

Genetic parameters of French beef breeds used in crossbreeding for young bull production

I. - Live performance

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Summary

The genetic parameters of fattening performance in the main French beef breeds were estimated from 2 sets of data on progeny testing carried out by 2 A.I. units. In the 1st station, 3098 progeny of 199 sires of *Blond d'Aquitaine* (BA), *Charolais* (Ch), *Limousin* (Li) and 2 synthetic sire lines, *Coopelso 93* (BA × Ch × Li) and *Inra 95* (BA × Ch), were tested. In the 2nd station, 699 progeny of 42 *Charolais* sires were tested. These progeny were young crossbred bulls and were fattened on a high plane of nutrition up to a final weight of about 540 kg. Growth rate was characterized by daily weight gain during fattening and by final age. Data were also available on young bull morphology — fleshiness and skeletal scores at end of fattening — as well as on their weight and birth conditions. The coefficients of heritability and of genetic correlation were computed by the usual methods from estimated paternal and residual components of variances and covariances.

The coefficients of heritability were homogeneous between the 2 data sets and had the following mean values : growth rate .38, fleshiness .26, skeletal development .15, birth weight .31 and dystocia .08. The coefficients of genetic correlation were not as homogeneous but marked trends were evident. A very strong genetic relationship was found between direct effects on birth weight and dystocia. Selection on growth rate would cause a significant increase in birth weight and dystocia and would favor large skeletal-sized animals rather than heavily fleshed animals when these criteria are estimated at constant weight. These estimated genetic parameters showed that genetic variability is sufficient for selection on stations of individual performances to be efficient, except in the case of birth difficulty, for which it would be necessary to use progeny testing to integrate information on birth weight.

Key words : Genetic parameters, beef breeds, live performance.

Résumé

*Paramètres génétiques des races à viande françaises utilisées en croisement
pour la production de taurillons. I. Performances en vif*

Les paramètres génétiques des performances d'engraissement dans les principales races à viande françaises ont été estimés à partir de 2 fichiers constitués par les données de

contrôles sur descendance réalisés par 2 centres de production de semence. Dans la station du premier centre furent contrôlés 3 098 descendants de 199 pères des races *Blonde d'Aquitaine* (BA), *Charolaise* (Ch), *Limousine* (Li), et de 2 lignées mâles synthétiques *Coopelso 93* (BA \times Ch \times Li) et *Inra 95* (BA \times Ch). Dans la station du second centre furent contrôlés 699 descendants de 42 pères *Charolais*. Ces descendance sont constituées de veaux mâles croisés et conduits classiquement pour une production intensive de taurillons jusqu'à un poids final d'environ 540 kg. La vitesse de croissance est caractérisée par le gain moyen quotidien pendant l'engraissement et par l'âge final. Des informations sont également disponibles sur la morphologie des taurillons — notes de pointage du développement de la charnure et du squelette en fin d'engraissement — ainsi que sur leur poids et leur condition de naissance. Les coefficients d'héritabilité et de corrélation génétique ont été calculés classiquement à partir des estimées des composantes paternelles et résiduelles des variances et covariances.

Les coefficients d'héritabilité sont homogènes entre les 2 fichiers et ont pour valeurs moyennes : la vitesse de croissance 0,38, la charnure 0,26, le développement squelettique 0,15, le poids à la naissance 0,31 et la fréquence des naissances dystociques 0,08. Les coefficients de corrélation génétique ne sont pas aussi homogènes mais des tendances marquées apparaissent cependant. Une très forte liaison génétique a été mise en évidence entre les effets directs sur le poids et les difficultés à la naissance. Une sélection sur la vitesse de croissance doit entraîner une augmentation sensible du poids et des difficultés à la naissance, et doit favoriser les animaux à grand développement squelettique au détriment des animaux à forte charnure lorsque ces critères morphologiques sont évalués à poids constant. Ces paramètres génétiques estimés mettent en évidence une variabilité génétique suffisante pour qu'une sélection sur performances individuelles en station soit efficace, mis à part pour les difficultés à la naissance pour lesquelles un contrôle sur descendance qui intègre l'information apportée par le poids à la naissance s'avère nécessaire.

Mots clés : Paramètres génétiques, races à viande, performances en vif.

I. Introduction

In France, the selection of beef breed sires used in terminal crossing by artificial insemination is based on integrated programs which include a first selection on pedigree by planned mating, followed by selection on station performance testing and finally progeny testing. The efficiency of such programs as well as that of each step within the programs depend on the genetic parameters of the traits involved in the selection objectives in the population concerned. Studies in French beef breeds initiated by VISSAC (1964) and continued by POUJARDIEU & VISSAC (1968) and FOULLEY *et al.* (1978) determined the genetic parameters of traits related to farm veal calf production which, at that time, was the type of production aimed for in selection programs. These studies also permitted the profit of such programs to be ascertained (MOCQUOT & FOULLEY, 1973). But with the inevitable decline in traditional veal calf production, the early commercialization of dairy crossbred calves and the increase in young bull production, some A.I. units reorganized their selection programs (FOULLEY & MENISIER, 1982) by carrying out in station progeny testing of sires on intensively fattened young bulls.

To improve the selection strategy of the new programs it was necessary to determine the genetic variability and relationships between traits involved in this new production which concerns different professionals : calf producer, young bull feeder and butcher. The data collected in these progeny testing stations have been used to estimate genetic parameters of fattening performance which particularly concern far-

mers fattening young bulls. Information on the birth of these calves on their original farms have also been analysed to incorporate any effects of improved growth performance at the level of the calf producers. Analysis of slaughter traits, which particularly interest the butcher, will be presented in another paper.

II. Material and methods

The data analysed were provided by 2 stations for progeny testing of sires of French beef breeds used in terminal crossing by artificial insemination. In the 1st station - Midatest A.I. unit - 199 sires from different specialized breeds or lines were progeny-tested : 65, 36 and 38 from *Blond d'Aquitaine* (BA), *Charolais* (Ch) and *Limousin* (Li) breeds and 38 and 21 from the synthetic sire lines, *Coopelso 93* (BA × Ch × Li) and *INRA 95* (BA × Ch) ; the lasti line is based on double-muscled cattle. In the 2nd station - Oger A.I. unit - 42 *Charolais* sires were progeny-tested. The sires in both stations were tested in different annual batches (9 at Midatest and 3 at Oger). These sires were previously in station performance tested and were selected on an index combining their growth rate and fleshiness score. In both A.I. units the culling rate was about 50 p. 100 on the basis of that index. The batches within station may be compared by the use in each one of a control group of 3 reference sires : *Blond d'Aquitaine* sires at Midatest and *Charolais* sires at Oger. Progeny groups involved approximately 20 bull calves born from some 100 artificial inseminations randomly spread over many dairy herds (one per herd) throughout the year. *Frisonne* dams were used at Midatest and *Normande* dams mainly at Oger. Soon after birth, these bull calves were put in nurseries 4 at Midatest and 1 at Oger — where they stayed 4 to 5 months before entering the station to be tested on intensive young bull production. The young bulls were fattened in age-groups on corn silage distributed *ad libitum* and supplemented with protein feed. Fattening was finished when the young bulls reached a fixed slaughter weight within batches. This final weight was 515 kg in the first batch in both stations, and increased to 585 kg and 545 kg in the last batch at Midatest and Oger.

Three types of data were available on these progenies :

— *data from farm of origin* : birth weight and birth difficulty ; the latter was characterized by frequency of dystocia — hard pull or cesarian ;

— *data on growth rate* : weaning weight adjusted by interpolation for mean age at leaving the nursery — 4 months at Midatest, 5 months at Oger ; average daily weight gain during fattening and age at the end of fattening ;

— *data on live morphology* : weaning fleshiness score on leaving the nursery — sum of scores, based on 7, on evaluation of muscular development of shoulder, back and hind limb ; fleshiness score at end of fattening — sum of scores, based on 10, on evaluation of muscular development of shoulder, width and depth of back, width and round of thigh ; skeletal size score at end of fattening — sum of scores, based on 10, on evaluation of skeletal development through size of shank bones, length of back and pelvis, width of hips and overall development score. A single experienced technician in each station gave the scores.

Statistical analyses of the data were separately conducted in each station. Genetic and phenotypic parameters — heritability, genetic and phenotypic correlation

coefficients — were calculated by the usual methods using paternal and residual components of variances and covariances estimated by applying method 3 of HENDERSON (HENDERSON, 1953) to a crossed mixed model including the following fixed effects : calving parity of dam, batch \times age-group, nursery (Midatest) and dam breed (Oger). At Midatest a sire breed effect was also included in the model and components of variance were estimated pooled within sire breed. Since comparison at the end of fattening had to be carried out at constant weight, the estimates of variance and covariance components of scores were corrected for variations in final weight, according to the formulas in the appendix.

Approximate of standard errors of genetic parameters were calculated from estimates of variance and covariance components, according to the derivation principle of KENDALL & STUART (1958) and using the formula of GROSSMAN & NORTON (1974) for the genetic correlation coefficients.

III. Results and discussion

A. Means and phenotypic variability

The least-squares means as well as the phenotypic standard deviations and coefficients of variation (tabl. 1) were obtained using the previously described models. In both stations the batch \times age-group effect was highly significant on all traits, except the frequency of dystocia. The importance of this effect emphasizes that a good distribution of the progeny between age-groups is wished for a better sire evaluation and that the control sires are useful for between batches comparisons. Calving parity had no significative effect, excepted on birth weight, since the dams were adult females which did not suckle their calves. At Midatest growth performance were significantly affected by nursery effect. At Oger dam breed (*Frisonne v. Normande*) had no effect.

Live morphological scores were significantly and positively correlated with weight. The coefficients of partial regression were of the same order of magnitude as those computed by POUJARDIEU & VISSAC (1968) and FOULLEY *et al.* (1978) on 75-day farm veal calves, progenies of *Charolais*, *Limousin* or *Blond d'Aquitaine* sires, by GOGUE (personal communication, 1975) on 18-month old *Charolais* heifers at a progeny testing station on maternal aptitudes and by RENAND (1983) on 16-month old *Charolais* bulls at performance testing stations. These positive relations show that the scorers did not evaluate animal morphology independently of animal weight. It was necessary to eliminate this additional variability in order to compare conformation of animals of different weight or to analyse relations between morphological criteria and other performances.

The phenotypic variability of the variables was quite homogenous between the 2 data sets. At the same weight, fleshiness scores showed higher variability than those of skeletal development or growth performances. The decision to end fattening at a fixed weight clearly reduced the variability of final weight but without eliminating it entirely.

TABLE 1

Means, phenotypic standard deviations and coefficients of variation of live traits.
Moyennes, écarts-types et coefficients de variation phénotypiques des performances en vif.

Live traits	Station							
	Midatest				Oger			
	Mean	Standard deviation	Coefficient of variation	Regression coefficient (d)	Mean	Standard deviation	Coefficient of variation	Regression coefficient (d)
<i>Birth</i>	(2 673)				(647)			
Birth weight (n) (kg)	47.7	± 6.2	13.5	—	50.2	± 6.9	13.7	—
Birth difficulty (%)	10.4	± 28.9	278.8	—	11.1	± 26.8	241.6	—
<i>Growth</i>	(3 098)				(699)			
Weaning weight (a) (kg)	138	± 19	14.1	—	194	± 26	13.2	—
Daily gain (g/d)	1 149	± 160	14.0	—	1 250	± 155	12.4	—
Final age (d)	477	± 43	9.0	—	429	± 38	8.8	—
Final weight (kg)	539	± 28	5.1	—	530	± 21	3.9	—
<i>Morphology</i>	(3 098)				(699)			
Weaning fleshiness (b) (/100)	—	—	—	—	87.1	± 15.7	18.1	+ .019
Final fleshiness (c) (/100)	62.5	± 10.8	17.3	+ .015	63.8	± 10.5	16.6	+ .010
Skeletal size (c) (/100)	67.0	± 5.7	8.4	+ .015	62.4	± 7.0	11.1	+ .009

(a) Weight adjusted to 4 months in Midatest station and 5 months in Oger station.

(b) Score regressed on weaning weight.

(c) Score regressed on final weight.

(d) Partial regression coefficient on live weight, standardized to phenotypic deviation of the dependant variable.

(n) Number of young bulls tested.

TABLE 2
*Least squares means of sire breed effects on live traits in Midatest station, expressed relative to Charolais.
 Moyennes des moindres carrés des effets du type génétique paternel sur les performances en vif à Midatest,
 en écart au Charolais.*

Live traits	Sire breed					Sire breed F-value (c)
	Charolais	Blond d'Aquitaine	Limousin	Coopelso 95	Imra 95	
<i>Birth</i>	(394)	(1 259)	(324)	(449)	(253)	
Birth weight (n)						
Birth weight (kg)	47.0	— 1.0	— 3.3	— 1.8	— .6	6.3 **
Birth difficulty (%)	12.5	— 3.3	— 4.5	— 2.4	— .7	1.2 NS
<i>Growth</i>	(403)	(1 390)	(485)	(548)	(272)	
Weaning weight (a) (kg)	145	— 10	— 16	— 10	— 3	22.1 **
Daily gain (g/d)	1 205	— 50	— 117	— 98	— 16	17.0 **
Final age (d)	461	+ 17	+ 40	+ 28	— 1	24.6 **
Final weight (kg)	546	— 7	— 11	— 11	— 7	5.8 **
<i>Morphology (b)</i>	(403)	(1 390)	(485)	(548)	(272)	
Final fleshiness (/100)	63.8	— 5.2	— 1.7	— 1.2	+ 1.5	17.8 **
Skeletal size (/100)	64.7	+ 4.0	+ 2.7	+ 2.8	+ 2.0	25.2 **

(a) Weight adjusted to 4 months.

(b) Scores regressed on final weight.

(c) Level of significance : NS ($P > .05$), * ($P < .05$), ** ($P < .01$).

(n) Number of young bulls tested by sire breed.

B. Sire breed effects

At Midatest all traits, except birth difficulty, were significantly affected by sire breed (tabl. 2). As the sample of tested sires was not random within breeds, the analysis of sire breed effects must not be interpreted as a breed comparison. Young bulls from *Charolais* sires showed the highest growth — 5 p. 100 and 10 p. 100 higher than *Blond d'Aquitaine* and *Limousin* crossbred young bulls. The effects of synthetic sire lines were intermediate between those of the other 3 sire breeds. The same was true for birth weight and about the same for frequency of dystocia. Such an hierarchy of direct effects of these different sire breeds confirms the results of experiments comparing breeds carried out in France (BIBE *et al.*, 1973, 1976; ROBELIN *et al.*, 1978; PATTIE & MENISSIER, 1980; FREBLING *et al.*, 1982; MENISSIER *et al.*, 1982), Argentina (MIQUEL *et al.*, 1974 a, b), New Zealand (CARTER, 1975; EVERITT *et al.*, 1978, 1980), Denmark (ANDERSEN *et al.*, 1976, 1977; LIBORIUSSEN *et al.*, 1982), U.S.A. (SMITH *et al.*, 1976 a, b) and Canada (FREDEEN *et al.*, 1982 a, b).

Charolais crosses, and especially Inra 95, had the best fleshiness scores, while *Blond d'Aquitaine* crosses were characterized by large skeletal size and poorer fleshiness at the same live weight. The other genetic types were intermediate. BIBE *et al.* (1976) have already reported this morphological difference in live *Charolais* and *Blond d'Aquitaine* cattle.

C. Heritability coefficients

The estimates of heritability coefficients and their standard errors are shown in table 3. The values obtained were homogeneous between the 2 data sets in spite of differences in the genetic material used and the differences in the precision of these estimates related to the number of animals used for analyses. Thus the mean values of heritability (\bar{h}^2) presented in the following text and calculated by weighting both estimates by the corresponding degrees of freedom of sire effect may represent the mean genetic variability expressed during progeny testing of this type of cattle.

The heritability coefficient of birth weight was $\bar{h}^2 = .31$. This value was comparable to that estimated recently by GALLARD *et al.* (1982) in *Charolais* breed but was clearly higher than previous French values estimated in *Blond d'Aquitaine*, *Charolais*, *Limousin* breeds by POUJARDIEU & VISSAC (1968) and FOULLEY *et al.* (1978) based on progeny test data for veal calf production, despite similar conditions, i.e. usually 1 calf per herd. While FOULLEY *et al.* (1978) noted a probable decline in genetic variability of birth weight between 1968 and 1978 due to the selection program applied, the present higher values of the heritability coefficients must be explained by an increase of the genetic variability due to the use of a new type of breeding sires. However, our results are slightly less (by .10 point) than the mean heritability coefficient calculated from data in the literature (PRESTON & WILLIS, 1970; WOLDEHAWARIAT *et al.*, 1977; BUCHANAN, 1979; RENAND, 1983).

The heritability coefficient of the frequency of dystocia ($\bar{h}^2 = .08$) was clearly lower than that of birth weight. This value is comparable to results reported in France and elsewhere (RENAND, 1983) which almost all indicate that it is difficult to detect intrabreed genetic variability of direct effects on birth difficulty. As the heritability

of these effects increases with the frequency of dystocia, estimates of heritability coefficients are thus higher when sires are tested using heifers than adult cows (BRINKS *et al.*, 1973; BURFENING *et al.*, 1979; PHILIPSSON *et al.*, 1979). But since sire testing is carried out mainly on adult females, selecting sires only on frequency of dystocia in their progeny is certainly not very effective for reducing direct effects on calving difficulty, unless a large number of progeny are used.

TABLE 3

Coefficients of heritability for live traits.

Coefficients d'héritabilité des performances en vif.

Live traits	Station			
	Midatest		Oger	
	Heritability	± s.e.	Heritability	± s.e.
<i>Birth</i>				
Birth weight31	± .06	.32	± .12
Birth difficulty09	± .04	.05	± .07
<i>Growth</i>				
Weaning weight21	± .05	.18	± .09
Daily gain34	± .05	.41	± .13
Final age41	± .06	.32	± .12
<i>Morphology (a)</i>				
Weaning fleshiness	—	—	.21	± .10
Final fleshiness28	± .05	.21	± .10
Skeletal size14	± .04	.18	± .09

(a) Scores regressed on live weight.

Between birth and fattening, the heritability coefficients of growth performance reach a minimum value at the end of nursery ($\bar{h}^2 = .20$). ANDERSEN (1977) and OSIEGLOWSKI (1981) reported such age changes in heritability of growth criteria in bull-calves of dual purpose breeds. In the present case, this process may express increased environmental variability related to the difficulties of rearing and weaning calves in nurseries where the number of animals and their spaced arrival in time may cause health problems.

Growth rate criteria during fattening — average daily gain and final age — had rather consistent heritability coefficients ($\bar{h}^2 = .38$) which were slightly higher than

those estimates by GOGUE (personal communication, 1975) and MENISSIER (1976) on 18-month old *Charolais* heifers in station testing : $\bar{h}^2 = .21$ for postweaning daily gain and $\bar{h}^2 = .33$ for weight at 18 months. The management of these heifers — on pasture for reproduction — could explain the lower expression of growth potential variability compared to the present intensive system of young bull fattening. PETTY & CARTWRIGHT (1966) reported in their bibliographical review that heritability coefficients for growth performance were lower when measured on pasture than in feedlots. The values obtained in the present study, although similar to the most frequent estimates in the literature (PRESTON & WILLIS, 1970 ; WOLDEHAWARIAT *et al.*, 1977 ; BUCHANAN, 1979 ; RENAND, 1983), are slightly less (by .10 point) than the mean of those estimates. The genetic variability of the samples analysed here was certainly reduced by previous selection of the performance-tested sires and it has been shown that the bias in the computed value of variance components is higher when estimation is based on classical analysis of variance type procedure, as performed here, than through Maximum Likelihood (ML) type procedure [ROTHSCHILD *et al.* (1979), THOMPSON (1982), MEYER & THOMPSON (1984)]. In presence of selection the multivariate Restricted Maximum Likelihood (REML) has been shown to provide unbiased estimates if the selection criteria is included in the multiple trait analysis [SCHAEFFER & SOONG, 1978 ; MEYER & THOMPSON (1984)]. In our case such procedure would need to incorporate performance test results of all sires to the selected sires' progeny data and would require much more computational time. To get an estimation of the « true » value of genetic parameter, *a posteriori* corrected for the sires' selection effect, the formulae given by RAHNEFELD *et al.* (1973) and ROBERTSON (1977) were developed to a selection by truncature on the index combining growth rate and fleshiness score of sires. For a culling rate of 50 p. 100 the bias in the estimated value of heritability of growth rate criteria was estimated to be included between —0.04 and —0.07 point for different probable values of the « true » genetic parameters.

The heritability coefficients of morphological scores were lower than those of growth rate. The mean heritability coefficient of fleshiness was $\bar{h}^2 = .26$. Taking into account the selection of sires, this coefficient was shown to be underestimated by less than —0.04 point. Bibliographic reviews of results in North America show a difference (.20 point) between mean heritability of conformation score and that of weight at end of fattening : $h^2 = .35$ *v.* $h^2 = .55$ (PETTY & CARTWRIGHT, 1968 ; PRESTON & WILLIS, 1970 ; BUCHANAN, 1979). On the other hand, estimates obtained in France on farm veal calves showed a mean heritability for fleshiness, not adjusted for weight differences ($h^2 = .20$) slightly higher than for final weight ($h^2 = .15$) (POUJARDIEU & VISSAC, 1968 ; FOULLEY *et al.*, 1978). Considering the large diversity in testing conditions, production type and judgement criteria, it is impossible to elucidate these differences, but live fleshiness score seems generally to be only moderately heritable. Genetic variability of the skeletal size score was apparently even lower ($h^2 = .15$). This lesser value could probably be explained by the fact that the scores of the different criteria of skeletal development have lower repeatability coefficients (between .5 and .7) than those of fleshiness (higher than .9) (RAOULT & REHBEN, 1983). This difference certainly reflects the greater difficulty of the scorers in determining a basis of comparison for evaluating skeletal dimensions. The estimates of heritability coefficients obtained by MENISSIER (1976) on 18 month old *Charolais* heifers showed the same deviation, with higher values ($h^2 = .48$ for fleshiness and $h^2 = .31$ for skeletal size), but these scores were not adjusted for weight differences.

TABLE 4

*Coefficients of phenotypic (r_p) and genetic ($r_g \pm s.e.$) correlations among live traits.
Coefficients de corrélations phénotypique (r_p) et génétique ($r_g \pm e.s.$) entre les performances en viv.*

r_g (a) \pm s.e.	Birth		Growth				Morphology (b)		
	Birth weight	Birth difficulty	Weaning weight	Daily gain	Final age	Weaning fleshiness	Final fleshiness	Skeletal size	
<i>Birth</i>									
Birth weight	—	.80 \pm .18	.46 \pm .16	.50 \pm .12	— .53 \pm .11	—	— .03 \pm .16	.23 \pm .22	
Birth difficulty . .	.29	.66 \pm .57	.25 \pm .34	.15 \pm .29	— .29 \pm .29	.12 \pm .33	.38 \pm .28	.06 \pm .32	
	.27	—	.50 \pm .25	.61 \pm .20	— .56 \pm .19	—	— .12 \pm .23	.45 \pm .30	
		—	.19 \pm .44	.06 \pm .36	— .37 \pm .37	.49 \pm .39	— .05 \pm .38	— .26 \pm .40	
<i>Growth</i>									
Weaning weight . .	.18	.05	—	.42 \pm .13	— .65 \pm .09	—	— .10 \pm .15	— .11 \pm .19	
Daily gain11	— .01	—	.54 \pm .25	— .76 \pm .17	— .08 \pm .37	— .04 \pm .36	.90 \pm .29	
Final age24	.09	.14	—	— .88 \pm .03	—	— .13 \pm .19	.30 \pm .16	
	.18	.07	.23	—	— .94 \pm .05	—	— .17 \pm .30	.39 \pm .28	
	— .26	— .09	— .43	— .78	—	—	— .10 \pm .13	— .21 \pm .16	
	— .20	— .07	— .59	— .81	—	.45 \pm .30	.15 \pm .32	— .55 \pm .27	
<i>Morphology (b)</i>									
Weaning fleshiness	—	—	—	—	—	—	—	—	
Final fleshiness . .	.04	.07	.17	— .04	— .07	—	— .57 \pm .27	— .26 \pm .35	
Skeletal size00	.03	— .01	.17	— .16	—	—	— .36 \pm .18	
	.08	.06	.03	.22	— .23	.33	—	— .31 \pm .37	
	.05	.07	.02	.02	— .01	—	.19	—	
	.14	— .02	.15	.18	— .22	— .05	.13	—	

(a) Upper line : Midatest coefficients, lower line : Oger coefficients.

(b) Scores regressed on live weight.

D. Genetic and phenotypic correlation coefficients

Estimates of genetic and phenotypic correlation coefficients are shown in table 4. Considering the differences in the numbers of sires and young bulls tested, the significance of the genetic correlation coefficients was clearly better at Midatest than at Oger. To get a wider approach of the underlying biological relationships between traits, the discussion will not be limited only to estimates significantly different from zero. When estimates are homogeneous between the 2 data sets, a « mean » value (\bar{r}_p and \bar{r}_g) weighted by the degrees of freedom of sire effect was calculated using the Z-transformation and presented in the following text.

As often observed, phenotypic correlation coefficients between growth performance were lower than those of genetic correlation. Both measurements of growth rate during fattening — daily gain and final age — were closely related phenotypically, and especially genetically ($\bar{r}_p = -.79$ and $\bar{r}_g = -.89$); any one can be used to characterize the growth potential of young bulls. While phenotypic correlation coefficients between these 2 measurements and birth weight were comparable for the 2 data sets ($\bar{r}_p = +.24$), estimates of genetic correlations diverged markedly between the 2 : $r_g = +.53$ at Midatest and only $\bar{r}_g = +.22$ at Oger. It would be interesting to be able to determine exactly if this difference is related to the genetic material studied or simply due to higher sampling errors at Oger; results in the literature have usually shown that selection on growth significantly increases birth weight due to marked genetic correlations between these criteria : mean \bar{r}_g between $+ .50$ and $+ .60$ (PRESTON & WILLIS, 1970; WOLDEHAWARIAT *et al.*, 1977; BARLOW, 1978; BUCHANAN, 1979; KOCH *et al.*, 1982; RENAND, 1983). On this relationship will depend the efficiency of the selection programs set up to change the shape of the growth curve through improving genetic effects on postnatal growth rate without increasing effects on prenatal growth.

Such a restriction on changes in birth weight may be desired because, as birth weight increases, calving difficulties would increase due to positive genetic correlations between frequency of dystocia and growth rate ($r_g = +.59$ at Midatest and $r_g = +.22$ at Oger) or birth weight ($\bar{r}_g = +.80$ at Midatest and $\bar{r}_g = +.66$ at Oger). These latter estimates confirm the high values obtained in France by BELIC & MENISSIER (1968), FOULLEY *et al.* (1978), GAILLARD *et al.* (1982) in *Charolais*, *Limousin* and *Blond d'Aquitaine* breeds in terminal crossing. Moreover, considering the respective heritabilities of birth condition score and weight, these results emphasize the usefulness of birth weight in evaluating the direct effects of sires on dystocia in their calves under actual testing conditions in France (FOULLEY & MENISSIER, 1982).

At the end of fattening and at the same weight, there was a marked genetic opposition between fleshiness and skeletal size scores ($\bar{r}_g = -.35$) which did not appear phenotypically ($\bar{r}_p = +.18$). GOGUE (personal communication, 1975) had previously noted a slight genetic opposition in 18-month old *Charolais* heifers ($r_g = -.18$) but this opposition was more clear when the scores were adjusted for weight differences ($\bar{r}_g = -.52$). It is thus possible to characterize animal morphology independently of animal weight by classifying the animals into 2 extreme types : compact, thick animals and tall, slim ones. The growth potential of the latter was higher than that of the former because growth rate showed a positive genetic correlation with skeletal size ($\bar{r}_g = +.30$) and a slightly negative one with fleshiness ($\bar{r}_g = -.12$). This later slightly negative coefficient may be induced by the selection of the sires on their

growth rate and fleshiness score. Taking into account the probable heritability coefficients of both traits, the « true » genetic correlation, corrected for selection bias, has to be close to zero. In the literature, results indicate a generally positive genetic relation of about $r_g = +.35$ between conformation score and weight at end of fattening (North American summaries : PETTY & CARTWRIGHT, 1966 ; BUCHANAN, 1979) as well as between fleshiness score and weight of 75-day old farm veal calves (French results : POUJARDIEU & VISSAC, 1968 ; FOULLEY *et al.*, 1978). These positive values, for the most part, certainly express the fact that all animal dimensions increase simultaneously with weight rather than a morphological change. BAILEY *et al.* (1971) noted a slightly lower conformation in Hereford selected on weight or even on conformation score at one year when the results were corrected for the correlated effect related to weight increase. Thus, if, for some reason, the aim is to change the morphological frame of cattle, this weight effect must be taken into account and the estimated genetic parameters considered after elimination of that effect.

IV. Conclusion

This study presents first French results on genetic parameters of live performance of young bulls of the French beef breeds fattened in feed lot. Apart from birth difficulty, all the traits, and particularly growth rate during fattening, showed marked genetic variability. This variability was high enough so that a significant genetic improvement of live fattening performance may be expected through selection of intensively reared bulls in performance-test stations. Progeny testing would theoretically not be necessary for the growth and conformation traits except from estimating the direct genetic effects of sires on frequency of dystocia, the precision of which would be clearly improved by using birth weight data. Since the results indicated an expected correlated increase in birth weight and birth difficulty in calves of selected sires, a restriction on birth weight could be incorporated in selection programs. On the other hand in station, progeny testing would be useful, first, to evaluate more precisely the breeding value of sires intensively used in artificial insemination or the top bull sires used for planned mating, and, second, to check the efficiency of selection after performance-testing.

Received March 8, 1984.

Accepted July 23, 1984.

Acknowledgements

The author wishes to thank Mrs DAIFUKU for providing the English translation of the manuscript.

Appendix

Method of computing genetic parameters of variables in models with or without covariate

In livestock data analyses the following situation may exist : a 1st group of variables (x) for which the model includes no covariate, and a 2nd group of variables (y) which have to be regressed on an independent variable (w). If the genetic parameters in each group of variables can be directly computed from the estimated components of variance in the corresponding models, the estimation of the genetic and phenotypic correlation coefficients between variables of different groups needs some more computation. In point of fact all parameters can be estimated using only the estimated components in the models without covariate.

In our situation, the mixed models include fixed effects (b), random sire effects (u) and eventually live weight as a covariate (w).

The models of the (x) and (w) variables are :

$$\begin{aligned} x &= Xb_x + Zu_x + e_x \\ w &= Xb_w + Zu_w + e_w \end{aligned}$$

If no adjustment is carried out, the model of the (y) variable is :

$$y = Xb_y + Zu_y + e_y$$

But the (y) variable has to be adjusted for the (w) covariate :

$$\begin{aligned} y &= Xb_y^* + Zu_y^* + w\beta_y + e_y^* \\ &= Xb_y^* + Zu_y^* [Xb_w + Zu_w + e_w] \beta_y + e_y^* \end{aligned}$$

Therefore the comparison of both models of the (y) variable gives :

$$\begin{cases} u_y = u_y^* + \beta_y u_w \\ e_y = e_y^* + \beta_y e_w \end{cases}$$

As $\beta_y = \frac{\sigma_{e_{wy}}}{\sigma^2 e_w}$ the variances and covariances in the complete model can be

computed from the estimated values of variances and covariances of (y) in the models without covariate, as follows :

— paternal variance component of (y) :

$$\sigma^2 u_y^* = \sigma^2 u_y \left[1 + \left(\beta_y \frac{\sigma u_w}{\sigma u_y} \right)^2 - 2 \left(\beta_y \frac{\sigma u_w}{\sigma u_y} \right) r_{gwy} \right]$$

— phenotypic variance of (y) :

$$\sigma^2 y^* = \sigma^2 y \left[1 + \left(\beta_y \frac{\sigma w}{\sigma y} \right)^2 - 2 \left(\beta_y \frac{\sigma w}{\sigma y} \right) r_{pwy} \right]$$

— paternal covariance component between (y) and an unadjusted (x) variable :

$$\sigma_{yx}^* = \sigma_{yx} \left[1 - \left(\beta_y \frac{\sigma u_w}{\sigma u_y} \right) \frac{r_{gwx}}{r_{gyx}} \right]$$

— phenotypic covariance between (y) and an unadjusted (x) variable :

$$\sigma_{yx}^* = \sigma_{yx} \left[1 - \left(\beta_y \frac{\sigma w}{\sigma y} \right) \frac{r_{pwx}}{r_{pyx}} \right]$$

where r_g and r_p are the genetic and phenotypic correlation coefficients between the variables in the models without covariate.

The genetic parameters can be computed as follows :

— heritability coefficient of variables (y) adjusted by regression :

$$h_y^2 = h_y^2 \frac{1 + \zeta_y^2 - 2\zeta_y r_{gwy}}{1 + \eta_y^2 - 2\eta_y r_{pwy}}$$

— genetic correlation coefficient between a variable (y) adjusted by regression and an unadjusted variable (x) :

$$r_{gyx}^* = \frac{r_{gyx} - \zeta_y r_{gwx}}{\sqrt{1 + \zeta_y^2 - 2\zeta_y r_{gwy}}}$$

— genetic correlation coefficient between 2 variables (y, z) both adjusted by regression on covariable (w) :

$$r_{gyz} = \frac{r_{gyz} - \zeta_y r_{gwx} - \zeta_z r_{gwy} + \zeta_y \zeta_z}{(1 + \zeta_y^2 - 2\zeta_y r_{gwy})(1 + \zeta_z^2 - 2\zeta_z r_{gwy})}$$

— phenotypic correlation coefficients are computed by replacing in the preceding formulas r_g by r_p and ζ by η .

where h_y^2 is the apparent heritability coefficient of (y) variable in the model without covariable.

where

$$\zeta_y = \beta_y \frac{\sigma u_w}{\sigma u_y}$$

$$\eta_y = \beta_y \frac{\sigma w}{\sigma y} = \frac{h_y}{h_w} \zeta_y$$

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