48. Alternative models to predict residual feed intake in Hereford breed and effects on their breeding values accuracy

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Abstract

Residual feed intake (RFI) is a relevant trait, but expensive to measure so few candidates are phenotyped and have accurate GEBVs. Genetic evaluation corresponds to a single trait evaluation, where RFI are the residual from a lineal regression on feed intake on performance traits during feed-test. This study evaluates two approaches to predict a GEBV for RFI. First combing feed performance traits in a multitrait model to calculate a single measure of RFI using selection index, and 2nd the inclusion of weaning weight (WW) as an indicator trait combined with previous model. The GEBVs for the alternatives proposed were equivalent to conventional RFI. Using WW as a predictor trait on reference animals and candidates could be an inexpensive way to increase the accuracy of GEBVs. It allows to remove possible bias due to preselection of animals that participate on feed test and to extend prediction to more selection candidates.

Introduction

Residual feed intake (RFI) has been included in breeding programs with the aim of reducing feed intake without compromising animal performance. Because it is an expensive and labor-intensive to measure trait, only a small percentage of selection candidates are phenotyped Traditional genetic predictions for the rest of candidates relies on pedigree relationships with animals with records and have low accuracies. Although genomic selection is a promising tool for difficult to measure traits, accuracies depend on reference populations sizes. Using easily recordable predictor traits on both reference animals and candidates without RFI phenotypes could be another inexpensive way to increase accuracy. This approach also allows to remove possible bias due to preselection of animals that participate on feed test and to extend predictions to other selection candidates.

Conventional genetic evaluation of RFI is a two-step process. First, RFI is obtained as the residual from a lineal regression for DMI that includes metabolic liveweight (MWT), average daily gain (ADG), and ultrasound back fat (UBF) measured in feed intake tests. Breeding values are then estimated based on this phenotypic RFI in a genetic univariate model (Ravagnolo *et al.*, 2018). An alternative approach to calculate genetic merit for RFI would be by combining feed intake, growth and backfat in a multi-trait model to calculate a single measure of RFI using selection index theory (Kennedy *et al.*, 1993). Another approach proposed in this work is to use weaning weight (WW) as an indicator trait, which is already available and easily recordable in all animals, combined with DMI, ADG, MWT and UBF in a multi-trait model to calculate RFI using selection index as in previous model. The objective of this work is to analyze and compare the new approaches with the conventional methodology used in the Hereford breed in Uruguay.

Materials & methods

Animals and data. Phenotypic DMI, ADG, MWT and UBF data of 780 Hereford bulls were recorded in 9 postweaning 70-day feed intake tests, using an automated system (Growsafe) for DMI recording and following Beef Improvement Federation guidelines (BIF, 2010). Three generations of pedigree (26,572 animals), as well as genomic information of 5,439 animals imputed to the 50k SNP (BovineSNP50, Illumina San Diego, CA), were included in the analysis.

Methods. Three models were used for the estimation of genomic breeding values (GEBV) for RFI. In Model 1, RFI was first obtained as the residual of the following regression model:

$$DMI = CG + b_1\, ADG + b_2\, MWT + b_3\, UBF + RFI \tag{1}$$

where CG is the feed intake test contemporary group (Test×Pen, n-15), DMI, ADG, MWT and UBF were defined previously, and b_1, b_2 y b_3 the partial regression coefficient of each trait on DMI. Then, GEBV for RFI (RFIg1) were obtained using GBLUP as implemented in BLUPF90 (Misztal *et al.*, 2016).

The genetic model was:

$$Y = Xb + Z_u + e \tag{2}$$

where Y is RFI obtained from (1), X is the incidence matrix for fixed effects (age of the animal in days at start of test as a covariable, age of dam as five class variable), Z is the matrix linking animals to phenotypes, u is the vector of genetic breeding values, and e is the vector of residual effects. It was assumed that $u_{RFI} \sim N(0, H\sigma^2_u)$ and $e \sim N(0, I\sigma^2_e)$, where H is the combination of pedigree-based relationships and differences between pedigree-based and genomic-based relationships (Aguilar *et al.*, 2010).

Model 2 is a 4-multi-trait model which included all traits used for RFI calculation (DMI, ADG, MWT and UBF):

$$\begin{bmatrix} Y_1 \\ Y_2 \\ Y_3 \\ Y_4 \end{bmatrix} = \begin{bmatrix} X_1\beta_1 \\ X_2\beta_2 \\ X_3\beta_3 \\ X_4\beta_4 \end{bmatrix} + \begin{bmatrix} Z_1u_1 \\ Z_2u_2 \\ Z_3u_3 \\ Z_4u_4 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \\ e_3 \\ e_4 \end{bmatrix} \tag{3}$$

where Y_{1-4} are DMI, ADG, MWT, UBF, and X and Z are the incidence matrices previously described. Solutions for GEBV for each trait were obtained, and the estimated breeding value for RFI (RFIg2) was calculated using selection index theory as follows:

$$RFI_{g2} = u_1 - b_2u_2 - b_3u_3 - b_4u_4 \tag{4}$$

where 1-4 are the GEBVs solutions for DMI (u_1), ADG (u_2), MWT (u_3), UBF(u_4) predicted from the model [3], and the RFI index coefficients calculated as:

$$V^{-1}C = \begin{bmatrix} b_2 \\ b_3 \\ b_4 \end{bmatrix}, \quad V = \begin{bmatrix} \sigma_2^2 & \sigma_{u2u3} & \sigma_{u2u4} \\ \sigma_{u2u3} & \sigma_3^2 & \sigma_{u3u4} \\ \sigma_{u2u4} & \sigma_{u3u4} & \sigma_4^2 \end{bmatrix}, \quad C = \begin{bmatrix} \sigma_{u1u2} \\ \sigma_{u1u3} \\ \sigma_{u1u4} \end{bmatrix} \tag{5}$$

where V are the genetic variances and covariances for ADG (σ_2^2), MWT(σ_3^2), and UBF (σ_4^2), C the genetic covariances between DMI with ADG ($\sigma_{u1,u2}$), with MWT ($\sigma_{u1,u3}$), and with UBF ($\sigma_{u1,u4}$) (Table 1a), which were estimated using AIREML (Misztal *et al.*, 2016)

For Model 3, WW of the 780 animals with DMI, ADG, MWT and UBF data and 4,930 animals presented in their 235-contemporary groups (only with WW) at weaning were included in a 5-multi-trait model to estimate genetic (co)variances. Representation matrix is similarly to model (5). Genetic variances and covariances estimates are presented in Table 1(b). Solutions for the five traits were obtained, but only GEBVs for DMI, ADG, MWT and UBF were combined as in (4) for the estimation of RFIg3.

Table 1. Genetic co-variance components and genetic correlations obtained for 4-trait model used in $RFIg_2$ (a), and 5-trait model used in $RFIg_3$ (b).

a)	DMI (kg)	ADG (kg/d)	MWT (kg)	UBF (mm)	b)	WW (kg)	DMI (kg)	ADG (kg/d)	MWT (kg)	UBF (mm)
					WW	249.6	6.65	1.47	72.46	3.24
DMI	**0.36**	0.06	2.67	0.19	DMI	0.54	**0.61**	0.11	4.63	0.24
ADG	0.68	**0.02**	0.35	0.03	ADG	0.57	0.83	**0.03**	0.88	0.04
MWT	0.78	0.44	**32.66**	2.33	MWT	0.66	0.85	0.78	**48.43**	2.22
UBF	0.39	0.23	0.51	**0.64**	UBF	0.40	0.61	0.43	0.62	**0.26**

Additive genetic variance in diagonal, genetic covariances above and genetic correlations below the diagonal.

Accuracy. Individual GEBV accuracies were calculated using prediction error variances (PEV) from the inverse of the mixed model equations, as: $r = \sqrt{1- PEV/(1+F)\sigma_g^2}$, where σ_g^2 is the genetic variance of RFIg1 ($\sigma_g^2 = 0.08$). For multi-trait analysis, the accuracies for RFI_2 and RFI_3 were calculated using PEV and PEC (prediction error covariances) (Tier and Meyer, 2004).

Bias and re-ranking. Slopes of regression and Spearman rank correlations between the alternative GEBV obtained from the different models were computed to investigate bias and changes in the ranking of animals.

Results & discussion

The high correlation coefficient and the regression slope of 1 between RFIg1 and RFIg2 (Figure 1a) indicated that Models 1 and 2 are equivalent, as described by Kennedy *et al.* (1993). The comparison of GEBVs by Model 1 and Model 3 showed some changes in ranking (Figure 1b), although the correlation between both was high. The regression slope in this case was above one indicating an underestimation of GEBVs when conventional Model 1 is used, which is corrected by Model 3. Based on Pszczola *et al.* (2013), we can assumed that RFIg3 are less biased than RFIg1 due to: (1) it enables the model to more accurately predict the level of the breeding value of an evaluated animal relative to the reference animals because records of own phenotypes for predictor traits on the evaluated animals give information about the Mendelian sampling, and (2) it accounts for differences between the evaluated animals (animals with scarcely trait records) and the reference population where all animals had the predictor trait record.

Higher standard deviations were observed for RFIg2 (0.18) and RFIg3 (0.23), in comparison with RFIg1 (0.17). This should be consequence of the genetic variances components of all traits considered in the multi-trait model. The mean of RFIg2 (0.016), and RFIg3 (0.021) where higher than RFIg1 (0.014), as result of the underestimation of predicted GEBVs mentioned above.
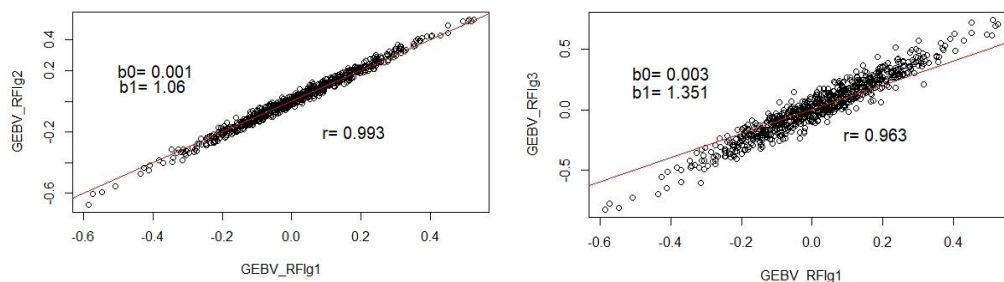

Figure 1. Correlations (r), intercept (b0) and slope of regression (b1) between alternatives GEBVs for RFI for the group of animals with phenotypes. (a) RFIg1 vs RFIg2, (b) RFIg1 vs RFIg3.

A small increase of GEBV accuracy was observed in Figure 2a for RFIg2 in relation with RFIg1, but when WW was considered in the multi-trait analysis (RFIg3, Figure 2b) the mean accuracy improved 39%. The mean accuracies for RFIg1, RFIg2 and RFIg3 for animals with phenotypes were 0.33, 0.36 and 0.46 respectively, meanwhile for contemporary animals without phenotypes nor genotypes the mean accuracies were 0.08, 0.09 and 0.11 for the three approaches, respectively. An improvement in accuracy was expected as WW is highly correlated with DMI and the other traits considered in the calculation of RFIg3.
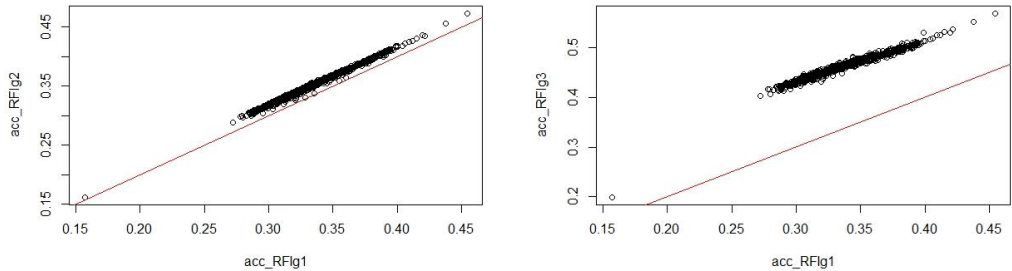

Figure 2. Correlations between accuracy of alternatives GEBVs for RFI for the group of animals with phenotypes. (a) acc_RFIg1 vs acc_RFIg2, (b) acc_RFIg1 vs acc_RFIg3.

Our results show the benefits of considering a multi-trait model including a predictor trait such as WW to predict breeding values for RFI, which were less bias and more accurate than considering a univariate model. This study will be complemented with validations analysis.

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