



TOWARDS IMPROVEMENT OF RUMINANT BREEDING THROUGH GENOMIC AND EPIGENOMIC APPROACHES

NEWSLETTER

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Table of contents

01	Editorial2 By Eric Pailhoux, RUMIGEN Coordinator
02	News3 Final Consortium Meeting Final Joint Event RUMIGEN Game Final video Book of abstracts New Practice Abstracts Webinar eBis on Rumigen results
03	Meet the consortium7 The whole team
04	RUMIGEN at work8 Approaches for societal dialogue on animal breeding
05	Publications9
06	Popular articles11
07	Upcoming events14 EcoGen Webinar Series



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Editorial

Eric Pailhoux

RUMIGEN Coordinator



Dear RUMIGEN Partners,

As a famous French singer would say: 'That's it, it's over...' or almost! However, it's the 'almost' that can make all the difference, so we need to stay focused until the final review on 31 August. The RUMIGEN adventure officially ends this week, but we still need to summarise, explain and share all the results gathered during this project, which has involved rich scientific exchanges and deeply inspiring human connections.

What can I say in this final editorial? I'm at a loss for words – or perhaps there's simply too much to say. In my mind, I'm reliving the early days of this project and the planning meetings surrounding the SFS-13-2020 call for proposals, which was briefly titled 'Genome and epigenome-enabled breeding in terrestrial livestock' (a short title, but one with vast implications...). I'm rereading one of the first files labelled 'first draft' from April 2019, as well as the agenda for the first meeting at Roissy-Charles de Gaulle Airport (a magical place if ever there was one!) on 13 September 2019. What a long journey it has been, and how many more magical places we've discovered and shared with you, the dedicated members of this consortium — scientists from all walks of life who have not only formed a consortium, but also made it effective, supportive and friendly throughout this project.

This editorial will be brief, but I would like to thank each and every one of you sincerely for making this European project a record of achievements, and above all an album of fond memories that I will revisit for years to come. I would especially like to thank the members of the ExCom, with whom I exchanged information most frequently during our bimonthly meetings. Thank you to the work package leaders for flawlessly executing the project's various tasks. Thank you to my INRAE colleagues, Jean-Luc and Didier, for their invaluable coordination support. Finally, I would like to express my deepest gratitude to our project manager, Anne Jarousse, for her unwavering support, and to our project officer, Colombe Warin, for her understanding, professionalism and kindness.

I am concluding this project with a sense of accomplishment and pride in a job well done. I hope you all feel the same way, and that your time on the RUMIGEN project has strengthened you in your respective endeavours. It has been a pleasure to share this journey with you, and I wish you all the best for the future.



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Final Consortium Meeting

The final RUMIGEN consortium meeting took place in Brussels on 14th April 2026, preceding the joint final conference held on 15 April with its sister project GERONIMO. The meeting provided an opportunity for partners to present and discuss the latest project results, reflect on key achievements and share lessons learned throughout the project. It also allowed for constructive exchanges on remaining challenges and future perspectives. Despite reaching the final phase of the project, the high level of engagement and commitment from partners remained evident, contributing to a productive conclusion of the consortium's work.



Final Joint Event

RUMIGEN final event, organised together with its sister project GERONIMO, was held in Brussels on April 15, 2026. It marked the conclusion of the project and brought together researchers, policymakers and stakeholders to discuss the future of gene editing and advanced breeding tools in livestock. The event provided a cross-disciplinary platform, with contributions from science, social sciences, industry and policy, reflecting the wide range of expertise needed to address scientific, societal and regulatory dimensions of new breeding technologies.

Discussions covered the state of scientific readiness of gene editing, epigenetic approaches and next-generation selection strategies, as well as their relevance for traits linked to animal health and welfare, disease resistance, climate adaptation and efficiency. A shared understanding emerged that gene editing can be considered a complementary tool to conventional breeding, while its practical use will depend on integration into breeding programmes and practical applicability. Other aspects such as animal welfare considerations, and societal acceptance should only be considered once there is a legislative proposal in and for Europe and depending on the different production and market realities.

The conference also highlighted a growing international acceptance for gene-edited animals and products, with several non-EU countries already with enabling legislative frameworks for these types of innovations.



As part of the cluster, EcoGen is running a webinar series focused on interdisciplinary collaboration, showcasing cutting-edge research, and engaging diverse stakeholders in the future of sustainable livestock production. This series highlights groundbreaking innovations that reduce environmental impact, improve animal health, and enhance productivity.

In this context, speakers warned that the lack of a coherent EU pathway for livestock applications may create uncertainty for research and innovation and weaken the sector's long-term competitiveness. Overall, the discussions reinforced the importance of continued dialogue between science and policy to support the development of clear, science-based regulatory approaches for emerging breeding technologies.

The event was a great success, both in terms of content and participation. It worth mentioning that it was an honour to welcome MEP Jessika van Leeuwen in our panel and Valerio Abadessa from DG AGRI among the speakers, alongside a keynote speech from Professor Alison Van Eenennaam from UC Davis. All speakers demonstrated a high level of professionalism and expertise, contributing to a rich and engaging programme. The event gathered around 100 participants in person and an additional 170 online, reflecting the strong interest in the topic across the community.

Read the press release [here](#)

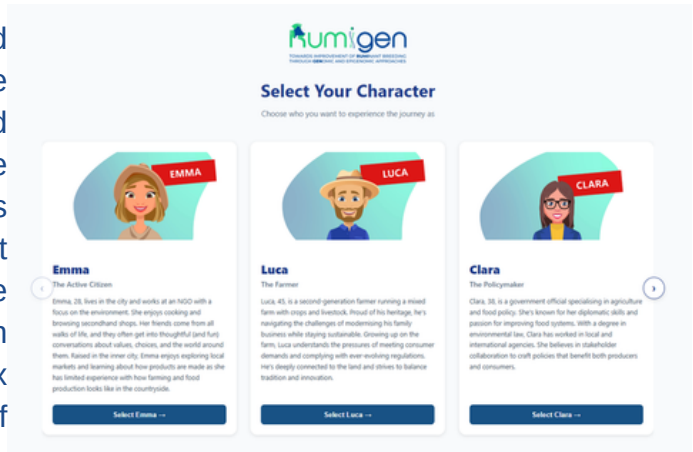




RUMIGEN Game

How might today's food choices shape the future of farming? As part of the communication activities, RUMIGEN developed an interactive online simulation game designed to spark discussion and increase awareness around sustainability, food systems and livestock production.

Through different characters and storylines, players are invited to make decisions on topics linked to food consumption and farming, while discovering the potential trade-offs and impacts of their choices. Aimed at policymakers, stakeholders and the wider public, the game offers an engaging way to explore the complex challenges surrounding the future of ruminant production and sustainable agriculture.

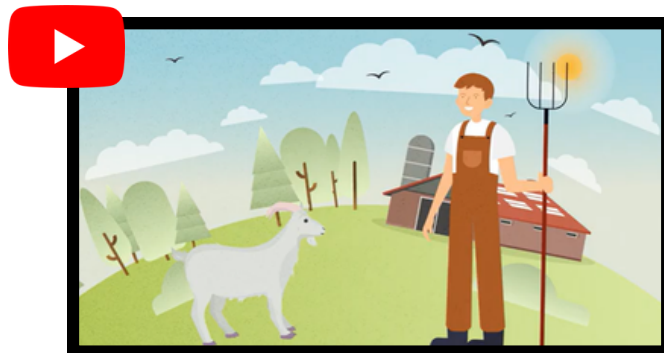


Try the game [here](#). 

Final Video

The final video of RUMIGEN is also available, presenting the project's overall impact and main achievements in an accessible format for a wider audience. The video highlights RUMIGEN's objectives, key research results and contributions toward more sustainable ruminant production systems, while showcasing how collaboration and innovation can support the future of livestock farming in Europe.

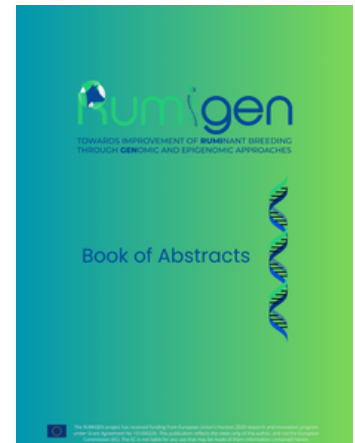
Watch now and learn how science and collaboration are shaping the future of ruminant production:





Book of abstracts

The *Final RUMIGEN Project Book of Abstracts* brings together a comprehensive collection of the most significant abstracts produced throughout the project's lifetime. It showcases the scientific contributions of all project partners, including presentations delivered at international conferences and peer-reviewed publications. This volume reflects the collaborative effort, innovation, and dedication that have driven the project forward, offering a valuable overview of its achievements and impact within the scientific community. We extend our sincere gratitude to all contributors for making this journey in science both productive and inspiring.



Read the full book of abstracts



New Practice abstracts

A dedicated compilation of Practice Abstracts has been developed within the RUMIGEN. The collection gathers concise and practice-oriented summaries of the project's main results and recommendations, translating research outcomes into accessible information for farmers, breeders, advisors and other stakeholders. It provides an overview of practical approaches and insights developed throughout the project to support more sustainable ruminant production systems.

Read them [here](#).



Webinar eBis on Rumigen results



UMT eBIS (INRAE, Idele and Eliance) organised a series of webinars on results obtained within the Rumigen project.

In particular, the webinars covered topics such as heat tolerance in dairy cattle, the impact of genomic selection on the genetic diversity of regional breeds, and recent research developments related to the Epi Chip and epigenetics within RUMIGEN and complementary French projects.

Watch them online [here](#).





MEET THE CONSORTIUM

Thanks to the whole team

For this final RUMIGEN EU newsletter, we want to dedicate the “Meet the Consortium” section to the partnership as a whole, whose collective expertise and commitment have driven the project forward over the past years.

We wish to recognise the strength of the consortium as an integrated team, where each partner has contributed essential knowledge, effort, and collaboration to achieve the shared objectives.

In particular, we extend our sincere appreciation to the project coordinator Eric Pailhoux and the project manager Anne Jarousse, for their outstanding leadership, steady guidance, and unwavering commitment throughout the project’s lifetime, ensuring cohesion, progress, and the successful delivery of RUMIGEN EU’s goals.

We warmly thank all partners for their invaluable contributions and invite you to reach out to us for any further information.

See the [RUMIGEN consortium](#) 





RUMIGEN AT WORK

Approaches for societal dialogue on animal breeding

By Rasmus Mikkelsen

RUMIGEN project presented a new model for societal dialogue on animal breeding, designed to help ensure that future ruminant breeding approaches are developed in ways that are socially legitimate, ethically responsible, and aligned with European stakeholder and citizen expectations. Rather than treating public acceptance as a simple “yes or no” response to specific technologies, the deliverable introduces the innovative “Room of Acceptance” (RoA) framework, which views acceptance as conditional, context-dependent, and shaped by interacting concerns such as animal welfare, environmental sustainability, transparency, governance, fairness, and the distribution of risks and benefits. The model combines literature review, stakeholder engagement, scenario development, and large-scale citizen consultations across Europe to identify both negotiable trade-offs and non-negotiable societal boundaries. By integrating these perspectives into an ex-ante and ex-post acceptance framework, the deliverable provides RUMIGEN and future breeding initiatives with a practical tool for guiding responsible innovation and strengthening trust between researchers, industry, policymakers, and society. Approaches for societal dialogue on animal breeding.

Read the full results [here](#).





PUBLICATIONS

Pangenome-based association testing between a structural variant located upstream of the KIT gene and head depigmentation across a diverse panel of cattle breeds.

Sorin, V., Sanchez, M.P., Drouilhet, L. et al. Genet Sel Evol 58, 17 (2026)

This research-study investigated the genetic basis of white-headed coat colour patterns in cattle using advanced pangenome-based genomic analysis. The researchers identified a structural variant located upstream of the KIT gene that is strongly associated with head depigmentation across several cattle breeds. By combining long-read genome assemblies with large-scale short-read sequencing data, the study demonstrated how pangenome approaches can detect complex structural variants that are often difficult to resolve with conventional linear reference genomes. Beyond pigmentation traits, the research highlights the broader value of pangenome methodologies for improving the identification of structural variants linked to important livestock traits, including health, adaptation, and production performance.



Assembly of a pangenome uncovers novel non-reference unique insertion sequences in cattle highlighting their genetic diversity

Sorin, V., Besnard, F., Capitan, A. et al. J Animal Sci Biotechnol 17, 47 (2026)

This study used pangenome assembly approaches to better capture the genetic diversity present across cattle breeds. By analysing high-quality genome assemblies from multiple French cattle breeds, the researchers identified more than 100,000 structural variants, including thousands of previously unknown DNA sequences that are absent from the current cattle reference genome. Several of these newly identified variants were linked to economically important traits such as milk production and morphology, highlighting their potential functional relevance. The study demonstrates how pangenome-based genomics can reveal important genetic variation that is missed by conventional reference genome approaches, while also emphasizing the importance of incorporating breed diversity into future livestock genomic research and breeding strategies.





Impact of genomic selection on genetic diversity in 5 local European cattle breeds.

Bonifazi, R., Meuwissen, T. H. E., Croiseau, P., Restoux, G., Minéry, S., Vandenplas, J., & Windig, J. J. (2026). Journal of Dairy Science.

This study investigated how the introduction of genomic selection (GS) is influencing genetic diversity in several European local cattle breeds. While genomic selection has improved the speed and efficiency of breeding programmes, concerns remain about its potential impact on inbreeding in smaller populations. By analysing pedigree and genomic data from five local cattle breeds across the Netherlands, Norway, and France, the researchers examined changes in population structure, sire usage, kinship, and inbreeding following the implementation of GS. The study found that genomic selection reduced generation intervals and enabled a broader and more balanced use of breeding sires, but its effects on genetic diversity differed between breeds. In some populations, inbreeding rates increased, while in others they decreased, suggesting that long-term outcomes depend strongly on breeding and population management strategies rather than on genomic selection alone. The research highlights the importance of continuously monitoring genetic diversity to ensure the sustainability of local cattle breeding programmes.





POPULAR ARTICLES

The RUMIGEN EpiChip: a new tool for integrating epigenetics into dairy cattle breeding

*Published on 05/03/2026 by Marie-Pierre Sanchez (INRAE).
[Original text in French.](#)*

Research carried out by INRAE (GABI and BREED research units) and Eliance shows that adding epigenetic information, alongside conventional genetics, could improve the prediction of dairy cow performance.

Context: Why going beyond genetics?

Since the pioneering work of Theo Meuwissen and colleagues, genomic selection has profoundly transformed genetic improvement in dairy cattle. It allows breeders to predict the genetic value of animals early in life and with high accuracy. However, part of the differences observed between cows — in milk production, fertility, health, and other traits — cannot be explained by genetics alone. Many complex traits are also influenced by environmental factors such as feeding, herd management, sanitary conditions, and the physiological status of the animal. This is where epigenetics, and particularly DNA methylation, becomes important. Without modifying the DNA sequence itself, these chemical marks can influence gene expression levels. They act as an interface between the genome and the environment and may therefore explain part of the “missing” variability not captured by genetics alone.

The EpiChip

Most epigenetic studies in cattle remain expensive and difficult to implement at large scale. To address this challenge, a dedicated tool was developed within the European RUMIGEN project: the EpiChip. The EpiChip enables standardized, large-scale measurement of DNA methylation levels at more than 43,000 sites across the bovine genome, focusing on regions that vary epigenetically between individuals or may be relevant to dairy cow performance.

4,484 Holstein cows analysed

The chip was used on blood samples collected from 4,484 French Holstein cows born between 2013 and 2023. For each cow, researchers combined:

- conventional genomic data (DNA sequence variation),
- epigenetic data (DNA methylation measured with the EpiChip),
- and phenotypic data from the national genetic evaluation system.

In total, 33 traits were analysed, including:

- milk production and milk composition,
- fertility traits (insemination success rate, calving-to-insemination interval, etc.),
- udder health (somatic cell score),
- and morphological traits (chest width, body depth, udder attachment, leg conformation, and others).



Two prediction models were compared:

- a model using only genetic information,
- and a model combining genetic and epigenetic information.

What did the study show?

1. DNA methylation explains part of the differences between cows

On average, DNA methylation explained around 12% of the observed variation between animals, depending on the trait studied.

More specifically:

- 6–14% for milk production traits,
- 7–13% for fertility traits,
- 11% for udder health,
- and 9–20% for morphological traits.

In other words, a measurable part of cow performance is associated with epigenetic variation beyond genetics alone.

2. Improved prediction accuracy

When methylation data were added to genomic data, prediction accuracy improved for 18 traits, with gains ranging from 0.6% to 5%. The largest improvements were observed for certain morphological traits (such as chest width and body depth) and for a fertility trait (non-return rate in cows), which are typically traits with low heritability. Although the gains remain modest at the individual level, even small increases in prediction accuracy can have significant economic impacts at the scale of a national breeding population.

How should these results be interpreted?

The study suggests that DNA methylation partly captures the effects of environment and physiological status on cow performance. It therefore provides complementary information to conventional genetics and may be particularly useful for low-heritability traits such as fertility and health, which are more difficult to improve through traditional selection methods.

However, several limitations should be considered. DNA methylation was measured in blood, which may not fully reflect biological processes occurring in tissues directly linked to the trait of interest, such as the mammary gland. In addition, the long-term stability of these epigenetic marks and their possible transmission across generations remain insufficiently understood.

Conclusion

The RUMIGEN EpiChip represents a promising new tool for large-scale epigenetic studies in dairy cattle breeding. While genomic selection remains highly effective, adding epigenetic information improves prediction accuracy for certain traits.

These results open new perspectives for understanding the biological mechanisms underlying milk production, fertility, and morphology, as well as the influence of environmental factors on these mechanisms. In the longer term, epigenetic information could help enrich and refine future breeding strategies.



Using RUMIGEN Epigenotyping chip data to predict dairy cow performance

Published on 06/01/2026 by Marie-Pierre Sanchez (INRAE).

[Original text in French.](#)

The EpiChip, developed for cattle within the H2020 RUMIGEN project, makes it possible to obtain genome-wide DNA methylation data from a specific tissue. It provides a powerful approach for understanding the epigenetic factors that influence dairy cow performance. In this study, the RUMIGEN EpiChip was used on blood samples from 3,087 Holstein cows to evaluate how epigenetic biomarkers can help predict animal performance.

Traits related to milk production, fertility, udder health, and morphology were analysed. The objectives were to estimate:

1. the respective contributions of genetics and DNA methylation to trait variability, and
2. the improvement in prediction accuracy provided by the EpiChip for predicting cow performance.

The study showed that DNA methylation explained between 1% and 15% of the variability for 14 of the 34 traits analysed. The affected traits included milk production (1%), udder health (3%), fertility (3%), and morphology traits (between 1% and 15% depending on the trait).

In addition, a model including both epigenetic and genetic effects improved prediction accuracy for 8 of the analysed traits, with gains ranging from 0.5% to 6.7% depending on the trait.

These results open new opportunities for using EpiChip data to improve predictive capacity beyond conventional genetic and environmental factors. This provides a more comprehensive framework for animal performance management and may support more informed breeding and management decisions aimed at improving the efficiency and sustainability of cattle farming.



UPCOMING EVENTS

ECOGEN Webinar Series

EcoGen is a collaborative research cluster led by [HoloRuminant](#) in partnership with [Re-Livestock](#), [3D'Omics](#), [RUMIGEN](#), and [GERONIMO](#). Together, these five Horizon projects are redefining sustainable livestock production by exploring innovative breeding strategies, microbiome research, and advanced technologies.

As part of its activities, the EcoGen cluster is running a webinar series focused on interdisciplinary collaboration, showcasing cutting-edge research, and engaging diverse stakeholders in the future of sustainable livestock production.

See the previous episodes [here](#) 

Do not miss it!

The next EcoGen webinars will be on **June 3, from 10:30 – 11:30 CEST.**, titled “Mitigation and Resilience in Livestock Production”.

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.



The graphic features the ECOGEN logo at the top, followed by logos for HoloRuminant, Re-Livestock, GERONIMO, RUMIGEN, and 3D'Omics. The main title is 'WEBINAR SERIES: EPISODE 9' with the subtitle 'Mitigation and Resilience'. Below this are three circular portraits of the speakers: Mario Calus, Martin Škrlep, and Aurelie Vinet. At the bottom, it states 'OUR SPEAKERS', 'WEDNESDAY, 3 JUNE', '10:30-12:00 CEST', and 'ONLINE'. A 'REGISTER NOW' button is overlaid on the bottom right, with a hand cursor icon pointing to it. A small European Union logo and 'Funded by the European Union' text are also present.

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