



**HAL**  
open science

## **Rumigen: new breeding tools in a context of climate change**

S. Mattalia, A Vinet, M P L Calus, H A Mulder, M J Carabaño, C Diaz, M Ramon, S Aguerre, J Promp, R Vallée, et al.

### ► **To cite this version:**

S. Mattalia, A Vinet, M P L Calus, H A Mulder, M J Carabaño, et al.. Rumigen: new breeding tools in a context of climate change. 74th Annual Meeting of the European Federation of Animal Science, INRAE, Aug 2023, Lyon, France. 10.3920/978-90-8686-936-7 . hal-04195840

**HAL Id: hal-04195840**

**<https://hal.inrae.fr/hal-04195840>**

Submitted on 4 Sep 2023

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

**RUMIGEN: new breeding tools in a context of climate change**

S. Mattalia<sup>1</sup>, A. Vinet<sup>2</sup>, M.P.L. Calus<sup>3</sup>, H.A. Mulder<sup>3</sup>, M.J. Carabaño<sup>4</sup>, C. Diaz<sup>4</sup>, M. Ramon<sup>5</sup>, S. Aguerre<sup>1</sup>, J. Promp<sup>1</sup>, R. Vallée<sup>1</sup>, B.C.D. Cuyabano<sup>2</sup>, D. Boichard<sup>2</sup>, E. Pailhoux<sup>6</sup> and J. Vandenplas<sup>3</sup>

<sup>1</sup>Idele, Domaine de Vilvert, 78350 Jouy en Josas, France, <sup>2</sup>INRAE, GABI, Domaine de Vilvert, 78350 Jouy en Josas, France, <sup>3</sup>Wageningen University & Research, Animal Breeding and Genomics, P.O. Box 338, 6700 AH Wageningen, the Netherlands, <sup>4</sup>INIA, Departamento de Mejora Genética Animal, Ctra. de La Coruña km 7.5, 28040 Madrid, Spain, <sup>5</sup>IRIAF, 13300, Valdepeñas, Spain, <sup>6</sup>INRAE, BREED, Domaine de Vilvert, 78350 Jouy en Josas, France; [sophie.mattalia@idele.fr](mailto:sophie.mattalia@idele.fr)

RUMIGEN is a project financially supported by the EU that aims to develop breeding programs able of managing the trade-offs between efficient production and resilience to extreme climate conditions. RUMIGEN is designed under a multi-disciplinary approach that mixes competencies in both genetics and social sciences. The genetic approach aims to enhance genomic selection using three levers: quantitative genetics, genome editing, and epigenetics. One of the objectives of RUMIGEN is to enlarge selection criteria and to provide genomic tools to select heat tolerant dairy cows. Studies are dedicated to the definition of heat-tolerance traits based on production, reproduction and health records, as well as to the study of the trade-offs between these traits, and with those already included in selection indexes. In France, Spain and the Netherlands, performances recorded in commercial herds (i.e. milk production traits, somatic cell scores and conception rate after first AI) were combined with meteorological data obtained from the nearest weather stations, and analysed in order to measure the impact of heat stress. First results obtained for different breeds and in a large range of farming and climatic scenarios showed that the combination of both types of information was relevant at the population level. Some differences between thresholds for optimal THI were observed between countries for some traits, which could be explained by different factors (farm management, exposure to outside temperatures, mitigation practices, etc.). However a decrease was observed on all performance traits with increasing temperatures, with consistent patterns of slopes between breeds and countries. Therefore this approach appears relevant to define novel traits related to heat tolerance for different breeds and different climates.

**The genetic basis of ruminant microbiomes – contribution of the HoloRuminant project**

Y. Ramayo-Caldas<sup>1</sup>, I. Mizrahi<sup>2</sup>, P. Pope<sup>3</sup>, C. Creevey<sup>4</sup>, J.P. Sanchez<sup>1</sup>, R. Quintanilla<sup>1</sup> and D. Morgavi<sup>5</sup>

<sup>1</sup>IRTA, IRTA Torre Marimon, 08026, Spain, <sup>2</sup>Ben-Gurion University of the Negev, Department of Life Sciences, Negev, Be'er-Sheva, 8443944, Israel, <sup>3</sup>Norwegian University of Life Sciences, Faculty of Biosciences, Elizabeth Stephansens v. 15, 1430, Norway, <sup>4</sup>Queen's University Belfast, School of Biological Sciences, Institute for Global Food Security, Belfast, BT9 5DL, United Kingdom, <sup>5</sup>Université Clermont Auvergne, INRAE, VetAgro Sup, UMR Herbivores, Saint-Genès-Champagnelle, 63122, France; [yulixaxis.ramayo@irta.cat](mailto:yulixaxis.ramayo@irta.cat)

Microbiome-host interactions have profound effects on metabolic functions and physiological processes that influence growth, production efficiency, animal welfare, and the robustness of the ruminant holobiont. Interactions between the host and its microbiome are influenced by both external and host-specific factors. While the influence of the external environment has long been recognised, it has also been reported that some rumen microbes in the core microbiome are transferred from dam to offspring, with the heritability of the rumen microbiome being low to moderate. In addition, genetic variants and candidate genes associated with individual variation in microbial traits have been reported in the host ruminant genome. However, existing information is scarce, based on reduced numbers of animals and mainly focused on the rumen microbiome. In HoloRuminant, we plan to assess the host genetic influence on microbiomes by using a holistic multi-omics approach to characterise the establishment and dynamics of microbiomes from different body sites during key life events. Planned activities also include the development of an open access database (HoloR) of existing and novel data, together with a repository (HoloR tools) of standardised bioinformatics and analytical pipelines developed in the project. Hologenomic data collected at multiple meta-omics levels will then be used to explore associations between microbial functions and host phenotypes, as well as links between host genetics, microbial, and host traits. The results of the project will improve our understanding of the mechanisms driving host-microbiome interactions in ruminants and may enable the implementation of novel conservation and breeding programs from a holobiont perspective.