

Genetics parameters and crossbreeding effects of prolificacy in three commercial lines of Iberian pigs

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Summary

The aim of this study was to estimate the variance components and the crossbreeding effects on prolificacy in a full diallelic cross between three Iberian pig lines with the aim of developing appropriate breeding strategies. We used phenotypes (total number of piglets born – TNB- and number born alive –NBA-) from 2.771 sows (10,936 parities) representing a 3 × 3 full diallelic experiment involving Retinto (RR), Torbiscal (TT) and Entrepelado (EE) populations. Data were analyzed with a Bayesian repeatability multi-breed animal model that include the crossbreeding parameters of the Dickerson model (direct and maternal line effects and heterosis between line pairs) and used a pedigree of 3158 individuals. The expected performance of each combination was calculated as the sum of direct, maternal and the heterosis effects. The results indicated that heritability was heterogeneous between populations, ranging from 0.04 to 0.14 for TNB and 0.02 to 0.12 for NBA. In addition, the crossbreeding parameters showed relevant differences between lines. The direct effects for the RR line for TNB and NBA were higher than for the E and T lines, whereas maternal effects were very heterogeneous, ranging between -0.32 for TNB and -0.28 for NBA (RR population) to + 0.31 for TNB and + 0.25 for NBA (EE population). The results for heterosis were clearly positive and they range between 0.26 (E × R) to 0.80 (E × T) piglets for TNB and between 0.24 (E × R) to 0.76 (E × T). Given the crossbreeding parameters, the R (paternal line) × E (maternal line) was the best cross for both TNB and NBA with a posterior probability 0.74 for TNB and 0.73 for NBA.

Keywords: prolificacy, diallelic cross, genetic parameters, crossbreeding, Iberian pig

Introduction

The Iberian pig strains are worldly recognized as some of the populations with best meat quality. This is a key factor for its preservation, as they have lower growth and feed efficiency (Barea et al., 2011) or prolificacy (Silió et al., 2001) when compared with other commercial pig populations. Nevertheless, the Iberian pig-meat sector has suffered a profound transformation involving the disappearance of traditional producers and their replacement by intensive management farms. Under this scenario, the improvement of the reproductive efficiency becomes relevant for its future economic viability.

Genetic improvement of litter size can be achieved with two non-exclusive strategies:

1) within line selection and 2) appropriate crossbreeding between lines to exploit heterosis. Traditionally, the genetic improvement for litter size in the Iberian population has been scarce (Fernández et al., 2008) and the Iberian pig producers have not used crossbreeding as they breed exclusively one of the available lines within the Iberian breed (Martínez et al., 2000). This is in strong divergence with other commercial pig populations, where selection efforts for prolificacy has been huge in dam lines during the last decades, and crossbreeding is a standard procedure (Dekkers et al., 2011).

The aims of this study were to perform a 3 x 3 diallelic experimental design (Hayman, 1954) between 3 contemporary commercial lines of Iberian pig, under intensive managements conditions, as well to estimate additive genetic variation and heritability and crossbreeding parameters (direct, maternal, and heterosis) on prolificacy as defined by the Dickerson model (Dickerson, 1969). The final objective of the results is to contribute to the definition of appropriate genetic improvement strategies within a pyramidal breeding program.

Material and methods

All animal procedures were performed according to the Spanish Policy for Animal Protection RD1201/05, which meets the European Union Directive 86/609 about the protection of animals used in experimentation, and were previously approved by the research ethics committee of the Institute for Food Research and Technology (IRTA).

Animals and experimental design.

The data sets used in this study consist of 10,936 records for *TNB* (Total Number Born) and *NBA* (Number Born Alive) from 2,771 sows. They were generated in a full diallelic experiment between three stains of Iberian pig (Retinto [RR]- Torbiscal [TT] and Entrepelado [EE]) and their reciprocal crosses (Retinto × Torbiscal [RT], Torbiscal × Retinto [TR], Retinto × Entrepelado [RE], Entrepelado × Retinto [ER], Torbiscal × Entrepelado [TE] and Entrepelado × Torbiscal [ET]). The number of sows and data and their breed distribution is presented in Table 1, and a more detailed description of their characteristics is given by Ibañez-Escriche et al. (2006). In addition, the pedigree for each animal was traced back 3 generations and 3158 individuals were included in the analysis.

Statistical analyses.

The statistical analyses of *TNB* and *NBA* were performed using a repeatability multi-population model, following the procedure described by Garcia-Cortés and Toro (2006), which divide the additive genetic effects into separate fractions depending on their genetic origin. The model was:

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \sum_{i=1}^3 \mathbf{Z}_i \mathbf{a}_i + \mathbf{W}\mathbf{p} + \mathbf{e}$$

where \mathbf{y} is the vector of observations (*NBA* or *TNB*), \mathbf{b} is a vector of systematic effects (order of parity, farm-year-season, male breed and line, maternal and heterosis effects), \mathbf{a} is the vector of additive genetic effects nested within genetic line (3,158 levels), \mathbf{p} is the vector of the permanent effect of the sow (2,771 levels), and \mathbf{e} is the residual error vector; \mathbf{X} , \mathbf{Z} , and \mathbf{W} are known incidence matrices related, respectively, fixed and random effects with vector \mathbf{y} .

The prior distributions for the random effects (\mathbf{a} , \mathbf{p} and \mathbf{e}) were multivariate Gaussian distributions. Bayesian analyzes were carried out by a *Gibbs sampling* algorithm with a single chain of 525,000 iterations and a period of "burn-in" of 25,000 iterations.

Results and Discussion

Variance components.

The statistical model used "multi-population" based on the method of García-Cortés and Toro, (2006), allowing the additive variance to split into separate independent parts depending on the genetic origin of the animals. Thus, posterior estimates of heritability for each strain (EE, RR, TT) for TNB and NBA are given in Table 2. The EE line has greater heritability (0.14 for TNB and 0.12 for NBA), followed by TT (0.11 and 0.10, respectively). These estimates were higher than those obtained in the Iberian populations (Pérez-Enciso and Gianola., 1992; García-Casco, et al, 2012), and within the range as those estimated for the most common breeds of white pig (Bidanel, 2011). However, the estimated heritabilities in line RR were lower, and similar to the obtained by Pérez-Enciso and Gianola (1992). With regards to coefficient of permanent environmental effect (p^2), we obtained a posterior mean estimate of 0.04, lower than the estimates of García-Casco et al. (2012).

Cross-breeding parameters.

The results of the crossbreeding parameters (Table 3) showed relevant differences between lines. The RR line presented the highest direct effects, whereas the EE population was clearly the best in the maternal effects. The posterior estimates of heterosis were always positive, although the ET combination was clearly the one with the highest values. When combined, the results indicated that the RE combination was the one with the highest expected performance for TNB (+0,59) and NBA (+0,54) with probability of 0.744 and 0.733, respectively, with respect to the mean of the estimated marginal posterior means of the differences in genetic types effect. The range of the differences of the 8 genetic types with respect to RE was between -1.34 (TT) and -0.29 (ET) for NT. Similar values were obtained for NV. The EE line has a difference with respect to RE of -0.83 NT and -0.73 NV. The differences of the RR line with respect to RE were -0.56 NT and -0.51 NV.

Conclusion

The results of this study indicate that there is enough genetic variability for selection for litter size in the EE and TT populations and that crossbreeding can provide a substantial improvement of reproductive efficiency. Moreover, they also suggest that the RE cross maximize the reproductive performance. This study reinforces the idea of the importance of implementing a pyramidal scheme for the genetic improvement of the Iberian pig populations.

*Table 1. Distribution of the number of sows (number of parities) by cross type in the diallelic experiment: pure lines (EE, RR, TT) in the diagonal and crossed (ER, ET, RE, RT, TE, TR) * outside the diagonal.*

Paternal ↓ / Maternal →	Entrepelado (EE)	Retinto (RR)	Torbiscal (TT)
Entrepelado (EE)	365 (1164)	247 (674)	172 (526)
Retinto (RR)	86 (255)	645 (2971)	402 (1597)
Torbiscal (TT)	34 (96)	359 (1537)	448 (2116)

* Paternal Line × Maternal Line

Table 2. Mean of the estimated marginal posterior means of heritability (h^2) for the total number of piglets born (TNB) and born alive (NBA). Values between brackets are the corresponding posterior SD.

Traits	Entrepelado (EE)	Retinto (RR)	Torbiscal (TT)
TNB	0.14 (0.033)	0.034 (0.016)	0.11 (0.026)
NBA	0.12 (0.031)	0.020 (0.013)	0.10 (0.024)

Table 3. Mean of the estimated marginal posterior distribution of the differences for the direct effect (L) and maternal (M) of the Entrepelada (EE), Torbiscal (TT) and Retinto (RR) lines, referring to the effects average of the three lines, and the heterosis (H) from crosses between these lines for TNB and NBA traits. Values between brackets are the corresponding posterior SD.

TRAITS	L _{EE}	L _{TT}	L _{RR}	M _{EE}	M _{TT}	M _{RR}	H _{ET}	H _{ER}	H _{TR}
TNB	-0.215 (0.242)	-0.420 (0.189)	0.635 (0.157)	0.313 (0.132)	0.010 (0.114)	-0.323 (0.086)	0.795 (0.186)	0.260 (0.146)	0.472 (0.111)
NBA	-0.099 (0.236)	-0.485 (0.186)	0.584 (0.148)	0.247 (0.131)	0.029 (0.113)	-0.277 (0.083)	0.755 (0.185)	0.240 (0.143)	0.507 (0.110)

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