

# The genetic basis of ruminant microbiomes - contribution of the HoloRuminant project

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**EAAP 2023, Lyon, 31<sup>st</sup> August 2023**



## I. Introduction

- Microbial-host coevolution
- Host-genetic and microbiomes
  - Heritable microbiomesWhereto and to what extent?



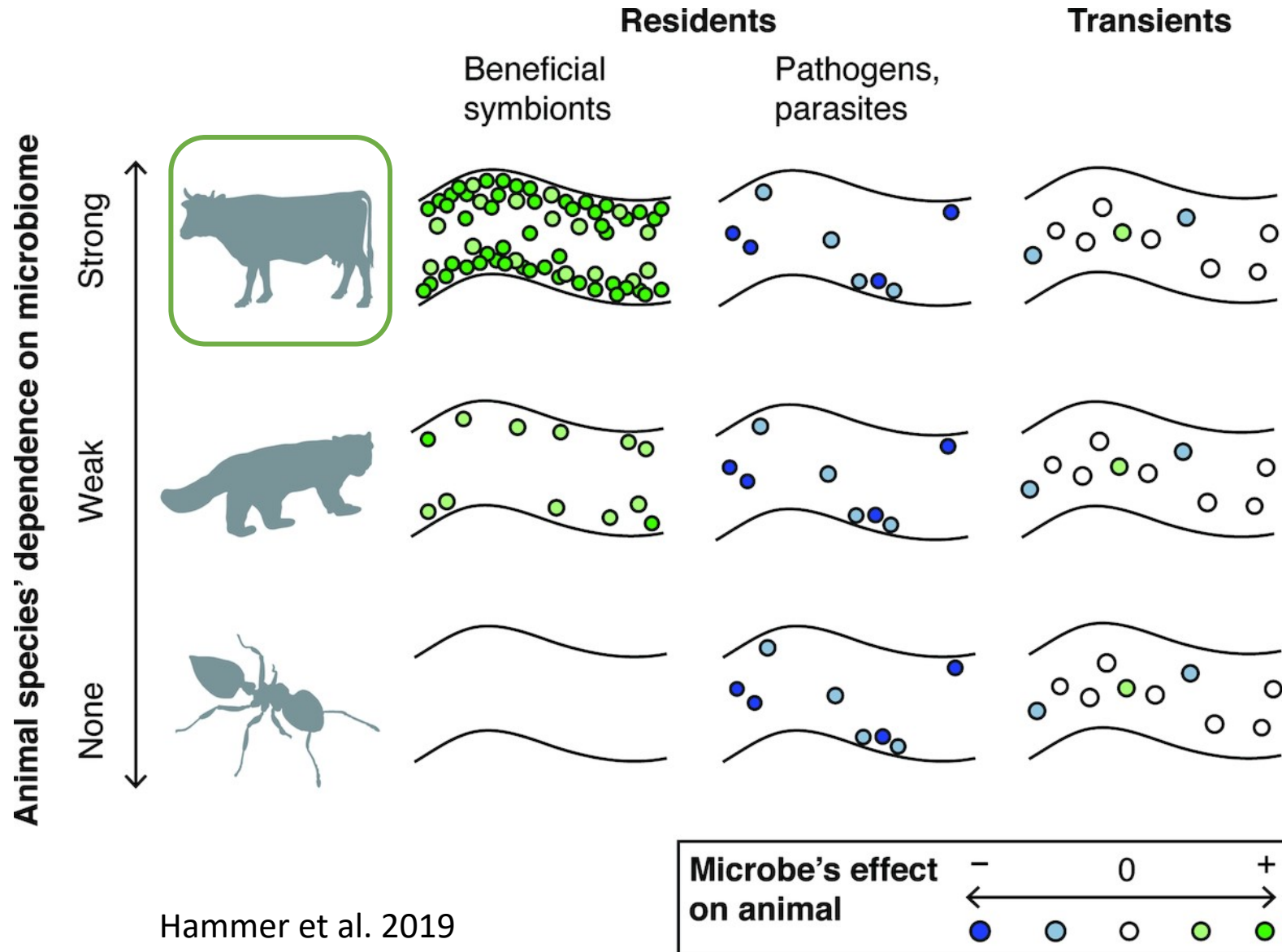
# Microbiomes matters



- Improving livestock sustainability
- Reduction of environmental impact
- Discovery of new bioactive metabolites
- Reduction in the use of antibiotics
- Animal health and welfare



# Host-microbial dependencies



## Diet

Starch-based

↑ fiber

VS.

Western-diet

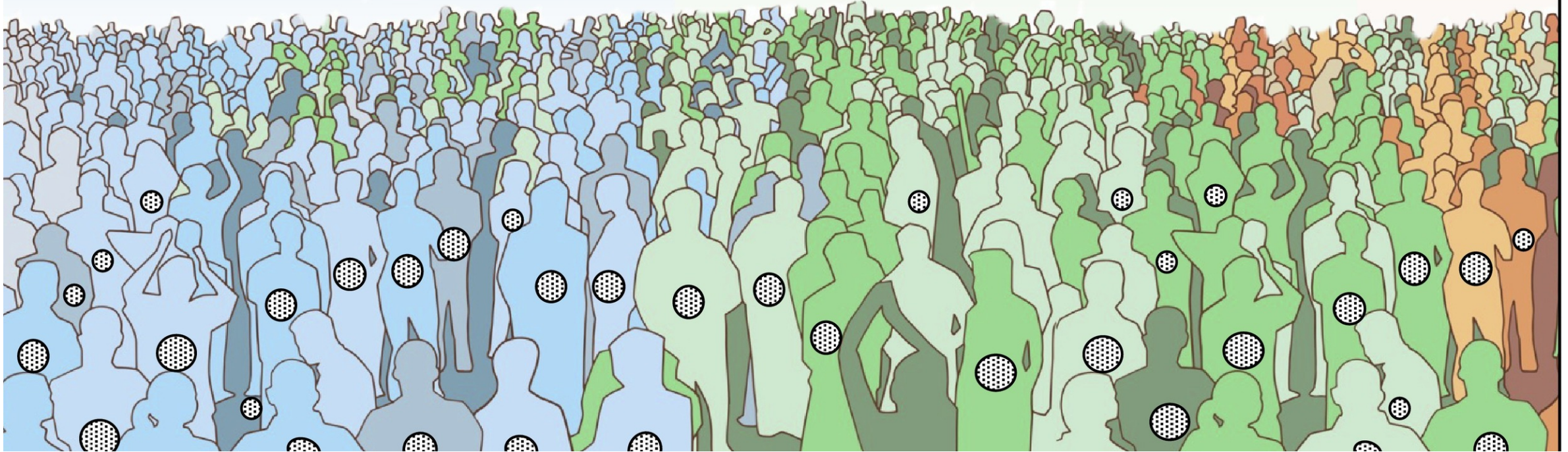
↓ fiber, ↑ fat/sugar

## Lifestyle

- Rural vs urban environment
- Exposure to farm and pet animals
- Family size
- Social Interactions

## Host

- Relatedness
- Selected genes  
*LCT*  
*ALDH1L1*  
*PLD1*  
*AMY1*

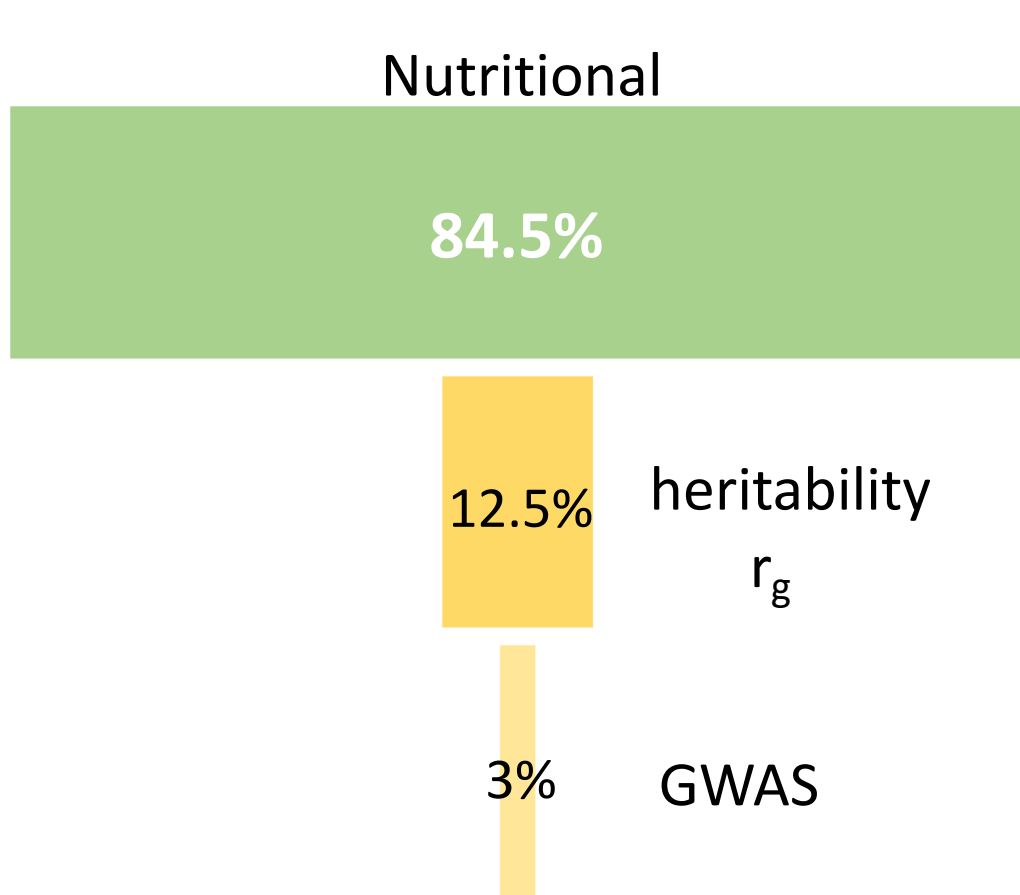


Parizadeh & Arrieta, 2023

# Livestock Microbiomes

- Domestication
- Partner fidelity
- Dietary control
- Breeding programs
- Environmental control





PubMed



based on a state-of-the-art review, July, 2023



## A heritable subset of the core rumen microbiome dictates dairy cow productivity and emissions

R. John Wallace<sup>1\*†</sup>, Goor Sasson<sup>2†</sup>, Philip C. Garnsworthy<sup>3</sup>, Ilma Tapio<sup>4</sup>, Emma Gregson<sup>3</sup>, Paolo Bani<sup>5</sup>, Pekka Huhtanen<sup>6</sup>, Ali R. Bayat<sup>4</sup>, Francesco Strozzi<sup>7‡</sup>, Filippo Biscarini<sup>7§</sup>, Timothy J. Snelling<sup>1</sup>, Neil Saunders<sup>3</sup>, Sarah L. Potterton<sup>3</sup>, James Craigan<sup>3</sup>, Andrea Minuti<sup>5</sup>, Erminio Trevisi<sup>5</sup>, Maria L. Callegari<sup>8||</sup>, Fiorenzo Piccoli Cappelli<sup>5</sup>, Edward H. Cabezas-Garcia<sup>6||</sup>, Johanna Vilkkii<sup>4</sup>, Cesar Pinares-Patino<sup>4</sup>, Kateřina O. Fliegerová<sup>9</sup>, Jakub Mrázek<sup>9</sup>, Hana Sechovcová<sup>9</sup>, Jan Kopečný<sup>9</sup>, Aurélie Bonin<sup>10</sup>, Frédéric Boyer<sup>10</sup>, Pierre Taberlet<sup>10</sup>, Fotini Kokou<sup>2</sup>, Eran Halperin<sup>11</sup>, John L. Williams<sup>7#\*\*</sup>, Kevin J. Shingfield<sup>4\*\*\*††</sup>, Itzhak Mizrahi<sup>2\*\*\*</sup>



## Host genetic control on rumen microbiota and its impact on dairy traits in sheep

Guillermo Martinez Boggio<sup>1\*†</sup>, Annabelle Meynadier<sup>1</sup>, Albert Johannes Buitenhuis<sup>2</sup> and Christel Marie-Etancelin<sup>1</sup>



## Host Genome Influence on Gut Microbial Composition and Microbial Prediction of Complex Traits in Pigs

Amelia Camarinha-Silva,<sup>\*,1</sup> Maria Maushammer,<sup>\*,1</sup> Robin Wellmann,<sup>\*</sup> Marius Vital,<sup>†</sup> Siegfried Preuss,<sup>\*</sup> and Jörn Bennewitz<sup>\*,2</sup>

GENETICS



## Use of Bayes factors to evaluate the effects of host genetics, litter and cage on the rabbit cecal microbiota

María Velasco-Galilea<sup>1,2\*</sup>, Miriam Piles<sup>1</sup>, Yuliaxis Ramayo-Caldas<sup>1</sup>, Luis Varona<sup>3</sup> and Juan Pablo Sánchez<sup>1</sup>



$$h^2 = 0.2 - 0.6$$

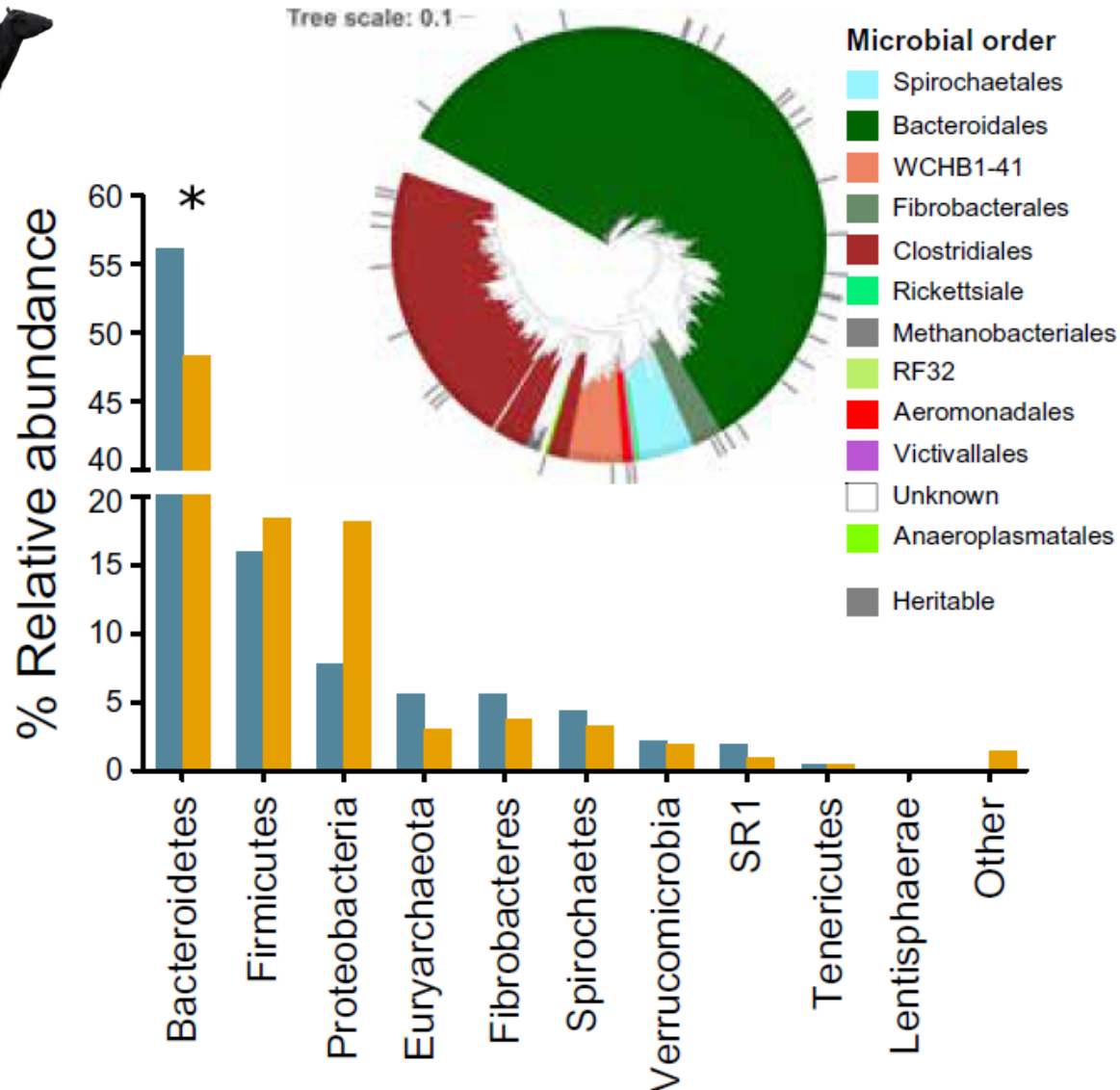
$$h^2 = 0.1 - 0.29$$

$$h^2 = 0.32 - 0.57$$

$$h^2 = 0.18 - 0.35$$



# Heritable core microbiomes



Phylogenetically closely related

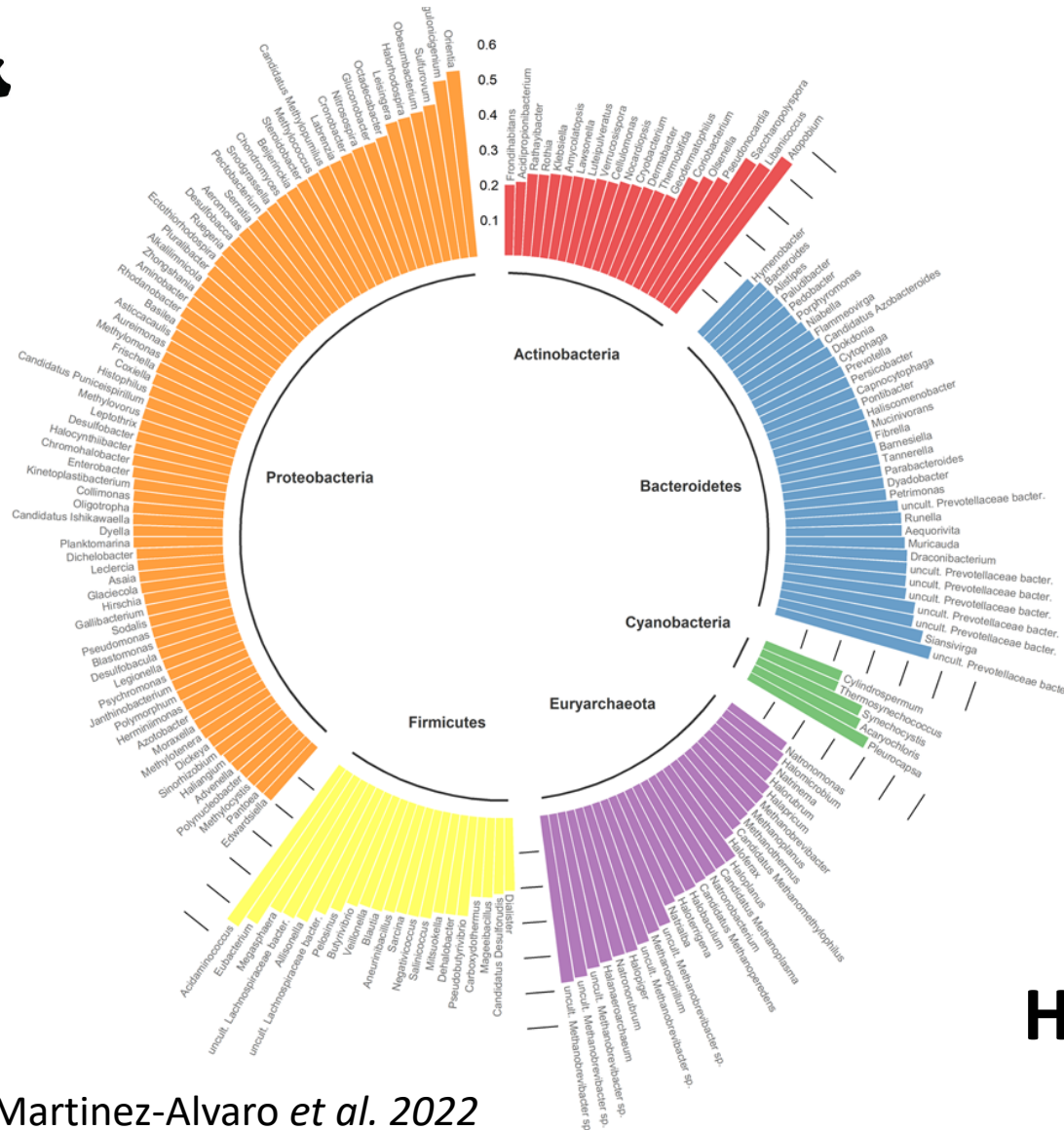
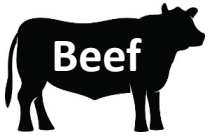
30-60% of the overall abundance

Keystone in microbial network

Associated with host phenotypes  
(CH<sub>4</sub>, SCFA, milk composition)

Adapted from *Wallace et al. 2019*

# Heritable microbiomes



b

$$h^2 = 0.12 - 0.61$$

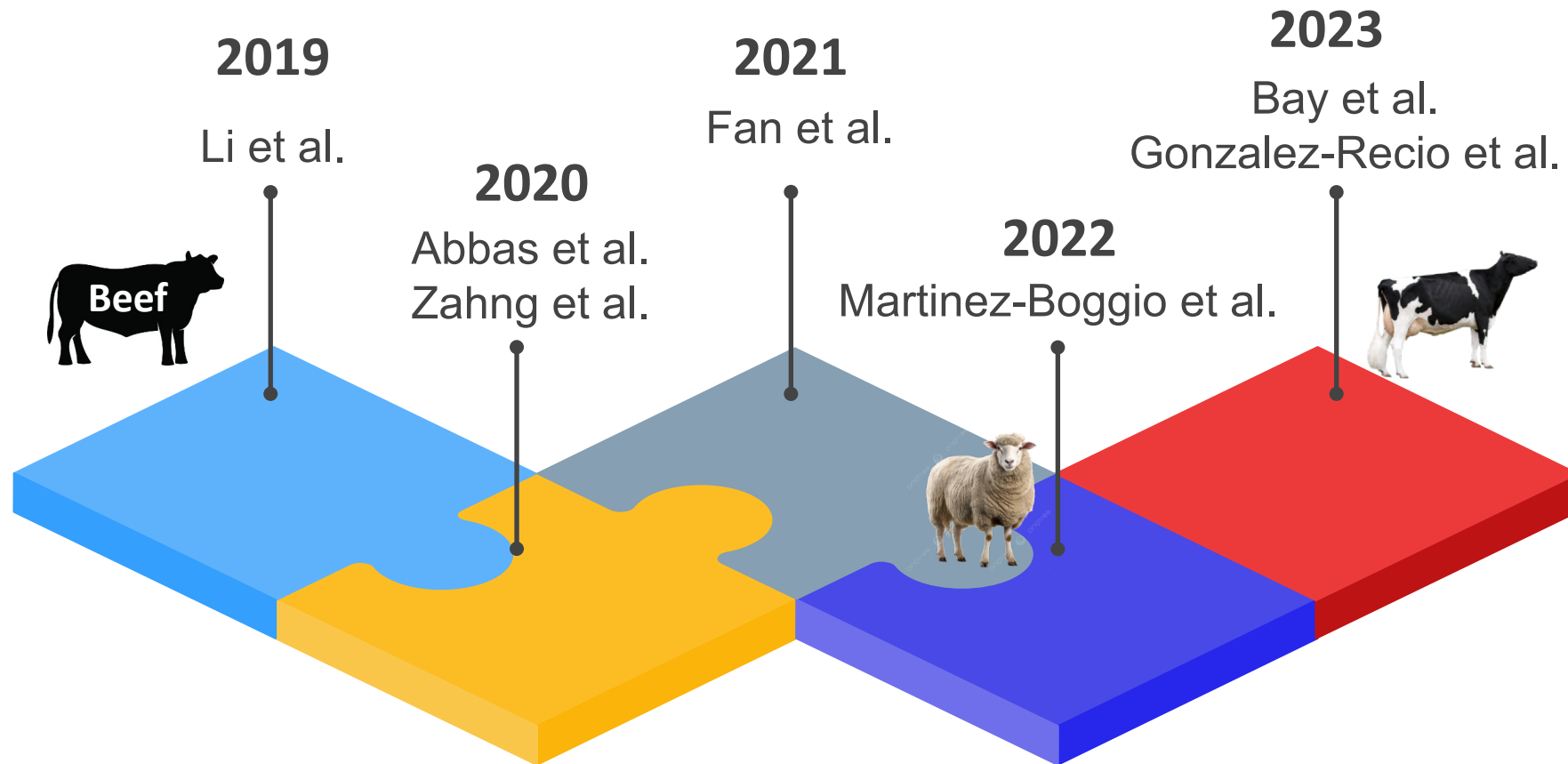
$$r_{gCH_4} = 0.59 - 0.93$$

$$r_{gFA} = 0.39 - 0.87$$



Heritable and related to host-traits

Adapted from Martinez-Alvaro *et al.* 2022



# GWAS (state-of-art)



qilme2

Fan et al

Bay et al

qilme  
Quantitative Insights  
v.1.9

Abbas et al

qilme  
Quantitative Insights  
v.1.9.1

LotuS

Zahng et al

Li et al

Type



Gonzalez-Recio et al

SqueezeMeta



Taxonomy database



GreenGenes



Silva db



Feces



Rumen



Foot skin

# GWAS (state-of-art)

Assessment of variation in microbial community amplicon sequencing by the Microbiome Quality Control (MBQC) project consortium

nature reviews  
microbiology

Identifying and Overcoming Threats to Reproducibility, Replicability, Robustness, and Generalizability in Microbiome Research



Reporting guidelines for human microbiome research: the STORMS checklist

nature  
medicine



**Standardize methodologies**

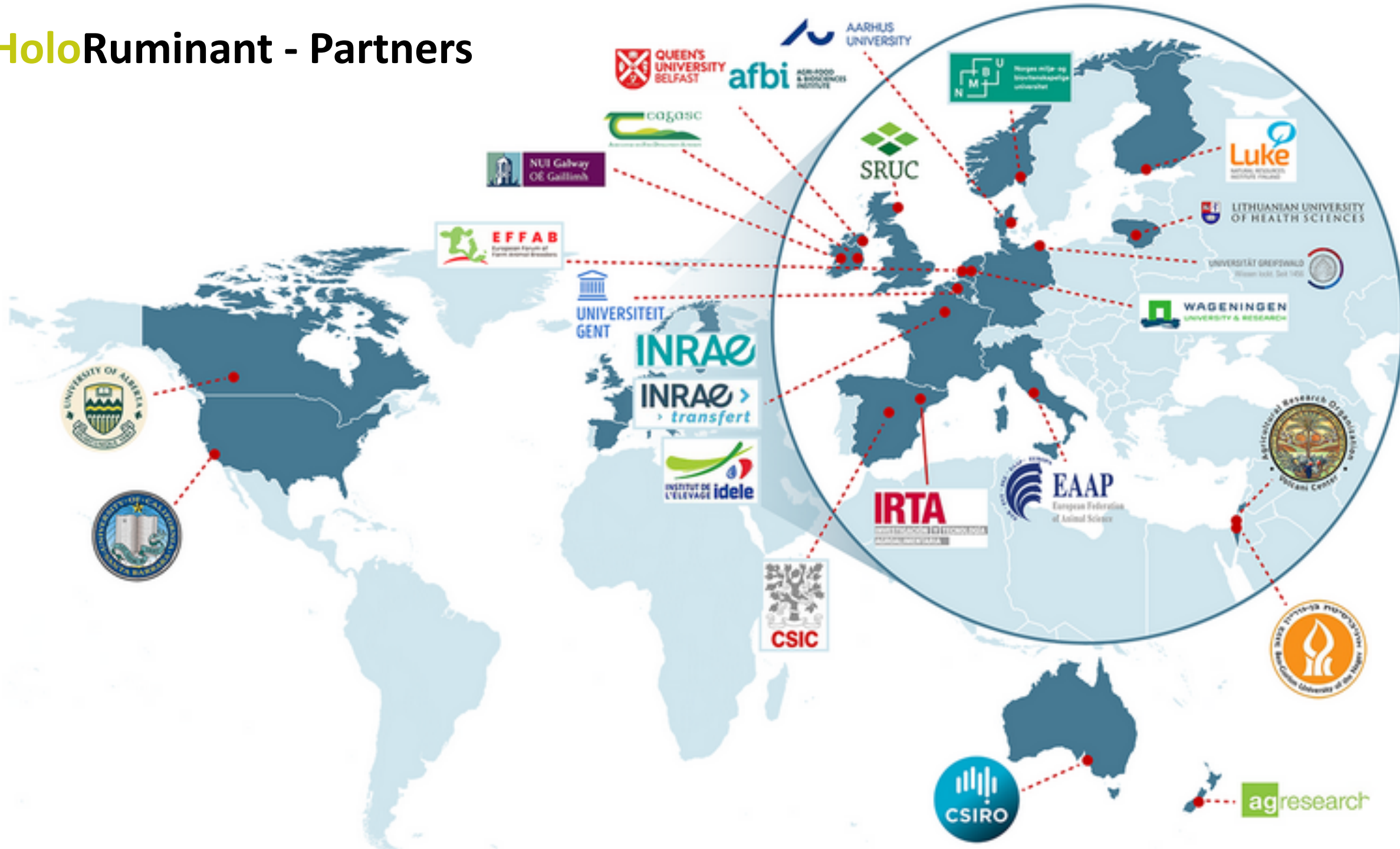




# HoloRuminant

Understanding microbiomes of the ruminant holobiont

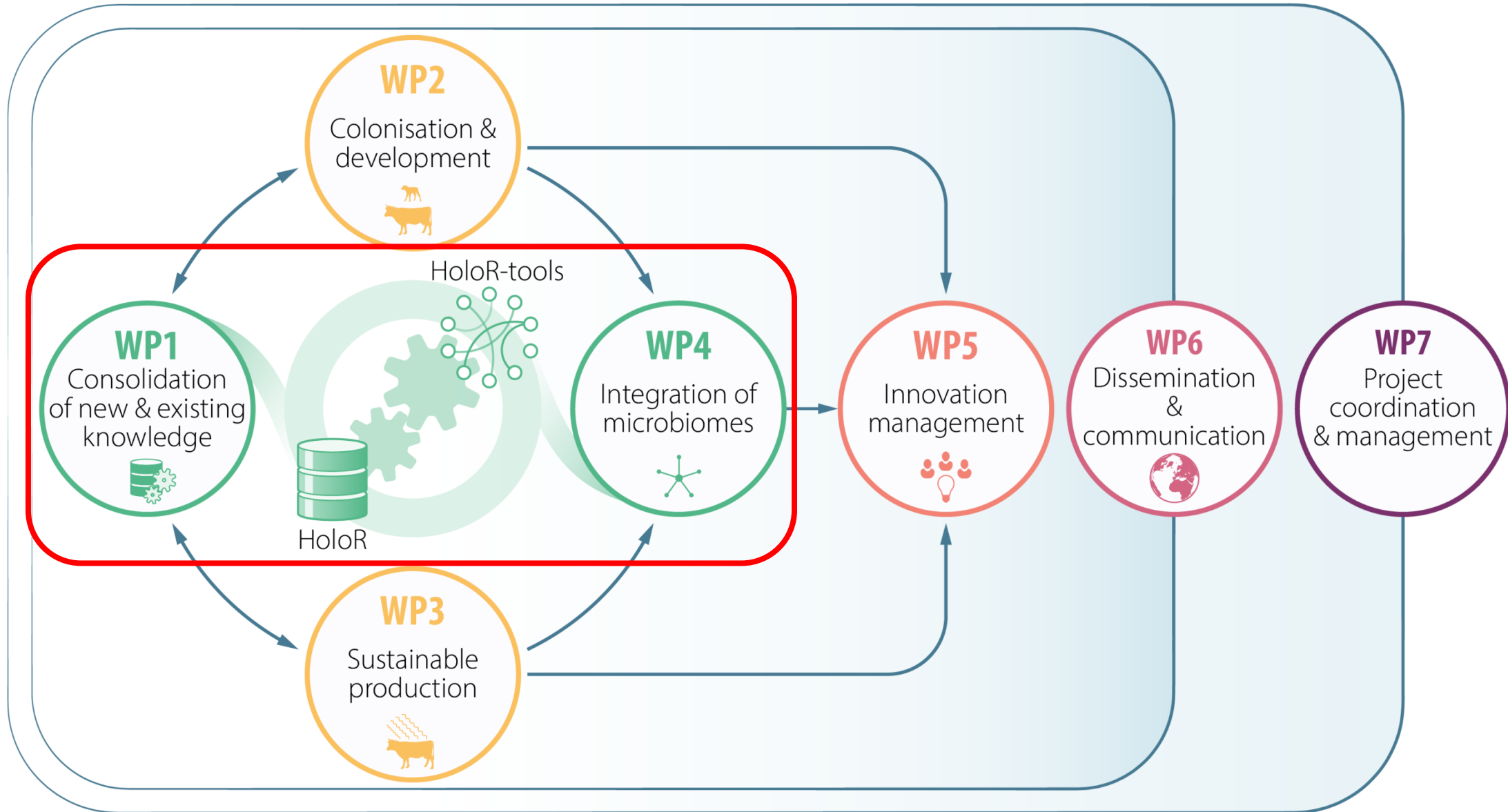
# HoloRuminant - Partners



To elucidate the role of ruminant-associated microbiomes and their interplay with the host animal in early life and throughout fundamental life events

**HoloRuminant will:**

- Characterize the establishment and **dynamics** of ruminant microbiomes
- Determine the connectivity between microbiomes from **different body sites**;
- their **genetic basis** , and influence on the host's **key performance indices** (KPIs)
- Facilitate the **adoption** of the proposed innovations by **end-users**



# WP1. Consolidation of existing and development of novel knowledge



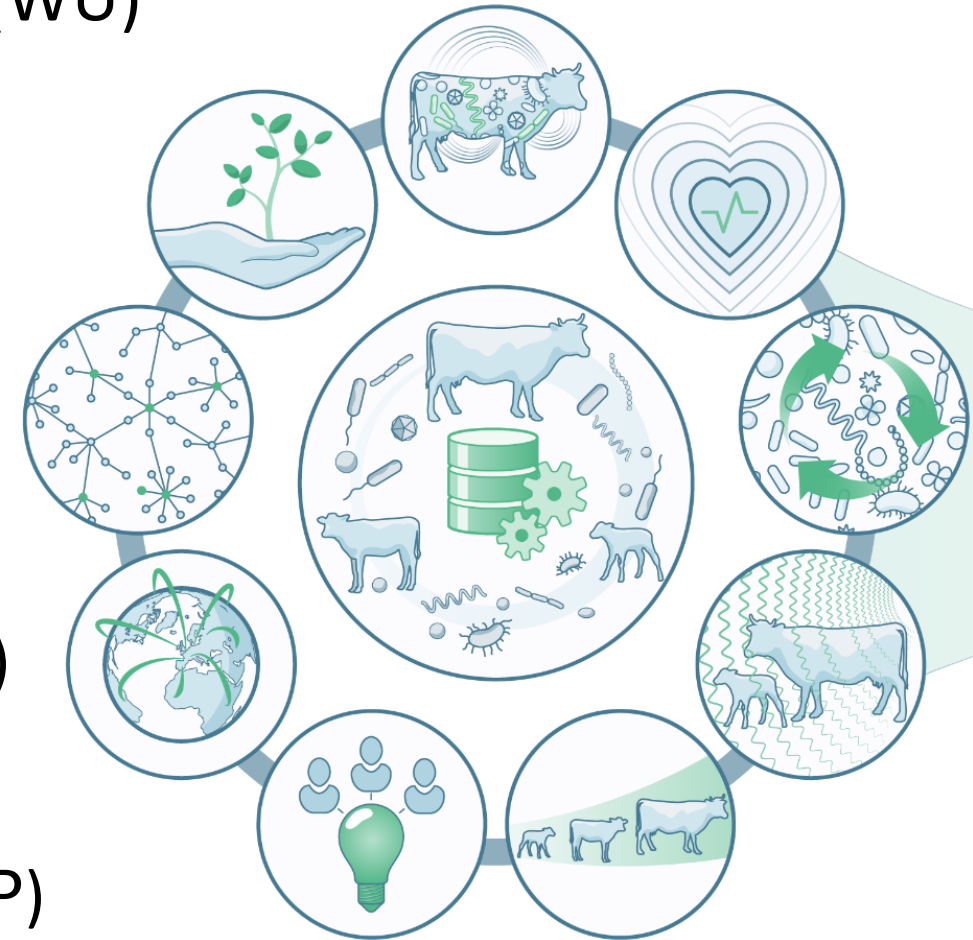
**WP leaders:** Chris Creevey (QUB) & Hauke Smidt (WU)

**Task 1.1:** Standardised methodologies

**Task 1.2:** Consolidation of metataxonomic studies

**Task 1.3:** Consolidation of microbial genomes (metaG)

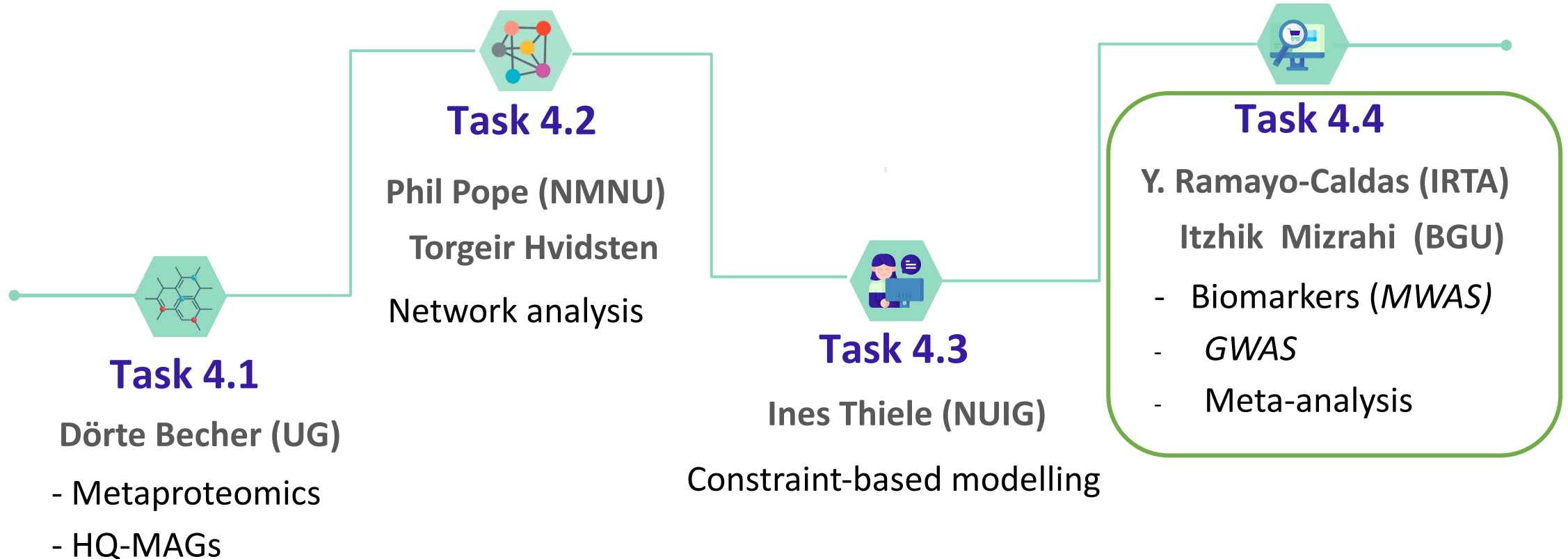
**Task 1.4:** Generation of novel data (HQ-MAGs, metaP)



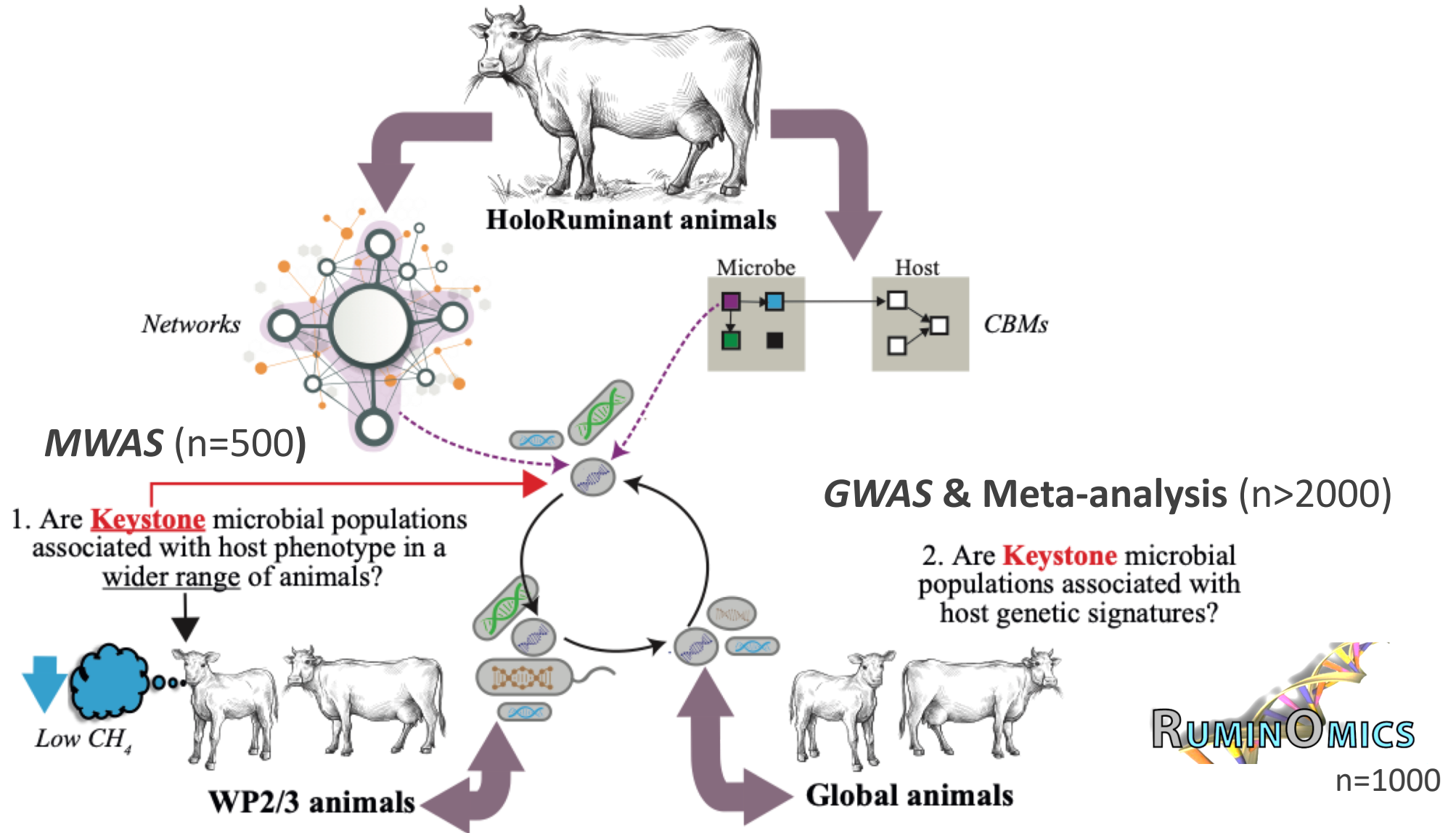
## WP4. Integrating microbiomes for improving ruminant performance



**WP leaders:** Phil Pope (NMBU) & Dörte Becher (UG)



## Task4.4 Step 2- GWAS and Meta-analysis



- Database (**HoloR**) and repository (**HoloR-tools**) of standardized pipelines
- Microbial signatures associated to host key performance indices (KPIs)
- Host genetic (**pleiotropic**) variants linked to KPIs and microbial signatures
- New insights into mechanisms driving host-microbiome interactions



# Thank you for your attention!



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EAAP 2023, Lyon, August 31st, 2023



[www.holoruminant.eu](http://www.holoruminant.eu)