

Using collective feed intake data to select for feed efficiency on full or restricted feeding regimen

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ABSTRACT

Variance components of average daily gain (ADG) on both full and restricted feeding regimen (FF and RF), and average daily feed intake (ADFI) on FF of kits raised in collective cages were estimated for each week of the fattening period by using a multiple-trait model analysis. Data from a total of 6,264 kits from 1,317 litters housed in 812 cages along 14 batches were used for the analysis. Results indicate that weighted estimate of heritability for ADG was 0.47 (0.03) and 0.40 (0.03) on FF and RF, respectively, but genetic variance was much smaller on RF. The interaction between the genotype and feeding regimen was 13% of the mean phenotypic variance of both traits. Heritability of $ADFI_{FF}$ was 0.28 (0.06). Breeding values of ADG_{RF} conditional on ADG_{FF} represents the effects of genes only involved in feed efficiency. The heritability of this trait is equal to that for $ADFI_{FF}$ conditional on ADG_{FF} (a different measurement of feed efficiency) but its genetic variation is lower. The genetic correlation between them was nearly null which indicates that these traits are related to different components of feed efficiency.

Key words: Feed efficiency, feeding regimen, GxE interaction, genetic parameters, collective data

INTRODUCTION

Despite of its importance direct selection for feed efficiency (**FE**) is not performed in most breeding programs because of the problems associated to individual recording of feed intake (**FI**) which is involved in the definition of FE. Thus, for example, selection for residual feed intake is defined as the difference between actual FI and that predicted based on requirements for production and maintenance. Recently, selection for increased average daily gain on restricted feeding (ADG_{RF}) has been proposed as selection criteria to improve FE since variation in this trait is directly related with variation in FE because of constant FI. Therefore, individual records of FI are no needed. In rabbit, there are currently two experiments of selection to improve FE by selecting for increased ADG_{RF} or reduced RFI on full-feeding, respectively (Drouilhet et al., 2013). In both experiments animals were kept in individual cages in order to individually record (or control) FI whereas, under commercial conditions, kits are raised in collective cages. In these conditions feeding behaviour is different due to social interactions among individuals sharing the same cage which in turns affects FI and ADG, and could lead to a GxE interaction effect on FE. In addition, the magnitude of the interaction between the genotype and the feeding regimen (**FR**) is still unknown in rabbit, and therefore the effect of selection under restricted feeding on animals fed *ad libitum* or vice versa.

In this paper we propose a model for a joint fit of individual ADG and cage average daily feed intake ($ADFI$), when data come from kits raised in collective cages on full (**FF**) or restricted feeding (**RF**). The objective is to estimate genetic parameters for these traits and the interaction between the genotype and FR, as well for different measurements of FE which can be obtained from variance components of ADG and ADFI.

MATERIALS AND METHODS

Animals and experimental design

A total of 6,264 kits from a rabbit sire line (Caldes line, Gómez et al., 2002), currently selected for ADG with *ad libitum* feeding during the fattening period (from 32 to 60 d of age), were used for the experiment. Animals were bred under the same environmental and management conditions except feeding regime which was FF or RF. In both cases kits were fed the same standard pellet diet from weaning (32 d) to slaughter age (67 d). After weaning, kits were randomly assigned to one of these two treatments. In order to get homogeneous groups regarding animal size, kits were assigned to two different groups within treatment based on their body weight: Large Size kits (LS; above the batch mean) and Small Size kits (SS; under or equal to batch mean). For every week the amount of food offered to animals on RF was equal to 0.75% of *ad libitum* feed intake FI, which was computed as the average FI of animals during the week before in the same batch and size class combination, multiplied by a factor to account for the increase in FI from week to week due to animal growth (this factor was computed from data of a previous experiment). Actual feed restriction was on average 75.3% for heavy kits and 74.1 % for light kits. Water was always available. A maximum of two kits per litter were allocated in the same cage with the intention of minimizing the maternal and pre-weaning environmental effects on behaviour and growth performance. Only data from cages containing the initial 8 kits at the end of the fattening were used for the analysis. Those data corresponded to 6,264 kits from 1,303 litters produced along 14 batches and housed in 783 cages. Individual BW of all kits and total feed intake (TFI) of kits fed *ad libitum* in the same cage were weekly recorded always on the same day of the week.

Statistical Analysis

A multiple-trait analysis of weekly ADFI in cages on FF ($ADFI_{FF}$) and individual ADG both under FF (ADG_{FF}) and FR (ADG_{RF}) was conducted. Thus 12 traits were considered: 3 traits x 4 weeks. The analysis was performed using gibbs1f90 program (Misztal et al. 2002). For each week, individual ADG was computed as the difference in BW at the beginning and end of that week divided by 7; $ADFI_{FF}$ was defined as the average amount of feed daily consumed by a kit in a cage and computed as $ADFI = TFI / (7 \times 8)$. The model for all traits included the fixed factors of batch (14 levels), animal size (2 levels), litter size at birth (7 levels), parity order (4 levels: 1, 2, 3 and >3), the random environmental factors of litter and cage, the additive genetic effect and the residual. In the case of $ADFI_{FF}$ this model can be written as:

$$y_{ijo} = B_i + S_j + \mathbf{x}'_{Po} \mathbf{P} + \mathbf{x}'_{LSo} \mathbf{LS} + \mathbf{z}'_{lo} \mathbf{l} + \mathbf{z}'_{ao} \mathbf{a} + c_o + e_{ijo}$$

where, $y_{ijklmno}$ is the ADFI of the o^{th} cage, in the batch i^{th} and in the group of size j^{th} ($j=BS,SS$), \mathbf{x}'_{Po} , \mathbf{x}'_{LSo} , \mathbf{z}'_{lo} and \mathbf{z}'_{ao} contain the proportion of the different levels among the 8 animals in the o^{th} cage; these vectors will have the same length as the number of levels of each factor. B_i is the effect of the i^{th} batch, S_j is the effect of the j^{th} group of size, c_o is the effect of the o^{th} cage, \mathbf{P} is the vector (size 4) of parities effects, \mathbf{LS} is the vector (size 7) of litter sizes effects, \mathbf{l} is the vector (size 1,303) of the litter effects, \mathbf{a} is the vector (size 7701, number of animals in the pedigree) of breeding values and e_{ijo} is residual term. Variance components (VC) for $ADFI_{FF}$ and ADG_{RF} , conditioned on ADG_{FF} , were computed following the indications given by Strathe et al. (2014). These conditional variables can be then interpreted as average daily residual feed intake and the part of ADG_{RF} independent of ADG_{FF} ($ADG_{RF|ADG_{FF}}$), respectively. In addition weekly VC on both FR were summarized in single parameter by computing the weighted average across all weeks, being the weighting factor the proportion of data in each week.

RESULTS AND DISCUSSION

The pattern of growth was different for animals on FF or RF (Figure 1). Post-weaning growth was decelerated after first week for animals on FF whereas it accelerated until week 3 and then remained constant for animals on RF. Therefore, in order to avoid making assumptions on longitudinal trajectories, ADG and ADFI on different weeks and FR were considered to be different but correlated traits for the subsequence analysis. Data from the 5th week were excluded from the analysis because in the last week a different diet was provided.

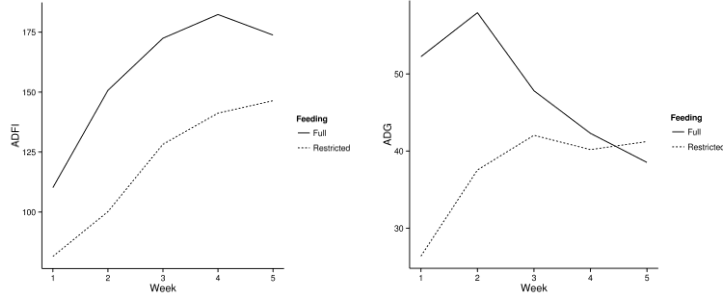


Figure 1: Weekly average daily feed intake (ADFI) and body weight gain (ADG) for animals feed on full or restricted feeding

Heritability for post weaning ADG computed from weighted averages of VC was high and similar for both FR (Table 1). The magnitude of this parameter is much higher than the corresponding to each week; this was due to genetic covariances among weeks which were much higher than the phenotypic covariances. For ADFI_{FF}, a much lower heritability was observed (Table 1), which was fairly equal to the raw average of weekly heritabilities, indicating a similar magnitude of both genetic and phenotypic weekly covariances. The weighted genetic correlation between ADG in both FR was 0.71(0.07) (Posterior mean(posterior standard deviation)), clearly different from 1, indicating an important interaction effect (Mathur, 2002) between the genotype and FR, this interaction supposes 14% of the weighted average across weeks phenotypic variance for both FR.

Table 1: Weekly estimates of ratios of phenotypic variance of feed intake (FI), average daily gain (ADG) and residual feed intake (RFI) for animals on full (FF) or restricted (RF) feeding regimen

		ADG					FI				
	P ¹	W1	W2	W3	W4	avg	W1	W2	W3	W4	avg
FF	σ^2	80.91 (2.48)	97.50 (3.45)	86.48 (3.44)	88.70 (3.78)	34.89 (1.33)	399.15 (46.83)	936.24 (130.31)	1046.39 (145.60)	1644.86 (222.48)	304.15 (31.05)
	h^2	0.28 (0.04)	0.36 (0.04)	0.27 (0.04)	0.17 (0.04)	0.47 (0.03)	0.42 (0.09)	0.18 (0.05)	0.20 (0.06)	0.18 (0.05)	0.28 (0.06)
	c^2	0.08 (0.01)	0.09 (0.01)	0.18 (0.02)	0.18 (0.02)	0.05 (0.01)	0.07 (0.02)	0.09 (0.03)	0.10 (0.03)	0.06 (0.02)	0.11 (0.03)
	σ^2	52.55 (1.89)	56.60 (2.02)	72.15 (2.74)	81.73 (3.57)	23.19 (0.94)					
	h^2	0.29 (0.04)	0.19 (0.03)	0.21 (0.04)	0.19 (0.04)	0.40 (0.03)					
RF	c^2	0.14 (0.02)	0.15 (0.02)	0.17 (0.02)	0.20 (0.03)	0.09 (0.02)					

¹Parameter: σ^2 = phenotypic variance, h^2 = heritability; c^2 = ratio of phenotypic variance due to cage effect; ²W = week of the fattening period. ³FF = full feeding; RF = restricted feeding

ADFI_{FF} conditioned on ADG_{FF} can be interpreted as a FE measurement equivalent to RFI despite maintenance needs hasn't been considered. The weighted heritability for this trait is high (Table 2), in

agreement with previous estimates of heritability for feed conversion ratio in the same population of rabbits (Piles et al., 2004). ADG_{RF} can also be interpreted as a FE trait, despite its high heritability genetic variability for this trait is was much lower than for $ADFI_{FF}|ADG_{FF}$ which might limit the possibilities of response to selection for this trait.

Conditioning ADG_{RF} on ADG_{FF} removes the covariance between ADG across FR. Therefore, predicted breeding value for $ADG_{RF}|ADG_{FF}$ represent the effect of genes exclusively involved in ADG_{RF} and not involved in ADG_{FF} . Thus the letter could better indicate the effect of FE genes. The heritability of this conditional trait is equal to that for $ADFI_{FF}|ADG_{FF}$ but its genetic variation is lower. The genetic correlation between $ADFI_{FF}|ADG_{FF}$ and $ADG_{RF}|ADG_{FF}$ was nearly null (-0.16(0.20)) which suggests that they define different components of FE. It has to be noted that $ADFI_{FF}|ADG_{FF}$ does not account at all for maintenance needs, while both ADG_{RF} and $ADG_{RF}|ADG_{FF}$ explicitly do.

Table 2: Weekly estimates of ratios of phenotypic variance of average daily gain on restricted feeding (ADG_{RF}) and average daily feed intake on full feeding ($ADFI_{FF}$) conditional on average daily gain on full feeding (ADG_{FF}).

P ¹	ADG _{RF} ADG _{FF}					ADFI _{FF} ADG _{FF}				
	W1	W2	W3	W4	avg	W1	W2	W3	W4	avg
σ^2	44.55 (1.67)	51.45 (1.88)	67.57 (2.65)	77.35 (3.45)	18.95 (0.92)	311.72 (33.78)	885.94 (124.90)	1002.14 (143.05)	1542.93 (220.87)	266.87 (26.05)
h^2	0.09 (0.03)	0.06 (0.02)	0.10 (0.03)	0.09 (0.03)	0.24 (0.05)	0.12 (0.04)	0.12 (0.04)	0.12 (0.04)	0.13 (0.04)	0.24 (0.06)
c^2	0.17 (0.02)	0.17 (0.02)	0.18 (0.02)	0.21 (0.03)	0.10 (0.02)	0.01 (0.01)	0.03 (0.02)	0.02 (0.01)	0.04 (0.01)	0.06 (0.02)

¹Parameter: σ^2 = phenotypic variance, h^2 = heritability; c^2 = ratio of phenotypic variance due to cage effect; ²W = week of the fattening period.

CONCLUSIONS

It is feasible to use collective data of feed intake in order to select for feed efficiency. Selection would be slightly more effective when animals are on full than on restricted feeding. However due to the existence of an interaction between the genotype and the feeding regimen, it is advisable to select animals on the same conditions as for production. Full-feeding feed intake conditional on full-feeding growth can be interpreted as a measurement of RFI; this trait shows a moderate heritability and allows to capture genetic effects different from those involved in growth on restricted feeding.

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