A PIPELINE FOR THE INTEGRATION OF GROWTH, FEED EFFICIENCY AND GREENHOUSE-GAS EMISSION DATA IN ITALIAN HOLSTEIN

*F. Tiezzi[1], **R. Finocchiaro**[2], L. Benzoni[2], G. Invernizzi[3], J.B.C.H.M. van Kaam[2], M. Marusi[2], G. Savoini[3], R. Bozzi[1], and M. Cassandro[2,4]*

[1]*Department of Agriculture, Food, Environment and Forestry (DAGRI), University of Florence - Italy;*
[2]*Associazione Nazionale Allevatori della Razza Frisona, Bruna e Jersey Italiana (ANAFIBJ) - Italy;*
[3]*Dipartimento di Medicina Veterinaria e Alimentazione Animale (DIVAS), University of Milan - Italy;*
[4]*Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), University of Padova, - Italy*

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INTRODUCTION

- Dairy cattle is known to be impactful on greenhouse gasses (GHG) emissions with its enteric emissions for over 10% of the emissions from livestock sector globally (*Gerber et. Al., 2013*).

- Methane (CH_4) and carbon dioxide (CO_2) emissions have been shown to be heritable, providing the basis for applying genetic selection for their reduction (*Cassandro et al., 2010*).

- Selection could be applied by selecting directly for breath measurements, or using indirect selection including indicator traits such as feed intake (de Haas et al., 2017; Niero et al., 2020).

- How to record and streamline all the needed phenotype?

INTRODUCTION

Livestock Production Science, 32 (1992) 189–202 189
Elsevier Science Publishers B.V., Amsterdam

Genetic relationships between feed intake, efficiency and production traits in growing bulls, growing heifers and lactating heifers

G.J. Nieuwhof, J.A.M. van Arendonk, H. Vos and S. Korver
Department of Animal Breeding, Wageningen Agricultural University, Wageningen, Netherlands

(Accepted 27 January 1992)

OBJECTIVE

- Describe the collection protocol for growth, feed efficiency and greenhouse gas (GHG) emissions in young Italian Holstein bulls;
- These phenotypes collected are used to estimate genetic parameters for verifying the feasability of (direct and indirect) selection for reduced GHG emissions in Italian Holstein cattle;
- Creation of a streamline of this data;
- Extension of the estimation of GHG emissions at population level.

MATERIAL AND METHODS

Animals:

- 221 young genotyped Italian bulls undergoing progeny test at ANAFIBJ Genetic Center;
- 171-541 days of age (growing animals);
- 61,591 SNP available after editing.

Equipment:

- Roughage Intake Control system units (*RIC; Hokofarm Group, Voorsterweg, The Netherlands*);
- Automated Head-Chamber System (AHCS; GreenFeed C-Lock Inc.,Rapid City, SD,USA).

MATERIAL AND METHODS

Data from animals:

- Body weight (WEI);
- Body Condition Score (BCS);
- Heart girth (HG);
- Height (HEI).

RIC DATA:

- Visits at the feeder per day (NVF);
- Average intake at the feeder (AIF);
- Average time at the feeder (ATF).

Data from GreenFeed:

- Number of visits (NVG);
- Carbon-dioxide daily emissions (CO_2);
- Methane daily emission (CH_4);
- Average airflow (AIR);
- Average time (ATG).

STATISTICAL ANALYSIS

$$Y = Xb + Z_d d + Z_p p + Z_a a + e$$

Y = phenotypic records;
X = incidence matrix for **the fixed effects (age at phenotyping, date of birth);**
b = vector of solutions for the fixed effects (age at phenotyping, date of birth);
Z_d = incidence matrix for the «date of recording» uncorrelated random effect;
d = vector of solutions for the «date of recording» uncorrelated random effect;
Z_p = incidence matrix for the animal permanent environmental uncorrelated random effect;
p = vector of solutions for the animal permanent environmental uncorrelated random effect;
Z_a = incidence matrix for the animal additive genetic random effect (with genomic relationship matrix);
a = vector of solutions for the animal additive genetic random effect (with genomic relationship matrix);
E = random residuals

RESULTS

Descriptive statistics

Trait	Metric	N	Mean	SD
WEI	kg	885	309.3	77.5
BCS	score	849	3.0	0.3
HG	cm	715	157.3	14.2
HEI	cm	714	125.5	7.7
EFFICIENCY TRAITS				
NVF	**count**	**7,150**	**26.0**	**11.6**
AIF	**kg**	**7,150**	**0.3**	**0.1**
ATF	**s**	**7,150**	**317.0**	**117.1**
GREENFEED TRAITS				
NVG	count	2,817	3.9	1.7
CO_2	g/d	2,817	6198.2	1103.9
CH_4	g/d	2,817	223.6	51.8
AIR	L/s	2,817	29.2	4.0
ATG	s	2,817	329.3	87.5

Trait	h^2	Animal p.e.	Date of recording
WEI	0.45 (0.24)	0.428 (0.212)	0.039 (0.015)
BCS	0.51 (0.20)	0.266 (0.168)	0.023 (0.010)
HG	0.44 (0.25)	0.433 (0.223)	0.045 (0.018)
HEI	0.39 (0.23)	0.438 (0.196)	0.005 (0.004)
NVF	0.31 (0.12)	0.115 (0.072)	0.287 (0.029)
AIF	0.17 (0.15)	0.377 (0.105)	0.059 (0.008)
ATF	0.29 (0.18)	0.374 (0.142)	0.044 (0.008)
NVG	0.36 (0.11)	0.076 (0.066)	0.090 (0.015)
CO_2	0.48 (0.21)	0.258 (0.164)	0.082 (0.017)
CH_4	0.40 (0.17)	0.159 (0.113)	0.078 (0.015)
AIR	0.45 (0.09)	0.099 (0.053)	0.439 (0.049)
ATG	0.24 (0.11)	0.072 (0.057)	0.127 (0.020)

Genetic correlations

	WEI	BCS	HG	HEI	NVF	AIF	NVG	CO_2	CH_4	AIR
WEI		0.84	0.75	0.64						
BCS	0.84		0.72	0.55						
HG	0.75	0.72		0.11						
HEI	0.64	0.55	0.11							
NVF						0.75				
AIF					0.75					
NVG								0.70	0.77	0.92
CO_2							0.70		0.81	0.81
CH_4							0.77	0.81		0.83
AIR							0.92	0.81	0.83	

Genetic correlations

	WEI	BCS	HG	HEI	NVF	AIF	NVG	CO_2	CH_4	AIR
WEI		0.84	0.75	0.64	0.95	0.99				
BCS	0.84		0.72	0.55	0.90	0.98				
HG	0.75	0.72		0.11	0.90	0.98				
HEI	0.64	0.55	0.11		0.90	0.97				
NVF	0.95	0.90	0.90	0.90		0.75				
AIF	0.99	0.98	0.98	0.97	0.75					
NVG								0.70	0.77	0.92
CO_2							0.70		0.81	0.81
CH_4							0.77	0.81		0.83
AIR							0.92	0.81	0.83	

Genetic correlations

	WEI	BCS	HG	HEI	NVF	AIF	NVG	CO_2	CH_4	AIR
WEI		0.84	0.75	0.64	0.95	0.99				
BCS	0.84		0.72	0.55	0.90	0.98				
HG	0.75	0.72		0.11	0.90	0.98				
HEI	0.64	0.55	0.11		0.90	0.97				
NVF	0.95	0.90	0.90	0.90		0.75	0.73	0.63	0.67	0.69
AIF	0.99	0.98	0.98	0.97	0.75		0.67	0.55	0.58	0.61
NVG					0.73	0.67		0.70	0.77	0.92
CO_2					0.63	0.55	0.70		0.81	0.81
CH_4					0.67	0.58	0.77	0.81		0.83
AIR					0.69	0.61	0.92	0.81	0.83	

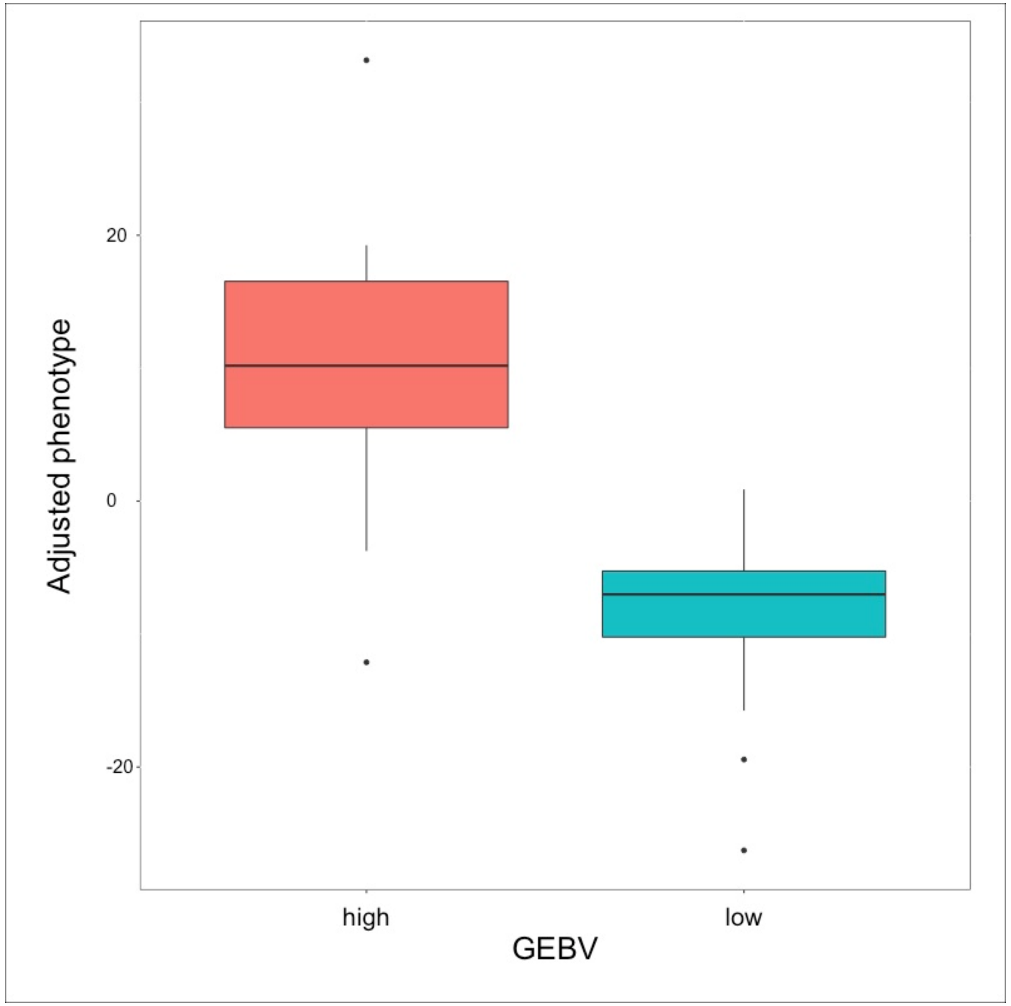
Genetic correlations

	WEI	BCS	HG	HEI	NVF	AIF	NVG	CO_2	CH_4	AIR
WEI		0.84	0.75	0.64	0.95	0.99	0.93	0.92	0.92	0.94
BCS	0.84		0.72	0.55	0.90	0.98	0.97	0.93	0.93	0.95
HG	0.75	0.72		0.11	0.90	0.98	0.94	0.90	0.90	0.94
HEI	0.64	0.55	0.11		0.90	0.97	0.95	0.92	0.92	0.95
NVF	0.95	0.90	0.90	0.90		0.75	0.73	0.63	0.67	0.69
AIF	0.99	0.98	0.98	0.97	0.75		0.67	0.55	0.58	0.61
NVG	0.93	0.96	0.94	0.95	0.73	0.67		0.70	0.77	0.92
CO_2	0.92	0.93	0.90	0.93	0.63	0.55	0.70		0.81	0.81
CH_4	0.92	0.93	0.90	0.92	0.67	0.58	0.77	0.81		0.83
AIR	0.94	0.95	0.94	0.95	0.69	0.61	0.92	0.81	0.83	

Genetic correlations

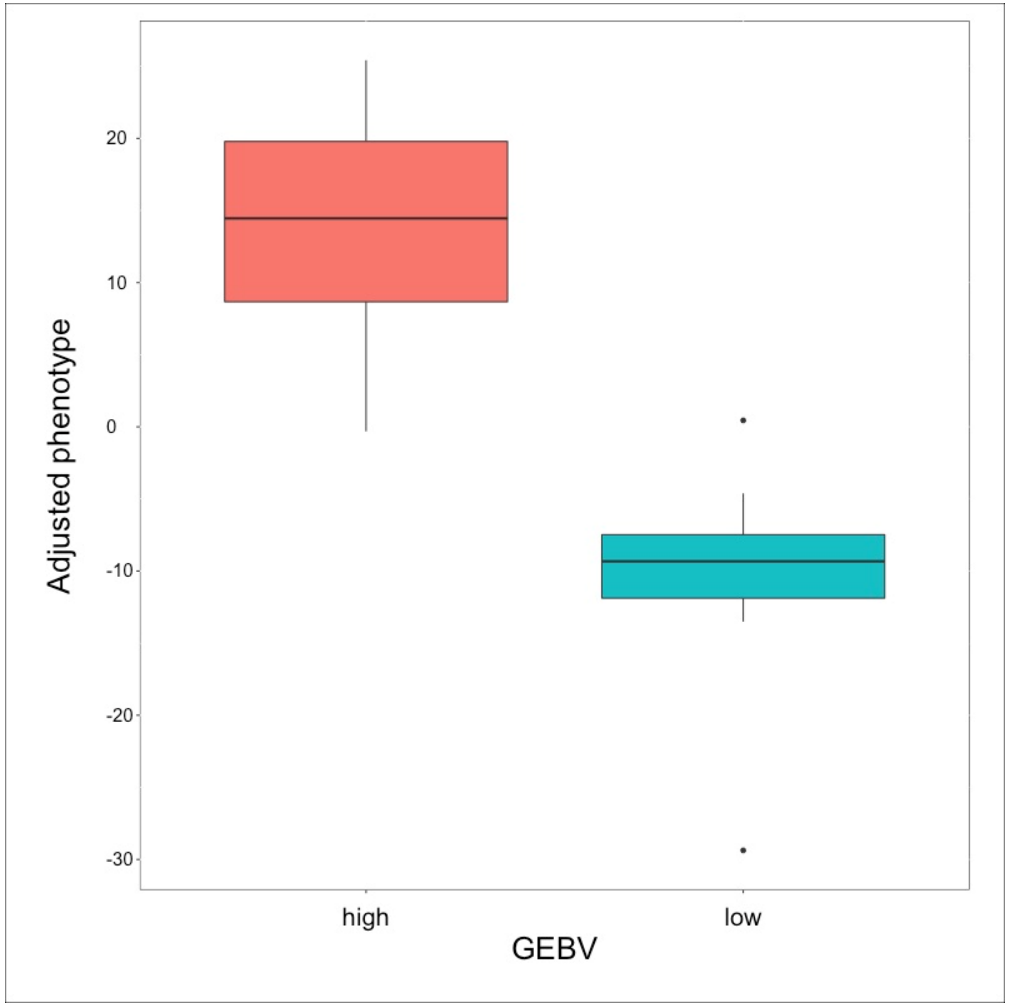
	WEI	BCS	HG	HEI	NVF	AIF	NVG	CO_2	CH_4	AIR
WEI		0.84	0.75	0.64	0.95	0.99	0.93	0.92	0.92	0.94
BCS	0.84		0.72	0.55	0.90	0.98	0.97	0.93	0.93	0.95
HG	0.75	0.72		0.11	0.90	0.98	0.94	0.90	0.90	0.94
HEI	0.64	0.55	0.11		0.90	0.97	0.95	0.92	0.92	0.95
NVF	0.95	0.90	0.90	0.90		0.75	0.73	0.63	0.67	0.69
AIF	0.99	0.98	0.98	0.97	0.75		0.67	0.55	0.58	0.61
NVG	0.93	0.96	0.94	0.95	0.73	0.67		0.70	0.77	0.92
CO_2	0.92	0.93	0.90	0.93	0.63	0.55	0.70		0.81	0.81
CH_4	0.92	0.93	0.90	0.92	0.67	0.58	0.77	0.81		0.83
AIR	0.94	0.95	0.94	0.95	0.69	0.61	0.92	0.81	0.83	

CH_4



20
0
-20
Adjusted phenotype
high
low
GEBV

CO_2



20
10
0
-10
-20
-30
Adjusted phenotype
high
low
GEBV

DISCUSSION

- We used daily records.
- We could have used:
  - Single-visit records
  - Overall performance-test average

DISCUSSION

Single-visit records

- Pros:
  - Multiple records per animal per day
  - Possibility to reduce noise by modeling
- Cons:
  - Individuals with more visits get more records..
  - Number of visits shows heritable variation

DISCUSSION

Overall performance-test average

- Pros:
  - Possibility to calculate residual feed intake
  - All individuals have the same number of observations
- Cons:
  - Impossible to disentangle genetic from perm. env. eff.
  - Average value might contain noise

CONCLUSIONS

- Selection indices could be built in order to reduce GHG emissions without compromising growth, BCS, stature and feed intake;
- Feed efficiency and GHG emissions need to be adjusted by growth, size and production records from cows that are sibs of the tested bulls;
- Test some daughters of these bulls and re-estimate genetic correlations between bulls and cows → Cooperation is needed…

MANAGING GENETIC DIVERSITY IN DAIRY CATTLE

WORKSHOP

thursday 14th of July 2022

REGISTRATION DEADLINE JUNE 30th

HYBRID MEETING

ON-SITE attendance:
ANAFIBJ - CREMONA - ITALY
via Bergamo, 292
REGISTRATION FEE 80€
&
ON-LINE attendance:
REGISTRATION FEE 50€

zoom

attendance certificate

info and registration please contact clararapazzoli@anafi.it

PROGRAM

10:00 Prof. Martino Cassandro *General Manager ANAFIBJ - ITALY*
THE EVOLUTION OF ARTIFICIAL INSEMINATION (AI) IN ITALY

10:40 Prof. Christian Maltecca *North Carolina State University - USA*
LIVESTOCK INBREEDING IN THE GENOMIC ERA

11:20 Mr. Emmanuel Lozada Soto *North Carolina State University - USA*
GENETIC DIVERSITY IN FIVE NORTHERN AMERICAN DAIRY BREEDS

12:00 Dr. Michela Ablondi *Università di Parma - ITALY*
GENOME-WIDE SCAN REVEALS GENETIC DIVERGENCE IN ITALIAN HOLSTEIN COWS BRED WITHIN PDO CHEESE PRODUCTION CHAINS

12:40 / 14:00 LUNCH BREAK

14:00 Dr. Christian Persichilli *Università del Molise - ITALY*
EXPLORING GENOME-WIDE DIFFERENTIATION AND SIGNATURES OF SELECTION IN ITALIAN AND NORTH AMERICAN HOLSTEIN POPULATIONS

14:40 Dr. Jan-Thijs van Kaam *ANAFIBJ - ITALY*
HOLSTEIN EFFECTIVE POPULATION SIZE REDUCING

15:00 Dr. Saija Tenhunen *Arhus University and VikingGenetics - DENMARK*
INBREEDING MANAGEMENT IN NORDIC HOLSTEIN

15:40 / 16:00 Prof. Martino Cassandro *General Manager ANAFIBJ - ITALY*
Conclusions

THANKS FOR THE ATTENTION!