

Single step genomic evaluation of residual feed intake in growing Holstein heifers

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Summary

Over the last two years, STgenetics has been collecting data on feed intake and weights on several thousand Holstein heifers at the Ohio Heifer Center. In this particular evaluation, only heifers between 200 and 400 days of age were considered. The final dataset included 1939 heifers with an average age of 301 days. Data collection was organized in trials of 70 days. The hardware comprised 80 GrowSafe bunks in 10 pens. On average, 8 animals were allowed to enter a pen per GrowSafe bunk. Daily feed intake was recorded using the GrowSafe bunks whereas body weight was recorded at entry and exit of the trial and, on average, 3 additional times during the trial. Average daily feed intake ranged from 11.48 to 64.40 with a mean of 40.78 pounds of fresh feed per day. Body weight ranged from 292.3 to 1087 with an average of 650.4 pounds. Average daily gain was estimated by a linear regression of body weight against days of age and averaged 2.153 pounds per day, ranging from 0.01 to 7.63. QC measures comprised minimum valid feed intake days (12), minimum valid weightings (2), minimum days on trial (30) and positive average daily gain.

Residual feed intake was defined as the residuals from a linear model on daily feed intake comprising the fixed effects age, metabolic body weight, pen-year-season and average daily gain. Those residuals subsequently entered 2 different genetic and genomic evaluation models: An animal model whereas the covariance across individuals was defined by the numerator relationship matrix (Pedigree only) and the same model with the combined genomic and additive genetic relationship matrix (Single Step GBLUP). All models were fitted in a Bayesian framework using Gibbs sampling. Posterior means (and standard deviations) for the heritability estimates were 0.21 (0.06) for the traditional animal model and 0.16 (0.03) for the single step GBLUP model. Reliabilities of all 6718 individuals of the most recent 5 generations of the pedigree ranged from 0.02 to 0.7 with a mean of 0.16. The highest reliabilities were achieved by sires and grandsires having a high number of daughters and/or granddaughters that went through the trials. Correlations between the genomic breeding values of residual feed intake and traits currently evaluated by the USDA were small with the only exception being an unfavorable correlation between residual feed intake and PTAT.

Keywords: feed efficiency, genomic prediction, single step

Introduction

The efficient utilization of scarce resources will be of ever increasing importance in the future. In order to maintain the supply of high quality nutrients the focus of the livestock industry is projected to be on feed efficiency, meaning maximizing the output of a consumable end product given the available resources or minimizing the input given a production goal (Hayes *et al.*, 2013). Over time, feed efficiency has tacitly occurred through the reduction in the number of dairy cattle to produce a certain amount of milk. This is a consequence of genetic improvement of milk production traits and thereby skewing the relationship between maintenance requirements and production. Negative genetic correlations of milk yield with other traits of recent economic importance led to a redefinition of breeding goals reflected in the major indexes around the world (e.g. NMS) putting less emphasis on production traits. Therefore, increasing milk yield as a sole means to increase feed efficiency, has limitations and it will be important to work on traits more directly related to feed efficiency of growth and milk production. STgenetics has established extensive phenotyping capabilities at the Ohio Heifer center in order to start a genomic breeding program tailored towards feed efficiency.

Materials and Methods

The dataset consisted of 1939 growing Holstein heifers between 200 and 400 days of age. Data collection took place between 2015 and 2017. Daily feed intake was measured using 80 GrowSafe bunks (GrowSafe Systems Ltd, Airdrie, AB) across 10 pens in trials taking place for 70 days each. Body weights were recorded at entry and exit of the trial and additional three times during the trials on average.

The linear model for residual feed intake was:

where \mathbf{y} is the random vector of average daily feed intake and $\mathbf{X}\boldsymbol{\beta}$ a vector of fixed effects comprising an intercept, age in days, pen-year-season, metabolic body weight and average daily gain. The residuals of this model (\mathbf{e}) entered 2 different animal models as response vectors and represent residual feed intake.

1570 of the heifers had genotypic information available in the form of SNP data. The majority of animals were genotyped with either the GeneSeek GP3 or GP4. After quality control, 22670 SNPs remained in the final dataset. All animals were imputed using *Eagle* (Loh *et al.*, 2016).

In order to incorporate all individuals in a genomic prediction model, a combined additive genetic and genomic relationship matrix was used, resulting in a single step GBLUP model (Legarra *et al.*, 2009, Aguilar *et al.*, 2010):

where \mathbf{y} is the random vector of residual feed intake, μ is an intercept and $\mathbf{X}\boldsymbol{\beta}$ is a vector of additive genetic or genomic effects (breeding values) with \mathbf{e} .

The covariance matrix \mathbf{V} is either the numerator relationship matrix (\mathbf{A}) or the combined additive genetic and genomic relationship matrix (\mathbf{G}).

The inverse of \mathbf{V} can be created as:

where G is a genomic relationship matrix with dimension equal to the number of genotyped animals (see e.g. VanRaden, 2008).

Results and Discussion

Posterior means (and standard deviations) for the heritability estimates were 0.21 (0.06) for the traditional animal model and 0.16 (0.03) for the single step GBLUP model (Table 1). Those heritabilities are somewhat lower than the ones reported by Pryce et al. (2012).

Table 1: Estimated variance components and heritabilities (with standard deviations) for residual feed intake.

Model	Additive genetic variance	Residual variance	Heritability
Pedigree only	4.86 (1.55)	18.63 (1.39)	0.21 (0.06)
Single Step GBLUP	3.62 (0.79)	19.52 (0.92)	0.16 (0.03)

Reliabilities of all 6718 individuals of the most recent 5 generations of the pedigree ranged from 0.02 to 0.7 with a mean of 0.16. The highest reliabilities were achieved by sires and grandsires having a high number of daughters and/or granddaughters that went through the trials.

Of importance for the future genetic work on feed efficiency are the genetic correlations to other traits of economic importance which are currently under selection. Table 2 gives a summary of the raw correlations of the genomic breeding values of residual feed intake and the most important traits of the US evaluations.

Table 2: Correlations of genomic breeding values across traits.

	Residual feed intake
Tpi	0.02
NM\$	-0.01
Cheese Merit	-0.01
Milk	0.06
Protein	0.06
Fat	-0.01
Productive Life	-0.05
PTAT	0.14

DPR -0.08

Generally, correlations between genomic breeding values were low to moderate with the maximum being 0.14 for residual feed intake and PTAT, indicating that feed efficiency decreases with higher breeding values for type traits.

This study investigated residual feed intake in growing Holstein heifers which is the first trait in an effort to cover feed efficiency evaluations at every stage of life in dairy cows. The genetic variance and moderate heritabilities in conjunction with the low genetic correlations with other traits reveals a tremendous potential to make fast genetic progress for residual feed intake in the future.

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