MINISTERIO DE CIENCIA E INNOVACIÓN
INIA Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria

ICAR 2023 TOLEDOSPAIN 22nd to 26th May 2023
Breeding for resilience: transitioning diverse livestock farming systems into the future

SESSION 4.1: CLIMATE CHANGE MITIGATION STRATEGIES

The Spanish strategy to reduce methane emissions through breeding in dairy cattle

Óscar González-Recio, J. López-Paredes, A. García-Rodríguez

Departamento de Mejora Genética Animal - INIA

Madrid, SPAIN

Accesibility

Sufficiency

Sustainability and adaptability /social acceptance

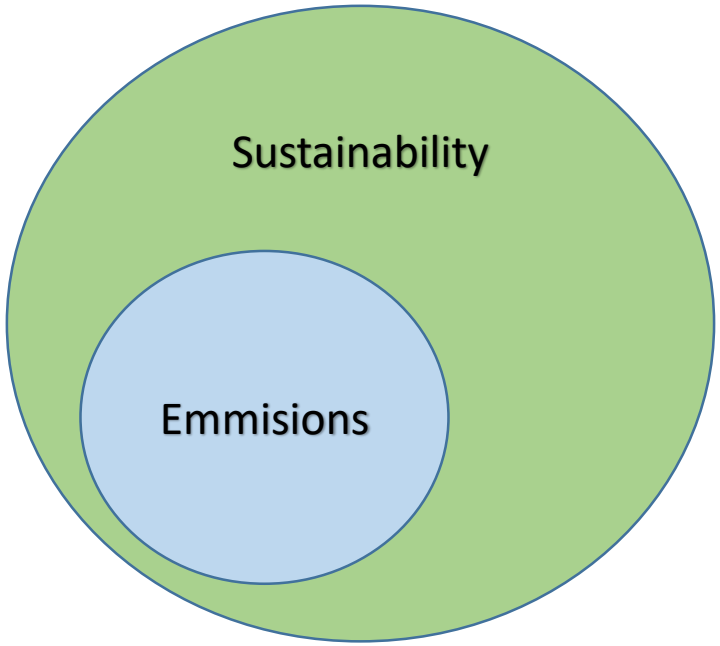
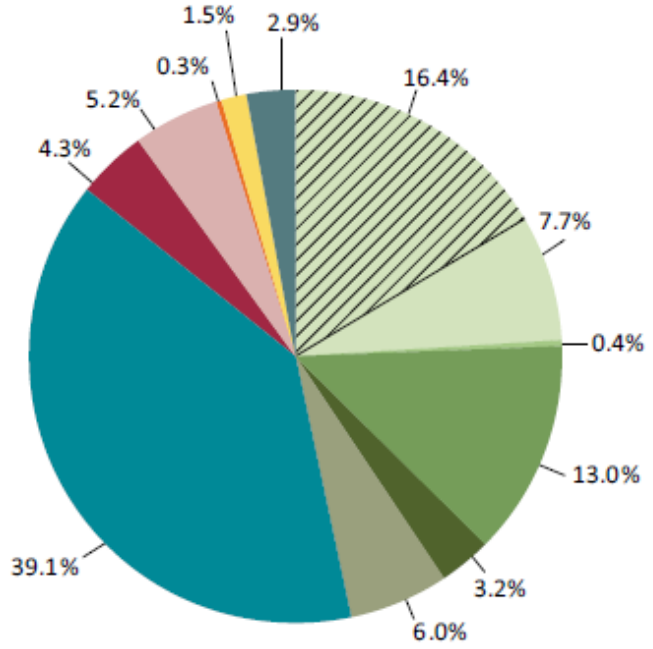


FIGURE 4. Global emissions from livestock supply chains by category of emissions



FAO (2013)

Alfaro & Mejias (2022) in ISBN-13: 978-84-95531-63-6 from FAO (2016)

Methane as an opportunity

- Methane is an important GHG from enteric fermentation

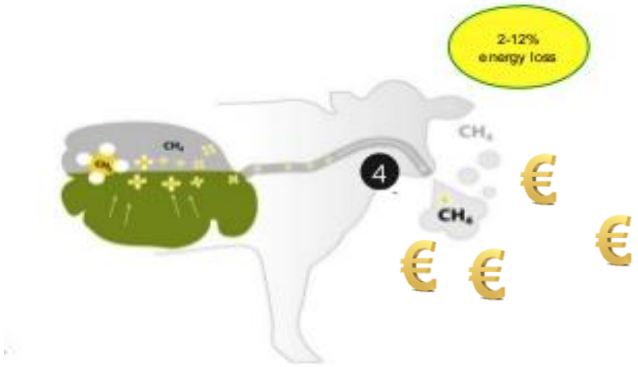
28-34x

- It has a short life in the atmosphere (10-20 yrs)
- Important mitigation potential

Efficient mitigation

COP26

- It is an energy sink, and a cost for the farmer



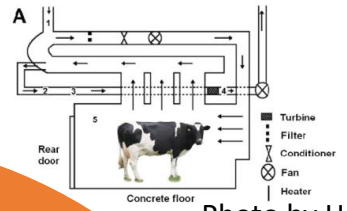


Photo by Hernandez Cabezas-Martinez

Photo by Idoia Goiri

Photo by Unknown author

Photo by Idoia Goiri

Photo by Mark Thiessen

- **Green Feed vs RC**

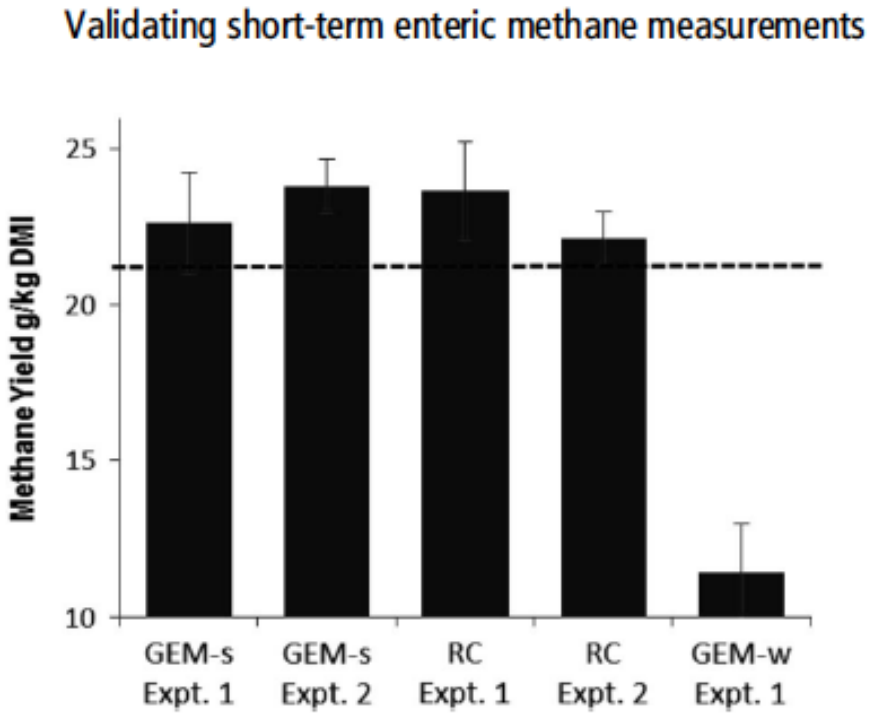


Figure 4 Methane yield results (g/kg dry matter intake (DMI)) by method (GreenFeed Emission Monitors (GEM) dispensing supplement (GEMs) or water (GEMw) or respiration chamber (RC)) and by experiment with 95% confidence interval. Dotted line corresponds to the predicted methane yield based on IPCC, 2006.

Velazco et al. (2016) Animal

- **Green Feed (g/d) vs Sniffers (ppm)**
  - Genetic correlation ~0.77 (van Breukelen et al. 2023, JDS)
  - More consistent results when averaging per week
    - Higher heritabilities (~0.36)
    - Higher repeteabilities (~0.61)

- **Sniffers (2018-2023)**
- **Advantages**
  - Do not interact with normal behaviour
  - Affordable (ready to be installed in farms per 10k-12k €)
  - Allow a large number of records per animal
  - Portable
  - Produce heritable phenotypes, correlated with other measurements and traits DMI, MY, RFI,…
- **Limitations**
  - Do not measure flux (**yet**…)
  - Require AMS or closed feed bin where all cows pass by

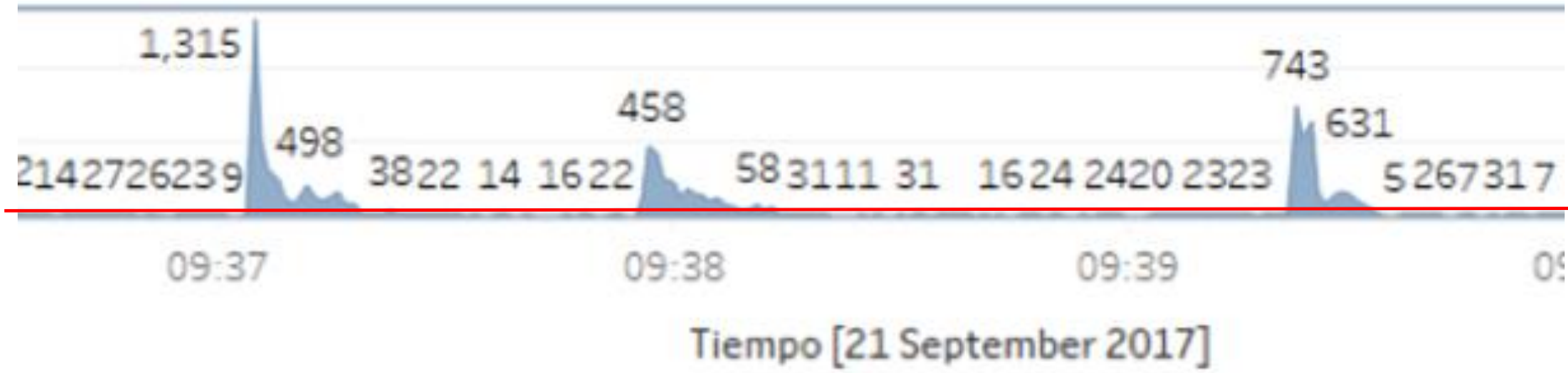
METHAGENE

All devices produce proxies. Even RC are not true representatives because they preclude natural behaviour. Methagene was a really important COST action that allowed a lot of international collaboration and learning!

Importance of trait standardization within and accross countries

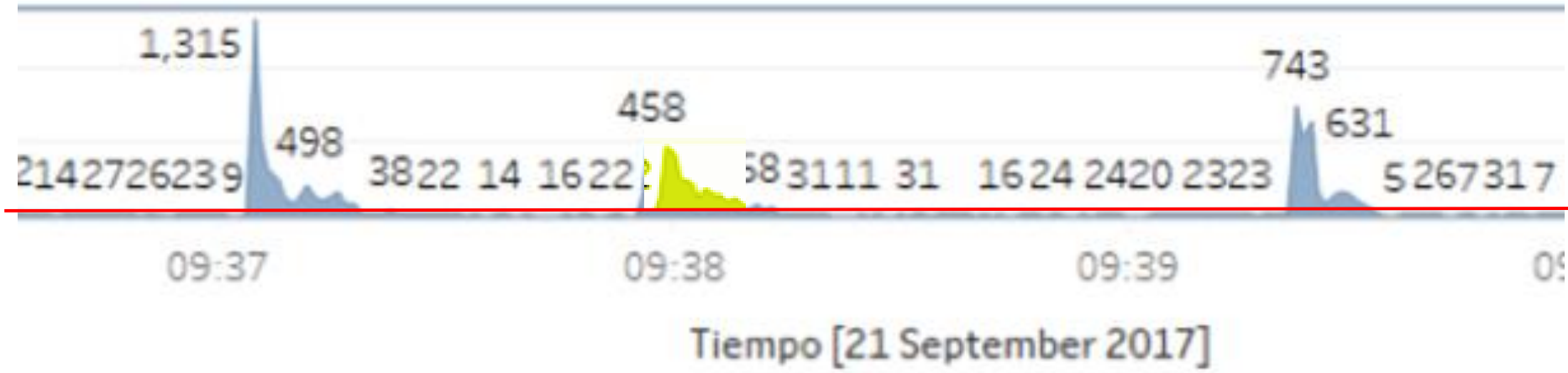
Example of eructation pattern from sniffers

Example of eructation pattern



-Mean: Average all values above the baseline

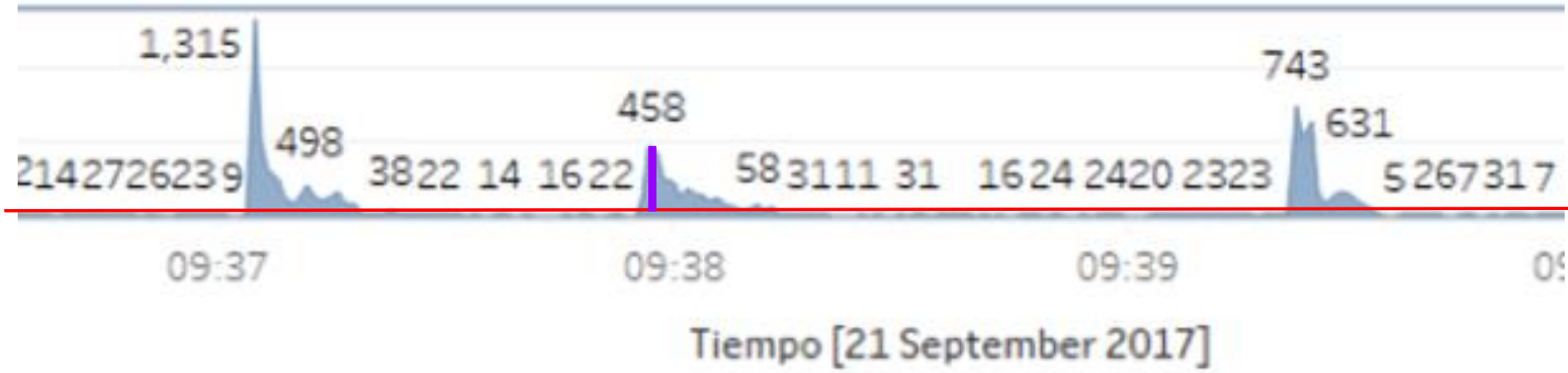
Example of eructation pattern



baseline

-Mean: Average all values above the baseline
-mean AUC per minute: Area of eructation events

Example of eructation pattern



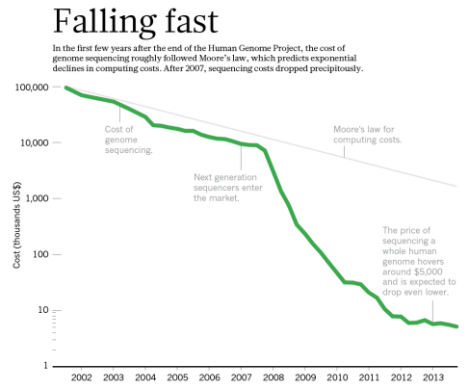
baseline

-Mean: Average all values above the baseline
-mean AUC per minute: Area of eructation events
-Average value of peaks magnitude per minute

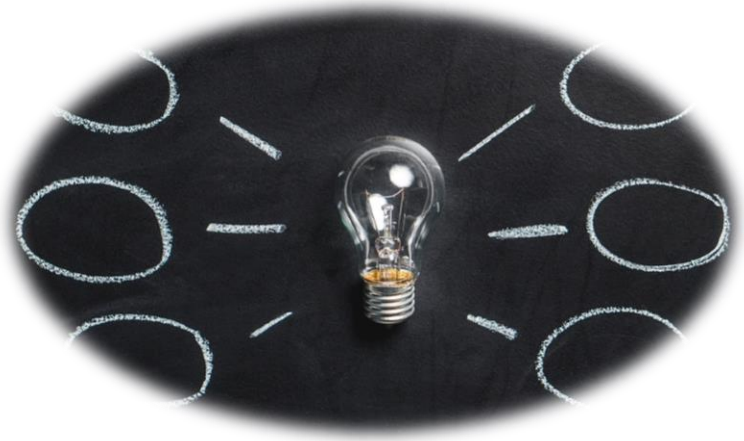
- **We need consensus on how to treat the measurements from sniffers (Research needed)**

ICAR THE GLOBAL STANDARD FOR LIVESTOCK DATA

- **We can solve most of limitations of sniffers <u>with computer science and statistics</u>, cheaper and worth it for a large scale phenotyping**



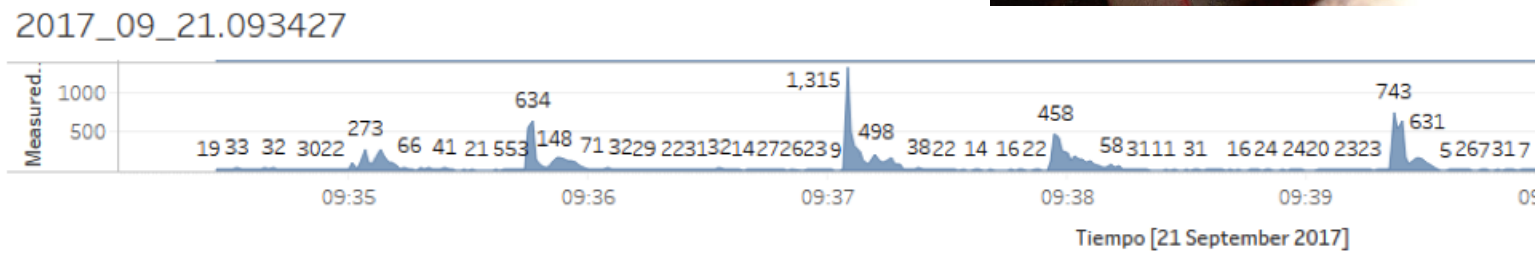
- **Sniffers 3.0**
  - Convert sniffers into greenfeeds-like
  - Measure or infer flux from respiration or eructation air volume.
  - Independent on regression on MY or LW (Changunda et al. 2009, Madsen et al. 2010)



DATA RECORDING ON FARMS

- 22 commercial farms with methane measurements >2300 cows)

Precision farming



Genotypes (50k SNPs)

Feed Efficiency

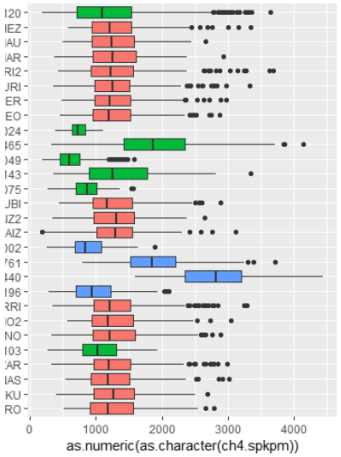
IRTA Institute of Agrifood Research and Technology

DATA RECORDING ON FARMS SINCE 2018

METHANE

- 2547cows (2018-2022)
- 27 farms (Northern Regions)

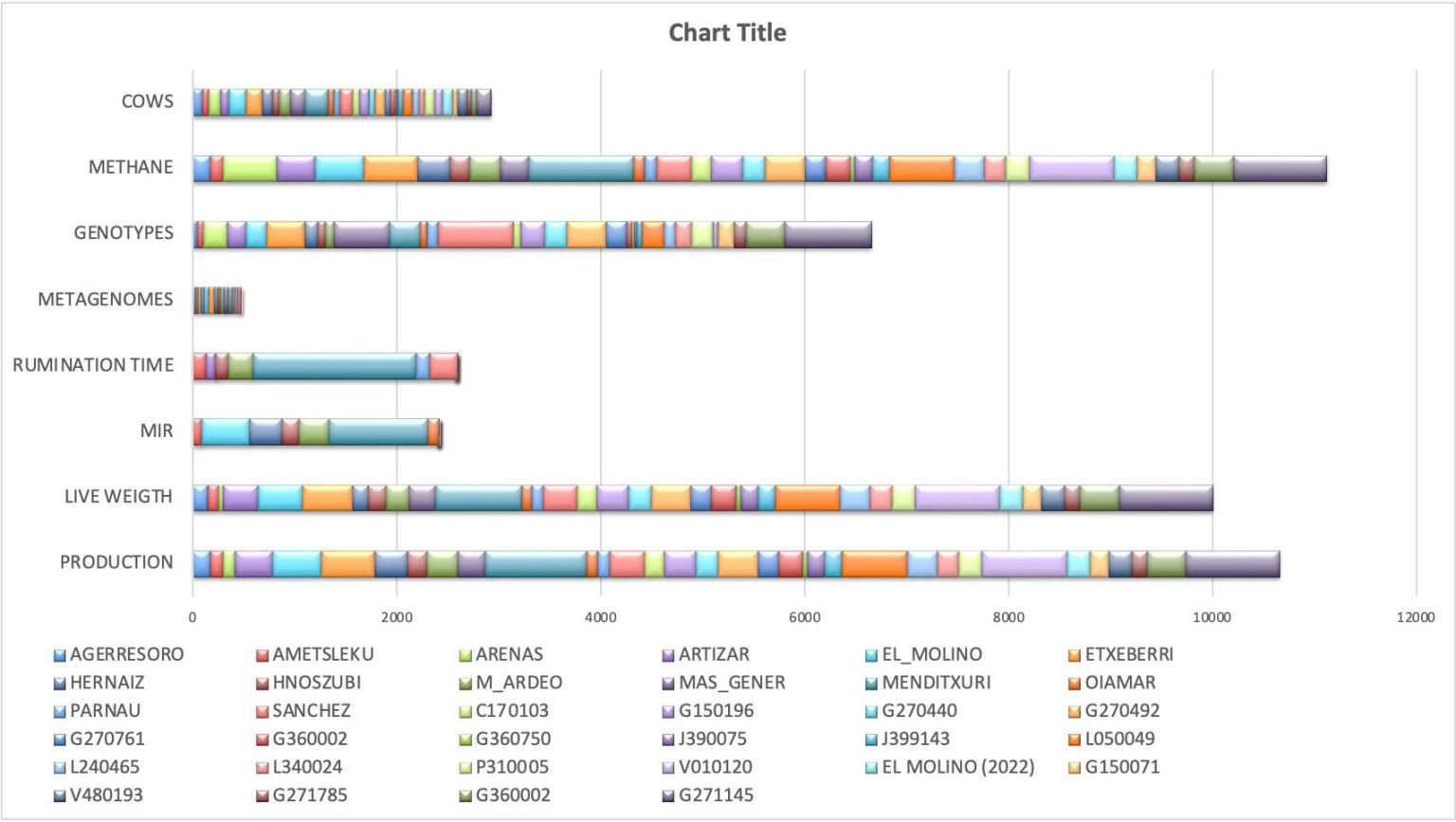
- 8,799 weekly averages



DRY MATTER INTAKE

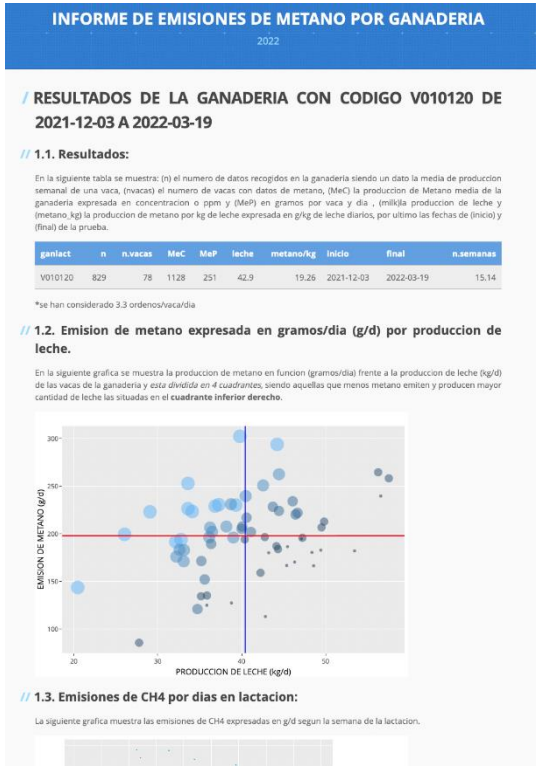
- 648 cows (2004-2020)
- 5 farms (Galicia, Asturias, Catalonia)
- 15,824 weekly averages

DATA RECORDED



FARM Report

- All collaborating farmers received free genotyping of all cows and heifers (funded by the project and CONAFE).
- Small compensation to acknowledge their work.
- A report is sent to the farmer after the measuring period



INFORME DE EMISIONES DE METANO POR GANADERIA

2022

RESULTADOS DE LA GANADERIA CON CODIGO V010120 DE 2021-12-03 A 2022-03-19

1.1. Resultados:

En la siguiente tabla se muestra: (n) el numero de datos recogidos en la ganaderia siendo un dato la media de produccion semanal de una vaca, (nvacas) el numero de vacas con datos de metano, (MeC) la produccion de Metano media de la ganaderia expresada en concentracion o ppm y (MeP) en gramos por vaca y dia , (milkla produccion de leche y (metano_kg) la produccion de metano por kg de leche expresada en g/kg de leche diarios, por ultimo las fechas de (inicio) y (final) de la prueba.

ganlact	n	n.vacas	MeC	MeP	leche	metano/kg	inicio	final	n.semanas
V010120	829	78	1128	251	42.9	19.26	2021-12-03	2022-03-19	15.14

*se han considerado 3.3 ordenos/vaca/dia

1.2. Emision de metano expresada en gramos/dia (g/d) por produccion de leche.

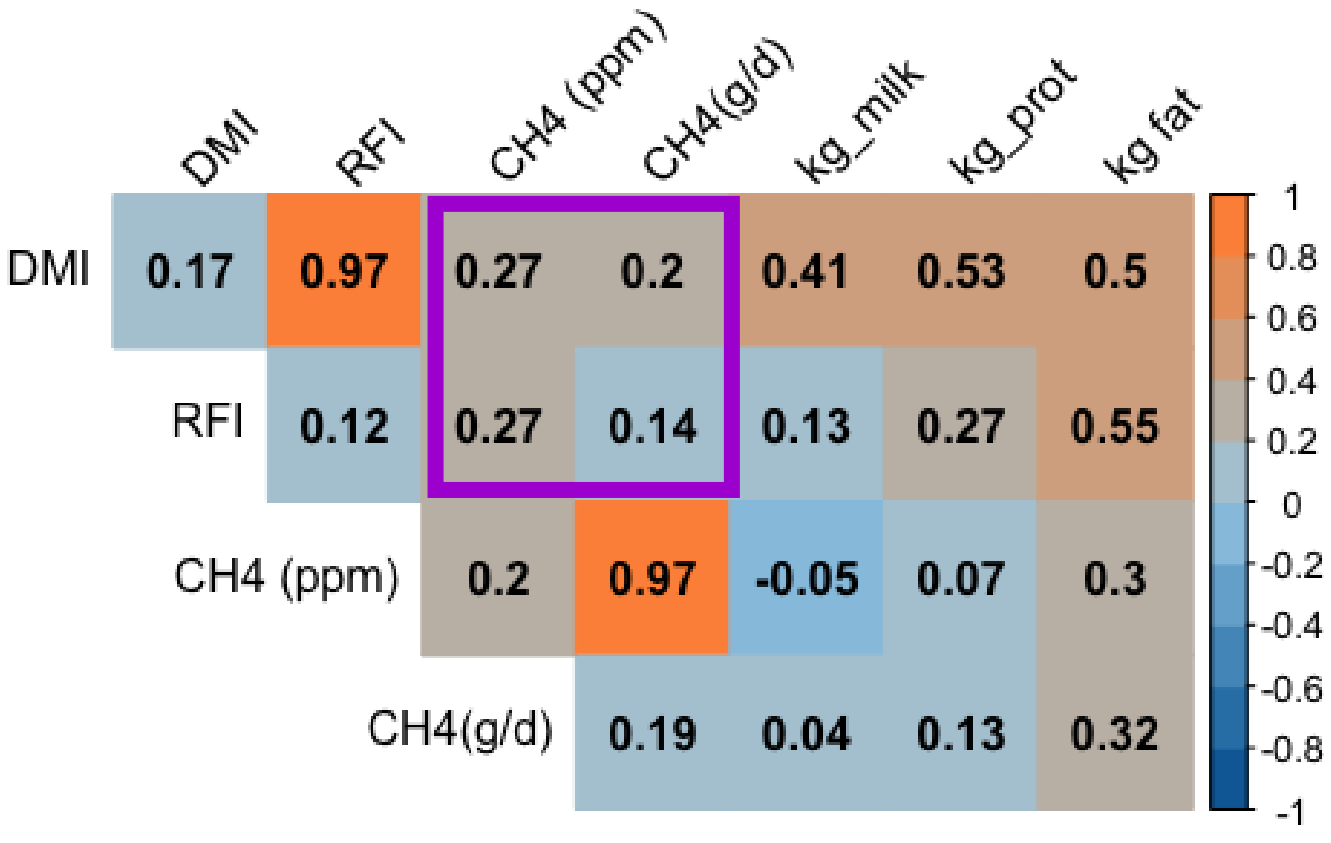
En la siguiente grafica se muestra la produccion de metano en funcion (gramos/dia) frente a la produccion de leche (kg/d) de las vacas de la ganaderia y *esta dividida en 4 cuadrantes*, siendo aquellas que menos metano emiten y producen mayor cantidad de leche las situadas en el **cuadrante inferior derecho.**

1.3. Emisiones de CH4 por dias en lactacion:

La siguiente grafica muestra las emisiones de CH4 expresadas en g/d segun la semana de la lactacion.

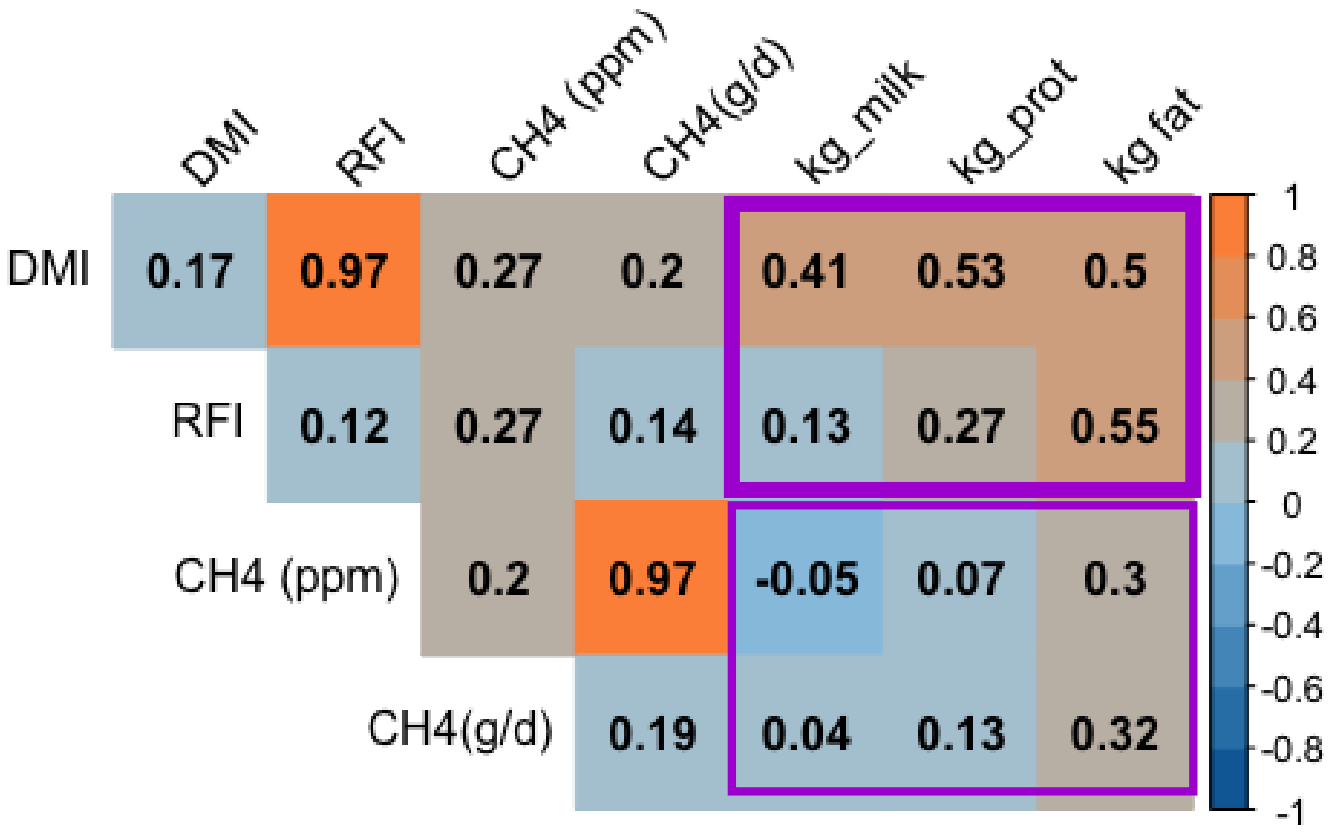
Bovine EURO12k

Genetic correlations



- Positive correlation between methane and feed efficiency.
- Larger intake levels →more methane emisions → less efficiency
- But different energy sinks

Genetic correlations



- More feed intake, more milk, but less efficiency.
- Methane is correlated with Fat yield (not prot or milk yield)

METHANE & GENETICS

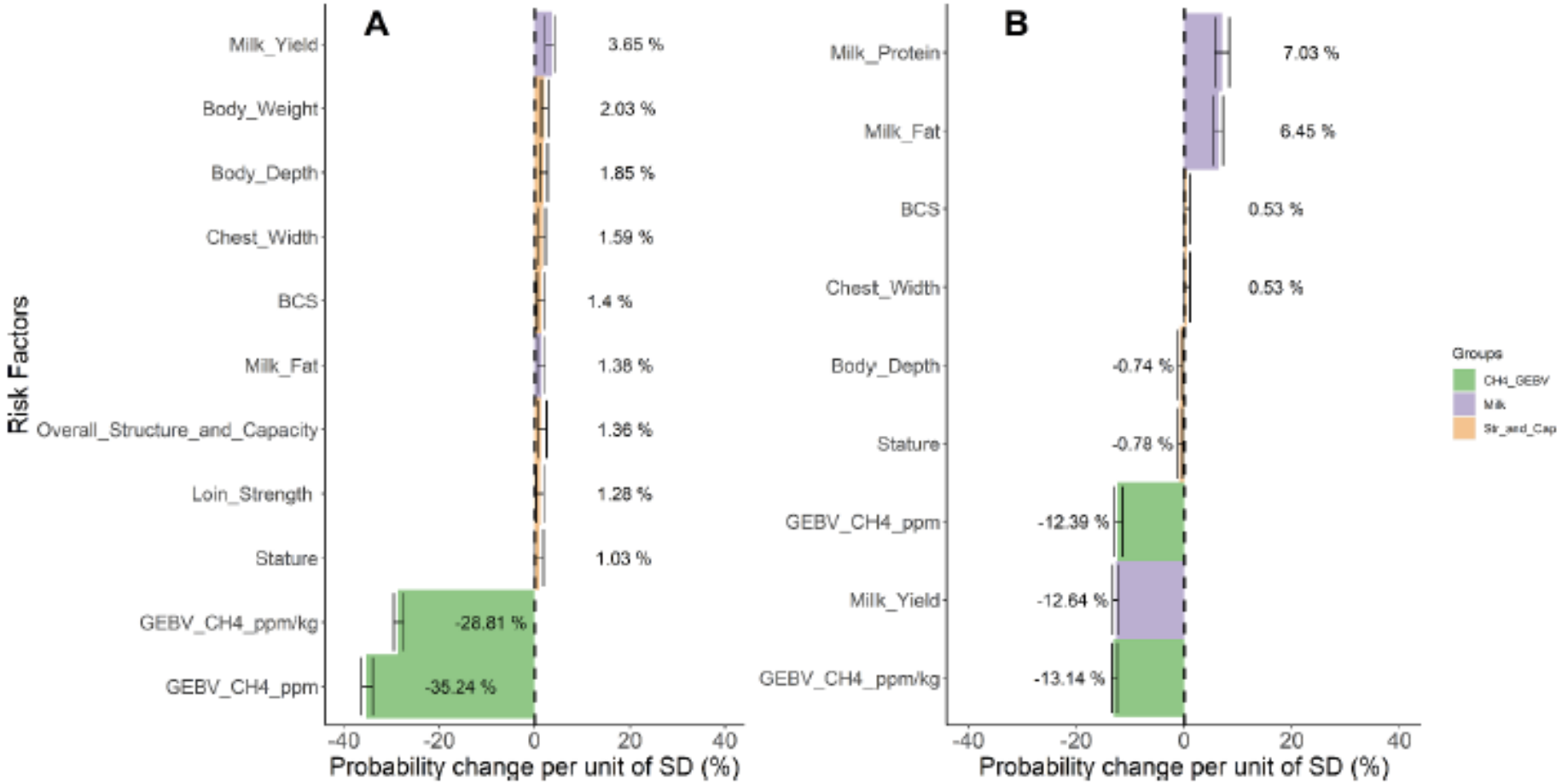
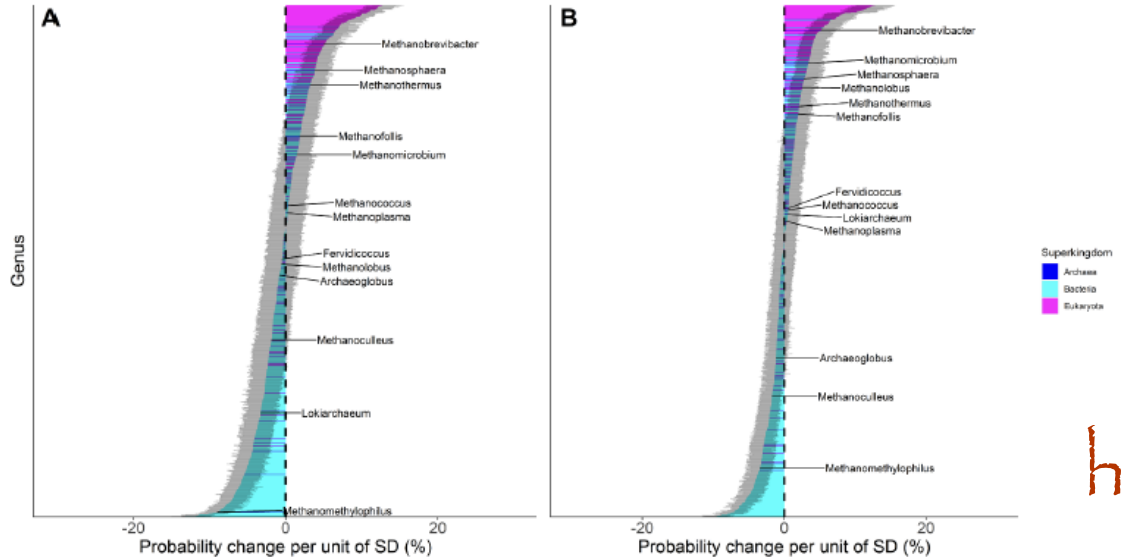


Fig. 1. Change in the probability of a cow being classified in the upper quartile for methane concentration (ppm CH_4) and methane intensity (ppm CH_4 / kg milk) per unit of increment in the risk factor corrected for standard deviation for methane concentration (A) and methane intensity (B). Black dashed lines indicate the baseline probability of being classified in the upper quartiles without any variable effect. Probability intervals are depicted for each risk factors. BCS=Body condition score, GEBV_CH4_ppm/kg= Genetic merit for methane intensity (MI), GEBV_CH4_ppm=Genetic merit for methane concentration (MET), CH4_GEBV=Genetic merit for methane traits, Milk=Milk related traits, Str_and_Cap= Structure and capacity related traits.

METHANE & GENETICS



h^2~0.10-0.40

Fig. 3. Change in the probability of being classified in the upper quartile for (A) methane concentration (ppm CH_4) and (B) methane intensity (ppm CH_4/kg milk) per unit of standard deviation for relative abundance (%) of 1240 genera colored by superkingdom. Black dashed line indicates the baseline probability of being classified in the upper quartiles without any genus effect. All the archaea genera are explicitly indicated. Probability intervals based on posterior standard deviations are depicted in gray for all genera.

Microbiota composition is heritable

- **Heritabilities (0.10-0.40)**

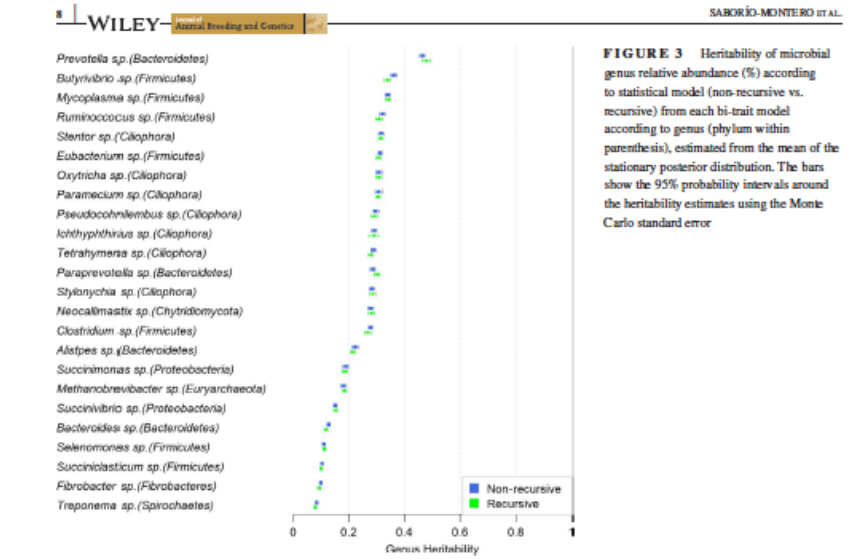
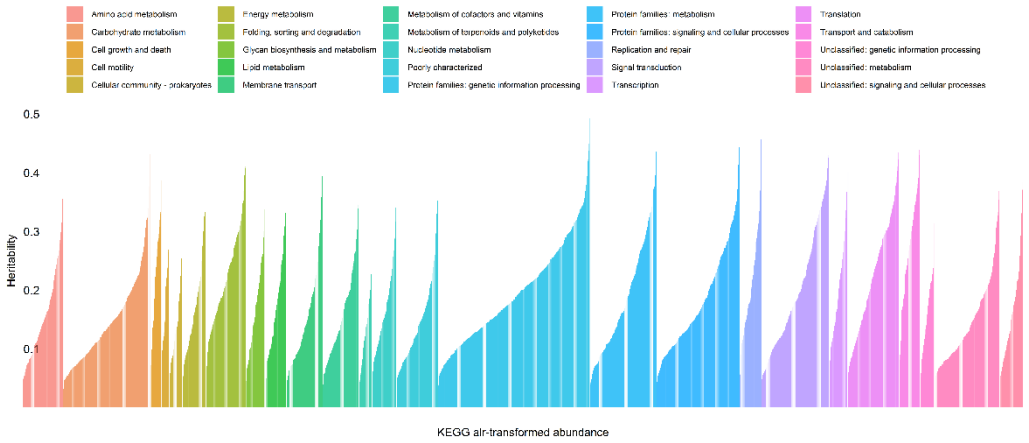
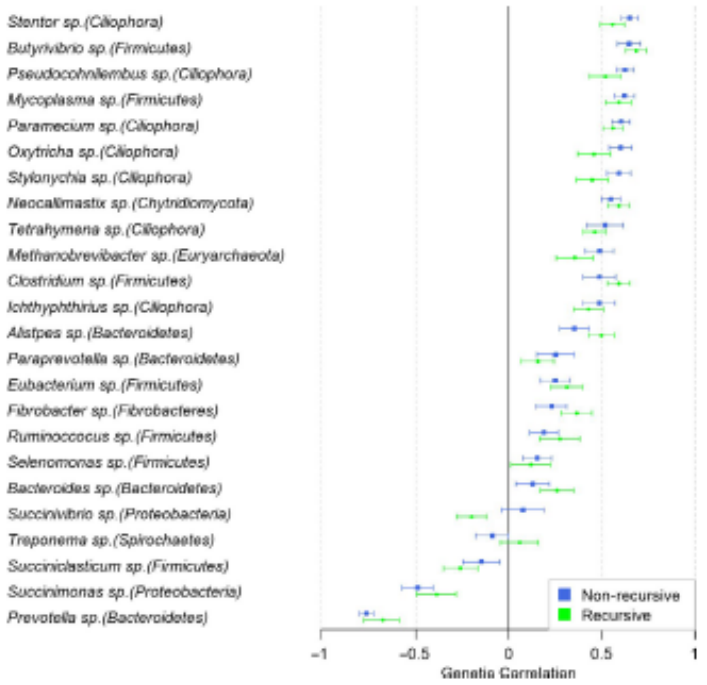


FIGURE 3 Heritability of microbial genus relative abundance (%) according to statistical model (non-recursive vs. recursive) from each bi-trait model according to genus (phylum within parenthesis), estimated from the mean of the stationary posterior distribution. The bars show the 95% probability intervals around the heritability estimates using the Monte Carlo standard error



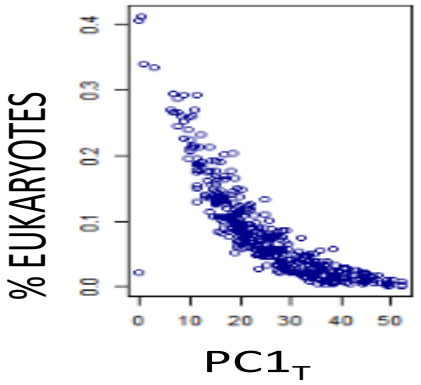
- **Fungi and protozoa are highly genetically correlated to methane emissions**

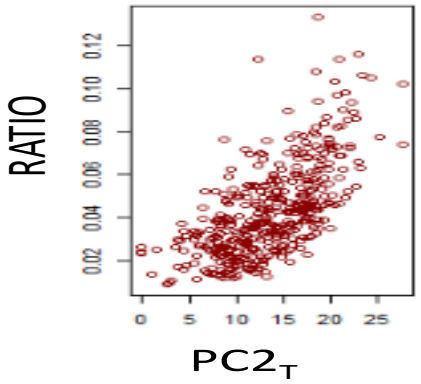
FIGURE 4 Genetic correlation between methane concentration (ppm) and microbial genus relative abundance (%) according to statistical model (non-recursive vs. recursive) from each bi-trait model according to genus (phylum within parenthesis), estimated from the mean of the stationary posterior distribution. The bars show the 95% probability intervals around the heritability estimates using the Monte Carlo standard error



Relationship with FE and microbiota

- **Considerations to breed for lower methane emissions (and feed efficiency)**
  - Breeding for lower methane may impact microbiota modulation ("organ").
  - What are the expected consequences?





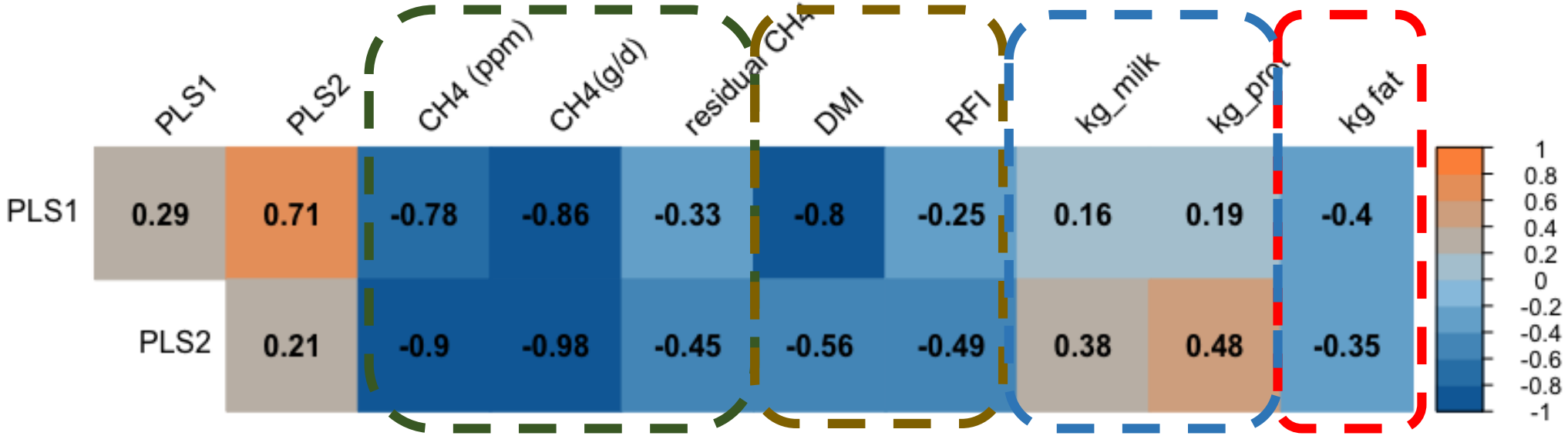
Relationship with FE and microbiota

INTERBULL BULLETIN NO. 56. Leeuwarden, The Netherlands, April 26 – 30, 2021

Dry matter intake, methane emissions and microbiome profiles as new traits for feed efficiency

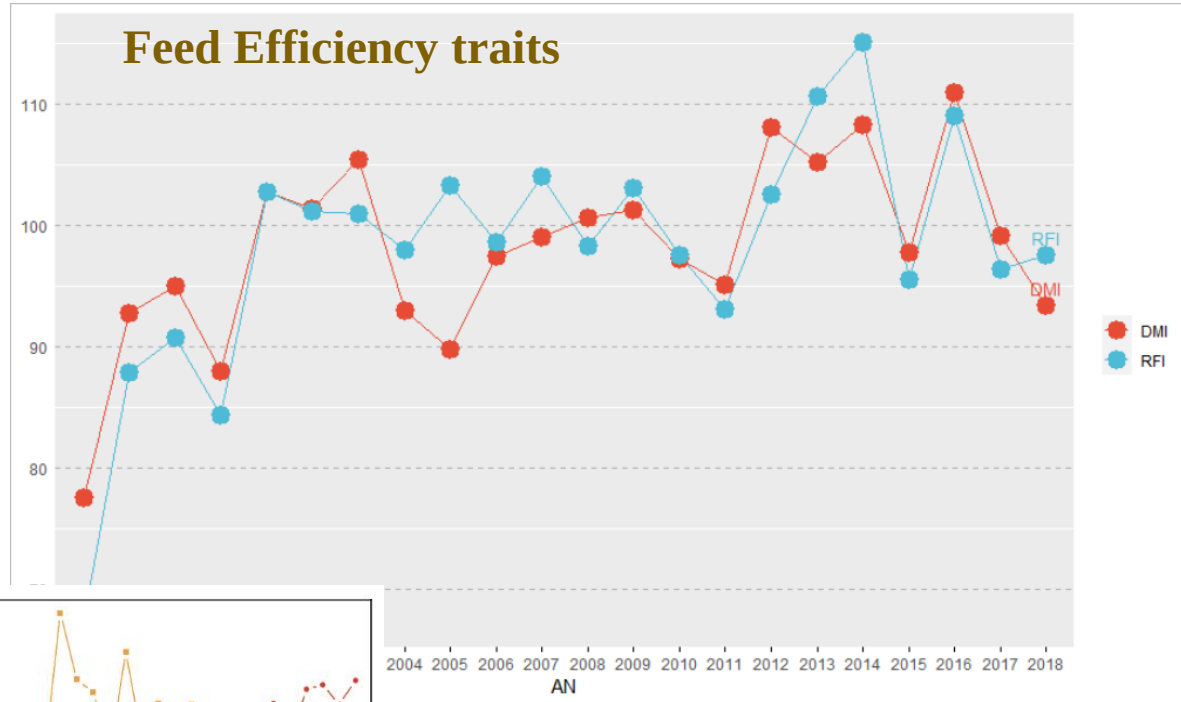
J. López-Paredes[1], A. Saborío-Montero[2], N. Charfeddine[1], J.A Jiménez-Montero[1] and O. González-Recio[23]

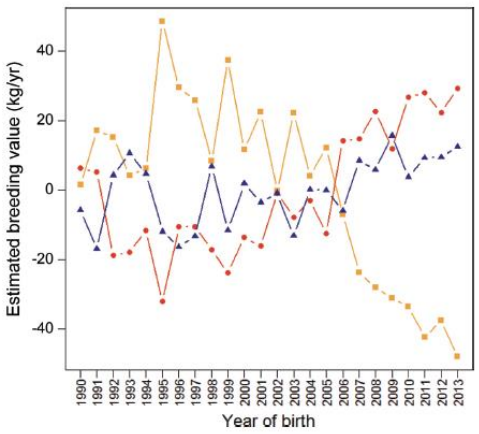
- **Microbiota composition is regulated by the cow genome**



- Microbes correlated to CH_4, are also correlated (in the same direction) with FE traits.
- And with increased MY and PY.
- Correlation with FY is antagonistic.

Genetic trends

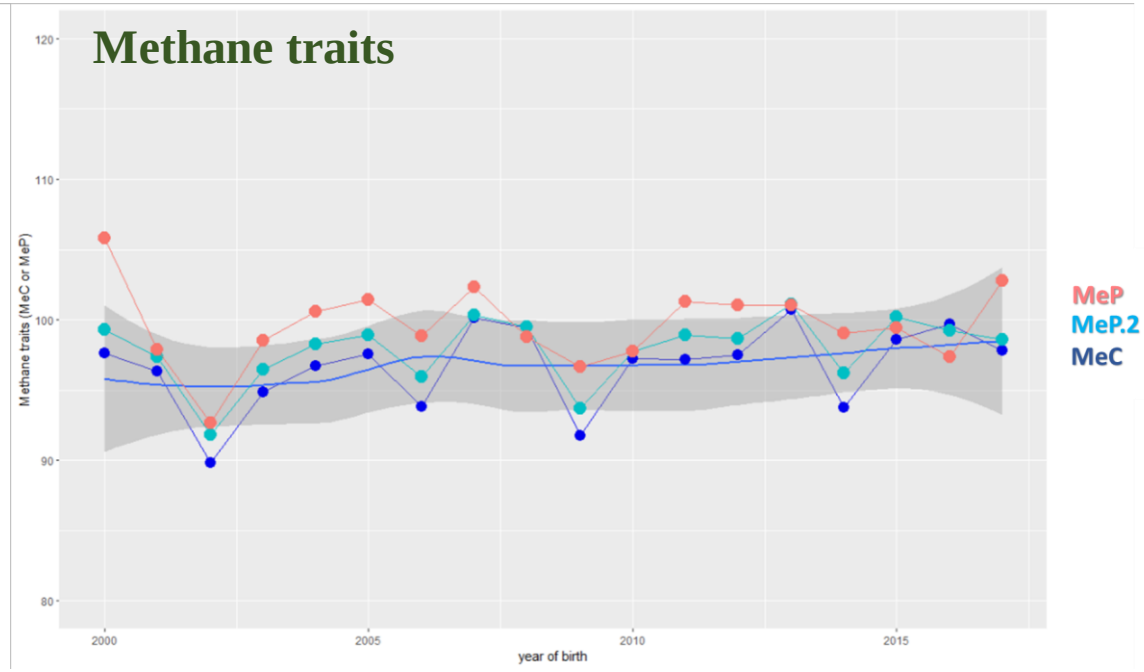




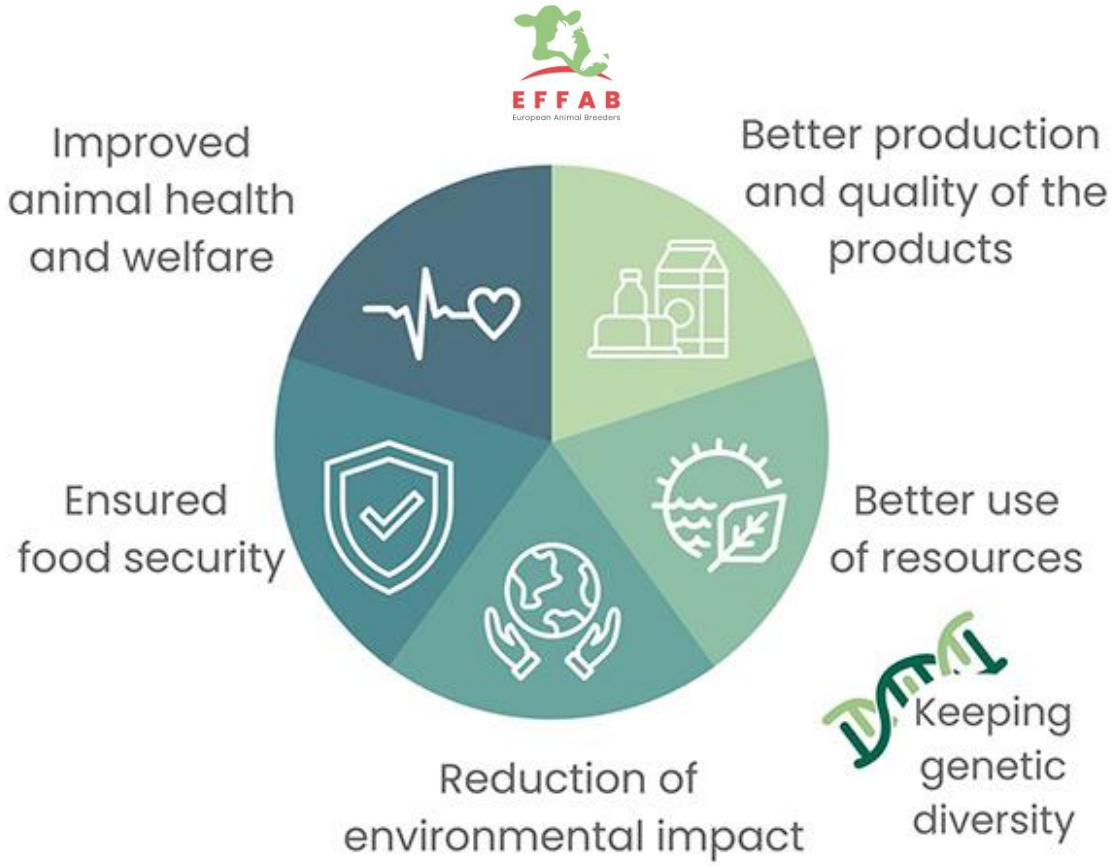
J. Dairy Sci. 98:7340–7350
http://dx.doi.org/10.3168/jds.2015-9621

Hot topic: **Definition and implementation of a breeding value for feed efficiency in dairy cows**

J. E. Pryce,*†[1] O. Gonzalez-Recio,* G. Nieuwhof,*‡ W. J. Wales,§ M. P. Coffey,# B. J. Hayes,*† and M. E. Goddard*‖



Methane and FE in selection indices



Considering traits in the selection indices

- **Feed Efficiency**
  - DMI, RFI, Feed Saved, Feed Efficiency ratio traits (per unit of product).
- **Methane**
  - MeC, MeP, RMeP, RMeC, MeI, MeY

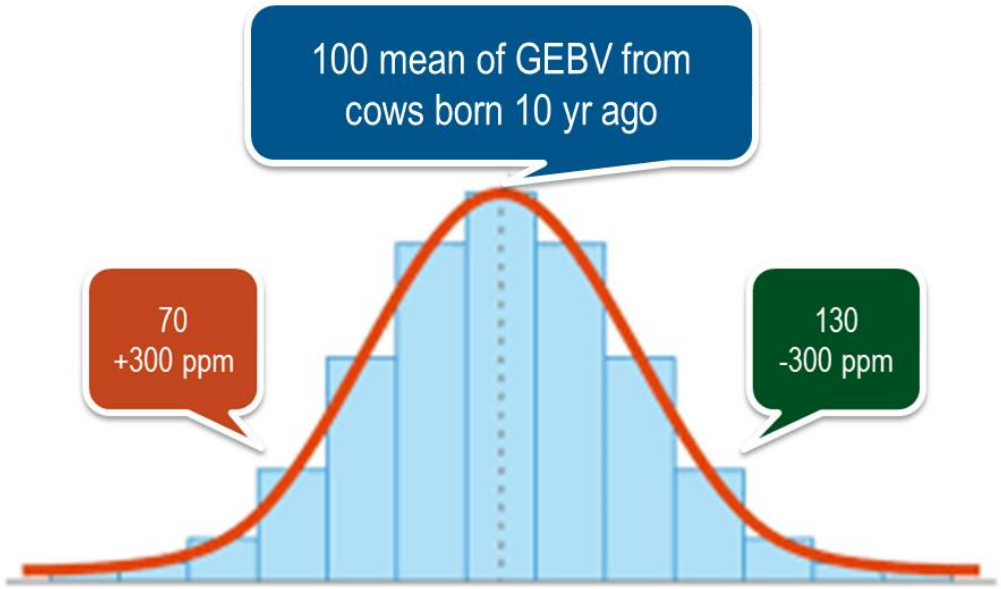
  - Avoid ratio traits (FE, MeI, MeY)
  - Weight traits appropiately
    - Economic weights easier to calculate
    - Lower genetic correlation with other economically important traits
    - Desired genetic response for methane
  - Microbiota

SPANISH METHANE OFFICIAL EVALUATION

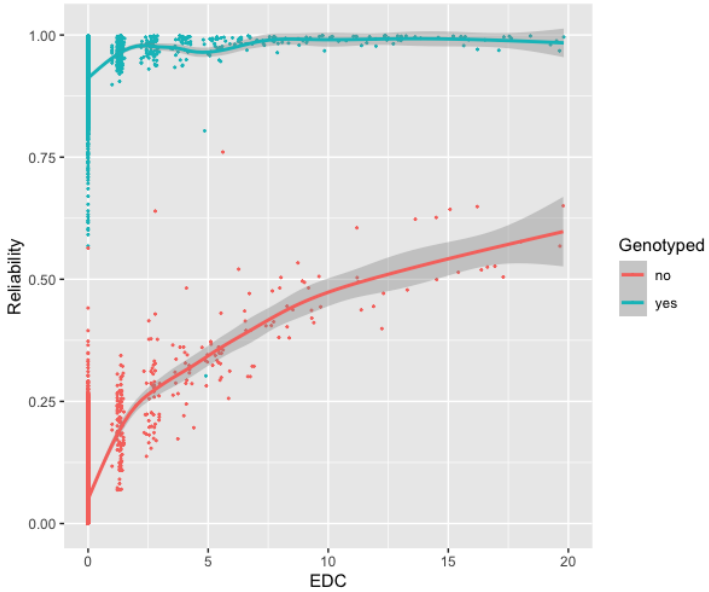
- **Based on direct measurements**
- **To be released on June 2023**

- **SingleStep Genomic BLUP**
  - CH4= m + Npar + HWR + DEL + MP + PERM + ADIT + e
  - h^2=0.17
  - r^2=0.66
- **360,000 evaluated animal (118,000 genotyped)**

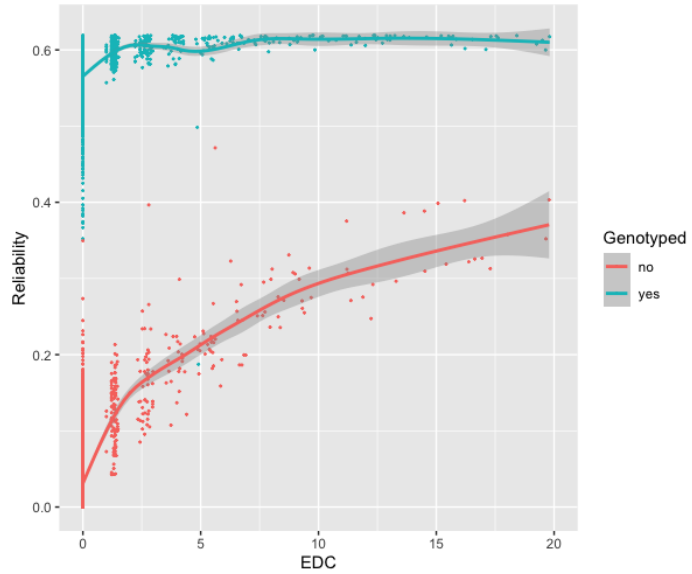
SPANISH METHANE OFFICIAL EVALUATION



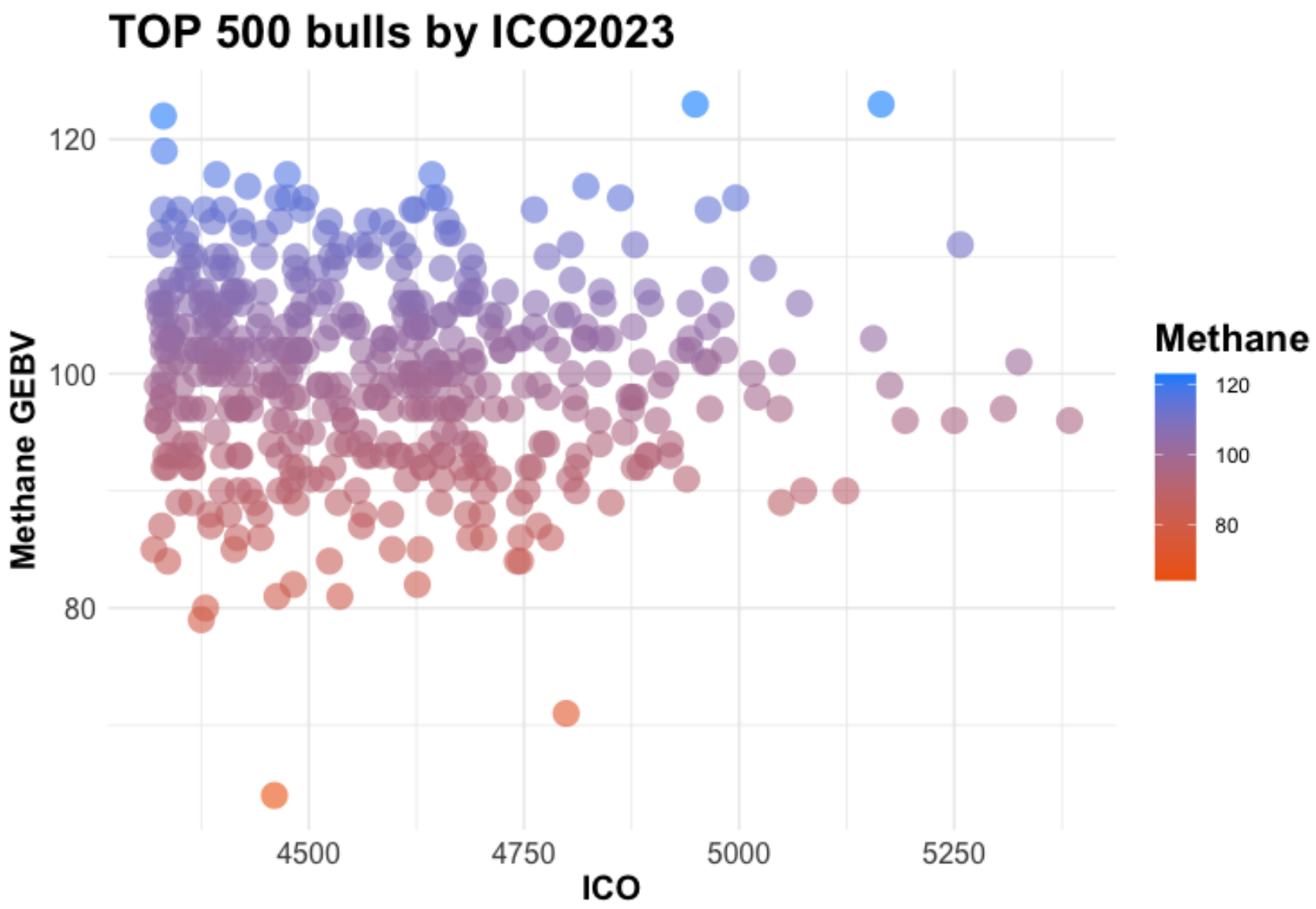
GEBV reliability



GEBV adjusted reliability

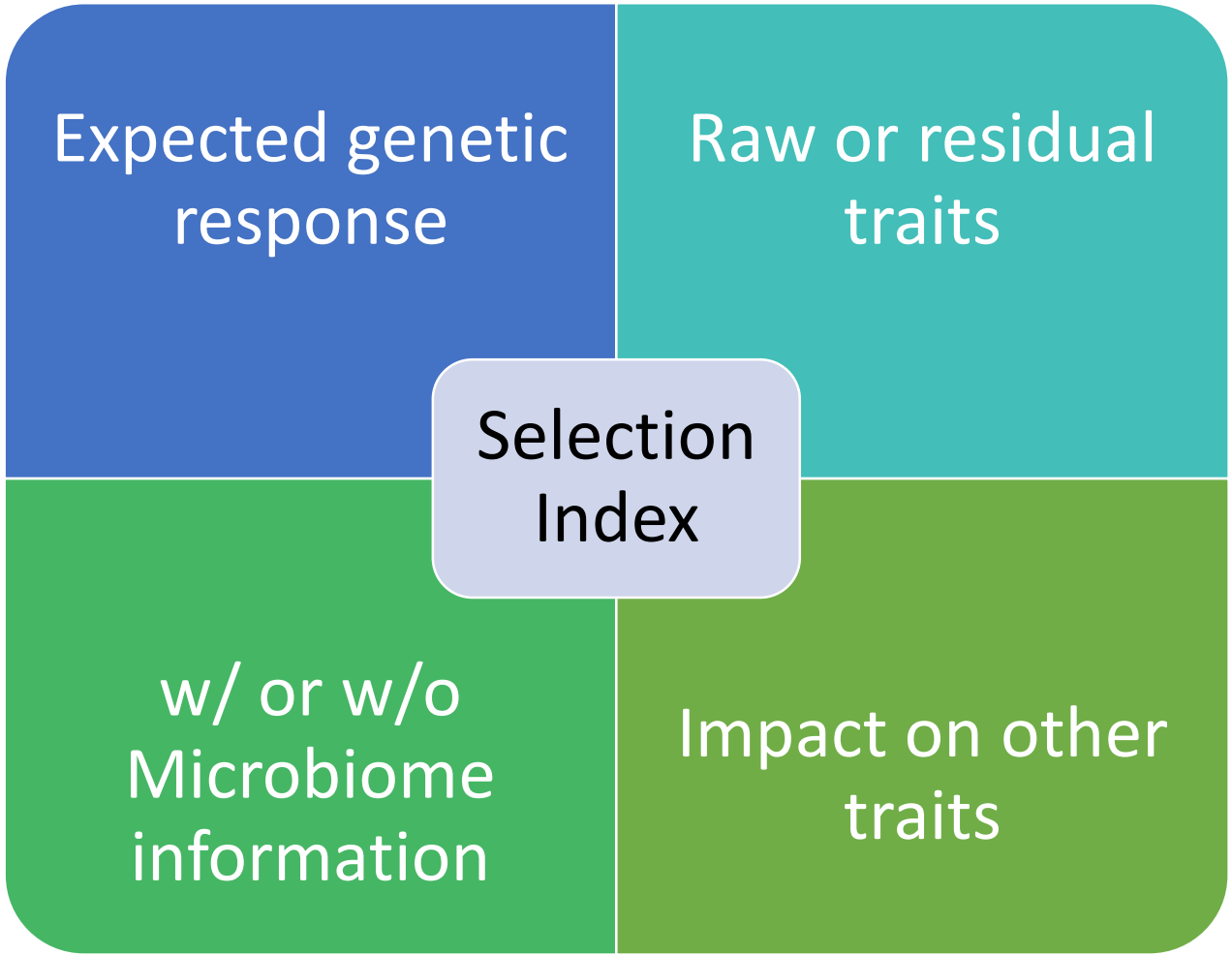


SPANISH METHANE OFFICIAL EVALUATION

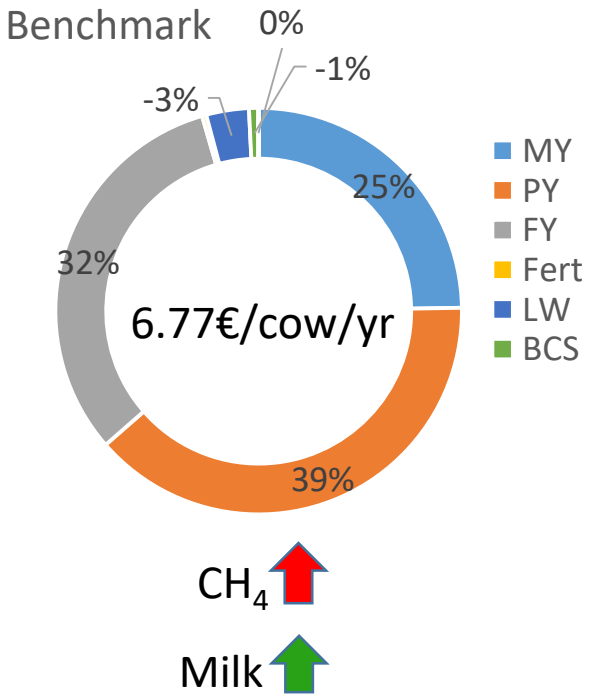


What is best trait(s) to select for?

(Disclaimer: Not official yet)



SELECTION INDICES



DMI, Methane
Production 63%
Fertility 3%
Size & BCS 16%
FE 14%
Methane 4%
51.77€/cow/yr

DMI, Methane, Microbiome
Production 42%
Fertility 5%
Size & BCS 18%
FE 7%
Methane 1%
Microbiome 25%
56.95 €/cow/yr

CH4 ↓
Milk ↓

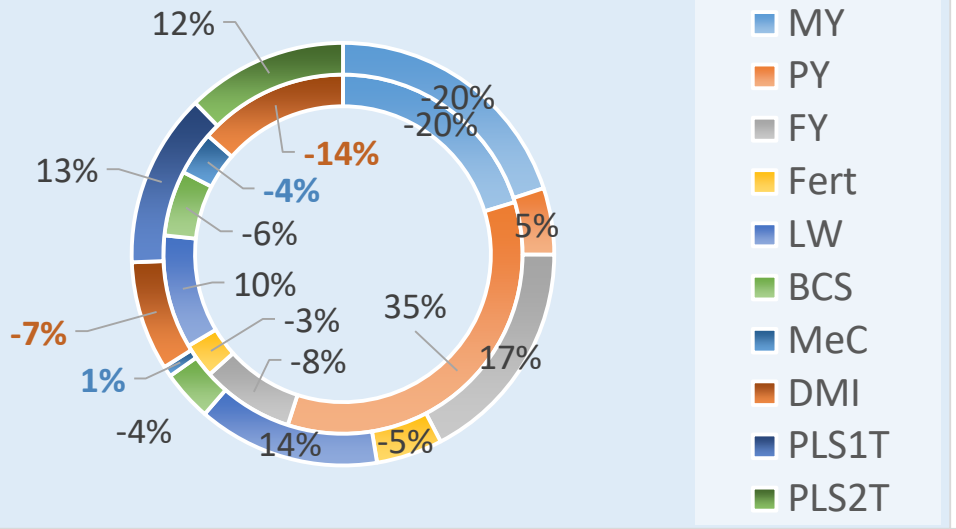
RFI, Residual CH4
Production 73%
Fertility 6%
Size & BCS 3%
FE 15%
Methane 3%
56.95€/cow/yr

RFI, Residual CH4, Microbiome
Production 68%
Fertility 6%
Size & BCS 3%
FE 12%
Methane 1%
Microbiome 10%
58.98 €/cow/yr

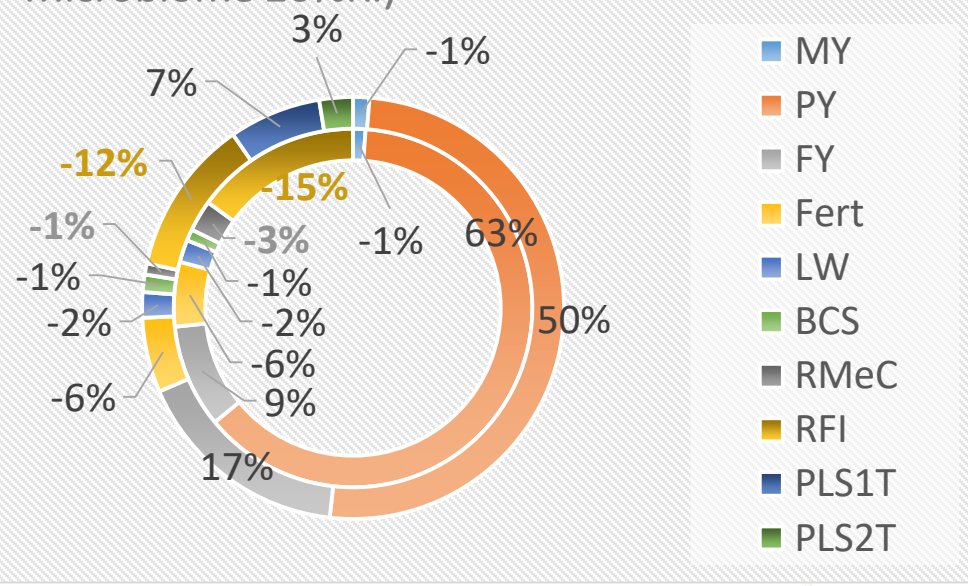
CH4 ↓
Milk ↑

Residual traits produce larger economic response, avoid negative selection on milk and fat yield, and including the microbiome select a more balanced (efficient and healthy) rumen microbiome

Benchmark+DMI+Methane
(+Microbiome 25%RI)



Benchmark+RFI+R.Methane
(+Microbiome 10%RI)



TAKE HOME MESSAGES

01

Measuring is going to be key

Sniffers → in-house farms.
Green feeds & SF6 → pastured based.
Sniffers that measure flux (**g/d**)

02

Monitor changes in the rumen microbiome to keep a healthy ruminotype

Research populations and genomic selection

03

Future sustainable selection indices must include: CH4 and FE

Residual traits seem more preferable in terms of genetic gains

04

Disseminate importance of sustainability within farmers

Adoption of sustainable selection indices

Acknowledgments

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I. Goiri

R. Atxaerandio

E. Ugarte

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