

# Examples of implementation of methane traits in breeding programs: Spain



Oscar González-Recio



# Overview of breeding programs

### Steps in a breeding program

### 1. Define breeding objectives

- Profit function, bioeconomical model, desired responses, etc
- Relative weight of traits to be selected in the overall breeding goal or selection index
- 2. Recording scheme
- 3. Create a reference population
  - Animals with genotype and phenotype (own records or progeny tests)
- 4. **Genetic evaluations** (genomic using molecular information)
  - Reference population
  - Genotyped animals in the candidate population (probably using imputation techniques if genotyping density differs from that of the reference population)
- 5. Selection of breeders for the next generation (dissemination)
  - sires of bulls
  - dams of bulls
  - sires of cows
  - dams of cows



# Overview of breeding programs

### Establishing a reference population for methane - Costs of phenotyping



J. Dairy Sci. 97:7905–7915 http://dx.doi.org/10.3168/jds.2014-8125 © American Dairy Science Association<sup>®</sup>, 2014.

### On the value of the phenotypes in the genomic era

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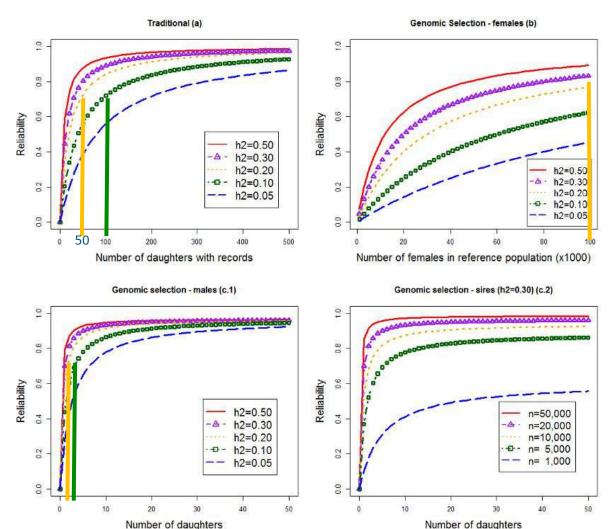
http://dx.doi.org/ 10.3168/jds.2014-8125

### Achieve 70% theoretical EBV reliability

Traditional breeding: progeny groups between 50-100 daughters

Genomic selection (sire reference population): progeny ~5 daughters

Genomic selection (cow reference population): 100k to 500k cows

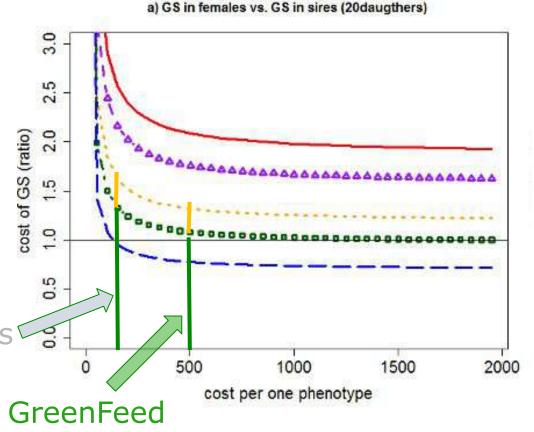




# Overview of breeding programs

Establishing a reference population for methane - Costs of phenotyping







# Situation in Spanish dairy breeding program

- Reference population
  - Holstein cows (~1000 cows per year, progeny groups for 200 sires)
  - Sires and cows genotyped
- •Genetic evaluations for methane traits (progress this far)

•Including methane in the breeding goal of Spanish Dairy Cattle (future perspectives)

### METHANE PHENOTYPING



# **3500 cows 37 farms**













Precision farming

Genotypes (50k SNPs)

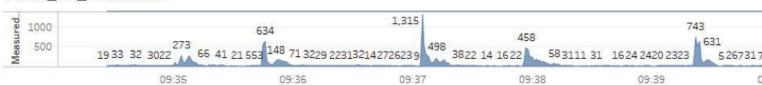


Genotypes (50k SNPs)





2017\_09\_21.093427



Tiempo [21 September 2017]

### METHANE PHENOTYPING

### 1. Recording methane in commercial and experimental farms



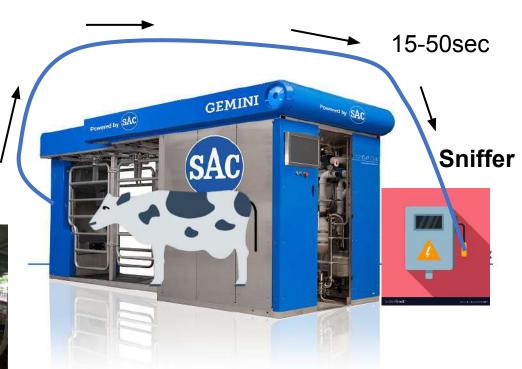




**Samples**= 3500 dairy cows in 37 farms

- Based on direct measurements
  - from sniffers in commercial farms
  - Extracted from of eructation events



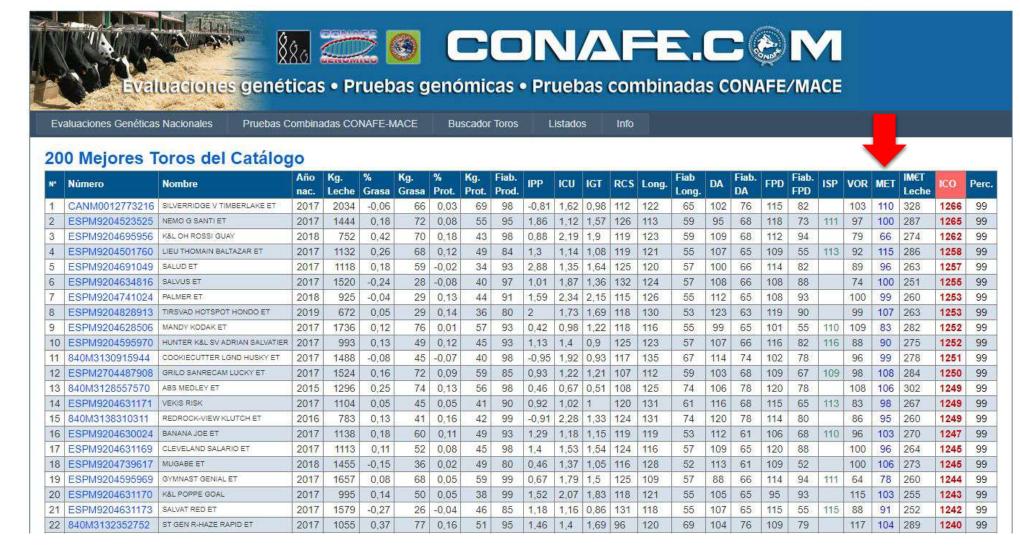


- SingleStep Genomic BLUP
  - CH<sub>Δ</sub>= μ + FatYield+Npar + Herd-Robot-Period+ DIM + MonthParity + PERM + ADIT + e
  - $h^2 = 0.17$
  - $r^2 = 0.66$
- ~3.500 animals as reference population (15.000 observations)
- 360,000 animals in pedigree (118,000 genotyped)





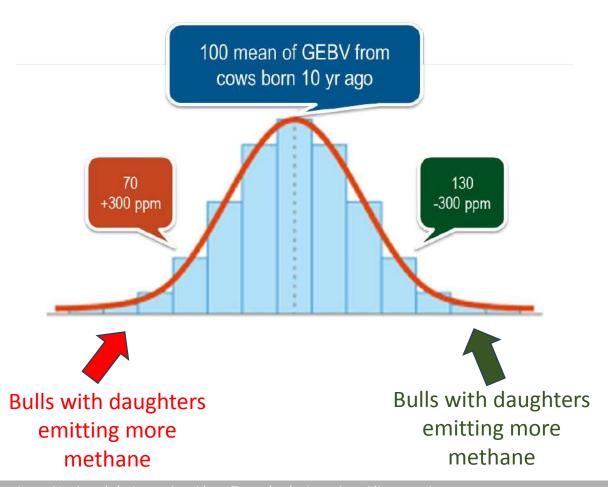
Published as an individual trait in the catalog.

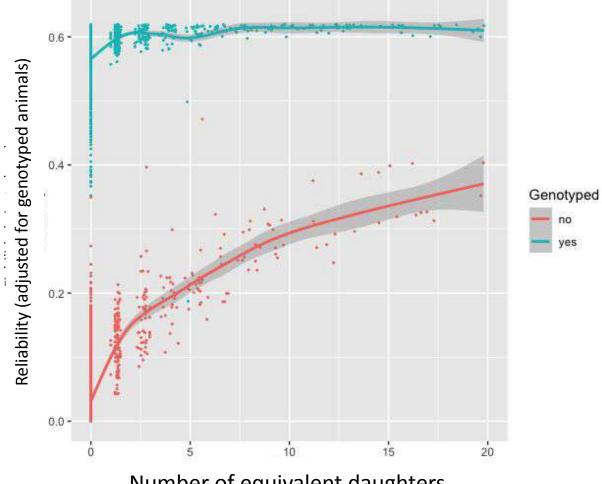






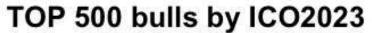
• GEBV published as mean=100 and sd=10

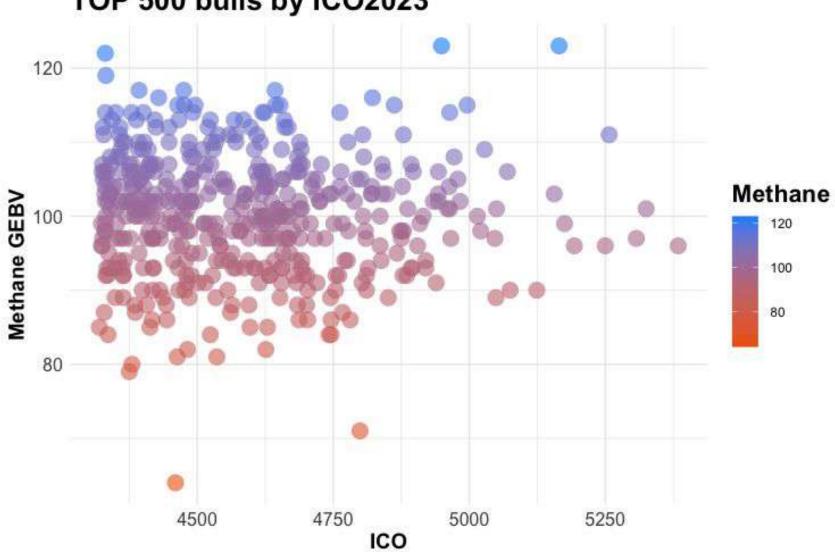






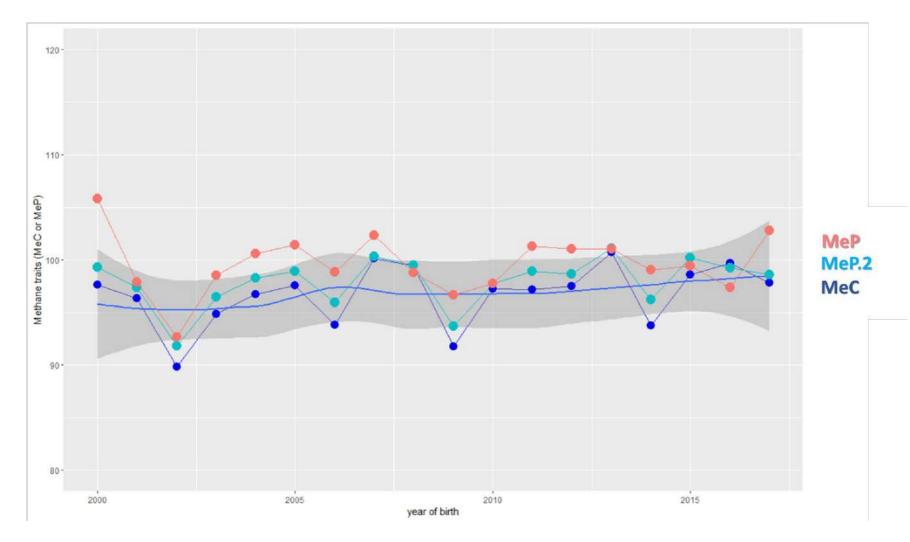






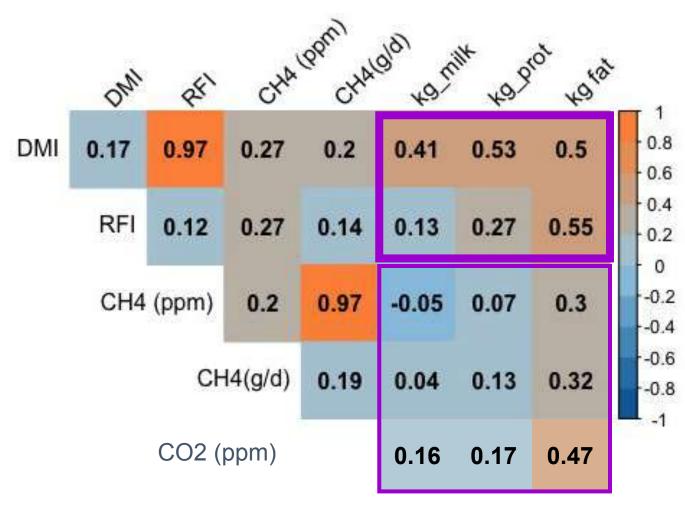
# Methane genetic trend

No genetic trend was observed

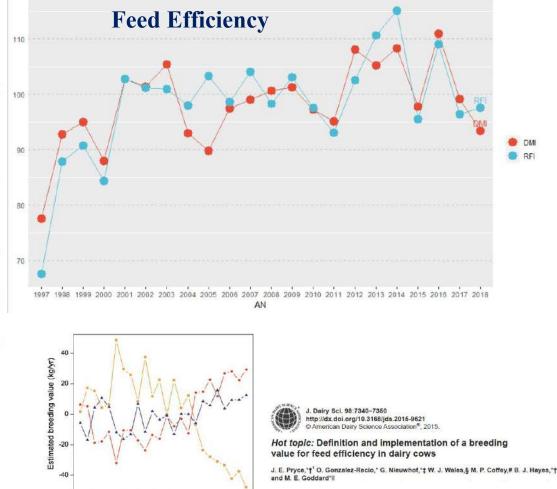


### Genetic correlations



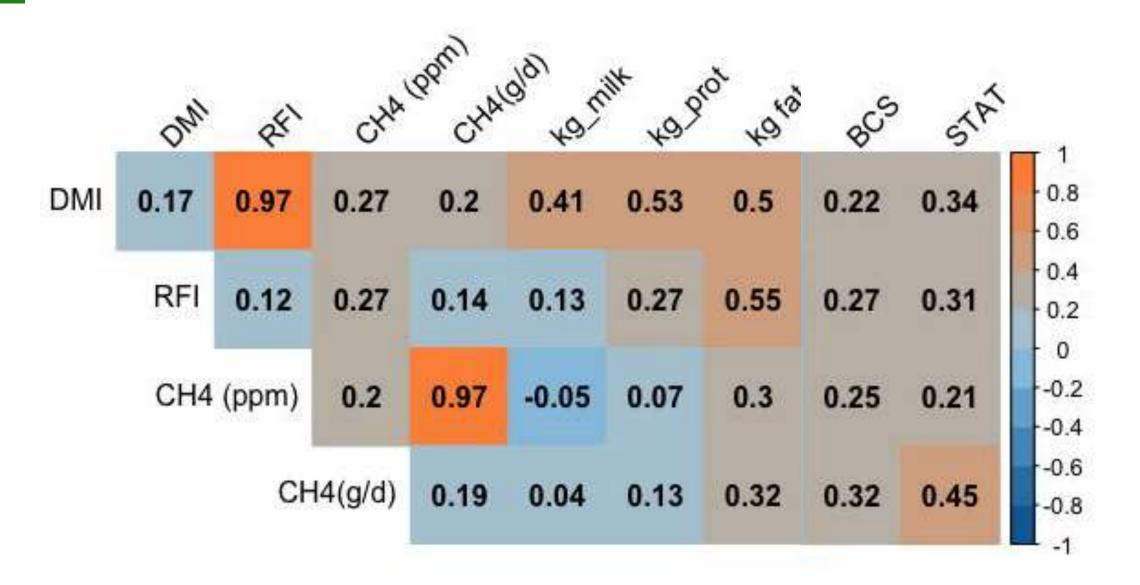


### Genetic trendsx



Year of birth

### Genetic correlations with other traits



### METHANE PHENOTYPING



- Phenotype definition (weekly averages)
  - 1. Mean  $CH_{\Delta}$  (by second and every 5 s)
  - 2. Sum of peaks CH<sub>4</sub> (by second and every 5 s)
  - 3. Sum of max peaks  $CH_{A}$
  - 4. Area under the curve (AUC CH<sub>4</sub>)
  - 5. Ratio of (mean)  $CH_4/CO_2$
  - 6. CH<sub>4</sub> grams per day (Madsen et al., 2010)

Prod CH<sub>4</sub>
$$\left(\frac{g}{d}\right) = 0.714 * ratio(ppm) * 180 * 24 * 0.001 * (5.6 * kg body mass0.75) +22 * ECM + 1.6*10-5 * days in pregnancy$$



7. CH<sub>4</sub> grams per day (in-house\*, based on observed CO2 and CH4/CO2 ratio, to be published)

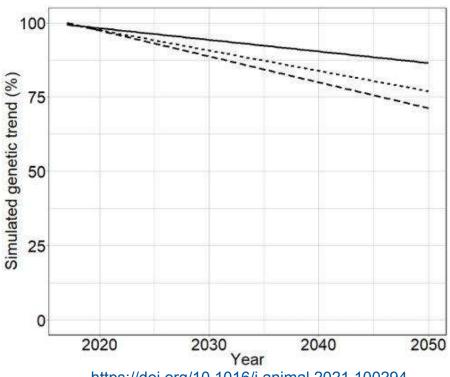
Large genetic correlation between phenotypes



# Animal breeding as a mitigation strategy

### Methane intensity (g/kg milk) & methane emissions (g/d)

- Current trend
- Combined selection for CH4 and other traits
- Theoretical maximum (exclusively focusing on methane)



https://doi.org/10.1016/j.animal.2021.100294 (de Haas et al. 2021)

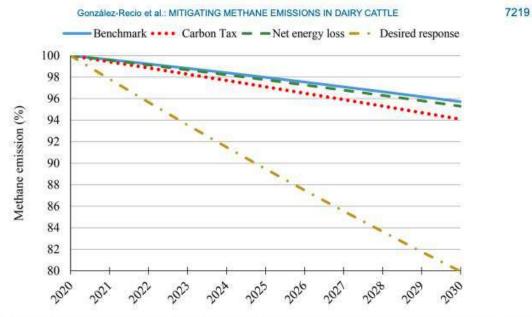
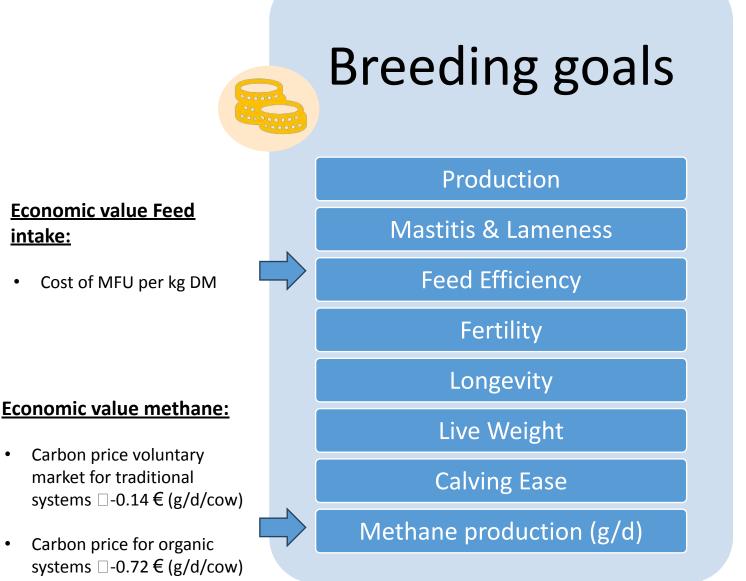


Figure 2. Expected reduction in percentage from current levels in methane emissions produced by Holstein cows in Spain based on genetic gain in methane emissions (MET; t/yr) under the 4 scenarios: benchmark, carbon tax, net energy loss, and desired response (i.e., number of cows × MET genetic gain × time/1,000). A decrease of 1.5% in the number of dairy cows was considered each year, following census data from the Spanish Holstein association: (http://www.conafe.com/VisorDocs.aspx?pdf=estadisticas\_CENSO\_DE\_ANIMALES.pdf).

# Economic Selection indices proposed in Spain (IM€T)

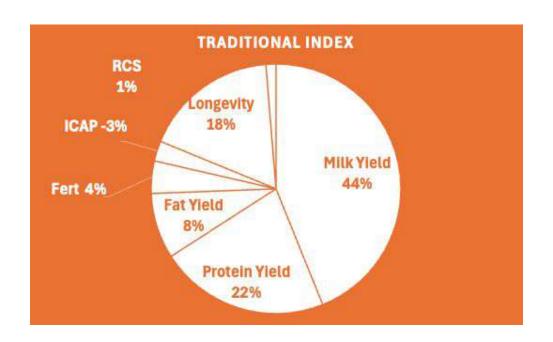
Traditional, Pasture-based, Cheese, Organic

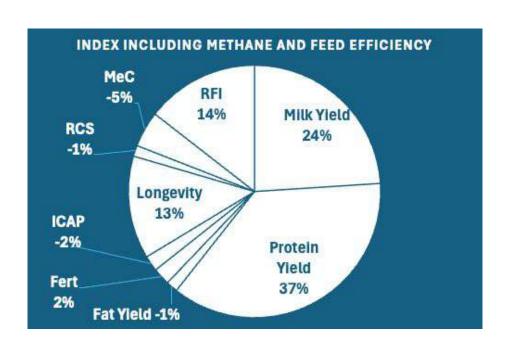


intake:

# Example of implementation

- - Efficiency and sustainability index in Spanish Dairy cattle
    - Subindex (will be integrated in the total merit index)



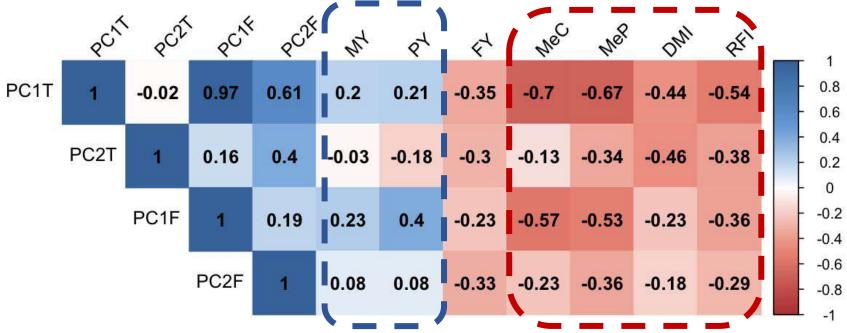


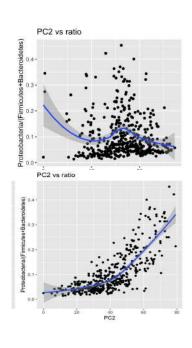
☐ Calculate expected genetic gain for each trait, including the correlated response on the microbial aggregated variables.



# Genetic correlations: Rumen microbiome community







- Aggregated microbial variables have heritabilites 0.20-0.30.
- Aggregated microbial variables are favorably genetically correlated with milk, protein, methane emissions and feed efficiency (unfavorable with fat).
- Inclusion of aggregated variables in the SI improved genetic response for production traits.
- Breeding for lower methane or feed efficiency may impact microbiota composition (dysbiosis)
- What are the expected consequences?

### TAKE HOME MESSAGE

01

Need large reference populations

02

In-depth discussion on methane reduction targets, and incentives to farmers and breeding programs

03

Rumen microbiome information is a suitable complementary phenotype for reducing methane emissions

Selecting for lower emissions and better feed efficiency may impact rumen microbiome health, and it should be controlled