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Genetics of body weight and length of Large White piglets and relationship to maternal performance

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Abstract

Body weight and body metrics of newborn piglets reflect their level of development. We studied a Large White population raised in a single experimental herd. Survival and growth performance of 10,101 piglets originating from 689 litters were analysed. In 440 of these litters, 1,320 piglets contrasting for birth weight were recorded for body length and circumference. At piglet level, the estimated direct and maternal heritability values were $h^2_d=0.02$ and $h^2_m=0.13$ for birth weight, $h^2_d=0.65$ and $h^2_m=0.21$ for the ponderal index and $h^2_d=0.23$ and $h^2_m=0.01$ for the ratio of circumference to body length. The genetic correlation between the ponderal index and litter size and gestation length tended to be negative.

Introduction

The developmental status of piglets at birth largely determines their survival and growth to weaning. Intrauterine growth retardation results in piglets that are weaker at birth due to the brain-sparing effect, which is highlighted by a higher brain to organ ratio. Morphometric measurements can be used to measure maturity in addition to birth weight, which is only a partial indicator of maturity at birth. Studies using head characteristics of newborns have shown that developmental delay is influenced by genetics (Matheson et al., 2018). Measurements that combine weight and different lengths of the animal are associated with developmental differences. We worked on objective morphometric measurements, body length and thoracic circumference, obtained by intra-litter sampling. Firstly, analyses at the piglet level allow to disentangle direct genetic from maternal genetic effects. Secondly, although the measurements are at piglet level, growth retardation could be considered as a property of the mother, partly due to her uterine capacity and nutritional status at the end of gestation. In a second step, genetic relationships with litter size and gestation length of the sow, and litter growth during lactation were analysed.

Materials & Methods

Animals and data. Data were collected from the purebred Large White population raised at the INRAE GenESI experimental farm (doi: 10.15454/1.5572415481185847E12). The project received financial support from the French National Agency for Research (PIPETTE project, ANR-18-CE20-0018). Sows were managed under a batch farrowing system, with three weeks interval. Farrowing was not induced, and interventions including cross-fostering were highly limited. Piglet death was recorded daily. Each individual piglet, regardless of whether it was stillborn or alive, was weighed within 24h after birth. At the same time, three born alive piglets per litter were measured for body length (crown to rump) and circumference (thorax): the lightest, the one closest to litter mean weight, and the heaviest one. All piglets were weighed again at 3 wks of age. In this period, their growth depended solely on milk intake.

The sows were inseminated with semen from AI Large White boars from the French national scheme, and for which variability was maximised after 2018, over the period when morphometric measurements were recorded. Piglets were weaned at 4 weeks of age. Two data sets were constructed. The first data set included individual birth weight (IBW) and weight at weaning (IW3) from which was calculated the individual daily weight gain from birth to 3 weeks, as $IWG0-3 = (IW3-IBW)/\text{age at 3 wks (20}\pm\text{3 days)}$. From weight and metrics were calculated the density index, the body mass index, the ponderal index (PI), and the ratio of circumference to body length (ratioL). Litter growth traits, i.e., litter mean birth weight (MBW) and weight at 3 wks (MW3) and daily weight gain (IWG03) were calculated from individual records. Gestation length was recorded, in full days, as farrowing date minus successful mating date. Prolificacy included the number of piglets born in total (TNB) and that survived until weaning (SURV).

The data set contained data on 385 sows with 10,101 piglets born in 689 litters, of which 7,019 were weighed twice and measured at birth. Among sows, 67% had their own weight performance at birth and 3 weeks of age. The data set was augmented with litter records (all but morphometrics) collected from older and contemporary sows, from end of 2015 to end of 2021. All sows considered were raised in the same housing system, i.e., crate; and with same management practices. The pedigree file, based on sow pedigree and sire pedigree included 20,666 animals. The second data set included sow and litter records.

Statistical analysis. All analyses were carried out with the REML procedure of the ASReml software (Gilmour et al., 2015). The goodness of fit was used to compare nested models following a chi-square statistics. Models for analyses included the fixed effect of parity (5 levels) and year-month (54 levels). The gender effect (2 levels at birth, 3 levels at 3 wks) was included in all piglet analyses. For piglet traits including IBW, IWG03 and PI, the complete model (possible simplified to reach convergence) was:

$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}_D\mathbf{a}_D + \mathbf{Z}_M\mathbf{a}_M + \mathbf{V}\mathbf{c} + \mathbf{W}\mathbf{l} + \mathbf{e}$ where \mathbf{y} is the vector of observations; \mathbf{X} , \mathbf{V} and \mathbf{W} are known incidence matrices; \mathbf{b} is a vector for fixed effects; \mathbf{a}_D is a vector of direct additive genetic effects, and \mathbf{a}_M is a vector of maternal genetic effects. The model accounted for a covariance between direct and maternal genetic effects, using the variance structure

$$\begin{bmatrix} \mathbf{a}_D \\ \mathbf{a}_M \end{bmatrix} \sim MVN \left(\mathbf{0}, \begin{bmatrix} \sigma_{A_D}^2 & \sigma_{A_{DM}} \\ \sigma_{A_{DM}} & \sigma_{A_M}^2 \end{bmatrix} \otimes \mathbf{A} \right) \text{ where } \mathbf{A} \text{ denotes the matrix of additive genetic}$$

relationships with $\sigma_{A_D}^2$ and $\sigma_{A_M}^2$ respectively the direct and maternal additive genetic variances and $\sigma_{A_{DM}}$ the co-variance between direct and maternal genetic effects. Next, \mathbf{c} is a

vector of random permanent environmental effects of the dam, $\mathbf{c} \sim N(0, \mathbf{I}\sigma_c^2)$; \mathbf{l} is a vector of

random litter effects, $\mathbf{l} \sim N(0, \mathbf{I}\sigma_l^2)$; and \mathbf{e} is a vector of residuals, $\mathbf{e} \sim N(0, \mathbf{I}\sigma_e^2)$. \mathbf{Z}_D

and \mathbf{Z}_M are known incidence matrices for the direct and maternal genetic effects. The

phenotypic variance was calculated as $\sigma_P^2 = \sigma_{A_D}^2 + \sigma_c^2 + \sigma_l^2 + \sigma_{A_M}^2 + \sigma_e^2$

Analyses with a direct-maternal model were applied. Genetic and phenotypic correlations between piglet traits and between a piglet trait and a litter trait (NBT or GEST) were obtained from sets of bivariate analyses. To overcome convergence difficulties, the model could be simplified to a maternal model, considering only the random effects of the dam, i.e., genetics

and permanent environment. At the sow level, the data were analysed using a bi-trait linear model for the combinations of mean morphometric measurement and sow performance.

Results

The distribution of piglet IBW and PI according to IBW of sampled piglets is given in Figure 1. IBW ($\bar{x}=1.37$ kg SD 0.37) and PI ($\bar{x}=96.35$ SD 13.9) were negatively correlated ($y=-0.33x+96$; $R^2=0.0001$; $N=1320$). Mean TNB was 15.7 (SD 3.4).

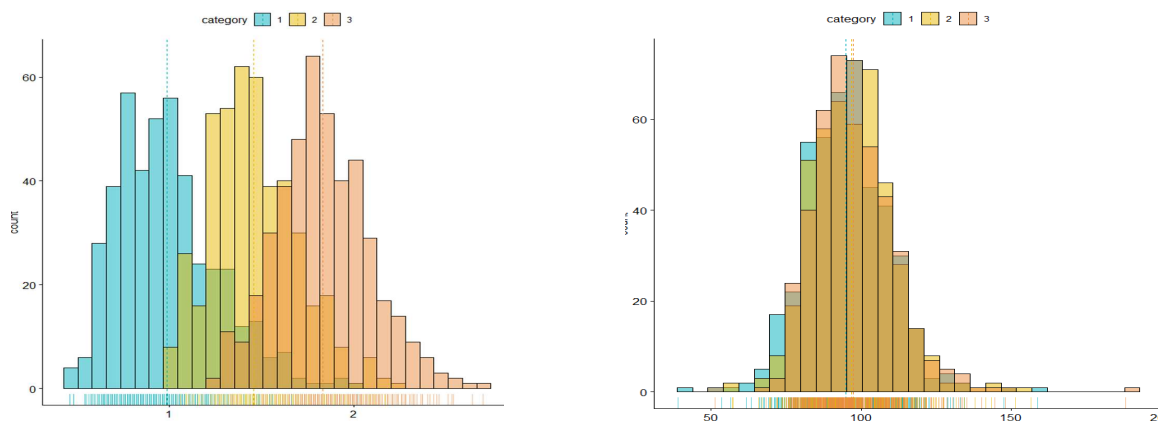


Figure 1. Distribution of piglet IBW (left graph) and PI (right graph) according to within-litter category (1: lightest, 2: mean, 3: heaviest in the litter).

The estimates of heritability and variance components for piglet traits are given in Table 1. Size of direct and maternal genetic effects on IWG03 was similar. The maternal heritability on IBW was higher than the direct heritability. Conversely, large direct genetic effects on PI were found, the piglet merit for achieving proper development at birth. Since PI depends on sow nutritional state in the end of the gestation phase, next we used models including only maternal effects.

Table 1. REML estimates of direct (h^2_d) and maternal (h^2_m) heritabilities and direct-maternal correlation (with SE) for piglet traits.

Estimates ^a	h^2_d	h^2_m	$r_{d,m}$	l^2 (%)	c^2 (%)
IBW	0.02 0.09	0.23 0.05	-0.22 0.61	11.2	1.4
IWG03	0.12 0.06	0.12 0.05	-0.35 0.28	6.7	6.4
PI	0.65 0.16	0.21 0.11	-0.76 0.01	ni ^b	7.8
ratioL	0.23 0.17	0.01 0.11	-0.01	13.9	0.5

^a l^2 and c^2 are respectively the part of phenotypic variance (%) that is explained by litter effects and sow permanent environment effects

^b effect not included (ni) in the model

Table 2. REML estimates of genetic (r_g) and phenotypic correlations (r_p) (with SE) between piglet PI (y_1 $h^2=0.09$ SE 0.05) and litter traits (y_2) from a sow model¹.

PI with	TNB	DGEST	MWB	MW3	DWG03	SURV
$r_{g\ y_1,y_2}$	-0.38 0.33	-0.33 0.33	-0.19 0.33	-0.31 0.37	-0.29 0.45	0.17 0.41
$r_{p\ y_1,y_2}$	-0.05 0.04	-0.04 0.03	0.04 0.04	0.05 0.04	0.02 0.03	-0.04 0.03
h^2 of y_2	0.26 0.09	0.28 0.08	0.30 0.09	0.20 0.07	0.12 0.03	0.17 0.08

¹ models for both traits included the fixed effects of parity and batch, and the random effects of the sow genetics and permanent environment

The estimates of genetic and phenotypic correlations between PI and sow traits are given in Table 2. The model for analyses included sow identity (i.e., maternal genetic effects) and permanent environment as random effects. Similar estimates were obtained with PI adjusted for litter size. At the genetic scale, although estimates were not precise, we observed a trend for the PI of piglets to be correlated positively with litter size at weaning. Negative relationships with litter growth were found. Litters with higher growth. The explanation may lie in higher losses in litters that include piglets of lower PI at birth. Sows with increased genetic merit for piglet PI have slower growth rate of their litter during lactation. PI was negatively correlated to NBT and DGEST at the genetic scale.

Discussion

The heritability for litter size was slightly higher than described in the literature. Heritability estimates for classic litter traits were in agreement with previous results (Banville et al., 2014; Matheson et al., 2018). We investigated new body measures with purposive intra-litter sampling. Unfortunately, many estimates were of low precision. The sampling of metric measurements limited our ability to test the effect of reach. Only the permanent environment of the mother (2-3 litters each) was considered. We obtained the first estimates for PI, a trait of interest that describes whether the newborn piglet was malnourished in utero, a metric also used in humans for diagnosing fetal growth disorders. Tabuaciri et al (2011) used different lines and averaged individual records (all measured litter piglets) in a litter trait. The heritability of PI on average was $h^2=0.07$ (0.08) and the antagonism with MBW was stronger than in the current study ($r_g=-0.56$ 0.61). Selection for litter size favours the production of piglets with lower PI, in agreement with the observation of delayed maturity in piglets born to Large White sows highly selected for prolificacy (Canario et al., 2007). Sows with genetic merit for longer gestation tend to produce piglets with lower PI.

Although known to be moderately heritable in adult pigs (Johnson and Nugent, 2003), we found very low heritability for the piglet density index ($h^2<0.01$) and that of the BMI was not estimable. Either these traits are not heritable in the current population or the sampling did not allow detecting their genetic component.

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