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USING COLLECTIVE FEED INTAKE DATA TO SELECT FOR
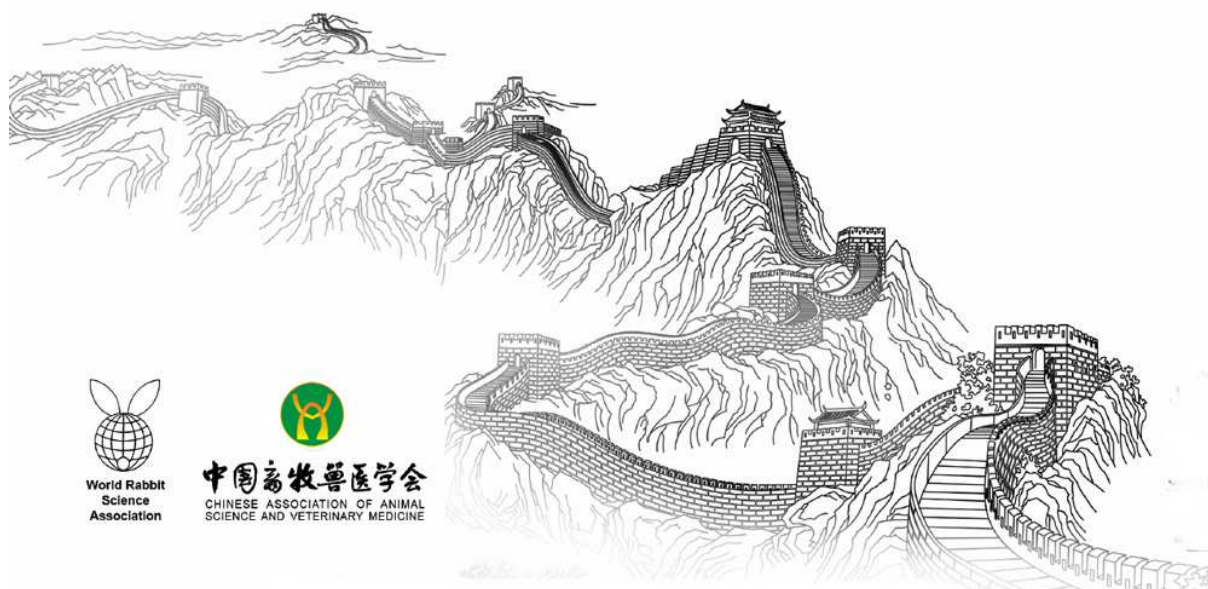FEED EFFICIENCY ON FULL OR RESTRICTED FEEDING REGIMEN.

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USING COLLECTIVE FEED INTAKE DATA TO SELECT FOR FEED EFFICIENCY ON FULL OR RESTRICTED FEEDING REGIMEN

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ABSTRACT

A multiple-trait model analysis of weekly average daily gain (ADG)of kits on both full and restricted feeding regimen (ADG$_{FF}$ and ADG$_{RF}$),and average daily feed intake on FF was performed (ADFI$_{FF}$). Data from a total of 6,264 kits from 1,317 litters housed in 812 collective cages along 14 batches were used. Variance component of two different feed efficiency traits were estimated from those corresponding to growth and feed consumption on both feeding regimens. Results indicate that weighted estimates of heritability for ADG were 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 14% of the mean phenotypic variance for 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 heritably 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 both traits was nearly null which indicates that they 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**), involved in the definition of FE. Thus, for example, residual feed intake (**RFI**) is defined as the difference between actual FI and predicted food 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 because variation in this trait is directly related with variation in FE due toconstant FI. One of the advantages of using this trait is that individual records of FI are not 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 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.On the other hand, the magnitude of the interaction between the genotype and the feeding regimen (**FR**), and therefore the effect of selection under restricted feedingon animals fed *ad libitum* or vice versa, is still unknown in rabbit.

In this paper we propose a model for a joint analysis 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 estimategenetic parameters for these traits and the interaction between the genotype and FR, as well as for different measurementsof 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) were used for the experiment.This line is currently selected for ADG with *ad libitum* feeding during the fattening period (from 32 to 60 d of age). After weaning, kits were randomly assigned to one of the two FR (FF or RF). A maximum of two kits from the same litter were allocated in the same cage to minimize the maternal and pre-weaning environmental effects on behaviour and growth performance. In order to get homogeneous groups regarding animal size, kits were assigned to two different groups within FR based on their weaning body weight: Big Size kits (**BS**; above the batch mean) and Small Size kits (**SS**; under or equal to batch mean). Animals were bred under the same environmental and management conditions except FR. In both cases kits were fed the same standard pellet diet from weaning (32 d) to slaughter age (67 d).For every week, the amount of food offered to animals on RF was equal to 75% of *ad libitum* FI, which was computed as the average FI of animals on FFduring 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 BS kits and 74.1 % for SS kits. Water was always available. 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 raised in 14 batches and housed in 783 cages. Individual body weight of all kits and total feed intake (**TFI**) of kits fed on FF 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. For each week, individual ADG was computed as the difference in body weight 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 x 8). The model for all traits included the fixed factors of batch (14 levels), animal size (2 levels), litter size at birth (7 levels: <6, 6, 7, … ,>10), 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_{ijo} is the ADFI of the cageo^{th},in the batch $i^{th}$and in the group of size jth(j= BS,SS); $\mathbf{x'}_{Po}$, $\mathbf{x'}_{LSo}$, $\mathbf{z'}_{lo}$ and $\mathbf{z'}_{ao}$ containthe proportion of the different levels among the 8 animals in the cageo^{th}; these vectors will have the same length as the number of levels of each factor; B_i is the effect of the batchi^{th}; S_j is the effect of the group of sizej^{th}; c_o is the effect of the cageo^{th};**P** is the vector (size 4) of parities effects;**LS** is the vector (size 7) of litter sizes effects;**l** is the vector (size 1,303) of the litter effects; **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 FRwere summarized in single parameter by computing the weighted average across all weeks, being the weighting factor the proportion of datain 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. 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.
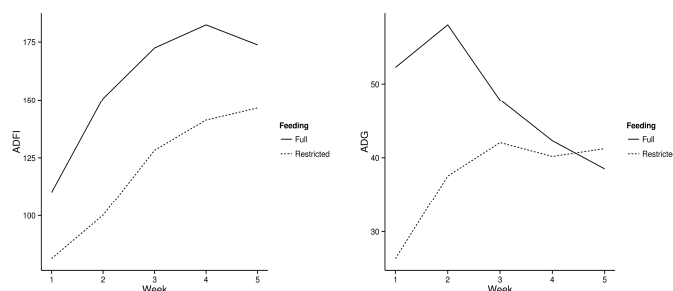
Figure 1: Weekly average daily feed intake (ADFI) and body weight gain (ADG) for animals feed on full or restricted feeding

Heritability for post weaning ADG computed from weighted averagesofVC washigh and similar for both FR (Table 1).The magnitude of this parameter is much higher than the corresponding to any week because of genetic co-variances among weeks were much higher than the phenotypic co-variances.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 posterior mean(posterior standard deviation) of weightedgenetic correlation between ADG in both FR was 0.71(0.07), clearly different from 1, indicating an important interaction effect (Mathur, 2002) between the genotype and FR; this interaction supposes 14% of mean of weighted averagesof phenotypic variance in both FR.

Table 1: Posterior mean (posterior s.d.) of ratios of phenotypic variation at different weeks for 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[a]	W1[b]	W2	W3	W4	avg[c]	W1	W2	W3	W4	avg
FF[d]	σ^2_P	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)
RF[d]	σ^2_P	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)					
	c^2	0.14 (0.02)	0.15 (0.02)	0.17 (0.02)	0.20 (0.03)	0.09 (0.02)					

[a]Parameter: σ^2_P = phenotypic variance, h^2 = heritability; c^2 =ratio of phenotypic variance due to cage effect; [b]W1, W2, W3, W4 = week of the fattening period;[c] Weighted averages;[d] FF = full feeding; RF = restricted feeding

ADFI$_{FF}$ conditioned on ADG$_{FF}$can be interpreted as a FE measurement similar to RFI,despite ofmaintenance needs has not been considered. The weighted heritability for this trait is high (Table 2), in agreement with previous estimatesof heritability forfeed conversion ratio in the same population of rabbits (Piles et al., 2004). ADG$_{RF}$ can also be interpreted as a FE trait. Despite of the high heritability for this trait,the possibilities of positive response to selection for this traitmight be limited due to its low genetic variability in comparison with that for ADFI$_{FF}$|ADG$_{FF}$.

Conditioning ADG_{RF} on ADG_{FF} removesthe covariancebetween 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}. Therefore,it could indicate better the effect of FE genes. The heritably 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 (PM = -0.16; PSD = 0.20)which suggeststhat they define different components of FE. It has to be noted that $ADFI_{FF}|ADG_{FF}$ does not account for maintenance needs, but both ADG_{RF} and $ADG_{RF}|ADG_{FF}$ would do it.

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	51.45	67.57	77.35	18.95	311.72	885.94	1002.14	1542.93	266.87
	(1.67)	(1.88)	(2.65)	(3.45)	(0.92)	(33.78)	(124.90)	(143.05)	(220.87)	(26.05)
h^2	0.09	0.06	0.10	0.09	0.24	0.12	0.12	0.12	0.13	0.24
	(0.03)	(0.02)	(0.03)	(0.03)	(0.05)	(0.04)	(0.04)	(0.04)	(0.04)	(0.06)
c^2	0.17	0.17	0.18	0.21	0.10	0.01	0.03	0.02	0.04	0.06
	(0.02)	(0.02)	(0.02)	(0.03)	(0.02)	(0.01)	(0.02)	(0.01)	(0.01)	(0.02)

[1]Parameter: σ^2 = phenotypic variance, h^2 = heritability; c^2 =ratio of phenotypic variance due to cage effect; [2]W = 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. Feed intake conditional on growth on full feeding 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.

ACKNOWLEDGEMENTS

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Feed-a-Gene

Adapting the feed, the animal and the feeding techniques to improve the efficiency and sustainability of monogastric livestock production systems

IRTA RECERCA I TECNOLOGIA AGROALIMENTÀRIES

Introduction

Strategies for genetic improvement of feed efficiency in rabbit

- As a **correlated response** to selection for daily gain or body weight at given age.
    - Easy to perform irrespective of the type of housing (individual or collective cages)
    - In some cases, less response than expected

- **Direct selection for** some measurement of feed efficiency of kits on full feeding computed before the genetic evaluation (e.g. residual feed intake)
    - Potentially more effective (Drouilhet et al 2016; JAS)
    - It requires the measurement of individual feed intake (FI) and body weight gain (BWG). Difficult and costly to perform
    - Do not account for variation over time in variances and correlations for BWG and FI (Strathe et al, 2014, 10th WCGALP)
    - Kits need to be in individual cages. Low response in commercial conditions when there is an interaction between the genotype and the feeding regimen and/or type of housing due to social effects

- **Direct selection** for some measurement of feed efficiency which do not need records on feed intake, as **growth rate on restricted feeding**
    - **Potentially effective** (Drouilhet et al 2016; JAS)
    - **Easy to perform**
    - **Possible genotype x feeding regimen interaction**
   - **Social-interaction effects** might be important:
        G x Type of housing interaction

Objectives

- To define a **model for direct selection for feed efficiency** which
    - Allows the **use of collective records** of feed intake
    - Accounts for **changes over time of genetic parameters** of feed intake and growth rate
- To estimate the **interaction between the genotype and the feeding regimen** for growth and feed efficiency **for kits in collective cages**

Material & Methods
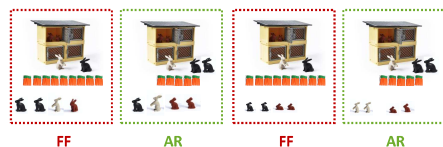
Feeding Regimens
FF: Full
RF: Restricted to 75% feed intake on FF

Same management & environmental conditions. 8 kits/cage. 4 families/cage

FF   AR   FF   AR

Weekly total feed intake of the cage (WTFI)

Individual body Weight (BW)   32d 39d 46d 53d 60d

6,264 kits
1,303 litters
14 batches
783 cages

$ADFI = WTFI / (7 \times 8)$

$ADG = (BW_{t+1} - BW_t) / 7$

Multiple-trait model for weekly data as different correlated traits

$ADFI_{FF}$: average daily feed intake on full feeding

ADG_{FF} : average daily gain on full feeding

ADG_{RF} : average daily gain on restricted feeding

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

Batch, Parity, Litter size, Body size, Litter, Cage, Additive genetic

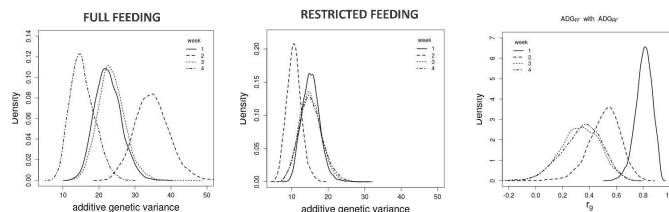Rate of the kits in the cage in each level of the factor

Bayesian analysis; gibbs1f90.

3 definitions of feed efficiency

- $ADFI_{FF} | ADG_{FF}$ feed intake conditioned on daily body gain on FF
- ADG_{RF} daily body gain on RF
- $ADG_{RF} | ADG_{FF}$: daily body gain on RF conditioned on daily body gain on FF

Results

Average Daily Gain on Full and Restricted Feeding Regimen

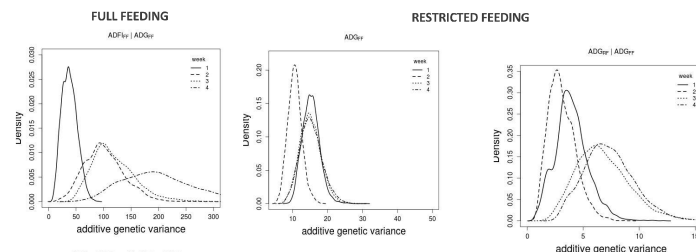FULL FEEDING   RESTRICTED FEEDING   ADG_RF with ADG_FF

Posterior mean (posterior s.d.) of ratios of phenotypic variation at different weeks for feed intake (ADFI), average daily gain (ADG) for growing kits on full (FF) or restricted (RF) feeding regimen

P [a]	ADG W1 [b]	ADG W2 [b]	ADG W3 [b]	ADG W4 [b]	ADFI W1 [b]	ADFI W2 [b]	ADFI W3 [b]	ADFI W4 [b]
FF [c] σ^2	80.91 (2.48)	97.50 (3.45)	86.48 (3.44)	88.70 (3.78)	399.15 (46.83)	936.24 (130.31)	1046.39 (145.60)	1644.86 (222.48)
h^2	0.28 (0.04)	0.36 (0.04)	0.27 (0.04)	0.17 (0.04)	0.42 (0.09)	0.18 (0.05)	0.20 (0.06)	0.18 (0.05)
c^2	0.08 (0.01)	0.09 (0.01)	0.18 (0.02)	0.18 (0.02)	0.07 (0.02)	0.09 (0.02)	0.10 (0.03)	0.06 (0.02)
RF [d] σ^2	52.55 (1.89)	56.60 (2.02)	72.15 (2.74)	81.73 (3.57)				
h^2	0.29 (0.04)	0.19 (0.03)	0.21 (0.04)	0.19 (0.04)				
c^2	0.14 (0.02)	0.15 (0.02)	0.17 (0.02)	0.20 (0.03)				

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

- Moderate heritability for ADG on FF and RF and ADFI on FF. Genetic correlation $\neq 1$
- Variance due to the genotype by feeding regimen interaction for ADG around 14% of the mean of phenotypic variances
- Bigger group effects for animals on RF than on FF at the beginning of fattening

Feed Efficiency on Full and Restricted Feeding Regimen

FULL FEEDING   RESTRICTED FEEDING
$ADFI_{FF} | ADG_{FF}$ ADG_{RF} $ADG_{RF} | ADG_{FF}$

$ADFI_{FF} | ADG_{FF}$ with $ADG_{RF} | ADG_{FF}$

Posterior means (posterior s.d.) of 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 [a]	$ADG_{RF}|ADG_{FF}$ W1 [b]	W2	W3	W4	$ADFI_{FF}|ADG_{FF}$ W1	W2	W3	W4
σ^2	44.55 (1.67)	51.45 (1.88)	67.57 (2.65)	77.35 (3.45)	311.72 (33.78)	885.94 (124.90)	1002.14 (143.05)	1542.93 (220.87)
h^2	0.09 (0.03)	0.06 (0.02)	0.10 (0.03)	0.09 (0.03)	0.12 (0.04)	0.12 (0.04)	0.12 (0.04)	0.13 (0.04)
c^2	0.17 (0.02)	0.17 (0.02)	0.18 (0.02)	0.21 (0.03)	0.01 (0.01)	0.03 (0.02)	0.02 (0.01)	0.04 (0.01)

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

- Low to moderate heritability for $ADFI_{FF}|ADG_{FF}$, $ADG_{RF}|ADG_{FF}$ and ADG_{RF}
- But very low additive genetic variance for $ADG_{RF}|ADG_{FF}$. Limited possibilities of response to selection for this trait
- Null genetic correlation between $ADFI_{FF}|ADG_{FF}$ and $ADG_{RF}|ADG_{FF}$ (PM = -0.16; PSD = 0.20) which suggests that they define different components of FE.

Conclusions

- It is feasible to use collective data of feed intake in order to select for feed efficiency when kits are fed on full feeding regimen
- Selection could be more effective on full than on restricted feeding.
- There is an interaction between the genotype and the feeding regimen when kits are housed in groups
- The three definitions of FE seem to involve different genetic effects

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