# Genetic Parameters For Direct And Maternal Effects On Litter Size And Weight Traits Of Iberian Pigs

*J. M. Corral*[*]*, M. Izquierdo*, J. Bazán*, D. Ayuso*,*
*N. Carolino†, L. T. Gama†, and J. A. Padilla‡*

## Introduction

The number of weaned pigs is related to litter size and litter homogeneity at birth, and it is of great economic interest for the Iberian pig industry. Genetic regulation of pig litter size is complex and the main component traits so far defined are ovulation rate, embryonic survival, uterine capacity, fetal survival and pre-weaning losses (Distl, 2007). Estimates of heritability of litter size are low. However, genetic variance for litter traits is large enough to expect them to be improved through selection (Chen et al., 2003). Also, genetic variation for preweaning piglet survival has been incorporated in some breeding programs (Cecchinato et al., 2008). The official breeding program of the Iberian pig breed does not include reproductive traits (Silió, 2000) but is considering to include them in the near future, because there is an important group of producers interested in improving these traits. For this reason, the Iberian Pig Breeder Association support this study, whose objetive is to estimate genetic parameters for litter size, litter survival and early piglet weights in the Iberian pig breed, in order to develop breeding strategies to improve litter size at weaning.

## Material and methods

**Data.** Litter size and weight records of purebred Retinto Iberian pigs were obtained from an experimental herd in SW Spain from 2005 to 2009. Data structure is described in Table 1 and includes a) reproductive traits: total number of piglets born (NBT), number of born alive (NBA) and number of weaned (NW); b) weight traits: litter weight at birth (LBW), individual birth weight (IBW), individual 21-day weight (W21), and individual weaning weight at 30 days of age (W30). Additionally, number of piglets born dead (NBD) and number of piglets dead before weaning (NWD) were computed. Animals were raised in extensive conditions and sows were confined in a farrowing crate facility for the farrowing and the lactation periods and no crossfostering was done. Data on W21 and W30 were collected exactly at the respective days of age. Data on piglet identification, sow age, birth date, sex and pedigree information were also collected.

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[*] Centro de Investigación Agraria Finca La Orden-Valdesequera, Junta de Extremadura. A-5, Km 372, Guadajira 06071 (Badajoz) Spain.

[†] Unidade de Investigação de Recursos Genéticos, Reprodução e Melhoramento Animal - INRB, I.P. Fonte Boa, 2005-048 (Vale de Santarém). Portugal.

[‡] Genética y Mejora Animal, Facultad de Veterinaria, Universidad de Extremadura. UEX Avda. de la Universidad s/n, 10071 (Cáceres) Spain.

**Statistical analyses.** Variance components and standard errors were estimated by restricted maximum likelihood (REML) using single trait animal models solved with the MTDFREML software (Boldman et al., 1995). Two animal models were used, one for litter traits (model 1), and a second model for individual piglet weights (model 2). Model 2 is similar to model 1 with the exception that maternal effects and the covariance between maternal and direct effects were computed.

***Model I:***

$$\boldsymbol{y = Xb + Za + Spe + e} \qquad [1]$$

Where:

$\boldsymbol{y}$ = vector of observations for litter traits on sows;

$\boldsymbol{X}$ = known incidence matrix relating observations in $\boldsymbol{i}$ to classes of fixed effects in $\boldsymbol{b}$;

$\boldsymbol{b}$ = vector of unknown contributions of fixed effects for classes of contemporary group, age of sow and sex of piglet;

$\boldsymbol{S}$ = known incidence matrix relating observations in $\boldsymbol{i}$ to classes in $\boldsymbol{pe}$;

$\boldsymbol{pe}$ = vector of unknown contributions of permanent environmental effects;

$\boldsymbol{Z}$ = known incidence matrix relating observations in $\boldsymbol{i}$ to classes in $\boldsymbol{a}$;

$\boldsymbol{a}$ = vector of unknown contributions of random additive genetic effects and

$\boldsymbol{e}$ = vector of unknown random residual effects;

Fixed effects included: a) contemporary group (year-season at farrowing), with 20 different classes, including 5 years (2005-2009) and 4 seasons; b) sow age at farrowing, with six classes (from 1 to 6 years; sows older than 6 years were included into class "6"); and c) sex of piglet, with two classes.

***Model II:***

$$\boldsymbol{y = Xb + Za + Wm + Spe + e} \qquad [2]$$

Where:

$\boldsymbol{y}$= vector of observations for individual piglet weights;

$\boldsymbol{W}$= known incidence matrix relating observations in $\boldsymbol{i}$ to classes in $\mathbf{m}$ and

$\boldsymbol{m}$= vector of random maternal additive genetic effects.

## Results and discussion

Many factors influence litter size at weaning, but the most important are birth weight, litter uniformity at birth (English and Morrison, 1984) and sow milk production. Results on the different traits studied are depicted in Table 1, which indicates a low mean for NBT, NBA and NW for this breed, in comparison with other breeds (Chen et al., 2003). Also NBD (1.32 piglets) and NWD (1.67 piglets) are high in this breed in comparison to results reported by, Chimonyo et al. (2006), who observed a mean NBD of 0.53 in the Mukota pig breed. The SD values for IBW, W21 and W30 indicate a phenotypic variation for these traits similar to those reported by other authors, who computed individual weights, as done in the present study. Thus, Chimonyo et al., (2006) reported a SD for IBW of 0.29 in Mukota breed and Damgaard et al., (2003) reported a SD for IBW and W21 of 0.23 and 1.07, respectively in purebred Yorkshire.

**Table 1: Means and standard deviations (SD) for different traits in the experimental herd of Iberian pigs**

| | NBT | NBA | NW | LBW (kg) | NBD | NWD | IBW (kg) | W21 (kg) | W30 (kg) |
|---|---|---|---|---|---|---|---|---|---|
| Mean | 8.75 | 7.43 | 5.96 | 10.30 | 1.32 | 1.67 | 1.21 | 4.72 | 6.52 |
| S.D. | 2.53 | 2.48 | 2.20 | 3.05 | 1.52 | 1.85 | 0.24 | 1.10 | 1.53 |
| N° of Observations | 654 | 654 | 635 | 654 | 654 | 635 | 2951 | 3774 | 3603 |
| N° of Sows | 261 | 261 | 216 | 253 | 261 | 216 | 237 | 255 | 251 |

Number of piglets born (NBT); Number Born Alive (NBA); Number Weaned (NW), Litter weight at birth (LBW); Number of piglets Born Dead (NBD); Number of piglets Dead before Weaning (NWD); Individual Birth Weight (IBW); Weight to 21 days of age (W21); Weaning Weight at 30 days of age (W30).

Results in Table 2 describe the different variance components and genetic parameters for the studied traits. Environmental variances of reproductive traits are large in relation to genetic variance, thus heritability estimates of these traits are low, as it was expected. Similar results were obtained by Chen et al. (2003) in Yorshire, Duroc, Hampshire and Landrace breeds, and by Fernández et al. (2008) in Iberian pigs. On the other hand, permanent environmental variances are medium-high in magnitude and therefore, there is a moderate repeatability for these trait as compared to repeatabilities reported by Chen et al. (2003). Permanent environmental variances for mortality traits are close to 0. Therefore, the heritabilities were similar to the repetabilities and very low in magnitude, similarly to the results obtained by Chimonyo et al. (2006). Permanent environmental variances also explain the average variance between families (Gama et al., 2004).

In relation to weights, the heredability estimate for IBW was lower than the values reported by Chimonyo et al., (2006). In contrast, the heritability estimates for W21 were similar to those reported by Fernández et al. (2008). Only a few studies reported the genetic correlation between direct and maternal effects for individual weights in piglets, because most of the studies computed litter weight instead of individual weights. In the present study, genetic correlations between direct and maternal effects for W21 and W30 were high in magnitude and negative, therefore, to select for sow maternal hability, maternal and direct components and the covariance between them should be included in the selection model.

## Conclusion

Although heritabilities for litter traits were low, these did not differ from results reported for other breeds and, thus genetic change can be expected when selecting for these traits. Repeatability for litter size traits were medium. Heritabilities for piglet weight were moderate, and similar to estimates from other breeds. However, the genetic covariance between direct and maternal effects were high in magnitude and negative and therefore, maternal effects should be included in the genetic model if genetic progress want to be achieved either for maternal hability or for piglet individual growth.

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**Table 2: Estimates of (co) variance components and genetic parameters of litter size and weight for univariate analyses using models [1] and [2]**

| | Model I | | | | | | Model II | | |
|---|---|---|---|---|---|---|---|---|---|
| | NBT | NBA | NW | LBW | NBD | NWD | IBW | W21 | W30 |
| $\sigma^2_a$ | 0.4220 | 0.0874 | 0.3685 | 0.4313 | 0.1803 | 0.2775 | 0.0057 | 0.2396 | 0.9181 |
| $\sigma^2_m$ | | | | | | | 0.0042 | 0.2527 | 0.4597 |
| $\sigma_{am}$ | | | | | | | 0.0003 | **-0.1738** | **-0.4795** |
| $\sigma^2_{pe}$ | 1.2789 | 1.1858 | 1.0339 | 2.1547 | 0.0050 | 0.0000 | 0.0054 | 0.1099 | 0.3091 |
| $\sigma^2_e$ | 4.1576 | 4.4555 | 3.4107 | 5.2982 | 2.0447 | 3.0653 | 0.0380 | 0.7688 | 1.2888 |
| $\sigma^2_p$ | 5.8584 | 5.7287 | 4.8131 | 7.8841 | 2.2300 | 3.3428 | 0.0536 | 1.1971 | 2.4963 |
| $h^2_a$ | 0.07 | 0.02 | 0.08 | 0.05 | 0.08 | 0.08 | 0.11 | 0.20 | 0.37 |
| | (0.07) | (0.05) | (0.07) | (0.06) | (0.05) | (0.06) | (0.05) | (0.06) | (0.09) |
| $h^2_m$ | | | | | | | 0.08 | 0.21 | 0.18 |
| | | | | | | | (0.06) | (0.08) | (0.08) |
| $r_{am}$ | | | | | | | 0.06 | **-0.71** | **-0.74** |
| | | | | | | | (0.52) | (0.19) | (0.14) |
| r | 0.2903 | 0.2222 | 0.2914 | 0.3280 | 0.0831 | 0.0830 | 0.2854 | 0.5030 | 0.6758 |

$^{\alpha}$ $\sigma^2_a$ Animal genetic variance; $\sigma^2_m$ maternal genetic effect; $\sigma_{am}$ covariance between animal genetic and maternal genetic effects; $\sigma^2_{pe}$ permanent environmental variance; $\sigma^2_e$ residual variance; $\sigma^2_p$ phenotypic variance; $h^2_a$ direct heritability; $h^2_m$ maternal heritability (standard error) in brackets; $pe^2$ fraction of variance due to permanent environmental effects; r repeatability; and $r_{am}$ genetic correlation between direct and maternal effects.

Number of piglets born (NBT); Number Born Alive (NBA); Number Weaned (NW), Litter weight at birth (LBW); Number of piglets Born Dead (NBD); Number of piglets Dead before Weaning (NWD); Individual Birth Weight (IBW); Weight to 21 days of age (W21); Weaning Weight at 30 days of age (W30).

## References

Boldman K.G., Kriese L.A., van Vleck L.D. *et al.* (1995). In A manual for use of MTDFREML. A set of programs to obtain estimates of variances and covariances [Draft], USDA-ARS, Lincoln, NE.

Cecchinato, A., Bonfatti, V. Gallo, L. *et al.* (2008). *J. Anim. Sci.*, 86 (10): 2486-95

Chen, P., Baas, T.J., Mabry, J. W. *et al.* (2003). *J. Anim. Sci.*, 81:46-53.

Chimonyo, M., Dzama, K., Bhebhe, E. (2006). *Livestock Science*, 105: 69-77.

Damgaard, L. H., Rydhmer, L., Lovendahl, P. *et al.* (2003). *J. Anim. Sci.*, 81: 604-610.

Distl, O. (2007). *Reprod. Domest. Anim.*, 42 Suppl 2: 10-6.

English, P.R., and Morrison, V. (1984). Causes and prevention of piglet mortality. *Pig News* Info, 5:369-376.

Fernández, A., Rodrigáñez, J. Zuzúarregui, J. *et al.* (2008). *Spanish Journal of Agricultural Research,* 6: 98-106.

Gama, L.T., Matos, C., Carolino, N. (2004). In Modelos mistos em melhoramento animal. Ed. Direcçåo Geral Veterinária. Arquivos Veterinários nº 7.

Silió, L., Iberian pig breeding programme. In Developing breeding strategies for lower input animal production environments. (2000) Galal S., Boyazoglu J., Hammond K. (eds) ICAR Technical Series, Roma, pp. 511-520.