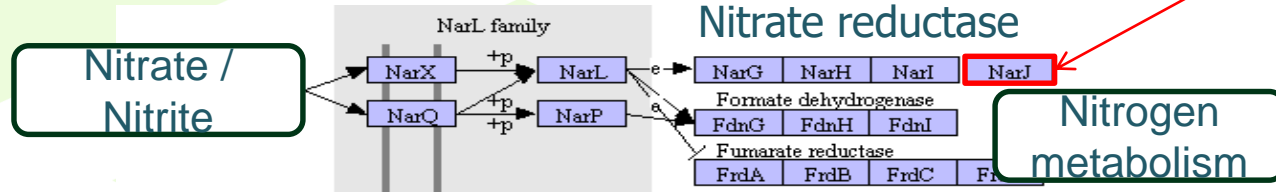
Methanogens

Microbial genes for DFI prediction

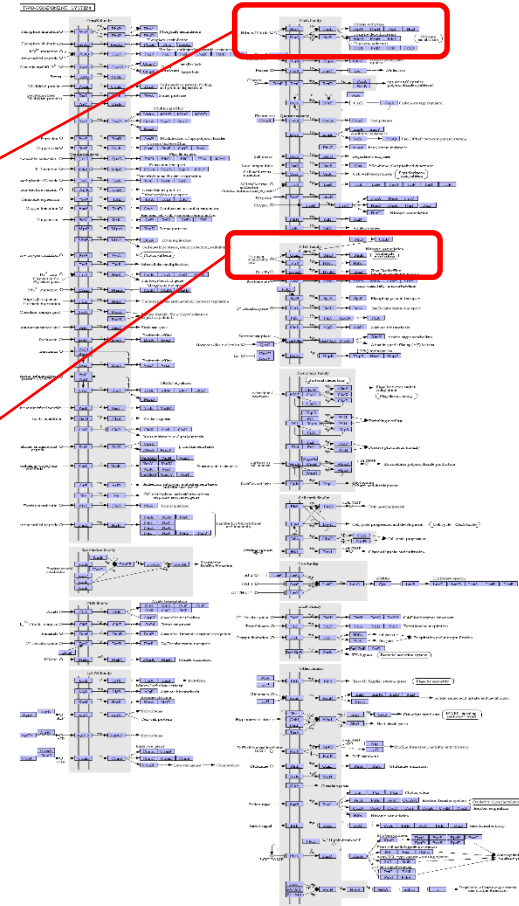
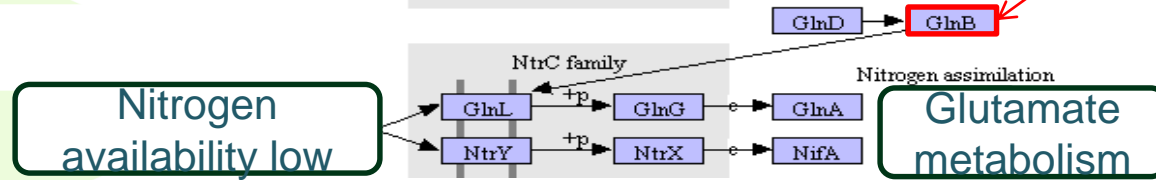


Function: **Environmental sensing**

⊖ *narJ* (Nitrate reductase 1, alpha subunit)



⊕ *glnB* (Nitrogen regulatory protein P-II 1)



Microbial genes for DFI prediction



Function: Metabolism of...

...Carbohydrates

⊕ *bglX* (beta-glucosidase)

...Amino acids

⊖ GATM (glycine amidinotransferase)

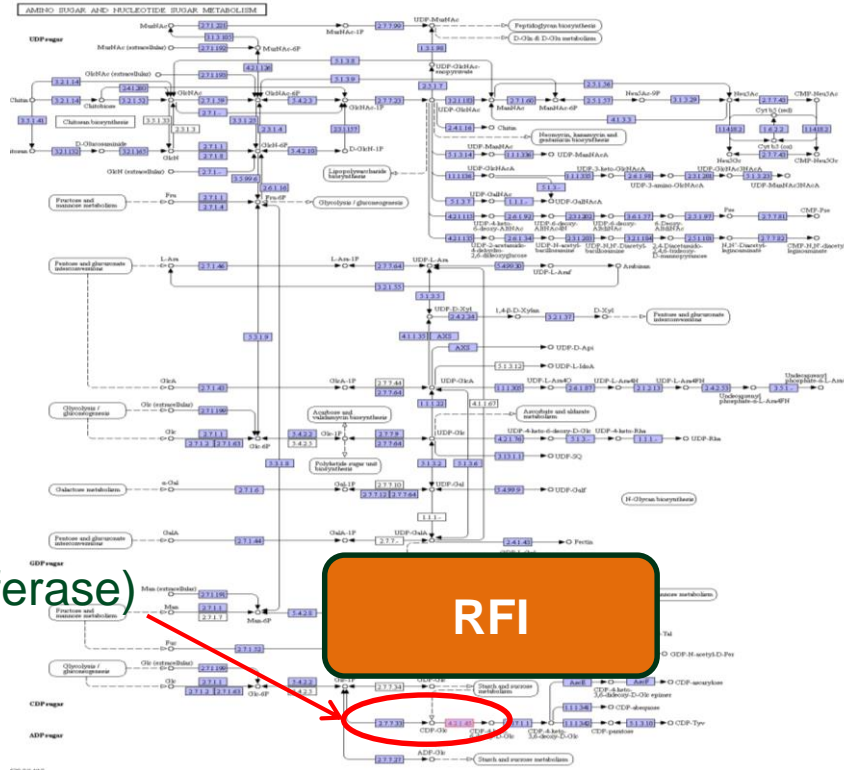
...Nucleotides

⊕ *rdgB* (XTP/dITP diphosphohydrolase)

...Amino sugar and nucleotide sugar / LPS

⊕ *rfaF* (Glucose-1-phosphate cytidyltransferase)

⊕ *rfaG* (CDP-glucose 4,6-dehydratase)



Conclusions



- **18 microbial genes explained 73% of the variance in feed intake**
- **Microbial genes associated with host feed intake participate in several different biochemical pathways**
- **Most candidate biomarkers were positively correlated to feed intake, but some showed negative correlation**

Relative abundances of microbial genes are potential **biomarkers of appetite** in beef cattle

Acknowledgements

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Identification of Rumen Microbial Genes Involved in Pathways Linked to Appetite, Growth, and Feed Conversion Efficiency in Cattle

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