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Growth, carcass and meat quality performance of crossbred pigs with graded proportions of Meishan genes

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Summary – Growth, carcass and meat quality traits were measured in 2 different experimental herds on male and female pigs produced from matings between Piétrain boars and 12 genetic types of sows with graded proportions of Large White (LW) and Meishan (MS) genes. Growth records (from 30–100 kg liveweight) were obtained on *ad libitum* feeding on a total of 1 640 pigs, among which 1 200 were submitted to carcass evaluation and meat quality measurements. Genetic type mean performance essentially varied according to the relative proportions of MS and LW genes in the dam and could hence be characterized by a single parameter, difference in crossbreeding (Δ_{MS-LW}^c), which measures the difference between MS and LW breeds used as dam breeds. Differences in crossbreeding were unfavourable to MS for all growth and carcass traits. Average estimates of Δ_{MS-LW}^c were -71 ± 16 g/d; 0.21 ± 0.07 ; $-2.4 \pm 0.3\%$; $-9.0 \pm 0.5\%$ for average daily gain (ADG) feed conversion ratio, killing out percentage and estimated carcass lean content (% M), respectively. However, significant herd differences were observed for ADG and %M. The 2 herd estimates were -51 ± 16 g/d and -92 ± 30 g/d for ADG, $-7.3 \pm 0.6\%$ and $-10.7 \pm 1.5\%$, for %M. Conversely, differences in crossbreeding for meat quality traits were in favour of MS, with an advantage of 1.1 ± 0.4 point in meat quality index over LW, *ie* one third of a phenotypic standard deviation.

pig / crossbreeding / Chinese breed / growth / carcass / meat quality

Résumé – Performances de croissance, de carcasse et de qualité de la viande de porcs comportant une proportion variable de gènes Meishan. Des performances de croissance, de carcasse et de qualité de la viande ont été mesurées dans 2 élevages expérimentaux sur des porcs mâles et femelles issus d'accouplements entre des verrats Piétrain et 12 types génétiques de femelles comportant des proportions variables de gènes Large White (LW)

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et Meishan (MS). Le contrôle de croissance (de 30 à 100 kg de poids vif) a été réalisé en alimentation à volonté sur un total de 1 640 porcs, dont 1 200 ont fait l'objet d'une évaluation de la qualité de la carcasse et de la viande. Les performances moyennes des différents types génétiques varient essentiellement en fonction des proportions relatives de gènes MS et LW chez la mère et peuvent donc être caractérisées par un paramètre unique, la différence en croisement (Δ_{MS-LW}^c), qui mesure l'écart entre les races MS et LW utilisées comme mères des produits terminaux. Les différences en croisement sont en défaveur de la MS pour l'ensemble des caractères de croissance et de carcasse. Les estimations moyennes de Δ_{MS-LW}^c s'élèvent à -71 ± 16 g/j; $0,21 \pm 0,07$; $-2,4 \pm 0,2\%$; $-9,0 \pm 0,5\%$ pour le gain moyen quotidien (GMQ), l'indice de consommation, le rendement et la teneur en muscle estimée (%M) de la carcasse, respectivement. Cependant, des différences significatives entre élevages sont observées pour ADG et %M. Les estimations des 2 élevages s'élèvent à -51 ± 16 g/j et -92 ± 30 g/j pour GMQ; $-7,3 \pm 0,6\%$ et $-10,7 \pm 1,5$ pour %M. À l'inverse, les différences en croisement pour les caractères de qualité de la viande sont en faveur de MS, avec un avantage de $1,1 \pm 0,4$ point d'indice de qualité de la viande sur LW, soit un tiers d'écart type phénotypique.

porcin / croisement / race chinoise / croissance / carcasse / qualité de la viande

INTRODUCTION

Some native porcine breeds from China, such as the Meishan breed, exhibit exceptional reproductive ability compared to currently used maternal genotypes and could be of great value for improving sow productivity (Legault and Caritez, 1983). However, these Chinese breeds are also characterized by very poor growth and carcass performance (Legault *et al*, 1985). Hence, their economic value will largely depend on the relative economic contributions of productive and reproductive traits.

Several crossbreeding schemes can be implemented in order to take advantage of these extreme genotypes (Sellier and Legault, 1986; Bidanel, 1990). Their economic value can be assessed using the knowledge of a limited number of crossbreeding parameters (Dickerson, 1969, 1973; Hill, 1982). Accordingly, an experiment was designed to estimate crossbreeding parameters relative to the cross between one of these Chinese breeds, the Meishan, and the most widely used French breed, the Large White, for the main traits of economic interest. Estimates of crossbreeding parameters for sow productivity and growth traits have been reported by Bidanel *et al*, (1989, 1990) and Bidanel (1993). The purpose of the present study was to evaluate the growth, carcass and meat quality performance of crossbred pigs with various proportions of Meishan genes and estimate the relevant crossbreeding parameters. Piétrain boars were used as terminal sires.

MATERIALS AND METHODS

Data and experimental design

The data originate from a crossbreeding experiment between Large White (LW) and Meishan (MS) pig breeds which took place between 1983–1989 at the INRA experimental research farm of Le Magneraud (Surgères, Charente-Maritime, referred to

as Le Magneraud). The 3-step design of the experiment was described in detail by Bidanel *et al* (1989). Briefly, the first step was a complete 2-breed diallel, which led to the production of 4 genetic types of females (MS, LW \times MS, MS \times LW, LW) and 3 genetic types of males (MS, LW, F₁ = LW \times MS or MS \times LW). In the second step, females chosen at random within each of the above-mentioned genotypes were mated to randomly chosen MS, LW and F₁ boars and produced 12 genetic types of litters. In the third step, randomly chosen females from these 12 genotypes were inseminated with semen from Piétrain boars in 5 successive parities. The data analysed in the present study include growth, carcass and meat quality performance of a random sample of the progeny of these females. The sow herd was managed under a batch farrowing system, with a 3-wk interval between contiguous batches. These batches then became postweaning and fattening batches of growing animals. The 12 genetic types of sows were not necessarily included in each batch. However, genetic types were allocated to batches so as to have a well connected design. Similar precautions were taken when allocating Piétrain boars to genetic types of sows. The pigs included in the present study were born between March 1986 and May 1988 in 29 different batches uniformly distributed over that period of time. One barrow and a minimum of 4 females per litter were randomly chosen at weaning. A total number of 1 640 pigs were chosen. They were raised at Le Magneraud, with the exception of 2 batches, which were transferred to another INRA experimental farm located in Rouillé, Vienne. This farm will be referred to as Rouillé hereafter. Le Magneraud is a closed herd with a good sanitary status, whereas Rouillé is an open herd and has a lower sanitary status. Buildings were closed in Le Magneraud and semi-open in Rouillé. The distribution of the 1 640 pigs according to genetic type, herd and sex is presented in table I.

Table I. Distribution of pigs by genetic type, herd and sex.

Dam genetic type ¹	No of dams	No of animals			
		Le Magneraud		Rouillé	
		Gilts	Barrows	Gilts	Barrows
MS	14	82	21	12	3
MS(LW \times MS)	12	78	20	30	9
MS(MS \times LW)	17	127	34	25	8
F ₁ \times MS	9	66	18	15	5
LW \times MS	10	109	37	13	2
MS \times LW	11	83	33	12	4
F ₁ (LW \times MS)	11	109	28	8	2
F ₁ (MS \times LW)	10	93	30	8	1
F ₁ \times LW	7	55	28	3	1
LW(LW \times MS)	9	68	22	12	1
LW(MS \times LW)	13	102	32	21	4
LW	13	107	59	—	—
Total	136	1 079	362	159	40

¹ LW = Large White; MS = Meishan; F₁ = LW \times MS or MS \times LW. The sire breed is mentioned first.

Measurements

Animals were transferred from the post-weaning building to the different fattening units \approx 30 kg liveweight. They were penned in groups of 8–10, with *ad libitum* access to water and to a pelleted diet formulated to contain 3 200 kcal digestible energy/kg and 16.5% crude protein. Each pen included animals from both sexes, but only one genetic type. Average daily gain and feed intake (on a pen basis) were measured from 30 kg liveweight to the day before slaughter.

Animals were slaughtered around 100 kg liveweight in a single slaughterhouse located \approx 55 km from Le Magneraud and 35 km from Rouillé. A sub-sample of 1 200 carcasses were cut for carcass and meat quality measurements. The day after slaughter, carcass weight, carcass length between the atlas and the anterior edge of the pulvian symphysis and backfat thickness at the levels of last lumbar vertebra (rump), last thoracic vertebra (back) and last cervical vertebra (neck) were measured. The right side of the carcass was weighed. This was considered the net half-carcass weight on which all subsequent calculations were based. They were then submitted to the standardized Paris-type cutting as described by Ollivier (1970). Muscle content of the carcass was estimated from the weight of 5 cuts, expressed as percentage of half carcass weight, according to the following equation (Pommeret and Naveau, 1979): percentage of muscle = $0.75 + 0.80$ (percentage of ham) $+1.06$ (percentage of loin) $+0.48$ (percentage of belly) -0.50 (percentage of backfat) -0.66 (percentage of leaf fat). Various meat quality criteria were also measured 24 h *post mortem*, including: 1) ultimate pH on longissimus dorsi, adductor femoris, gluteus superficialis and biceps femoris muscles; 2) water-holding capacity as assessed by the time (in tens of s) necessary for a piece of pH paper to get wet when put on the freshly cut surface of biceps femoris and gluteus superficialis muscles; and 3) reflectance of biceps femoris and gluteus superficialis muscles at 630 nm, using a Manuflex reflectometer (scale 0 at 1000). A meat quality index (MQI), showing a within-slaughter day correlation of 0.72 with the technological yield of cooked Paris ham processing (Jacquet *et al*, 1984), was computed as follows: $MQI = 53.7 + 5.9019$ (pH of adductor femoris muscle) $+0.1734$ (water holding capacity of biceps femoris muscle) -0.0092 (reflectance of biceps femoris muscle).

Statistical analyses

The data, with the exception of feed consumption and feed conversion ratio, were analysed using mixed model techniques (Henderson, 1984). When variances are known, best linear unbiased estimates of marginal means for main effects (averaged across appropriate interactions) and interactions can be obtained by solving mixed model equations. When variances are not known, as in the present case, they should be replaced by their restricted maximum likelihood estimates obtained from the data (Gianola *et al*, 1986). In the present study, dam (σ_d^2) and litter (σ_l^2) variances were estimated using Meyer's DFREML set of programs (Meyer, 1988, 1989). Estimation of fixed effects and hypothesis testing were then performed using the PEST computer package (Groeneveld and Kovac, 1990).

The assumed model for growth and carcass traits was as follows:

$$y_{ijklmnop} = E_i + B_{ij} + S_k + V_l + P_m + G_n + (EG)_{in} + (SG)_{km} + (PG)_{mn} + d_{no} + l_{nop} + cov + e_{ijklmnop} \quad [1]$$

where

$y_{ijklmnop}$ = an observable random variable;

E_i = fixed effect of the i th experimental herd ($i = 1, 2$);

B_{ij} = fixed effect of the j th batch, nested within the i th herd ($j = 1, 29$);

S_k = fixed effect of the k th sex (females of barrows);

V_l = fixed effect of the l th artificial insemination sire ($l = 1, 25$);

P_m = fixed effect of the m th parity of the dam ($m = 1, 5$);

G_n = fixed effect of the n th dam genetic type ($n = 1, 12$);

$(EG)_{kn}$ = fixed effect of the interaction between the i th herd and the n th genetic type;

$(SG)_{mn}$ = fixed effect of the interaction between the k th sex and the n th genetic type;

$(PG)_{km}$ = fixed effect of the interaction between the m th parity of the dam and the n th genetic type; and

d_{no} = random effect of the o th dam, nested within the n th genetic type. The vector \mathbf{d} of dam effects is $\mathbf{N}(\mathbf{0}, \mathbf{A}\sigma_d^2)$, where \mathbf{A} = matrix of additive relationships between dams,

l_{nop} = random litter effect, nested within the o th dam and the n th genetic type. The vector \mathbf{P} of litter effects is $\mathbf{N}(\mathbf{0}, \mathbf{I}\sigma_l^2)$, where \mathbf{I} = identity matrix, cov = covariable initial weight (for average daily gain) or final weight (for the other traits) and

$e_{ijklmnop}$ = residual effect. The vector \mathbf{e} of residuals is $\mathbf{N}(\mathbf{0}, \mathbf{I}\sigma_e^2)$.

Preliminary analyses indicated that the covariable did not differ ($P > 0.10$) according to the genetic type.

A similar model was used for meat quality traits except that the batch effect was replaced by the effect of slaughter date. Feed intake and feed conversion ratio data were analysed using a fixed linear model including the effects of experimental herd, batch within herd, dam genetic type and the linear regressions on pen sex ratio and final weight.

The same models were used to estimate crossbreeding parameters, except that genetic type effects were replaced by their decomposition according to adequately parameterized crossbreeding parameters. Not all usual crossbreeding parameters (Dickerson, 1969; 1973) could be estimated from the present set of data. It can be checked from table II that direct and maternal breed effects were confounded with $PI \times MS$ and $PI \times LW$ direct heterosis effects. This problem was solved by expressing genetic type means as a deviation from $PI \times LW$ mean $\mu_{PI \times LW}^c$ and by introducing a new parameter, difference in crossbreeding Δ_{MS-LW}^c (Bidanel, 1988). The expressions of $\mu_{PI \times LW}^c$ and Δ_{MS-LW}^c in terms of Dickerson's parameters are as follows:

$$\begin{aligned} \mu_{PI \times LW}^c &= 1/2g_{PI}^o + 1/2g_{LW}^o + g_{LW}^m + g_{LW}^n + h_{PI \times LW}^o \\ \Delta_{MS-LW}^c &= 1/2(g_{MS}^o - g_{LW}^o) + (g_{MS}^m - g_{LW}^m) + (h_{PI \times MS}^o - h_{PI \times LW}^o) \end{aligned}$$

where: $g_{LW}^o, g_{MS}^o, g_{PI}^o$ = direct effects of LW, MS and PI breeds, respectively; g_{LW}^m, g_{MS}^m = maternal effects of LW and MS breeds, respectively; g_{LW}^n = grand-maternal effect of LW breed; $h_{PI \times MS}^o, h_{PI \times LW}^o$ = direct heterosis effects for PI \times MS and PI \times LW crosses, respectively. It can be noticed that Δ_{MS-LW}^c also is the regression coefficient of performance on the percentage of MS genes.

Maternal epistatic recombination loss (Dickerson, 1969; 1973) was not included in final analyses because, as will be seen later, maternal non-additive effects were almost non-existent. The decomposition of the 12 genetic types according to reparameterized crossbreeding parameters is shown in table II.

RESULTS

Analyses of variance

Levels of significance of Fisher statistics for fixed effects are given in table III. A significant ($P < 0.05$) herd \times genetic type interaction (H \times G) was observed for carcass composition, particularly adiposity traits. The sex \times genetic type (S \times G) interaction was significant ($P < 0.05$) for average daily gain and killing out percentage. As will be seen later, these interactions were mainly due to herd or sex variations in breed differences. Parity \times genetic type interactions (P \times G) were also observed for average daily gain and various carcass traits. These P \times G interactions generally had a rather complicated structure and were associated with relatively minor differences in genetic type effects. On the whole, examination of subclass means suggested that interactions did not result in rank changes of genetic types and did not preclude examination of genetic type, herd and sex as main effects.

Differences among herd and batches (or slaughter date) were highly significant for most growth, carcass and meat quality traits. Animals raised in Le Magneraud grew faster (74 ± 13 g/d), had a better feed conversion ratio (-1.31 ± 0.05), leaner carcasses (-2.3 ± 0.8 mm average backfat thickness) and a better meat quality (2.50 ± 0.4 points of meat quality index). Conversely, they had a lower killing out percentage ($-1.1 \pm 0.3\%$) and shorter carcasses (-17 ± 5 mm). The sire effect was highly significant for all growth and carcass traits. It also influenced ultimate pH, but had no effect on reflectance and water holding capacity. Barrows grew faster (35 ± 6 g/d), had a higher killing out percentage ($0.5 \pm 0.2\%$) and better ultimate pH (from 0.03 ± 0.01 to 0.06 ± 0.02 according to the muscle) than gilts. On the other hand, females had leaner carcasses (3.7 ± 0.3 points of estimated carcass lean percentage) and consumed less feed (-0.25 ± 0.07 kg/d) than castrates. Parity differences were significant for initial and final weights, age at 100 kg and backfat thickness. The major part of weight differences was present at the beginning of the test period. Weight increased from the first to the third parity, then decreased slightly. Conversely, backfat thickness increased from the first to the fifth parity.

The effect of genetic type was significant for all growth and carcass traits except final weight and shoulder weight. With very few exceptions, genetic types with equal percentages of MS genes had very similar performance. As a consequence, 5 aggregate genetic types could be defined: 1/2 MS, 3/8 MS, 1/4 MS, 1/8 MS and 1/2 LW. For simplicity, only marginal means for these aggregate genotypes will

Table II. Decomposition of genetic type means according to crossbreeding parameters.

Genetic type ¹	Dickerson model ²										Reparameterized model ³			
	μ	g^o	g^m	g^n	h^o	h^m	h^m	$\mu_{PI \times LW}$	Δ_{MS-LW}^c	g_{MS-LW}^n	$g_{LW \times MS}^m$			
Sire Dam	μ	g^o	g^m	g^n	h^o	h^m	h^m	$\mu_{PI \times LW}$	Δ_{MS-LW}^c	g_{MS-LW}^n	$g_{LW \times MS}^m$			
PI MS	1	1/2	1/2	0	1	0	0	1	1	1	0			
PI MS(LW × MS)	1	1/2	3/8	1/8	3/4	1/4	1/2	3/4	3/4	1/2	1/2			
PI MS(MS × LW)	1	1/2	3/8	1/8	3/4	1/4	1/2	3/4	3/4	1/2	1/2			
PI F ₁ × MS	1	1/2	3/8	1/8	3/4	1/4	0	3/4	3/4	1	1/2			
PI LW × MS	1	1/2	1/4	1/4	1/2	1/2	1	1/2	1/2	1	1			
PI MS × LW	1	1/2	1/4	1/4	1/2	1/2	0	1/2	1/2	0	1			
PI F ₁ (LW × MS)	1	1/2	1/4	1/4	1/2	1/2	1/2	1/2	1/2	1/2	1/2			
PI F ₁ (MS × LW)	1	1/2	1/4	1/4	1/2	1/2	1/2	1/2	1/2	1/2	1/2			
PI F ₁ × LW	1	1/2	1/8	3/8	1/4	3/4	0	1/4	1/4	0	1/2			
PI LW(LW × MS)	1	1/2	1/8	3/8	1/4	3/4	1/2	1/4	1/4	1/2	1/2			
PI LW(MS × LW)	1	1/2	1/8	3/8	1/4	3/4	1/2	1/4	1/4	1/2	1/2			
PI LW	1	1/2	0	1/2	0	1	0	0	0	0	0			

¹ LW = Large White; MS = Meishan; F₁ = LW × MS or MS × LW. The sire breed is mentioned first. ² μ = overall mean; g_x^o, g_x^m, g_x^n = direct, maternal and grand-maternal effects of breed ($x = LW, MS$ or PI). $h_{PI \times LW}^m, h_{PI \times MS}^m$ = direct heterosis effects for $PI \times LW$ and $PI \times MS$ crosses, respectively. $h_{LW \times MS}^m$ = maternal heterosis effect for $LW \times MS$ cross. Epistatic recombination loss is not considered in the model (see text). ³ $\mu_{PI \times LW}^c$ = average performance of $PI \times LW$ pigs. Δ_{MS-LW}^c = Difference in crossbreeding between Meishan and Large White (see text). g_{MS-LW}^n = contrast (Meishan - Large White) for grand-maternal breed effects. $h_{LW \times MS}^m$ = maternal heterosis effect for $LW \times MS$ cross.

Table III. Levels of significance of Fisher tests of fixed effects in analyses of variance.

Trait	Source of variation									
	Herd (H)	Batch (B)	Sire (Si)	Sex (Se)	Parity of dam (P)	Dam genetic type (G)	G × H	G × Se	G × P	Cov ¹
Initial weight (kg)	***	***	***	***	***	**	*	NS	NS	-
Final weight (kg)	***	***	***	***	***	NS	NS	NS	NS	***
Average daily gain (g/d)	***	***	***	***	NS	**	*	**	NS	***
Age at 100 kg (d)	***	***	***	***	***	**	NS	*	NS	-
Feed intake (kg)	NS	***	-	+ ²	-	+	-	-	-	***
Feed conversion ratio	***	***	-	NS ²	-	**	-	*	-	NS
Killing out percentage (%)	***	***	***	NS	NS	**	NS	*	***	***
Carcass length (mm)	**	***	**	***	NS	***	+	NS	+	***
Backfat thickness (mm)										
Rump	**	***	***	***	NS	***	NS	NS	+	***
Back	NS	***	***	***	***	***	*	NS	NS	***
Neck	**	***	***	***	*	***	*	NS	NS	***
Half carcass weight (kg)	***	***	***	*	NS	**	NS	NS	NS	***
Loin	NS	***	NS	***	NS	***	NS	NS	**	***
Ham	***	***	***	***	*	***	**	NS	NS	***
Shoulder	NS	***	***	*	NS	NS	NS	NS	NS	**
Belly	NS	***	***	**	NS	***	*	NS	NS	***
Backfat	NS	***	***	***	NS	***	**	NS	NS	***
Leaf fat	+	***	***	***	NS	***	**	NS	NS	***
Leaf fat	NS	***	***	***	NS	NS	NS	NS	NS	***
Feet	NS	***	***	+	NS	***	NS	NS	NS	***
Head	NS	***	***	***	+	***	NS	NS	NS	***
Head	NS	***	***	***	NS	***	**	NS	NS	***
Carcass lean content (%)										
Ultimate pH of:										
Longissimus dorsi	***	***	**	**	NS	NS	NS	NS	***	NS
Adductor femoris	***	***	+	***	NS	NS	NS	NS	NS	NS
Gluteus superficialis	***	***	*	*	NS	*	NS	NS	NS	NS
Biceps femoris	***	***	*	NS	NS	NS	NS	NS	NS	NS
Reflectance of:										
Gluteus superficialis	***	***	NS	NS	NS	NS	NS	NS	**	NS
Biceps femoris	NS	***	NS	NS	NS	NS	NS	NS	NS	NS
Water holding capacity of:										
Gluteus superficialis	NS	***	NS	NS	**	*	NS	NS	NS	NS
Biceps femoris	*	***	NS	NS	NS	NS	NS	NS	NS	NS
Meat quality index	***	***	*	*	NS	NS	NS	NS	NS	NS

¹ cov = covariable. Initial weight for average daily gain. Final weight for the other traits. ² Pen sex ratio effect. NS: not significant ($P > 0.10$); + $P < 0.10$; * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.

be presented. Marginal means for growth and carcass traits are shown in tables IV and V, respectively. Genetic types had very similar initial and final weights, except 1/2 MS which were lighter ($P < 0.05$). Three groups could be defined with respect to growth rate. The 1/2 LW and 1/8 MS grew faster than 1/2 MS, with 3/8 MS and 1/4 MS being intermediate. Feed intake and feed conversion ratio were higher ($P < 0.05$) in MS and 3/4 MS than the other genetic types. Variations in carcass performance were essentially related to the relative proportions of LW and MS genes. Increasing proportions of LW genes were associated with higher killing out percentages, longer carcasses, lower backfat thickness, larger lean cuts weights and lower fat cuts, feet and head weights. As a result, estimated carcass lean content of 1/2 MS and 1/2 LW pigs differed by 7.6 points of percentage (*ie* about 17%).

Table IV. Estimates of genetic type marginal means for growth performance.

Trait	Genetic type ^{1,2}					SE ³
	1/2 MS	3/8 MS	1/4 MS	1/8 MS	1/2 LW	
Initial weight (kg)	28.8 ^a	30.0 ^b	30.0 ^b	29.4 ^{ab}	29.3 ^b	0.3–0.4
Final weight (kg)	97.3 ^a	100.1 ^b	99.5 ^b	99.6 ^b	100.3 ^b	0.6–0.9
Average daily gain (g/d)	696 ^c	736 ^b	738 ^b	767 ^a	777 ^a	8–14
Age at 100 kg (d)	186 ^c	180 ^b	181 ^b	175 ^a	173 ^a	1–2
Feed intake (kg)	2.31 ^b	2.31 ^b	2.23 ^a	2.24 ^a	2.24 ^a	0.03–0.06
Feed conversion ratio	3.19 ^b	3.17 ^b	3.07 ^a	3.02 ^a	3.00 ^a	0.03–0.05

¹ LW = Large White; MS = Meishan. ² Means with same letter do not differ at the 5% level. ³ Standard error of marginal means.

Genetic type marginal means for meat quality traits are shown in table VI. Significant differences were observed for all traits except ultimate pH of adductor femoris, reflectance and water holding capacity of biceps femoris. As previously discussed, these differences were essentially due to the relative proportions of LW and MS genes. Increasing amounts of MS genes were associated with a higher ultimate pH, a lower reflectance, a higher water holding capacity and, ultimately, a better meat quality index.

Crossbreeding parameters

Crossbreeding parameters for growth, carcass and meat quality traits are shown in tables VII, VIII and IX, respectively. Grand-maternal effects and maternal heterosis effects were significant for none of the traits. Hence, variations between genetic types were entirely due to differences in crossbreeding. MS genes led to a deterioration of growth rate (-71 ± 16 g/d). Yet, differences in average daily gain were much more important in barrows than in gilts (-92 ± 27 g/d *vs* -51 ± 16 g/d). A similar sex \times genetic type interaction was observed for killing out percentage. The use of MS genes was associated with a larger decrease in killing out percentage in females than in males (-2.8 ± 0.3 *vs* -2.0 ± 0.5 percentage points).

Table V. Estimates of genetic type marginal means for carcass traits.

Trait	Genetic type ^{1,2}					SE ³
	1/2 MS	3/8 MS	1/4 MS	1/8 MS	1/2 LW	
Killing out percentage (%)	79.5 ^c	80.3 ^b	80.6 ^b	81.0 ^a	81.5 ^a	0.2–0.4
Carcass length (mm)	906 ^c	917 ^{bc}	928 ^a	926 ^{ab}	931 ^a	3–6
Backfat thickness (mm)						
Rump	23.2 ^e	20.6 ^d	18.5 ^c	17.2 ^b	15.5 ^a	0.5–0.8
Back	27.0 ^b	25.6 ^b	23.1 ^a	22.7 ^a	21.8 ^a	0.5–0.8
Neck	46.1 ^c	44.9 ^c	40.6 ^b	40.4 ^{ab}	39.1 ^a	0.6–1.0
Weight (kg)						
Loin	10.03 ^e	10.65 ^d	11.23 ^c	11.58 ^b	12.01 ^c	0.07–0.2
Ham	8.55 ^e	8.96 ^d	9.32 ^c	9.64 ^b	9.88 ^a	0.05–0.08
Shoulder	6.22 ^a	6.28 ^a	6.31 ^a	6.21 ^a	6.34 ^a	0.05–0.08
Belly	4.52 ^d	4.35 ^c	4.17 ^b	4.11 ^b	3.99 ^a	0.04–0.06
Backfat	4.72 ^d	4.34 ^c	3.83 ^b	3.78 ^b	3.48 ^a	0.07–0.12
Leaf fat	0.84 ^b	0.80 ^b	0.63 ^a	0.61 ^a	0.59 ^a	0.02–0.03
Feet	1.07 ^c	1.00 ^b	1.02 ^b	0.96 ^a	0.93 ^a	0.01–0.02
Head	4.53 ^c	4.40 ^c	4.37 ^b	4.17 ^a	4.05 ^a	0.04–0.07
Estimated carcass lean percentage (%)	45.5 ^e	47.9 ^d	51.0 ^c	52.1 ^b	53.8 ^a	0.3–0.5

¹ LW = Large White; MS = Meishan. ² Means with same letter do not differ at the 5% level. ³ Standard error of marginal means.

MS genes highly impaired carcass composition. For instance, mean differences in crossbreeding for average backfat thickness (7.3 ± 1.0 mm) or estimated carcass lean content (-9.0 ± 0.5 points of percentage) represented 4 and 3 within-breed phenotypic standard deviations, respectively. However, differences varied according to the herd. The disadvantage of MS over LW for backfat thickness was 2–3-fold larger in Rouillé than in Le Magneraud. A similar pattern was observed for ham, belly and fat cuts weights and, as a consequence, estimated carcass lean content (table VIII).

The use of MS genes led to an increase of ultimate pH of gluteus superficialis and biceps femoris muscles and, to a lower extent in the longissimus dorsi and adductor femoris muscles (table IX). MS genes also had a favourable effect on meat colour of the gluteus superficialis and biceps femoris muscles and on water holding capacity of the gluteus superficialis muscle. On the whole, meat quality index was improved by 1.1 ± 0.4 point, *ie* \approx one third of the within-breed phenotypic standard deviation.

DISCUSSION

REML and BLUP techniques have seldom been used in the analysis of crossbreeding experiments, least-squares (LS) being the most widely used method. In fact, it may easily be shown that, for well designed experiments, using BLUP instead of LS leads to very few changes in point estimates of genetic types means or

Table VI. Estimates of genetic type marginal means for meat quality traits.

Trait	Genetic type ^{1,2}					SE ³
	1/2 MS	3/8 MS	1/4 MS	1/8 MS	1/2 LW	
Ultimate pH of:						
Longissimus dorsi	5.68 ^a	5.64 ^b	5.61 ^b	5.64 ^b	5.59 ^b	0.02–0.03
Adductor femoris	5.92 ^a	5.87 ^{ab}	5.84 ^b	5.83 ^b	5.87 ^{ab}	0.02–0.04
Gluteus superficialis	5.89 ^a	5.83 ^{ab}	5.80 ^{bc}	5.77 ^{cd}	5.73 ^d	0.02–0.03
Biceps femoris	5.82 ^a	5.76 ^{ab}	5.72 ^{bc}	5.71 ^{cd}	5.65 ^d	0.02–0.03
Reflectance of ⁴ :						
Gluteus superficialis	313 ^a	317 ^a	327 ^{ab}	333 ^b	329 ^{ab}	6–9
Biceps femoris	327 ^a	322 ^a	324 ^a	327 ^a	346 ^b	5–8
Water holding capacity of ⁵ :						
Gluteus superficialis	8.3 ^a	7.6 ^{ab}	6.5 ^{bc}	6.2 ^c	7.1 ^{abc}	0.5–0.8
Biceps femoris	12.0 ^a	12.1 ^a	11.9 ^a	12.3 ^a	11.7 ^a	0.5–0.8
Meat quality index	86.9 ^a	86.7 ^a	86.2 ^b	86.1 ^b	86.3 ^{ab}	0.2–0.4

¹ LW = Large White; MS = Meishan. ² Means with same letter do not differ at the 5% level. ³ Standard error of marginal means. ⁴ Scale 0 to 1 000. ⁵ Scale 0 to 20. Higher values denote better water holding capacity.

Table VII. Estimates of crossbreeding parameters (\pm SE) for growth traits.

Trait	Δ_{MS-LW}^c	Parameter ¹ g_{MS-LW}^n	$h_{LW \times MS}^m$
Average daily gain (g/d)	$-71 \pm 16^{***}$	4 ± 10	-14 ± 9
Males	$-92 \pm 27^{***}$		
Females	$-51 \pm 16^{**}$		
H ₁ ²	$-54 \pm 16^{***}$		
H ₂ ²	$-89 \pm 30^{**}$		
Age at 100 kg (d)	$8.5 \pm 2.5^{**}$	-0.6 ± 1.7	0.2 ± 1.6
Males	$10.7 \pm 4.4^*$		
Females	$6.3 \pm 2.5^{***}$		
Feed intake (kg)	0.07 ± 0.06	0.05 ± 0.04	-0.06 ± 0.04
Feed conversion ratio	$0.21 \pm 0.07^{**}$	0.05 ± 0.05	-0.03 ± 0.05

¹ Δ_{MS-LW}^c : difference (Meishan–Large White) in crossbreeding between Meishan and Large White breeds (see text); g_{MS-LW}^n : contrast (Meishan–Large White) for grand-maternal effects; $h_{LW \times MS}^m$: maternal heterosis effect; ² H₁: Herd 1 = Le Magneraud; H₂: Herd 2 = Rouillé; *: $P < 0.05$; **: $P < 0.01$; ***: $P < 0.001$.

crossbreeding parameters. Conversely, interval estimates are strongly affected. LS methods implicitly assume that individual records are independent. This is obviously not the case in most animal breeding situations. In the present case, both animals and dams were related. Ignoring these relationships leads to serious overestimation of the precision of genetic type means and crossbreeding parameters

Table VIII. Estimates of crossbreeding parameters (\pm standard error) for carcass traits.

Trait	Parameter ¹		
	Δ_{MS-LW}^c	g_{MS-LW}^n	$h_{LW \times MS}^m$
Killing out percentage (%)	$-2.4 \pm 0.3^{***}$	0.3 ± 0.3	0.3 ± 0.3
Males	$-2.0 \pm 0.5^{***}$		
Females	$-2.8 \pm 0.3^{***}$		
Carcass length (mm)	-10 ± 6	-5 ± 5	-2 ± 5
Backfat thickness (mm)			
Rump	$6.9 \pm 0.9^{***}$	0.5 ± 0.7	-0.3 ± 0.7
Back	$6.0 \pm 0.9^{***}$	0.7 ± 0.7	-0.4 ± 0.7
H ₁ ²	$3.9 \pm 0.9^{***}$		
H ₂ ²	$8.0 \pm 2.4^{***}$		
Neck	$8.9 \pm 1.1^{***}$	0.7 ± 0.8	0.2 ± 0.8
H ₁	$4.1 \pm 1.2^{***}$		
H ₂	$13.7 \pm 2.9^{***}$		
Loin	$-1.99 \pm 0.13^{***}$	0.05 ± 0.10	-0.05 ± 0.10
Ham	$-1.51 \pm 0.09^{***}$	$0.13 \pm 0.07^+$	0.03 ± 0.07
H ₁	$-1.24 \pm 0.10^{***}$		
H ₂	$-1.78 \pm 0.23^{***}$		
Weight (kg)			
Shoulder	-0.01 ± 0.08	0.01 ± 0.06	-0.00 ± 0.06
Belly	$0.62 \pm 0.07^{***}$	$-0.09 \pm 0.05^+$	0.01 ± 0.05
H ₁	$0.37 \pm 0.07^{***}$		
H ₂	$0.88 \pm 0.17^{***}$		
Leaf fat	$1.31 \pm 0.12^{***}$	0.06 ± 0.09	0.01 ± 0.09
H ₁	$0.92 \pm 0.13^{***}$		
H ₂	$1.75 \pm 0.31^{***}$		
Backfat	$0.33 \pm 0.04^{***}$	0.04 ± 0.03	-0.00 ± 0.03
H ₁	$0.21 \pm 0.04^{***}$		
H ₂	$0.45 \pm 0.10^{***}$		
Feet	$0.09 \pm 0.02^{***}$	0.02 ± 0.02	-0.01 ± 0.02
Head	$0.45 \pm 0.08^{***}$	0.04 ± 0.06	0.04 ± 0.06
Estimated carcass lean percentage (%)	$-9.0 \pm 0.5^{***}$	-0.2 ± 0.4	0.0 ± 0.4
H ₁	$-7.3 \pm 0.6^{***}$		
H ₂	$-10.7 \pm 1.3^{***}$		

¹ Δ_{MS-LW}^c : difference (Meishan–Large White) in crossbreeding between Meishan and Large White breeds (see text); g_{MS-LW}^n : contrast (Meishan–Large White) for grand-maternal effects; $h_{LW \times MS}^m$: maternal heterosis effect for Meishan \times Large White cross;

² H₁: Herd 1 = Le Magnereaud; H₂: Herd 2 = Rouillé; +: $p < 0.10$; ***: $p < 0.01$.

(Komender and Hoeschele, 1989). The main problem is then to know the variance components that should be used in the BLUP analysis. As shown by Gianola *et al* (1986), when variance components are not known, they should theoretically be replaced by their REML estimates. However, crossbreeding experiments often have a limited size, so that estimates of variance components have a limited precision. In the present case, approximate standard errors of σ_d^2/σ_p^2 (σ_d^2 = variance between dams; σ_p^2 = phenotypic variance) ranged between 0.06–0.09. Yet, it

Table IX. Estimates of crossbreeding parameters (\pm standard error) for meat quality.

Trait	Δ_{MS-LW}^c	Parameter ¹ g_{MS-LW}^n	$h_{LW \times MS}^M$
Ultimate pH of:			
Longissimus dorsi	0.07 \pm 0.04 ⁺	-0.01 \pm 0.03	-0.02 \pm 0.03
Adductor femoris	0.05 \pm 0.05	0.01 \pm 0.04	-0.03 \pm 0.04
Gluteus superficialis	0.11 \pm 0.04**	0.03 \pm 0.03	-0.02 \pm 0.03
Biceps femoris	0.14 \pm 0.04***	0.01 \pm 0.03	-0.01 \pm 0.03
Reflectance of ² :			
Gluteus superficialis	-27 \pm 10**	4 \pm 7	9 \pm 7
Biceps femoris	-19 \pm 9*	5 \pm 7	-5 \pm 7
Water holding capacity of ³ :			
Gluteus superficialis	2.9 \pm 1.1**	-0.9 \pm 0.8	-1.6 \pm 0.8 ⁺
Biceps femoris	-0.2 \pm 1.0	0.2 \pm 0.8	-0.3 \pm 0.8
Meat quality index	1.1 \pm 0.4**	-0.3 \pm 0.3	-0.3 \pm 0.3

¹ Δ_{MS-LW}^c : difference (Meishan-Large White) in crossbreeding between Meishan and Large White breeds (see text); g_{MS-LW}^n : contrast (Meishan-Large White) for grand-maternal effects; $h_{LW \times MS}^m$: maternal heterosis effect for Meishan \times Large White cross; ² scale 0-1 000; ³ scale 0-20. Higher values denote better water holding capacity; ⁺: $P < 0.10$; *: $P < 0.05$; **: $p < 0.01$; ***: $p < 0.001$.

should be noted that the impact of variations in variance component ratios on estimates of crossbreeding parameters is far less important than the effect of ignoring relationships among animals (Komender and Hoeschele, 1989). Another potential source of bias comes from the fact that there is *a priori* little reason to assume a homogeneous variance - covariance structure among genetic types. If so, standard errors of marginal means would be either overestimated or underestimated according to the genetic type. Methods for testing the homogeneity of variances and estimating variance components in situations of heteroscedasticity in the field of animal breeding have recently been developed (Foulley *et al*, 1990; San Cristobal, 1992). In many situations such as the present one, investigations on this aspect are unfortunately limited by the small size of experimental designs. The impact of heterogeneous residual variances should be rather low, as: 1) differences are rather small; 2) it has been shown that, for rather balanced designs, estimates of fixed effects are rather robust against the effects of unequal residual variances (see for instance Kendall and Stuart, 1976, for a discussion). Conversely, the heteroscedasticity of genetic variances might be more important, particularly for interval estimates.

The validity of equations such as those used for estimating carcass lean content or meat quality index may also be questioned. Indeed, performance of extreme genotypes such as Chinese breeds may be outside the range of values used to establish these equations. This should not be the case for MQI, as differences between MS and LW in meat quality traits are rather limited. Conversely, average carcass lean content of genetic types such as 1/2 MS or 3/8 MS are in the lower

range of values used by Pommeret and Naveau (1979). Hence, it is likely that the precision of estimated carcass lean content is a bit lower for 1/2 MS or 3/8 MS than for more standard ones such as 1/4 MS, 1/8 MS or 1/2 LW.

The results of the present study, referred to as study 3 hereafter, are rather consistent with those previously obtained by Legault *et al* (1985) on 1/4 MS pigs, referred to as study 1, and those of Guéblez *et al* (1987) on 1/4 MS and 1/8 MS pigs referred to as study 2. In the 3 studies, the use of MS as a component of the maternal genotype led to a moderate decrease in growth rate (differences in crossbreeding Δ_{MS-LW}^c for average daily gain were -56 g/d; -76 g/d and -52 g/d in studies 1, 2 and 3, respectively), an important deterioration of carcass lean content (-7% , -9.2% and -9% , respectively) and a small improvement of meat quality (1.0 pt, 0.4 pt and 1.1 pt, respectively). Somewhat more variable results were observed for feed conversion ratio (FCR) and killing out percentage (KO%). Differences in crossbreeding ranged from 0.10–0.46 for FCR and from 0.8–2.5% for KO%. Large differences between animals issued from the same dam genetic type and sired by either Duroc or Meishan boars were also reported by Young (1992a, b). Meishan-sired pigs had a lower average daily gain (-83 g/d; $P < 0.05$), a higher feed conversion ratio ($+0.24$; $P < 0.05$), a larger backfat thickness ($+8.6$ mm; $P < 0.05$) and a smaller longissimus muscle area (-8.6 cm²; $P < 0.05$) than Duroc-sired pigs.

As seen earlier, differences in crossbreeding Δ_{MS-LW}^c contain one-half of difference in direct breed effects, but also direct heterosis and maternal effects. Hence, breed differences cannot in general be estimated by extrapolating Δ_{MS-LW}^c . Direct estimates of breed differences for growth rate and feed conversion ratio (Bonneau *et al*, 1990; D'Agaro *et al*, 1990; Bidanel *et al*, 1991; Yen *et al*, 1991) are much larger than those inferred from differences in crossbreeding, thus suggesting that maternal effects are important and/or that heterosis effects are larger in the MS \times PI cross than in the MS \times LW cross. Conversely, both types of estimates are similar for carcass and meat quality traits (for instance, the MS – LW difference for estimated carcass lean content was estimated as -17.6% by Poilvet *et al* (1990) against -18% in the present study). This is not unexpected, as carcass and meat quality traits are known to have an essentially additive inheritance.

Yet it must be remembered that the MS pigs used in this experiment originated from a very limited sample of animals. Hence, any extrapolation to the MS breed as a whole is inadvisable. Then, it should be kept in mind that animals were fed *ad libitum* with a relatively high energy diet. As already emphasized by Legault *et al* (1985), *ad libitum* feeding maximizes the expression of breed differences for body composition. Thus, it is likely that the disadvantage of MS over LW would have been lower under restricted feeding. Similarly, as shown by Bidanel *et al* (1991), the use of repartitioning agents such as pST would reduce MS – LW differences.

In any case, based on the results of present study and on the economic weights used for the evaluation of terminal products in France (Anonymous, 1990), *ie* 0.174 FF per g average daily gain, -109.95 FF per point of feed conversion ratio, 4.48 FF per point of meat quality index and 20 FF ($> 50\%$ muscle) or 25 FF ($< 50\%$ muscle) for carcass lean content, the reduction in gross margin per pig can be evaluated as 200, 95 and 46 FF in 1/2 MS, 1/4 MS and 1/8 MS, respectively, compared to 1/2 LW. Assuming a constant sow maintenance cost of 4000 FF per year, individual piglet costs are reduced by 42 FF, 56 FF and 29 FF in MS, 1/2 MS

and 1/4 MS sows, respectively, compared to LW (Bidanel *et al*, 1989; Bidanel 1993). As a consequence, the economic balance clearly disfavors the use of MS pigs.

Yet, these assessments should be somewhat moderated due to the presence of genetic type \times herd interactions in growth rate and carcass composition. Such interactions were not evidenced in the study of Legault *et al* (1985), but this first study involved a much smaller number of pigs. There are numerous reports of genotype \times environment interaction in growth and carcass traits in swine (see for instance Davey *et al*, 1969). However, they mainly concern genetic type \times feeding regime interactions. This was not the case in the present study, as feeding regimes were the same in both herds. The difference in the sanitary level of the 2 herds might be another possible explanation for this genotype \times environment interaction. Slowly growing genetic types are more likely to be exposed to degraded sanitary conditions at the end of the test period. Such an interaction was also noticed by Kennedy and Quinton (1987).

In any case, this interaction will lead to large variations in the gross margin disadvantage of crossbred Chinese pigs (80, 40 and 20 FF per animal, respectively, for 1/2 MS, 1/4 MS and 1/8 MS slaughter pigs). However, even in the best situation, the economic balance remains clearly unfavourable to the MS breed.

CONCLUSION

The present study confirms the important disadvantage of crossbred Meishan pigs with respect to currently used genetic types for growth and carcass traits. This disadvantage can noticeably differ according to the herd. However, simple economic evaluations clearly show that there is no short-term interest for using the Meishan breed under intensive production systems in France. Things might change in the future. Due to its exceptional reproductive performance, higher selection intensities, shorter generations intervals and consequently higher genetic gains can reasonably be expected from selecting a pure or a composite Meishan line, provided that genetic parameters are not unfavourable. The economic value of such strategies remains to be evaluated. This should be achieved using more realistic economic models than that used in the present study. Such models should in particular account for variations in the production and maintenance costs of sows and of the culling price of animals at the different levels of the crossbreeding system.

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