HoloRuminant

Understanding microbiomes of the ruminant holobiont

NEWSLETTER

ISSUE 7

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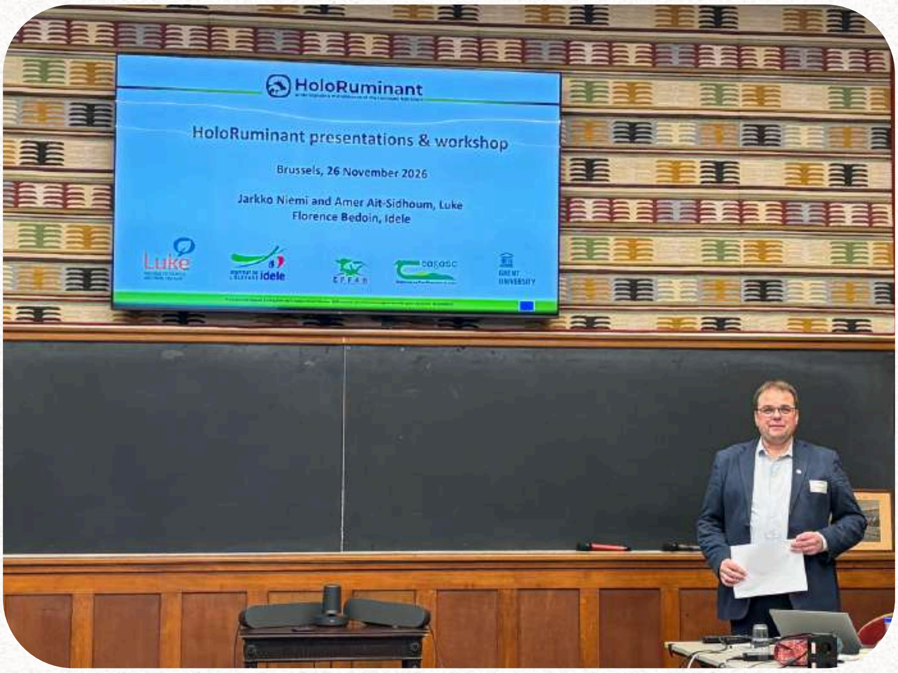
NEWS »»

HoloRuminant on Calf Scour and Unstable Gut Microbiome

HoloRuminant wrote an article for the Feed & Additive magazine, highlighting how calf scour arises from a vulnerable period in early immunity and an unstable gut microbiome, Sabine Scully from Teagasc Walsh and Geena Cartick from EFFAB - European Forum of Farm Animal Breeders outline management practices that support microbial balance to help calves resist disease. Read it here!



Connecting Stakeholders in Brussels

In November 2025, HoloRuminant gathered stakeholders across the livestock and research community for a productive stakeholder event.

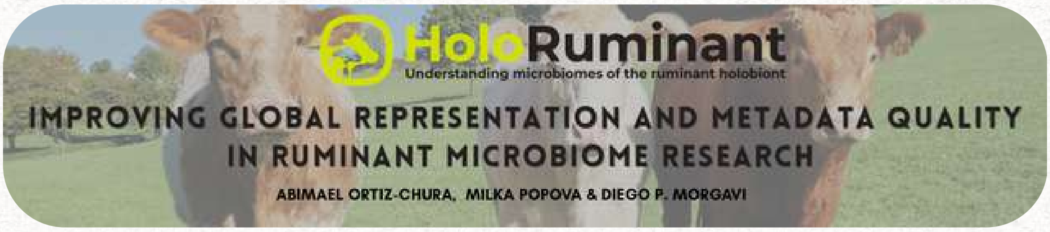
NEWS »»

Hosted at University Foundation, the event included three presentations sharing insights regarding HoloRuminant research results from:

- Sabine Scully (University College Dublin, Teagasc Walsh Scholar) on calf health & the microbiota: exploring early life to support life-long health and performance
- Prof. Veerle Fievez (Ghent University) on connecting rumen and faecal microbes to metabolic triad challenges in transition cows
- Joni Van Mullem (Ghent University & ILVO (Instituut voor Landbouw, Visserij- en Voedingsonderzoek)) on the effect of extruded linseed on methane emissions and rumen microbiota under two basal diets

Last on the agenda, we had an interactive workshop with our stakeholders where we discussed their priorities, possible adoption pathways & next actions.

Thank you to all who attended and participated for driving thoughtful, constructive discussions!



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IMPROVING GLOBAL REPRESENTATION AND METADATA QUALITY IN RUMINANT MICROBIOME RESEARCH

ABIMAEL ORTIZ-CHURA, MILKA POPOVA & DIEGO P. MORGAVI

Policy Paper: Improving Global Representation and Metadata Quality in Ruminant Microbiome Research

90% of all samples of ruminant microbiomes originate from Western Europe, North America, Australasia, and China. With over 40% of existing samples lack basic metadata (e.g., breed, age, sex). Limiting research based on these samples' applicability in regions where livestock productivity is lower, climate challenges are greater, and local breeds predominate. This new policy brief introduces recommendations on how to overcome this issue. Read it here.

NEWS »»

New Sampling Guideline Protocols by HoloRuminant

These protocols, developed by the HoloRuminant project partners, provide standardized methods for sampling different biological matrices in ruminants. Their aim is to support high-quality, comparable data generation for microbiome research. So far, five protocals have been released – with more to come soon! Access them below:

- Protocol for Rumen Fluid Sampling – Esophageal Tube Sampling
- Protocol for Faecal Sampling
- Protocol for Rumen Fluid Sampling – Flora Rumen Scoop
- Protocol for Milk Sampling
- Protocol for Nasopharyngeal Sampling

New Practice Abstract on Making Ruminant Microbiome Data Globally Representative and FAIR

Current microbiome datasets are heavily biased toward cattle in high-income countries, limiting their relevance for diverse production systems worldwide. This Practice Abstract showcases recommendations on how to overcome this problem based on a recent HoloRuminant study. Find out more here.

New Fact Sheet on the Perception of Calf Health Practices

While these practices are scientifically supported, their broader uptake depends on public acceptance—an area that remains under-explored in Europe. This study explored just this, the HoloRuminant project surveyed 3,220 citizens in Finland, France, Ireland, and Poland to assess acceptance of four microbiome-related calf health practices. Find out the results here!

IN CASE YOU MISSED IT »»

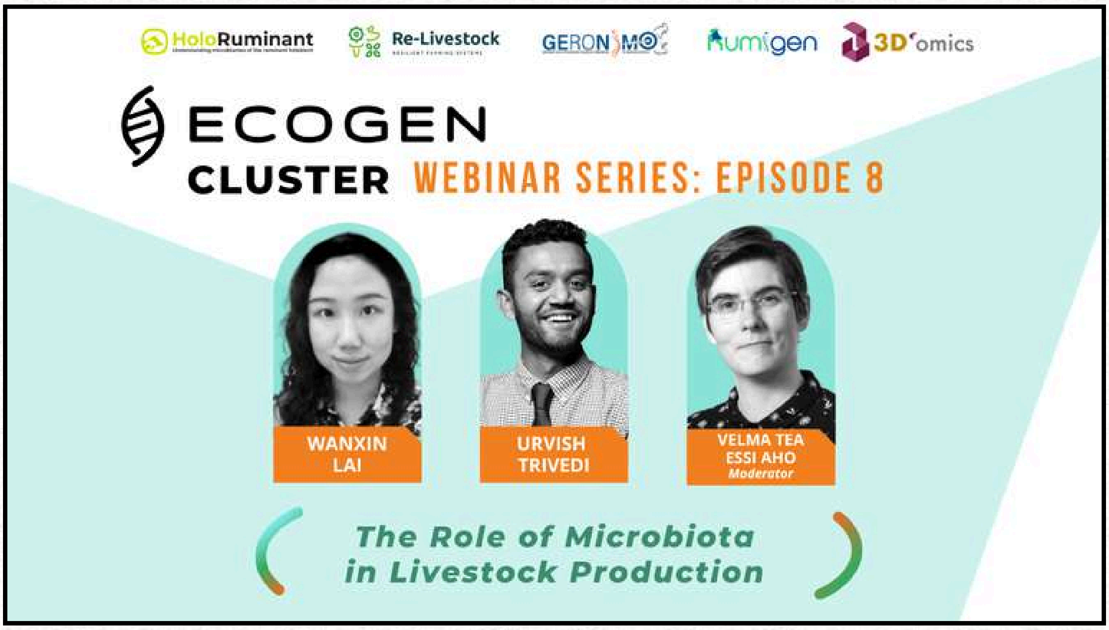
EcoGen webinar series Episode 6 - Beyond traditional breeding: Part 1

Episode 6 of the Ecogen explored how epigenetics, multi-omics, and holistic system thinking are transforming livestock breeding — turning biological insights beyond DNA into practical, on-farm decisions for improved health, resilience, methane reduction, and animal welfare. Watch it here!

EcoGen webinar series Episode 7 - Beyond traditional breeding: Part 2

In this second part of our deep dive into Beyond Traditional Breeding, we explore how genome and epigenome editing are reshaping the future of animal breeding, and why responsible innovation is essential as these technologies advance. Watch it here!

IN CASE YOU MISSED IT



EcoGen webinar series Episode 8 - The Role of Microbiota in Livestock Production

In this EcoGen webinar, we explored how microbial communities influence animal health, productivity, and environmental impact—from Salmonella–probiotic interactions to the metabolic pathways driving methane emissions in cattle. Watch it here!

MEET THE TEAM

PHIL POPE

WP4

Hi, I'm Phil (Phillip B.) Pope, a Professor of Microbiome Sciences whose research develops and applies advanced "omics" approaches (metagenomics, transcriptomics, proteomics and metabolomics) to understand—and ultimately manipulate—animal microbiomes to improve health, productivity and environmental outcomes. I earned my PhD in Metagenomics at Griffith University (Brisbane) and have built an international track record across Europe and Australia in microbiome science and bioinformatics.

In the EU Horizon 2020 HoloRuminant project, I co-lead Work Package 4 (WP4), "*Integrating microbiomes for improving ruminant performance*". As WP4 co-lead, I provide scientific and operational coordination across partners, ensuring that multi-omics datasets from different body sites, life stages and production systems are harmonised and integrated into robust models that link microbiome function to key ruminant performance indicators. Under my leadership, WP4 delivers core analytical outputs—including microbiome interaction networks, constraint-based metabolic models, and integrated MWAS/GWAS-style frameworks—alongside open, reusable toolsets (e.g., the HoloR-tools repository) to accelerate translation into breeding, diagnostics and management innovations.

YUKIAXIS RAMAYO

WP4

I obtained my degree in Veterinary Medicine and Animal Science from the University of Granma (Cuba) in 2006. In 2007, I was awarded an international scholarship from the Mediterranean Agronomic Institute of Zaragoza (CIHEAM-IAMZ) to pursue an MSc in Animal Genetic Improvement and Reproductive Biotechnology. In 2009, I received a Spanish Ministry of Education fellowship (FPU) to undertake my PhD at the Universitat Autònoma de Barcelona, which I completed in 2013.

I subsequently held a Marie Curie FP7 COFUND postdoctoral position at INRA (France), collaborating with the University of Copenhagen and the Beijing Genomics Institute on bioinformatics pipelines for de novo genome assembly and quantitative metagenomics, applied to pig gut and cattle rumen microbiomes. In 2017, I joined IRTA under a Marie Skłodowska-Curie fellowship, and in 2020 I was awarded a Ramón y Cajal contract.

At IRTA, I have established a research line focused on hologenomics and computational biology applied to animal production. Within the H2020 HoloRuminant project, I lead Task 4.4, which focuses on identifying and characterizing microbial guilds, studying their prevalence across geographies, and assessing environmental and host-related modulatory factors. This work also evaluates their impact on host physiology and genetic modulation, and develops strategies to integrate hologenomic data to improve the prediction accuracy of key livestock traits such as methane emissions and feed efficiency.

UPCOMING EVENTS

EcoGen Webinar: Mitigation and Resilience

How can breeding and management practices help livestock systems adapt to climate change? Join us for an in-depth look at heat stress, trait trade-offs, and sustainable rearing, from dairy cows in the Netherlands to heritage pig breeds in Slovenia.

With speakers:
- Aurelie Vinet, INRAE — researcher in bovine genetics on trade-offs between traits in the context of climate change

- Mario Calus, Wageningen University & Research — Chair of Animal Breeding and Genomics on the impact of heat stress on fertility traits in dairy cows in the Netherlands

- Martin Škrlep, Agricultural Institute of Slovenia — researcher in pig production and meat quality on the effects of reduced dietary protein and rearing practices on the Krškopolje pig breed

Register here!

- **Persistent auxiliary microbiome of early novel colonizers in the developing rumen with lasting functional significance.** Ori Furman, Gil Sorek, Sarah Moraïs, Liron Levin, Omar Eduardo Tovar-Herrera, Sarah Winkler, Itzhak Mizrahi, The ISME Journal, Volume 19, Issue 1, January 2025, wraf252, DOI: 10.1093/ismejo/wraf252 (12/25).

- **Core rumen microbes are functional generalists that sustain host metabolism and gut ecosystem function.** Tovar-Herrera, O.E., Grinshpan, I., Sorek, G. et al. Nat Ecol Evol (2025). DOI: 10.1038/s41559-025-02904-3 (12/25).

- **Characterisation of the bacterial and archaeal microbiota in fresh colostrum collected from a single, spring-calving dairy herd.** Scully S, Earley B, Smith PE, Finnie MSJ, McAloon C, Buckley F, et al. (2025). PLoS One 20(10): e0335718. DOI:10.1371/journal.pone.0335718 (10/25).

- **CompareM2 is a genomes-to-report pipeline for comparing microbial genomes**. Kobel, Carl M, Aho, Velma T E, Øyås, Ove, Nørskov-Lauritsen, Niels, Woodcroft, Ben J, Pope, Phillip B. Bioinformatics 2025. ISSN 1367-4811. DOI: 10.1093/bioinformatics/btaf517. (09/25).

- **Metabolic capabilities of key rumen microbiota drive methane emissions in cattle**. Lai W, Alberdi A, Leu A, de Leon AVP, Kobel CM, Aho VTE, Roehe R, Pope PB, Hvidsten TR. 0. mSystems 0:e00601-25. DOI: doi.org/10.1128/msystems.00601-25 (09/25).

- **A Comprehensive Review: Bovine Respiratory Disease, Current Insights into Epidemiology, Diagnostic Challenges, and Vaccination.** O'Donoghue, S.; Waters, S.M.; Morris, D.W.; Earley, B. Vet. Sci. 2025, 12, 778. DOI: 10.3390/vetsci12080778 (08/25).

- **Response of primary mammary epithelial cells to pathogen challenge in dairy cows with divergent genomic breeding values for udder health.** Terhi Iso-Touru, Daniel Fischer, Frank Panitz, Suvi Taponen, Zexi Cai, Goutam Sahana, Ilma Tapio, Johanna Vilkki, Genomics, Volume 117, Issue 5, 2025, 111102, ISSN 0888-7543, DOI: 10.1016/j.ygeno.2025.111102. (08/25).

- **Empowering bioinformatics communities with Nextflow and nf-core.** Langer, B.E., Amaral, A., Baudement, MO. et al. Genome Biol 26, 228 (2025). DOI: 10.1186/s13059-025-03673-9 (07/25).

- **Protozoal populations drive system-wide variation in the rumen microbiome.** Kobel, C.M., Leu, A., Vera-Ponce de León, A. et al. Nat Commun 16, 6238 (2025). DOI: 10.1038/s41467-025-61302-2 (07/25).

- **Co-occurring microbial guilds in pig fecal microbiota: key drivers and effects on host performance.** Vourlaki, IT., Rio-Lopez, R., Clavell-Sansalvador, A. et al. Genet Sel Evol 57, 27 (2025). DOI: 10.1186/s12711-025-00979-x. (06/25).

for more information about the HoloRuminant project, visit our website:

www.holoruminant.eu

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You can also follow us on our social media accounts:

and subscribe to our **mailing list!**

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