

A pipeline for the integration of growth, feed efficiency and greenhouse-gas emission data in Italian Holstein

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The objective of this study was to describe the collection protocol for growth, feed efficiency and greenhouse gas (GHG) emissions in young Italian Holstein bulls. The phenotypes will be used in genetic evaluations for the reduction of environmental impact in Italian Holstein.

Abstract

The animals involved in this study were young Italian Holstein bulls undergoing own performance test at the Genetic Center (GC) of Italian National Breeders Association for the Holstein, Brown and Jersey dairy cattle breeds (ANAFIBJ). Phenotypic data was provided for on 218 Holstein bulls between the age of 171 and 541 days. All bulls were genotyped using various SNP chips resulting in 69,127 SNP after imputation.

The phenotypic data can be summarized in three groups:

1. a group of traits describing growth and condition of the animal;
2. a dataset derived from measures taken with the Roughage Intake Control system (RIC; Hokofarm Group, Marknesse, The Netherlands) and
3. dataset derived from measures taken using the GreenFeed (C Lock Inc., Rapid City, SD, USA).

The group **A** included measures of body growth taken using electronic scales and stadiometers operated by qualified personnel. These included body weight (WEI), body condition score (BCS), heart girth (HG) and height (HEI). Group **B** included single-visit measures that were converted into daily measures and included: number of visits at the feeder per day (NVF), average intake at the feeder (AIF), average time at the feeder (ATF). Group **C** included single-visit measures then converted to daily records and included: number of visits (NVG), carbon-dioxide daily emission (CO₂), methane daily emission (CH₄), average airflow (AIR) and average time (ATG).

Variance components and genetic parameter estimation (heritability and genetic correlations) was carried out using a GBLUP mixed model that included a genomic relationship matrix built on the SNP markers.

The growth traits showed the largest estimates of heritability, close to 0.40. Heritability estimates for the RIC-derived traits were lower, ranging from 0.167 (AIF) to NVF (0.306). Estimates for emission traits ranged from 0.241 for ATG to 0.480 for CO₂.

Results suggest that selection indices could be built in order to reduce GHG emissions without compromising growth, condition, stature and feed intake. The upcoming research should be focused on the use of feed efficiency and relative GHG emission, as these components need to be adjusted by the growth and size of the animal. Subsequently a further data-set should include GC sire performance and their daughters', reared in dairy commercial farms.

Keywords: Greenhouse gas emissions, feed efficiency, genomic selection, Italian Holstein.

Introduction

Dairy cattle is known to be impactful on greenhouse gasses (GHG) emissions, with its enteric emissions accounting for over ten percent of the emissions from the livestock sector globally (Gerber *et al.*, 2013). Methane emissions are also energetically expensive because of the fermentation process (Appuhamy *et al.*, 2016) but this inefficiency could be reduced by steering the fermentation process, redirecting the energetic resources to reproduction and milk production (Haque, 2018). Methane and carbon dioxide emissions have been shown to be heritable, providing the basis for applying genetic selection for their reduction (Cassandro *et al.*, 2010; Cassandro M., 2013; Cassandro *et al.*, 2013; Pickering *et al.*, 2015; Lassen and Løvendahl, 2016). Such selection could be applied by selecting directly for breath measurements, but also using indirect selection *including* indicator traits such as feed intake (de Haas *et al.*, 2017; Niero *et al.*, 2020).

The objective of this study was to estimate genetic parameters for verifying the feasibility of (direct or indirect) selection for reduced GHG emissions in Italian Holsteins.

Material and methods

Animals and data

The animals involved in this study were young Italian Holstein bulls undergoing progeny test

in the genetic centre of the Italian National Breeders Association for the Holstein, Brown and Jersey dairy cattle breeds (ANAFIBJ) as reported by Callegaro *et al.* (2022). The ANAFIBJ genetic center is equipped with five Roughage Intake Control system units (RIC; Hokofarm Group, Voorsterweg, The Netherlands) distributed over three pens. One of the three pens is also equipped with the Automated Head-Chamber System (AHCS; GreenFeed C Lock Inc., Rapid City, SD, USA), an automated feeding station designed to measure daily CH₄ and CO₂ emissions (g/d) from ruminant's breath (Hristov *et al.*, 2015).

Phenotypic data was made available on 221 Holstein bulls between the age of 171 and 541 days. All bulls were genotyped using various SNP chips resulting in 69,127 SNP. Genomic data was edited using the preGSf90 software (Aguilar *et al.*, 2010), removing SNP with call rate below 0.90 and minor allele frequency below 0.05. After editing, 61,591 SNP were available.

The first set of traits included measures of body growth taken using electronic scales and stadiometers operated by qualified personnel. These included body weight (WEI), body condition score (BCS), heart girth (HG) and height (HEI). The second group of traits

included measures of feed intake and feeding behaviour assessed using the Roughage Intake Control system (RIC; Hokofarm Group, Marknesse, The Netherlands). Records were organized as daily measures: number of visits at the feeder per day (NVF), average intake at the feeder (AIF), average time at the feeder (ATF). The third group of traits included measures of greenhouse gasses emission and were obtained using the GreenFeed (C Lock Inc., Rapid City, SD, USA). Again, the single-visit measures were converted to daily records and included: number of visits (NVG), carbon-dioxide daily emission (CO₂), methane daily emission (CH₄), average airflow (AIR) and average time (ATG). A single dataset was created, containing all the phenotypic information. Individuals showed an average of 4 records for the growth traits, 36 records for the RIC-derived traits, 19 records for the GreenFeed-derived traits. For all records, the age at recording was calculated. In addition, the date of birth of the individual was transformed to numerical values as the difference, in days, from a fixed arbitrary date.

Estimates of variance components and genetic parameters were carried out using a linear mixed model that included a genomic relationship matrix constructed using the SNP markers. The model was defined as follows:

$$y = Xb + Z_d d + Z_p p + Z_a a + e \quad (1)$$

where **y** is the vector containing phenotypic records, **X** and **b** are the incidence matrix and vector of solutions for the fixed effects (age at phenotyping, date of birth), **Z_d** and **d** are the incidence matrix and vector of solutions for the 'date of recording' uncorrelated random effect, **Z_p** and **p** are the incidence matrix and vector of solutions for the animal permanent environmental uncorrelated random effect, **Z_a** and **a** are the incidence matrix and vector of solutions for the animal additive genetic random effect (with genomic relationship matrix), **e** is the vector of random residuals. The model was implemented for single-trait and two-trait analyses in order to obtain estimates of heritability and genetic correlations, using the gibbs2f90 software (Misztal *et al.*, 2002). Estimates of variance components and genetic parameters were obtained as posterior means and their dispersion was obtained as the posterior SD and the 95% confidence intervals. The heritability was expressed as the ratio between the additive genetic variance and the sum of the four variance components.

Statistical analysis

Descriptive statistics and heritability estimates for the studied traits are reported in table 1. The growth and condition traits showed the largest estimates, all being above or close to 0.40. While these traits are expected to be highly heritable, the estimates appear larger compared to those found in literature. This could be due to the relatively small sample size. On the other hand, heritability estimates for the RIC-derived traits were lower, ranging from 0.167 (AIF) to NVF (0.306). Heritability estimates for the emission traits were moderate to high, ranging from 0.241 for ATG to 0.480 for CO₂.

Genetic correlation estimates are reported in table 2. Among the growth traits, correlations were strong for WEI-BCS and BCS-HG, but weak for all the other combinations of traits. Correlations between NVF and AIF was 0.74, the genetic correlation between AIF and ATF was 0.98 (result not shown in table). Correlations among the GreenFeed-derived traits were moderate to strong, especially among CH₄, CO₂ and AIR, which were all above 0.70. NVG was moderately related to the other GreenFeed-derived traits, with correlations below 0.7. The genetic correlation between AIR and ATG was 0.95 (result not shown in table). Genetic correlations between the growth traits and the RIC-derived traits were all positive and strong, approaching unity

Results

(0.89 to 0.99). Genetic correlations between the growth traits and the GreenFeed-derived traits were also positive and strong, with values ranging from 0.90 to 0.96. Similarly, the genetic correlations between the GreenFeed-derived traits and the RIC-derived traits were positive and moderate to strong, with values from 0.60 to 0.73.

Discussion

Heading of subsection

The estimates show substantial genetic variation for all the studied traits. The CO₂ and CH₄ daily emissions show high heritability with the possibility of selection, therefore reduction of GHG emissions. The estimated values for the heritability of CH₄ and CO₂ are larger than values found in literature (Lassen and Løvendahl, 2016; Brieder *et al.*, 2018), although this could be due to the involvement of growing bulls rather than lactating cows and the limited sample size in the current study. The genetic correlations indicate that there is the possibility to select for less impactful animals. The genetic correlation between CO₂ and CH₄ emissions is strong (0.84), suggesting that selection for one component of the emissions would improve the other as well. Similarly, the AIR shows strong correlations with the GHG emissions, suggesting that this trait could be used as an indicator. Similarly, the NVG could serve as an indicator trait to reduce the emissions, although the achievable genetic progress would be limited due to the moderate genetic correlations (0.7-0.8). In fact, the value of 0.7 was indicated as the minimum acceptable value for achieving a relevant genetic progress in case of multiple-trait genomic predictions by Calus and Veerkamp (2011). Using this same criterion, NVF could reduce GHG emissions better than feed intake (AIF) given the stronger genetic correlations (0.74 vs ~0.65). Unsurprisingly, selection for larger animals will also lead to individuals that consume more feed with all correlations between growth traits and RIC-derived traits being close to 0.9. Similarly, selection for larger animals could lead to more GHG emissions (correlations close to 0.9). In general, selection indices could be built in order to reduce GHG emissions without compromising growth, condition, stature and feed intake. The upcoming research should involve the use of feed efficiency and relative GHG emission, as these components need to be adjusted by the growth and size of the animal.

Conclusion

Results suggest that selection indices could be built in order to reduce greenhouse gas emissions while still improving growth, condition, stature and feed intake. The upcoming research is involving the use of feed efficiency and relative GHG emission, as these components need to be adjusted by the growth and size of the animal as well as production records from cows that are sibs of the tested bull. Moreover, we will test these bull's semen in other experimental stations equipped with these precision instruments in order to register intake data and GHG data emission on some of the daughters of these bulls and re-estimate the genetic correlations between bulls and cows as proposed by other colleagues in the early nineties (Nieuwhof *et al.*, 1992)

Table 1. Descriptive statistics (posterior means with posterior standard deviation) and heritability estimates for the traits analysed.

Trait ¹	Metric	N	Mean	SD	h ²
WEI	kg	885	309.3	77.5	0.45 (0.24)
BCS	score	849	3.0	0.3	0.51 (0.20)
HG	cm	715	157.3	14.2	0.44 (0.25)
HEI	cm	714	125.5	7.7	0.39 (0.23)
NVF	count	7150	26.0	11.6	0.31 (0.12)
AIF	kg	7150	0.3	0.1	0.17 (0.15)
ATF	s	7150	317.0	117.1	0.29 (0.18)
NVG	count	2817	3.9	1.7	0.36 (0.11)
CO ₂	g/d	2817	6198.2	1103.9	0.48 (0.21)
CH ₄	g/d	2817	223.6	51.8	0.40 (0.17)
AIR	L/s	2817	29.2	4.0	0.45 (0.09)
ATG	s	2817	329.3	87.5	0.24 (0.11)

¹WEI: body weight; BCS: body condition score; HG: heart girth; HEI: height; NVF: number of visits at the feeder; AIF: average intake at the feeder; ATF: average time at the feeder; NVG: number of visits at the GreenFeed; CO₂ daily carbon dioxide emissions; CH₄: daily methane emissions; AIR: average airflow at the visit; ATG: average time at the GreenFeed.

Table 2. Estimates of genetic correlations¹ among the growth-related traits², the RIC-derived traits² and the GreenFeed-based traits².

	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	

¹Estimates of the genetic correlations are the posterior mean for the parameter. Values in bold indicate that the value '0' was not included within the 95% confidence intervals, therefore are to be considered significant for P<0.05.

²WEI: body weight; BCS: body condition score; HG: heart girth; HEI: height; NVF: number of visits at the feeder; AIF: average intake at the feeder; NVG: number of visits at the GreenFeed; CO₂ daily carbon dioxide emissions; CH₄: daily methane emissions; AIR: average airflow at the visit.

This study was supported by “Latteco2 project, sottomisura 10.2 of the PSRN Biodiversity 2020–2023” (MIPAAF. D.M. no. 465907 del 24/09/2021, project unique code 12C21004080005).

Acknowledgement

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