

GENETIC RELATIONSHIP BETWEEN FATTENING AND SLAUGHTER TRAITS IN PURE BRED CHAROLAIS YOUNG BULLS

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INTRODUCTION

Selection of AI beef sires in performance testing stations in France is aimed at improving muscle growth capacity. Initially, final test weight and muscularity scoring were the only traits recorded for predicting this capacity. In early eighties an experiment failed to prove any additional efficiency of scanning, using the devices available at that time for estimating body composition (Rehben, 1982). A new performance testing procedure has been applied since then, with the measurement of feed intake in order to include feed efficiency as a new selection criterion. Selection on that trait should improve the biological efficiency of fattening and was expected to participate in the improvement of muscle growth capacity (Ménissier *et al.*, 1986). To evaluate the actual utility of feed intake measurement, an experiment was conducted for estimating the genetic parameters of fattening traits together with slaughter traits, more specifically the genetic correlation between feed efficiency and body composition.

MATERIAL AND METHODS

Animals and traits. In an INRA experimental herd, pure bred Charolais cows were artificially inseminated with 80 Charolais sires over a 12 year period for procreating the 946 experimental young bulls used in this study. Sixty of these sires were previously selected among 510 bulls recorded in performance testing stations. They were ranked and selected on their own final test weight and feed efficiency: half (30) for high merit and half (30) for low merit. The remaining 20 sires were used specifically for breeding heifers.

Bull calves were weaned at 32 weeks of age and entered a fattening barn where they were fed a pelleted diet *ad libitum*. The following traits were recorded: final weight (FW), daily gain (DG) and daily feed intake (FI). Two feed efficiency traits were calculated: the feed conversion ratio (FCR) and the residual feed intake (RFI) that was the residual of a multiple regression between animals of FI on metabolic mid-test weight ($W^{0.75}$) and DG, using SAS package (SAS, 1989). Young bulls were slaughtered at fixed age: half at 15 months and half at 19 months. At slaughter carcass and offal were weighed. Carcass composition was estimated with a prediction equation developed by Robelin and Geay (1975) using the dissection results of the 6th rib and the weight of internal fat deposit. The following variables were analysed : dressing percentage (DP), muscle (M%) and Fat (F%) contents. The relative weights of the following organs in relation to the empty body weight were also recorded: empty digestive tract (DTrw), heart (Hrw) and lungs (Lrw).

Analysis models and estimation of genetic parameters. As most of the sires had been selected on their own performance, the estimation of genetic variability among the tested progeny required the information used for sire selection to be included in the analysis in order to avoid any selection bias. Three sire traits, final test weight, daily feed intake and daily gain,

were systematically included in all multitrait animal models, together with progeny traits that were analysed two by two. The model for sire performances included a contemporary group (10 groups) effect. The model for progeny performances included the following fixed effects : year (12 years), age of the dam (3, 4, 5, 6, over 6 years) and birth type (single or twin) and a regression on slaughter age.

Genetic parameters were estimated using the restricted estimation of maximum likelihood (REML) method (VCE 4.2 Package, Neumaier and Groeneveld 1998).

RESULTS AND DISCUSSION

The means and estimated genetic parameters of the three basic information recorded in both the sire test stations and the progeny experimental herd are reported in table 1.

Table 1. Means and genetic parameters of basic fattening traits in sire test station and progeny fattening unit.

traits	progeny	Final age (d)	FW (kg)	DG (g/d)	FI (kg/d)
sires	mean \pm s.d.	512 \pm 61	684 \pm 87	1449 \pm 192	10.9 \pm 1.3
Final age	494 \pm 29	$h^2 \pm s.e./r_g \pm s.e.$	0.33 \pm 0.03	0.30 \pm 0.03	0.33 \pm 0.04
FW	728 \pm 60	0.50 \pm 0.09	0.91 \pm 0.06	0.72 \pm 0.05	0.73 \pm 0.05
DG	1412 \pm 241	0.23 \pm 0.07	0.41 \pm 0.09	0.80 \pm 0.10	0.35 \pm 0.06
FI	11.7 \pm 1.1	0.37 \pm 0.09	0.97 \pm 0.02	0.31 \pm 0.20	0.76 \pm 0.10

Genetic parameters of progeny traits were more precisely estimated than sire traits. They were obviously within the range of most published results (Koots *et al.*, 1994a, 1994b). It is worth noticing the high genetic correlation coefficients between similar traits recorded either on sires or on progeny. The differences in environments may explain they were not higher, however.

These three traits were positively linked and selection of animals with the best growth capacity and the lowest nutrient requirements will require to use either classical FCR or RFI. The genetic parameters of these two feed efficiency criteria are reported in table 2.

Table 2. Means and genetic parameters of feed efficiency variables.

	mean \pm s.d.	$h^2 \pm s.e.$		FW	DG	FI
FCR (kg/kg)	7.59 \pm 1.10	0.38 \pm 0.04	r_p	-0.07	-0.52	0.44
			r_g	0.01 \pm 0.08	-0.56 \pm 0.08	0.57 \pm 0.07
RFI (kg)	0.00 \pm 0.83	0.33 \pm 0.04	r_p	0.02	0.01	0.72
			r_g	0.04 \pm 0.08	-0.21 \pm 0.12	0.73 \pm 0.04

FCR and RFI had similar heritability coefficient than other live performances and in the range of the results compiled by Archer *et al.* (1999) and higher than values estimated by Herd and Bishop (2000). They were phenotypically and genetically tightly related ($r_p = 0.70$, $r_g = 0.82 \pm 0.04$) and both independent of FW. As expected, RFI was closely related to FI. It was,

however, slightly negatively related to DG. A selection against FCR or RFI is expected to reduce FI and, simultaneously, to improve DG without any change in FW.

The correlation coefficients between the fattening traits and body composition at slaughter are reported in table 3. Among the three basic traits, FW was genetically independent of body composition (DP, M% and F%). DG and FI had opposite relationship with body composition : DG favourably related to DP and M%, while FI was positively related to F%. The two feed efficiency variables exhibited higher genetic correlation coefficients ($|r_g| \geq 0.5$) with carcass composition (M% and F%). In their review Koots *et al.* (1994b) found three references with an average genetic correlation of $r_g = -0.35$ between FCR and lean percentage. Herd and Bishop (2000) also found that RFI was negatively related ($r_g = -0.43$) to an estimate of lean content using backfat thickness scanning measures.

In the present experiment, the genetic ability of the animals to deposit predominantly muscle *versus* fat (or the opposite) was shown therefore to be a major component of feed efficiency in this system of production. The relatively high growth level supported by the fattening diet certainly reduced the incidence of differences in maintenance requirements between animals. Although there are literature evidences of genetic variability for maintenance requirements among growing cattle (Archer *et al.*, 1999) there was no available measurement of maintenance related traits in this experiment for estimating the impact of this component on feed efficiency.

Table 3. Correlation coefficient between fattening and body composition traits.

		DP	M %	F %	DTrw	Hrw	Lrw
h ²		0.54 ± 0.04	0.41 ± 0.04	0.36 ± 0.04	0.45 ± 0.04	0.23 ± 0.04	0.39 ± 0.04
FW	r _p	0.13	-0.18	0.27	0.01	-0.08	-0.25
	r _g	0.09 ± 0.11	-0.01 ± 0.12	0.05 ± 0.12	-0.21 ± 0.11	-0.13 ± 0.11	-0.15 ± 0.13
DG	r _p	0.20	-0.04	0.13	-0.03	-0.07	-0.19
	r _g	0.38 ± 0.10	0.35 ± 0.11	-0.36 ± 0.12	-0.45 ± 0.11	-0.16 ± 0.12	-0.15 ± 0.13
FI	r _p	-0.03	-0.33	0.41	0.15	0.04	-0.19
	r _g	-0.16 ± 0.11	-0.33 ± 0.10	0.39 ± 0.09	0.15 ± 0.09	0.06 ± 0.11	-0.27 ± 0.13
FCR	r _p	-0.24	-0.28	0.27	0.18	0.12	0.02
	r _g	-0.48 ± 0.09	-0.62 ± 0.08	0.68 ± 0.09	0.55 ± 0.10	0.18 ± 0.11	-0.10 ± 0.12
RFI	r _p	-0.18	-0.30	0.32	0.21	0.14	-0.03
	r _g	-0.32 ± 0.10	-0.48 ± 0.12	0.54 ± 0.06	0.42 ± 0.10	0.23 ± 0.11	-0.23 ± 0.13

Among internal organs, the relative weight of the empty digestive tract was however significantly related to fattening traits with large positive genetic correlation coefficients with FCR and RFI: the biggest the digestive tract the more feed was consumed in excess of growth requirements. Part of this increased intake was certainly used for fat accretion as shown above. Part was certainly related to the highest cost of protein turn-over in visceral as shown by Webster (1981) who estimated that 40% of heat production in a ruminant animal may be attributed to the metabolism in the intestinal epithelium and liver. The relationship with the relative weight of heart showed similar trend but less marked. The relationship with the relative

weight of lungs was opposite: animals genetically more efficient had relatively more developed lungs. Among the internal organs that were suspected to contribute significantly to maintenance requirements, the relative development of lungs appeared therefore to be slightly favourable to feed efficiency.

CONCLUSION

This study showed that if a selection only on final test weight in performance testing station would be effective for improving the global growth capacity of progeny, it would not be effective for promoting muscle growth over offal and fat accretion. A positive response on muscle weight simultaneously with reductions of fat content and residual feed intake was actually obtained when selecting on final test weight and feed efficiency in performance testing station as reported by Renand *et al.* (1998) in a preliminary analysis of this experiment.

Inclusion of a feed efficiency criterion, that requires the recording of feed intake, would be profitable for a genetic improvement of muscle growth capacity thanks to a selection of animals that retain energy preferably in muscle, which waste less energy in visceral organs and have superior respiratory capacity.

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