

Crossbreeding effects and genetic parameters on piglet survival from three Iberian strains

N. Ibáñez-Escriche*, L. Varona†, E. Magallon‡ and J.L. Noguera*

* IRTA, Catalonia, Spain, †Universidad de Zaragoza, Spain, ‡ Inga Food S.A. – Nutreco, Spain

ABSTRACT: Data from a 3 × 3 full diallelic cross experiment with three contemporary Iberian pig strains were used to study the genetic parameters and crossbreeding effects affecting piglet survival. The data set comprised 11,150 records of individual piglet mortality until weaning collected from 1,127 litters during 2010-2013. The three strains and their reciprocal crosses were represented in data set. The genetic analysis was performed using a Bayesian threshold model with three categories (survive until weaning, dead before weaning, stillbirth). Results showed a substantial genetic variability at the piglet and maternal level with heritabilities of 0.09 and 0.08, respectively. Crossbreeding parameters revealed important differences between lines for piglet survival. A positive heterosis was estimated for all crosses. The most outstanding example was the cross between *Entrepelado* and *Torbiscal* with a reduction of 5% and 8% on stillbirth and pre-weaning mortality, respectively.

Keywords: Piglet survival; Iberian pig; Genetics; Threshold model

Introduction

Piglet survival is an important trait from pig producer and animal welfare perspectives. It can be defined as the survival of fully formed piglets at the end of gestation until weaning and, includes therefore, farrowing and pre-weaning survival (Knol et al., 2002). It is known that direct and maternal genetic effects have influence in piglet survival (e.g., Arango et al., 2006; Su et al., 2008) and the relative importance of each source of genetic variation is variable among the different genetic lines (Ibáñez-Escriche et al., 2009). Additionally, differences of stillbirth incidence between purebred and crossbred litters have been reported before in the literature (reviewed by Blasco et al., 1995). In general, crossbred litters have a lower stillbirth incidence than purebred litters (eg. Bae and Park, 1985; Bidanel et al., 1989).

Iberian pig breed is an autochthonous population of the Iberian Peninsula which is mainly focused on obtaining the raw material for cured meat products of top quality and price (Fernández et al., 2003). The development of organized breeding programs is scarce and relatively recent in the Iberian pig breed (Silió, 2000). Moreover, the pyramid crossbreeding system that allow exploit both heterosis and line complementarity is practically absent in these populations. Its implementation Iberian pig breeding schemes has the potential to significantly improve its global perfor-

mance. Therefore, the aim of this study was to estimate the genetic parameters and crossbreeding effects of piglet survival using a threshold model from a 3 x 3 full diallelic cross experiment performed on three contemporary Iberian pig strains and under intensive management.

Materials and Methods

Populations and Data Source. The Research Ethics Committee of IRTA approved all management and experimental procedures involving live animals. The data sets used in this study came from a designed diallelic experiment involving three Iberian strains: *Retinto* (RR), *Torbiscal* (TT) and *Entrepelado* (EE) and their reciprocal crosses. During the experiment, animals were kept in intensive commercial pig breeding conditions. The complete data set consisted on piglet mortality records until weaning of 11,150 piglets collected from 1,127 litters during 2010-2013 and where the three strains and their reciprocal crosses were represented. The number of data, breed distribution and the summary statistics for all traits are presented in Tables 1 and 2.

Table 1. Distribution of litters and piglets (between brackets) by crosstype.

	Strain [§]	Boars		
		R	T	E
Sows	R	111 (949)	243 (2076)	82 (661)
	T	416 (3248)	146 (1122)	61 (488)
	E	22 (173)	9 (67)	37 (296)

[§]R: Retinto; T: Torbiscal; E: Entrepelado.

Table 2. Mean and coefficient of variation (CV) for total number of piglets born and percentage of mortality at birth (%MB) and from birth to weaning (%MBW).

Mean	CV	% MB	%MBW
8.06	19.84	5.79	10.72

Statistical analyses. A Bayesian threshold animal model with maternal genetic effects was fitted to analyze the piglet survival from birth to weaning of Iberian piglets in 3 × 3 diallelic experiment. The assumed model for the liability **l** of the piglet survival was,

$$l = Xb + Z_d a_d + Z_m a_m + W_l c_l + e$$

where \mathbf{b} represents the systematic effects of sex (male or female), year-season (20 levels), litter size (8 levels, less than 5, from 5 to 10, 11 or more piglets), order of parity (6 levels, first to fifth, sixth or more parities), and, according to the model of Dickerson (1969), direct line effect (3 levels), dam line effect (3 levels) and direct heterotic effects for the crosses (three levels), \mathbf{a}_d is the vector of direct additive genetic effects (11,150 levels), \mathbf{a}_m is the vector of maternal additive genetic effects (539 levels), \mathbf{c}_l is the vector of common litter effects (1,127 levels), \mathbf{e} is the vector of residuals, and \mathbf{X} , \mathbf{Z}_d , \mathbf{Z}_m and \mathbf{W} are known incidence matrices that link the fixed and random sources of variation to the liability, respectively. The response in the piglet survival at weaning (y) was modeled as:

$$f(y|l) = \prod_{i=1}^n f(y_i|l_i) = \prod_{i=1}^n [1(l_i < t_i)(y_i = 1) + 1(l_i > t_i)(y_i = 2) + 1(l_i > t_i)(y_i = 3)],$$

and

$$f(\mathbf{l}|\mathbf{b}, G, \sigma_e^2) = N(\mathbf{X}\mathbf{b} + \mathbf{Z}_d\mathbf{a}_d + \mathbf{Z}_m\mathbf{a}_m + \mathbf{W}\mathbf{c}_l, \mathbf{I}\sigma_e^2)$$

Where y_i ($i=1,2,\dots,n$) is the i th phenotypic observation with categories 1 (survive until weaning), 2 (dead before weaning) and 3 (stillbirth), n is the total number of data, l_i is its corresponding liability and t is the threshold that defines the categories of the response. Multivariate Gaussian distributions with mean 0 and variances $\mathbf{I}\sigma_{c_l}^2$, $\mathbf{A}\sigma_{ad}^2$ and $\mathbf{A}\sigma_{am}^2$ were assumed for \mathbf{c}_l , \mathbf{a}_d and \mathbf{a}_m , where \mathbf{I} and \mathbf{A} are the identity and numerator relationship matrix, respectively. The genetic correlation between \mathbf{a}_d and \mathbf{a}_m was fitted to zero because it was not identifiable due the absent of mother's records. Uniform bounded priors were assigned for \mathbf{b} and for the variance components. Bayesian analysis was implemented with a data augmentation step for the liability, following Sorensen et al. (1995). Marginal posterior distributions of all unknowns were estimated using the Gibbs sampling algorithm (Geman and Geman, 1984). After exploratory analyses, we used a total of 100,000 samples for each analysis, with a burning period of 10,000.

Results and Discussion

Genetic parameters. Estimates of the marginal posterior distributions of the heritabilities and the proportion of the phenotypic variance due to common litter effects for piglet survival in the Iberian strains are presented in Table 4. Results showed a substantial genetic variability at the piglet (0.09) and maternal level (0.08). The maternal heritability is in agreement with most of the studies in which farrowing survival and pre-weaning survival have been analyzed as a threshold model (e.g. Knol et al., 2002; Arango et al., 2006; Su et al., 2008). However, the piglet survival heritability is higher than in most of these studies, and is only in the range of the results reported by Roehe et al. (2009) under outdoor conditions and Ibañez-Escriche et

al. (2009) for farrowing survival in a Pietrain population. In our case, the experiment was performed in intensive commercial pig breeding conditions. Therefore, this result cannot be attributed to a higher genetic contribution to their survival under outdoor conditions. A most plausible explanation of our result is that the small litter size (8.06) of Iberian pigs would allow a higher piglet genetic ability to express survive than in the case of populations with large litter size (Knol et al., 2002; Ibañez-Escriche et al., 2009).

Table 3. Posterior mean (Mean) and standard deviation (sd) of the direct and maternal heritabilities (h_d^2 and h_m^2) and proportions of the phenotypic variance due to common litter effects (c_l^2) for piglet survival.

	h_d^2	h_m^2	c_l^2
Mean	0.09	0.08	0.10
sd	0.02	0.01	0.01

Table 4. Features of the estimated marginal posterior distribution of the crossbreeding effects for piglet survival: differences between direct line (gI) and maternal line effects (gM) and direct heterosis effect (hI).

Effect	Mean	sd	P*>0
gI _{E-T} [§]	0.99	0.52	0.97
gI _{E-R}	0.79	0.51	0.94
gI _{T-R}	0.20	0.23	0.81
gM _{E-T}	-0.98	0.38	0.01
gM _{E-R}	-0.82	0.36	0.02
gM _{T-R}	-0.16	0.16	0.84
hI _{ET}	0.88	0.26	1.00
hI _{ER}	0.25	0.21	0.88
hI _{TR}	0.21	0.10	0.98

[§]R: Retinto strain; T: Torbisical strain; E: Entrepelado strain.

*P>0: Probability of the posterior value being greater than zero.

Crossbreeding parameters. Results from crossbreeding parameters (Table 4) revealed important differences between lines for piglet survival in the liability scale. The E strain showed superior values of direct line effect than strains R and T. In contrast, E strain showed the lowest dam line effect whereas T strain showed the highest one. It would imply a higher mother ability of T strain in terms of piglet survival. At the same time, a positive direct heterosis (hI) was achieved for all crosses, being the cross between E and T strains which scored the highest posterior mean value with 0.88 in the liability scale. This hI represents a reduction of 5% and 8% on stillbirth and pre-weaning mortality, respectively, of the population studied. These results reveal a higher piglet survival on crossbred litters than in purebred one, in agreement with previous results reported in "white" pig populations (reviewed by Blasco et al., 1995). Further, our hI results were similar to those reported by Bidanel et al. (1989) in a crossbreeding experiment performed on distantly related breeds such as Meishan and French Large White. It could be explained to the high rate of inbreeding of these strains (Fabel et al., 2004) coupled with the presence of relevant non-additive effects in the genetic deter-

minism of the analyzed trait. However, further studies are needed in order to support these findings.

Conclusion

These results suggest the existence of a genetic determinism from both, the piglet and its dam, affecting piglet survival in these Iberian pig populations. Both, piglet and dam genetic effects showed a substantial genetic variability which support the feasibility of reducing piglet survival by selection. On the other hand, crossbreeding parameters showed significant differences between strains and crosses. These results suggest that the establishment of a suitable crossbreeding system in Iberian pig breeding schemes may be worthy. In this context, the ET cross showed a clear superiority for piglet survival due the direct heterosis effect achieved between these strains.

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