GENETIC PARAMETERS OF BEEF PRODUCTION AND MEAT QUALITY TRAITS OF YOUNG CHAROLAIS BULLS PROGENY OF DIVERGENTLY SELECTED SIRES

G. Renand*, P. Berge†, B. Picard#, J. Robelin#, Y. Geay#, D. Krauss§, F. Ménissier*

* Station de Génétique Quantitative et Appliquée, INRA, 78352 Jouy-en-Josas, France
† Station de Recherches sur la Viande, INRA 63122 Theix, France
# Laboratoire Croissance et Métabolisme des Herbivores, INRA, 63122 Theix, France
§ Domaine de Galle, INRA, 18360 Avord, France

SUMMARY

In a selection experiment, 317 *Charolais* young bulls, progeny of 58 sires divergently selected (2x29) on their own growth capacity and feed efficiency measured in performance testing stations, have been tested in an experimental herd. Carcass weight and composition have been measured as well as nine different biological characteristics of the *Longissimus dorsi* muscle related to meat quality.

The responses observed on the progeny show that the selection procedure applied in the performance testing stations is appropriate for improving the muscle growth capacity and does not change markedly the biological components of meat quality. These responses and the estimated genetic correlations show a tendency that higher muscle growth capacity is related to later physiological development. Selecting leanner animals will certainly have favourable effects on tenderness (higher thermal solubility of the collagene and higher proportion of rapid-white type of fibers) and a reduction of intramuscular lipid content. As heritability coefficients of most of these muscle characteristics are high enough, they can eventually be used as selection criteria in breeding programmes to improve related meat qualities as long as they can be easily measured.

INTRODUCTION

In general, muscle growth capacity is considered to be the primary selection objective for improving the efficiency of beef production from young growing cattle and consequently the economic margin of producers. With this purpose, bulls of specialized beef breeds used by artificial insemination in France are successively selected on their own performance in station and on progeny in feed-lot (Ménissier, 1988). The selection criteria in the performance testing stations combines the growth and the feed efficiency, that is expected to indirectly rank the bulls on their muscle growth capacity.

Although there is presently no clear economic incentive, meat quality has to be taken into account since white poultry and pork meats seriously compete with beef, at least in Europe. If this quality may largely depend on slaughtering and post-mortem maturing technics, it also originates from the biological characteristics of the muscles, characteristics that are certainly genetically controlled.

Therefore, as breeding programmes have to improve the efficiency of production and to keeep under control or even to improve meat quality, there is a need to estimate simultaneously the genetic parameters of production and quality traits. With this purpose, a prospective study has been engaged in France to analyse in a French beef breed the genetic variability of different biological characteristics of muscles related to organoleptic qualities, in relation to the genetic variability of muscle growth. These characteristics, contrary to organoleptic qualities that are subjectively appreciated on a limited number of animals, can be measured on a reduced sample of muscles at slaughter or even *in vivo* on a larger number of animals. Eventually, if needed and practicable, they may be integrated in breeding programmes as selection criteria.

MATERIALS AND METHODS

During 5 consecutive years (1986-90), 60 bulls have been selected among 510 *Charolais* bulls performance tested in two stations. The selection index (Is) was a combinaison of the final weight index adjusted for age (Iw) and a residual feed efficiency index (Ie) : Is = .426 Iw + .655 Ie - 8.1. In each station-year 6 bulls were selected : 3 among the bulls with superior indexes (Sup) and 3 among the bulls with inferior indexes (Inf). The actual selection differential was 3.38 standard deviations of the selection criteria.

These bulls have been used for inseminating *Charolais* cows of the INRA-Domaine de Galle herd. After weaning at 32 weeks of age, male calves are fattened with a complete condensated diet distributed *ad libitum* up to 15 or 19 months of age. They are slaughtered at the experimental INRA centre of Theix where the composition of their carcass is estimated after the 6^{th} rib has been dissected and the internal fat depots weighed (Robelin and Geay, 1975). On the *Longissimus dorsi* (LD) muscle of this 6^{th} rib, the following characteristics are measured : 24 hour pH, intramuscular lipid content (Ameth, 1972), heminic iron content (Hornsey, 1956), hydroxyproline content and thermal solubility (Bonnet and Kopp, 1984), protein to DNA ratio (Lowry et al., 1951; Labarca and Paigen, 1980), ICDH oxydative enzymatic activity (Briand et al., 1981), LDH glycolytic enzymatic activity (Ansay, 1974), type I myosin heavy chain proportion (Picard et al., 1994).

Up to now 317 bull calves of 58 sires (29 Sup. and 29 Inf.) have been measured from 1989 to 1993. However for some traits, data are still not available for the last slaughtered animals. Due to the sampling procedure of the sires, two models have been used to estimate the genetic parameters. Both models include a year-age of dam (YAD) effect and a slaughter age (AGE) effect. In the first model a selection group of sires (SEL) has been included, while not in the second model :

Model 1 : $y_{ijkln} = YAD_i + AGE_j + SEL_k + sire(SEL)_{kl} + e_{ijkln}$
Model 2 : $y_{ijln} = YAD_i + AGE_j + sire_l + e_{ijln}$

The genetic parameters have been computed from the estimated variances-covariances components of the sire and residual random effects in both models. A multitrait REML computing programme, provided by D. Boichard (personal communication), including the EM algorithm and a canonical transformation, has been applied to groups of variables with identical incidence matrix.

RESULTS AND DISCUSSION

The overall means and phenotypic standard deviations are reported in table 1. The coefficients of variation of carcass weight and composition are relatively low in this sample of cattle since they were measured in a well controlled environment. In comparison, except for pH, the coefficients of variation of the biological characteristics of the *Longissimus dorsi* muscle are clearly higher. Between 15 and 19 months there is a significant increase in carcass weight and fatness, simultaneously to an increase in the lipid and pigment contents in the LD muscle (table 1). With age, the oxydative enzymatic activity increases in the muscle, while the glycolytic enzymatic activity decreases. Although not significant, there is a tendency for a reduction with age of the collagene solubility and the proportion of type I myosin. All these changes are coherent with our knowledge on the developpement of the young cattle after puberty.

The selection of the sires appears to have a significative effect on carcass traits : carcass weight is improved and fatness reduced (table 1). These results show that the selection procedure applied in the performance testing stations leads to a significative response on muscle growth capacity, corresponding therefore to the selection objective. This selection does not change significantly the biological characteristics of the muscle, except a decrease in the intramuscular lipid content and a greater collagene solubility. Although the effect of the selection on muscle characteristics is relatively reduced, it is worth-while to note that this effect is generally opposed to the effect of age. Therefore, there is a tendency that animals with later physiological development are preferentially selected.

Table 1. Means, phenotypic coefficients of variation, age and selection effects, heritability coefficients

	n	overall mean		phenotypic C.V.	age effect 19 - 15 months		selection effect Sup. - Inf		h^2 model 1	h^2 model 2
Carcass traits										
Weight	317	408	kg	9 %	+88	***	+13	**	0.33	0.50
Lean %	317	71.7	%	3 %	-0.0	ns	+0.6	*	0.71	0.71
Fat %	317	13.6	%	16 %	+0.8	***	-0.8	**	0.56	0.56
Longissimus dorsi characteristics										
pH	317	5.55		3 %	+0.04	*	+0.01	ns	0.19	0.17
Lipid %	317	1.7	%	53 %	+0.4	***	-0.2	*	0.46	0.45
Heminic iron	317	13.0	µg/g	17 %	+2.7	***	-0.3	ns	0.73	0.73
Hydroxyprol.	317	644	µg/g	15 %	+10	ns	-0	ns	0.47	0.43
Hydrox. solub.	317	22.6	%	29 %	-1.0	ns	+1.6	t	0.12	0.11
Protein/DNA	244	517	mg/mg	22 %	-12	ns	+21	ns	0.09	0.12
LDH	237	117	nkat/g	16 %	-14	***	+2	ns	0.19	0.19
ICDH	245	160	nkat/g	32 %	+28	***	+1	ns	0.28	0.28
Myosin I	237	39.8	%	33 %	-1.2	ns	-0.4	ns	0.26	0.26

The heritability coefficients are reported in table 1. The carcass weight is the only trait which heritability coefficient depends on the statistical model used. The coefficient in the model without the selection effect (h^2= 0.50) is certainly too high since the selection introduced a supplementary genetic variability in the sample. On the other hand, the coefficient in the model with the selection effect (h^2= 0.33) is certainly too low since the genetic variability within group is reduced by the selection. The most probable value has to be comprised between these extremes. In such a sample under well controled environment, the heritability coefficients of carcass weight and composition are relatively large and coherent with the litterature (Renand et al., 1992). Except for the collagene solubility and the protein to DNA ratio, heritability coefficients of muscle characteristics are generally higher than h^2= 0.20 . The apparent genetic variability is therefore large enough to be used in selection programmes if needed.

The phenotypic and genetic correlation coefficients are reported in table 2. These coefficients are very similar whatever the model used for estimating the genetic parameters. Therefore these estimates are certainly representative of the genetic relationship among these traits. The genetic correlations are markedly larger than the phenotypic correlations. There are two clear genetic antagonisms. The first one is the classical opposition between carcass lean and fat content. The second one opposes the LDH glycolytic activity to both the ICDH oxydative activity and the proportion of type I myosin. Therefore the repartition of slow-red and fast-white fibers in the *Longissimus dorsi* muscle seems to be largely under genetic control. Logically these three muscle characteristics are genetically related to the pigment and the intramuscular lipid contents : negatively for the first one and positively for the two last ones.

Higher muscle to fat ratio is clearly associated with higher protein/DNA ratio (therefore with larger fibers), with lower intramuscular lipid and pigment contents, with higher thermal solubility of the collagene and higher glycolytic enzymatic activity. As rapid-white type of fibers have been shown to be related to higher post-mortem maturing rate of the meat (Valin, 1988), the genetic correlations presently estimated indicate that selecting leanner animals is certainly favourable as far as tenderness is concerned. However this selection will tend to reduce the intramuscular lipid content and therfore the associated flavour of the meat.

Table 2. Phenotypic and genetic correlation coefficients*

	CW	CL%	CF%	pH	Lip%	Pigm.	Hydr.	Solub	P/DNA	LDH	ICDH	Myo I
Carcass weight		+0.27	-0.19	+0.83	-0.25	-0.15	+0.36	-0.59	+0.28	-0.19	+0.45	+0.53
CW		+0.38	-0.33	+0.71	-0.29	-0.26	+0.38	-0.18	+0.54	+0.02	+0.23	+0.23
Carcass lean %	-0.06		-0.98	+0.56	-0.78	-0.55	-0.36	+0.18	+0.86	+0.26	+0.01	+0.02
CL%	-0.03		-0.98	+0.55	-0.79	-0.58	-0.36	+0.33	+0.85	+0.29	-0.04	-0.02
Carcass fat %	+0.23	-0.95		-0.41	+0.66	+0.50	+0.23	-0.12	-0.91	-0.19	+0.00	+0.05
CF%	+0.20	-0.95		-0.40	+0.66	+0.53	+0.23	-0.29	-0.90	-0.23	+0.05	+0.10
pH	-0.01	-0.00	-0.00		-0.69	-0.40	-0.16	-0.17	+0.52	-0.13	+0.66	+0.65
	-0.01	-0.00	-0.00		-0.70	-0.40	-0.25	-0.04	+0.36	-0.20	+0.68	+0.70
Lipid %	+0.19	-0.57	+0.61	-0.11		+0.77	+0.61	-0.53	-0.69	-0.76	+0.37	+0.27
Lip%	+0.17	-0.57	+0.61	-0.11		+0.78	+0.63	-0.62	-0.72	-0.77	+0.41	+0.30
Heminic iron	+0.01	-0.26	+0.23	+0.04	+0.18		+0.18	-0.59	-0.78	-0.77	+0.42	+0.46
Pigm.	-0.01	-0.27	+0.24	+0.04	+0.19		+0.18	-0.72	-0.84	-0.79	+0.48	+0.51
Hydroxyprol.	-0.04	-0.06	+0.02	-0.09	+0.08	+0.14		-0.65	-0.27	-0.41	+0.19	-0.21
Hydr.	-0.04	-0.06	+0.02	-0.09	+0.07	+0.14		-0.49	-0.22	-0.44	+0.18	-0.18
Hydrox. solub.	-0.05	+0.06	-0.06	-0.00	-0.10	-0.10	-0.08		+0.33	+0.91	-0.50	-0.67
Solub.	-0.02	+0.07	-0.07	-0.01	-0.10	-0.11	-0.08		+0.49	+0.93	-0.56	-0.74
Protein/DNA	-0.04	+0.06	-0.06	+0.05	-0.04	-0.11	-0.10	-0.00		+0.11	+0.07	-0.23
P/DNA	-0.02	+0.07	-0.07	+0.04	-0.05	-0.12	-0.10	+0.02		+0.20	-0.07	-0.33
LDH	+0.02	+0.04	+0.01	+0.09	+0.00	-0.25	-0.17	+0.19	+0.12		-0.83	-0.51
	+0.03	+0.04	+0.01	+0.09	+0.00	-0.26	-0.17	+0.20	+0.13		-0.85	-0.56
ICDH	-0.12	-0.06	+0.01	+0.15	+0.00	+0.32	+0.10	-0.09	-0.02	-0.26		+0.87
	-0.13	-0.06	+0.02	+0.15	+0.01	+0.33	+0.10	-0.10	-0.03	-0.26		+0.89
Myosin I	-0.04	-0.05	+0.04	-0.06	+0.00	+0.18	-0.07	-0.07	-0.06	-0.22	+0.35	
Myo. I	-0.05	-0.06	+0.05	-0.06	+0.01	+0.18	-0.06	-0.08	-0.07	-0.23	+0.35	

* Phenotypic correlations above and genetic correlations below the diagonal
Estimates with model 1 on the first line and with model 2 on the second line

REFERENCES

ANSAY, M. (1974) Ann. Biol. Anim. Bioch. Biophys., 14 : 471-486

ARNETH, W. (1972) Fleischwirtsch., 52 : 1455-1458

BONNET, M. and KOPP, J. (1984) Cahier Tech. INRA, 5 : 19-30.

BRIAND, M., TALMANT, A., BRIAND, Y., MONIN, G., DURAND, R. (1981) Eur. J. Appl. Physiol., 46 : 347-365

HORNSEY, H.C. (1956) J. Sci. Food Agric., 7: 534-540.

LABARCA, C. and PAIGEN, K. (1980) Anal. Biochem., 102 : 344-352

LOWRY, O.H., ROSEBROUGH, N.J., FARR, A.L., RANDALL, R.J. (1951) J. Biol. Chem., 193 : 265

MENISSIER, F. (1988) Proc. 3rd World Congr. Sheep and Beef Cattle Breed., 2 : 215-236.

PICARD, B., LEGER, J., ROBELIN, J. (1994) Meat Science, 36 : 333-343.

RENAND, G., PLASSE, D., ANDERSEN, B.B. (1992) In Beef cattle production. eds. Jarrige, R. and Béranger, C., Elsevier, 87-108.

ROBELIN, J. and GEAY, Y. (1975) Ann. Zootech., 24 : 391-402.

VALIN, C. (1988) Reprod. Nutr. Develop., 28 : 845-856