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GENETIC PARAMETERS OF LITTER NUMERICAL CHARACTERISTICS AND PREWEANING PIGLET GROWTH RATE IN FRENCH LANDRACE PIGS

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INTRODUCTION

Litter size at birth has considerably increased through selection in pig maternal lines over the last 15 years (e.g. Tribout et al.. 2003). but has been accompanied by a deterioration of perinatal and birth to weaning piglet survival. The correlative response on piglet preweaning growth rate remain incompletely known. though most studies report negative genetic relationships between litter size and preweaning growth rate (e.g. Damgaard et al.. 2003; Huby et al.. 2003). This is partly due to the complex determinism of preweaning piglets performances. which depends on their own genes as well as those of their genetic and foster mother(s). The use of crossfostering makes modelling and analyses more complex. but may also allow the respective contributions of genetic and foster dam(s) to be estimated.

The objective of this study was to estimate the relative contribution of piglets. genetic dam and foster dam genes to the genetic variation of piglet preweaning growth and their phenotypic and genetic correlations with litter numerical characteristics in a French Landrace population.

MATERIAL AND METHODS

Animals and traits. The data originate from a French Landrace Nucleus herd of 140 sows, distributed in 7 farrowing batches with a 3 weeks interval between successive batches. Sows were all inseminated. Parturitions were systematically induced on d113 of gestation. Assistance during farrowing was as limited as possible. The data set analysed comprised 1328 litters with 17778 piglets born, of which 13069 were individually weighed at birth and at weaning (not all litters and only piglet born alive were weighed). Crossfostering concerned 13% of piglets born alive. A total of 10 traits were analysed, i.e. the total number of piglets born (TNB), the number born alive (NBA) and weaned (NW), the number and proportion of stillbirths (NSB and SB%, respectively) and of dead piglets from birth to weaning (NDBW and DBW%, respectively), individual piglet weight at birth (BW) and at weaning (WW), as well as average daily gain from birth to weaning (ADG). Elementary statistics from the 10 traits studied are given in table 1.

Statistical analyses. The 7 litter numerical productivity traits were considered as sow traits and were analysed using linear animal models including farrowing batch and parity as fixed effects, sow additive genetic value and permanent environment as random effects. Mortality rates were also analysed used a logistic regression model with a logit link.

Piglet traits were analysed using linear animal models including birth batch, sex and dam parity as fixed effects, piglet, dam and nurse (except for BW) additive genetic values, as well as common birth litter as random effects, TNB (for BW) or the number of piglets fostered and age at measurement (WW and ADG) as covariates. Genetic parameters were estimated using multiple traits restricted maximum likelihood analyses with the VCE (4.5 version – Neumaier and Groeneveld, 1998) and ASREML (version 1.10 – Gilmour et al., 2003) softwares.

Table1. Number of pigs, means and phenotypic standard deviations (SD) of the 10 traits studied

Trait	Abbreviation	N	Mean	SD
Birth weight (kg)	BW	13609	1.40	0.34
Weaning weight (kg)	WW	12411	7.48	1.47
Average daily gain from birth to weaning (kg/d)	ADG	11753	0.23	0.05
Total number born/litter	TNB	1328	13.6	3.5
Number born alive/litter	NBA	1328	12.3	3.2
Weaned/litter	NW	1328	10.6	3.0
Number of stillbirths/litter	NSB	1284	1.3	1.6
Number of dead piglets from birth to weaning	NDBW	1282	1.7	1.8
Stillbirth rate (%)	SB%	1284	9.1	10.5
Birth to weaning mortality rate (%)	MBW%	1282	12.5	12.1

RESULTS AND DISCUSSION

Estimates of genetic parameters for litter productivity traits are given in table 2. Heritability values were low for the 7 traits analysed and in accordance with average literature estimates (Rothschild and Bidanel, 1998). Phenotypic and genetic correlations between litter size at birth and at weaning were highly positive (0.75 to 0.98). Conversely, correlations between stillbirth and birth to weaning mortality traits were close to zero or even negative (-0.39 to 0.19), showing that the two components of preweaning piglet mortality have a very different genetic determinism, as also shown by Huby et al. (2003) in Large White pigs.

Table 2 . Estimates[A] of heritabilities (permanent environmental effects) on the diagonal, phenotypic (below diagonal) and genetic (above diagonal) between litter traits

Traits[B]	TNB	NBA	NW	SB	ND	SB%	D%
TNB	**.10 *(.09)***	.88	.98	.36	.18	.46	.13
NBA	.88	**.10 *(.07)***	.91	ne[C]	-.36	.54	.21
NW	.75	.87	**.09 *(.05)***	-.14	-.31	-.70	-.06
SB	.41	-.06	-.09	**.08 *(.11)***	ne	.19	-.39
ND	.25	-.21	-.22	.95	**.05 *(.06)***	ne	-.22
SB%	.43	.45	.13	.04	-.03	**.08 *(.18)***	ne
D%	.30	.29	.01	-.04	.00	.81	**.04 *(.05)***

[A]Standard errors range from 0.01 to 0.03 for heritabilities, from 0.07 to 0.23 for genetic correlations; [B]See table 1 for trait definition; [C]non estimated due to convergence problems

Mortality traits also have different relationships with the three prolificacy traits, in accordance with the results of Huby et al (2003) and Canario et al. (2006). TNB has positive, i.e. unfavourable, phenotypic and genetic correlations with both stillbirth and birth to weaning mortality. NBA has low or even favourable relationships with stillbirth, but remains unfavourably associated with NDBW or MBW%. Finally, NW has negative, i.e. favourable relationships with both components of mortality.

Tableau 3. Estimates of variance components and genetic correlations between components of preweaning piglet growth

Trait[A]		BW			WW				ADG			
	Component[B]	D	M	C^2	D	M	N	C^2	D	M	N	C^2
BW	D	**.01**	-.13	-	.46	.10	-.36	-	-.71	.25	-.08	-
	M		**.21**	-	-.24	.26	.35	-	.44	-.74	.23	-
	C^2			**.08**	-	-	-	-	-	-	-	-
WW	D				**.02**	-.45	-.38	-	ne[C]	ne	ne	-
	M					**.06**	-.53	-	-	.86	-.58	-
	N						**.15**	-	-	-.58	.98	-
	C^2							**.10**	-	-	-	-
ADG	D								**.02**	-.38	-.61	-
	M									**.05**	-.45	-
	N										.13	-
	C^2											**.10**

[A] BW = birth weight ; WW = weaning weight ; ADG = birth to weaning average daily gain. [B] D, M, N= direct (piglet), mother and nurse genetic effects; C^2 = common birth litter effects. [C] Non estimated due to convergence problems

Genetic parameters estimated for piglet preweaning growth traits are shown in table 3. Piglet genes had a very limited influence on their growth up to weaning (< 2% of phenotypic variance). Maternal effects explained around 30% of the phenotypic variance of the 3 traits analysed, of which 2/3 were of genetic origin and 1/3 corresponded to common birth litter effects (which can include non additive gene effects). The effects of piglets dam remained significant up to weaning, but nurse effects explained the largest proportion of the phenotypic variance.

Estimates of genetic correlations were estimated with a low accuracy (standard errors ranging from 0.20 to 0.40) and consequently have to be interpreted with caution. Direct effects, which were very low, were removed from multivariate models used to analyse WW and ADG to improve convergence. The genetic correlations between the 3 genetic components were systematically negative; the antagonism was more pronounced at weaning than at birth (0.13 for BW, -0.38 to -0.53 for WW et -0.38 à -0.61 for ADG). Direct effects on BW and WW were positively correlated, but had antagonistic relationships with ADG (-0.71). The correlation pattern was similar for maternal effects (0.26 between BW and WW; -0,74 between BW and ADG). Correlations between dam and nurse effects on WW and ADG were strongly positive (0.86 and 0.98, respectively). Similarly, direct-maternal genetic correlations between traits were generally positive (0.10 and -0.24 between BW and WW; 0.25 and 0.44 between BW and ADG).

Genetic correlations between piglet growth and litter numerical productivity traits are given in table 4. Estimates also have a low accuracy and have to be considered with caution. Yet, they tended to indicate that direct effects have positive correlations with numerical productivity traits, whereas correlations involving dam or nurse effects were all negative, i.e. unfavourable.

Tableau 4. Estimates of genetic correlations between piglet weight at birth andat weaning and litter numerical characteristics

Trait[A]	Component[B]	TNB	NBA	NW	SB%	MRBW%
BW	D	0.99	0.98	0.98	0.01	0.77
	M	-0.29	-0.18	-0.01	-0.10	-0.39
WW	D	0.15	-0.34	0.6	-	-
	M	-0.63	-0.31	-0.22	-	-0.64
	N	-0.05	-0.25	-0.32	-	-0.48

[A] BW, WW =piglet weight at birth and at weaning, respectively. [B] D, M, N = direct, mother and nurse effects, respectively.

CONCLUSION

Though preliminary, this study contributes to an improved knowledge of the genetic variability of reproduction and pre-weaning growth. The complexity of trait associations and the major role played by maternal effects were estimated. Selecting on number born alive would help to decrease perinatal mortality, but would not allow birth to weaning survival to be improved.

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GENETIC PARAMETERS OF LITTER SIZE, PIGLET PREWEANING MORTALITY AND GROWTH RATE IN FRENCH LANDRACE PIGS. A. Bouquet*, L. Canario, B. Ligonesche and J.P. Bidanel. *INRA SGQA, 78352 Jouy-en-Josas, France.

Genetic parameters of litter productivity and piglet preweaning growth traits were estimated in a French Landrace population on a total of 1328 litters and 13609 piglets. The effects of piglet, mother and nurse genes on piglet growth were estimated. The analyses were carried out using REML methodology applied to multivariate animal models. Heritabilities of reproduction traits were low, below 0.10. Piglet genes explained less than 2% of the phenotypic variability of preweaning growth. Maternal effects globally explained 30% of this variability, of which 2/3 were of genetic origin. The effects of the foster mother were the most important during lactation and at weaning, but the effects of the genetic mother remained significant up to weaning. Litter size at birth showed a genetic antagonism with birth to weaning mortality and maternal effects on piglet growth rate during the lactating period.