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Genetic relationships between different measures of feed efficiency and its component traits in Wagyu (Japanese Black) bulls

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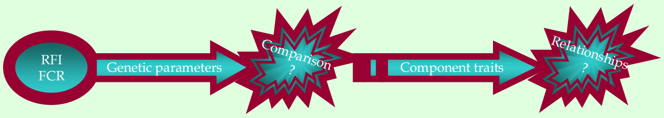
The feed resource for animals is a major cost determinant for profitability in livestock production enterprises, and thus any effort at improving the efficiency of feed use will help to reduce feed cost. It is, therefore, of interest to determine whether the inclusion of residual feed intake (RFI) or feed conversion ratio (FCR) in the selection program would improve efficiency of beef production.



Opportunities for improving production efficiency by exploiting genetic variation in feed efficiency depend not only on the existence of genetic variation within a target population but also on genetic correlations with other key production traits. We estimated genetic parameters for feed efficiency traits and their genetic relationships with its component traits.

Animals: A total of 740 Japanese Black bulls were tested for 112 days at the Okayama Animal Industry Center, Japan during the period from 1971-2002. The bull calves, collected from designated farms, were within the age limit of 7-8 months and body weight of 200-300 kg. Each year, 20 -30 bulls were selected on the basis of heavier body weight from approximately 200 bulls. After three weeks of being introduced to the feed, the bulls were provided *ad libitum* access to roughage; however feeding of concentrate was restricted to twice daily for 1 hour morning and evening.

Traits in study: The traits studied were daily gain (DG), metabolic weight (MWT), body weight at finish (BWF), feed intake (FI), RFI and FCR. The RFI was calculated as the difference between actual and expected FI by the residual of phenotypic (RFI_{phe}) and genetic (RFI_{gen}) regression from the multivariate analysis of FI on MWT and DG.

RFI_{phe} was calculated as: $RFI_{phe} = FI - \beta_w \times MWT - \beta_g \times DG$
where β_w & β_g = the phenotypic regression coefficients of FI on MWT and DG, respectively.

RFI_{gen} was calculated as: $RFI_{gen} = FI - \beta_w \times MWT - \beta_g \times DG$
where β_w & β_g = the genetic regression coefficients of FI on MWT and DG, respectively

Statistical analysis: The covariance components for all traits were estimated by the REML method with the VCE program. The analyzed traits are described by the following model:

$$Y_{ij} = F_i + b(A_j - A) + a_j + e_{ij}$$

where Y_{ij}=phenotype of j^{th} animal in i^{th} cohort; F_i=fixed effect of i^{th} cohort; b=linear regression coefficient of observation on age; A_j=age of the animals; A=average age of the animals; a_j=additive genetic effect; e_{ij}=random residual. The genetic parameters were estimated from bivariate analyses.

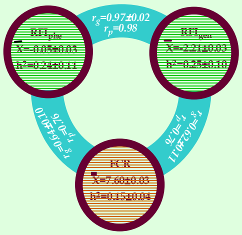


Figure 1 *Relations among feed efficiency traits*

- Both the RFI were moderately heritable and the h^2 for FCR was low.
- The r_g and r_p between RFI_{phe} and RFI_{gen} were >0.95, implying that they might be regarded as the same traits
- Corresponding correlations of FCR with RFI were high but less than unity, indicating that they should be regarded as distinct traits.
- The positive correlations between RFI and FCR indicate that lower RFI (higher efficiency) was associated with improved FCR.

Table 1 *Means, h^2 and correlations among FI and growth traits*

Traits	Means (kg) ±SD	Genetic parameters†			
		FI	DG	MWT	BWF
FI	9.26±0.04	**0.34±0.11**	0.87±0.08	0.74±0.15	0.88±0.11
DG	1.23±0.01	0.56	**0.20±0.10**	0.96±0.09	0.95±0.10
MWT	78.88±0.23	0.55	0.36	**0.49±0.09**	0.97±0.08
BWF	408.88±1.47	0.55	0.49	0.89	**0.47±0.10**

† h^2, genetic and phenotypic correlations are on, above and below the diagonal, respectively

- The r_g between FI and growth traits were high and r_p between them were moderate.
- The r_g among growth traits were in unity (>0.95) and the r_p between them were moderate to high.
- Estimated h^2 for DG was low, whereas for MWT and BWF were moderate.
- The h^2 of FI was moderate and higher than those for feed efficiency traits.

Table 2 *Phenotypic and genetic correlations between different measures of feed efficiency and its component traits*

Traits	Correlations †	FI	DG	MWT	BWF
RFI_{phe}	r_p	0.72	0.01	-0.01	-0.01
	r_g	0.78±0.06	0.25±0.16	0.16±0.13	0.19±0.15
RFI_{gen}	r_p	0.31	-0.13	-0.18	-0.18
	r_g	0.61±0.10	0.18±0.20	-0.07±0.14	-0.04±0.15
FCR	r_p	0.40	-0.52	0.14	0.11
	r_g	0.34±0.15	-0.58±0.24	-0.57±0.25	-0.52±0.25

† r_p and r_g denote phenotypic and genetic correlations, respectively.

- FI was positively correlated with all feed efficiency traits but was more strongly correlated with RFI than with FCR.
- By definition, RFI_{phe} should not be phenotypically correlated with its component traits, and the results confirmed this (i.e. r_p with MWT and DG were zero).
- RFI_{gen} was genetically independent of MWT, whereas low r_g was found between RFI_{gen} and DG.
- Favorable (negative) r_g and r_p were observed between FCR and its component traits, DG.

- Selection against RFI would lead to a large reduction in FI with small change in growth traits, and selection against FCR would lead to a small reduction in FI with small increase in growth traits.
- Reported literatures have suggested that the use of ratio traits (FCR) for genetic selection may cause problems associating to prediction of the change in the component traits in future generations.
- The weights of the component traits in RFI are determined by only biological covariances. However, profitability will be maximized when index weights on RFI, growth and other traits are determined by both biological and economic parameters, which need to be investigated.

Conclusion

RFI_{phe} was phenotypically independent of its component traits, and RFI_{gen} was genetically independent of MWT, while there was a weak genetic relationship between RFI_{gen} and DG. RFI was more heritable than FCR, and a stronger r_g was observed between RFI and FI than between FCR and FI. Due to these observations, and the favorable nature of RFI (linear index) we conclude that RFI should be included in beef breeding program for genetic improvement of feed efficiency.