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Feed intake can be predicted as quantitative or qualitative traits

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Abstract

Feed intake (FI) of ruminants is of high interest to study feed efficiency, greenhouse gas emissions and health traits. However, FI is a very expensive trait to record. Here, we investigated the genetic correlations between true average daily feed intake (ADFI) considered either as a continuous or categorical trait, and the correlations between simple predictions of FI based on body weights and growth with true ADFI. ADFI is genetically the same trait whether considered as a continuous or categorical trait. RFI calculated from categorical ADFI was genetically the same trait as RFI calculated from true ADFI. However, estimated ADFI from a simple model accounting for zootechnical traits, although positively correlated with true ADFI, led to reduced genetic correlations between categorical traits and ADFI: a maximum of 25% of misclassification of lambs is expected if qualitative predictions of ADFI or RFI have to be considered in future analyses.

Introduction

Feed efficiency (FE) is a key trait to improve in small ruminants, from an environmental to an economic point of view. Different criteria exist to define FE, the more popular being feed conversion ratio (FCR) and residual feed intake (RFI) that are considered the reference/gold standards. However, both require feed intake (FI) to be recorded. Different tools exist to record individual FI, but most of them cannot be used in commercial farms, either because they do not comply with animal management (e.g., individual crates) or because they are too expensive (automatic feeders or individual troughs). Many studies aim at identifying proxies of FI or Average Daily Feed Intake (ADFI, over a given period of time) such as metabolites or microbiota, with models also including feed characteristics. Pittroff and Kothmann (2001) reviewed models of quantitative predictions of FI applied to sheep, and concluded that additional studies and datasets were required. Predicting FI is still a challenge in livestock, as shown by recent studies on the relationships between FI and body weights (Lewis and Emmans, 2020). In physiological studies, animals are commonly grouped based on their ADFI to carry out different analyses, but to our knowledge, no genetic study looked at ADFI as a categorical trait; this could enable the application of other prediction models. The objective of this work is to study the genetic parameters of true and predicted ADFI (over an eight-week period) considered either as a quantitative or categorical trait, as well as RFI.

Materials & Methods

Animals and traits. Animals and traits have already been presented in Tortereau et al. (2020). Briefly, a total of 951 Romane male lambs were phenotyped under a 100% low-energy concentrate diet for body weights, feed intake and body composition traits during 8 weeks, starting from 3 months of age. Daily feed intake was averaged over the 8-week testing period to estimate the average daily feed intake (ADFI). The individual RFI was estimated as the residual of the multiple linear regression of ADFI on Average Daily Gain (ADG), BackFat Thickness and Muscle Depth at the end of the test to account for production requirements, and

on the metabolic BW (mBW) at the end of the test to account for maintenance requirements (proc reg; SAS Institute Inc., Cary, NC, USA).

Definition of alternate ADFI traits and RFI. We defined new traits based either on true ADFI or on estimated ADFI (eADFI). Estimated ADFI was defined based on the coefficients retrieved from the multiple linear regression of ADFI on ADG, mBW and age at the beginning of the test (startAge), on a subset of 465 lambs tested from 2009 to 2012. Then, this equation was applied to all individuals (2009-2016) to calculate eADFI. Mean (m) and standard deviation (sd) of ADFI and eADFI were calculated to define the thresholds between five categories of the new categorical traits ADFI_5 and eADFI_5 (Figure 1).

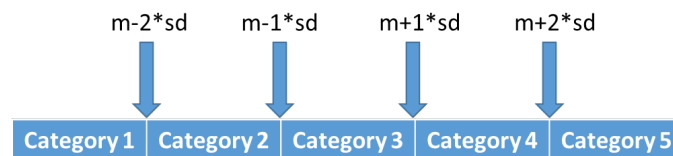


Figure 1. Definition of ADFI_5gr and eADFI_5gr categorical traits, with m (mean) and sd (standard deviation), for ADFI (m = 1962 g/d; sd = 249 g/d) and eADFI (m = 1929 g/d; sd = 231 g/d).

The average ADFI and eADFI were estimated for each of the five categories, and each lamb was assigned this average as a new trait value (ADFI5 and eADFI5, respectively).

An additional RFI trait (RFI5) was calculated with the same multiple linear regression as presented above applied to ADFI5. To summarize, each lamb had eight traits: ADFI, eADFI, RFI, ADFI_5gr, eADFI_5gr, ADFI5, eADFI5, and RFI5.

Estimation of genetic parameters. Heritabilities and genetic correlations between continuous traits were estimated with univariate and bivariate analyses between each pair of traits under an animal mixed model using the REML methodology implemented in the ASReml software (Gilmour et al., 2009). Genetic correlations involving categorical traits (ADFI_5gr and eADFI_5gr) were estimated with TM software developed by Legarra et al. (2011) which handles categorical traits. The fixed effects in the models fitted to each trait were the year (n = 8) and the pen (n = 7). Body weight at the beginning of the test was included as a covariate for ADFI, but not for RFI.

Results

With the subset of lambs born from 2009 to 2012, we defined the prediction equation of feed intake as $eADFI = -550 + 0.90 \cdot ADG + 114 \cdot mBW - 1.48 \cdot startAge$ ($R^2 = 0.80$).

With the full dataset, the phenotypic correlation between ADFI and eADFI was 0.78 ± 0.01 . A total of 74% of lambs were classified in the same ADFI and eADFI categories. Among the other 26% of lambs classified in different categories, all individuals but three were assigned to the group just before or just after (Table 1).

The average differences between ADFI and ADFI5 or eADFI5 (average values of ADFI or eADFI) of the category the animal belongs to) were 5.2% (± 3.7) and 6.8% (± 5.0), with a maximum difference of 14.6 and 30.2%, respectively.

Table 1. Distribution of lambs into five ADFI and eADFI categories

		eADFI_5gr				
		1 st categ.	2 nd categ.	3 rd categ.	4 th categ.	5 th categ.
ADFI_5gr	1 st categ.	11	10			
	2 nd categ.	20	85	33		
	3 rd categ.	2	77	540	41	
	4 th categ.			47	66	9
	5 th categ.			1	3	6

Heritabilities of traits related to ADFI and eADFI ranged from 0.10 ± 0.06 for eADFI5 to 0.33 ± 0.10 for ADFI_5gr (Table 2).

Table 2. Predicted traits: heritabilities and genetic correlations with true average daily feed intake and true residual feed intake.

<i>type of trait</i> ¹	ADFI	ADFI_5gr	ADFI5	RFI5	eADFI	eADFI_5gr	eADFI5
	<i>cont.</i>	<i>categ.</i>	<i>cont.</i>	<i>cont.</i>	<i>cont.</i>	<i>categ.</i>	<i>cont.</i>
h^2	0.28 (± 0.08)	0.33 (± 0.10)	0.16 (± 0.07)	0.20 (± 0.07)	0.22 (± 0.08)	0.27 (± 0.10)	0.10 (± 0.06)
genetic corr. with ADFI		1.00	1.00	0.68 (± 0.16)	0.62 (± 0.12)	0.63 (± 0.16)	0.54 (± 0.21)
genetic corr. with RFI	0.78 (± 0.08)	not different from 0	0.87 (± 0.11)	1.00	not different from 0	not different from 0	not different from 0

¹ Traits are either categorical (categ.) or continuous (cont.)

Genetic correlations indicate that ADFI, ADFI_5gr and ADFI5 are genetically the same trait. Similarly, RFI is the same trait whether estimated from true ADFI or from averaged values (RFI5) (Table 2). The genetic correlation between true and estimated ADFI was positive (0.62 ± 0.12). The categorical trait eADFI_5gr and the corresponding continuous trait eADFI5 showed significant positive genetic correlations with ADFI (0.63 and 0.54, respectively).

Discussion

The link between feed intake and body weight, growth and age is well known, and many studies aimed at predicting quantitatively feed intake (Pittroff and Kothmann, 2001). With Romane male lambs, we highlighted that ADFI is genetically the same trait when expressed as a categorical trait (ADFI_5gr) or as average values of feed intake (ADFI5). This makes it possible to consider a wider variety of prediction methods including qualitative prediction methods. Recently, in pigs, machine learning procedures were successfully applied on transcriptomic data to predict either categories of FE (with a 100% success of assignation) or FE values (with $R^2 = 0.80$ and $RMSE = 8\%$) (Messad et al., 2021). In our study, we highlight that RFI and RFI5 are genetically the same trait despite the 5% difference between ADFI and ADFI5. Moreover, RFI5 was less heritable than RFI (0.20 ± 0.07 vs. 0.45 ± 0.08 ; Tortereau et al., 2020). Additional studies of the impact of feed intake accuracy on RFI estimates and RFI

genetic parameters will be of high interest in order to better consider the phenotyping strategies of feed intake.

In our study, we tested different numbers of categories (from two to five based on ADFI and eADFI distributions) and results were similar to the ones we presented with five categories (results not shown). However, the genetic correlation between eADFI_5gr and ADFI is only 0.63, which is significantly different from 1.00: misclassification of a quarter of the individuals would have consequences for the genetic correlation with ADFI.

With a simple estimation of ADFI from age, mBW and ADG, we obtained a new trait, eADFI, significantly correlated with ADFI (Table 2). The distribution of lambs within five classes, eADFI_5gr, was still positively genetically correlated to ADFI. Even if the objective of this paper was not to analyse the prediction accuracy of ADFI from classical zootechnical traits, this result highlights that such a simple prediction might be proposed as a first prediction of ADFI. However, with such a prediction, RFI cannot be calculated given that eADFI represents the maintenance and requirements of ADFI, whereas it might be suitable for prediction of FCR. Most of the models considered in Pittroff and Kothmann (2001) rely on animal requirements and thus do not consider the residual part of feed intake. New proxies such as transcriptome, metabolites and microbiota have to be considered in order to better predict ADFI and RFI (Cantalapiedra-Hijar et al., 2018). With PLS-DA approaches carried out on ruminal microbiota data only, it was possible to discriminate high vs. low efficient animals, and high vs. low eating lambs, but with a poor prediction accuracy, particularly for RFI groups (Le Graverand et al. 2021). Therefore, future models combining new proxies and zootechnical traits might help in predicting ADFI or RFI in sheep, whether quantitatively or qualitatively.

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