Bayesian analysis of paternal and maternal gametic effects in a Reciprocal Cross between two Iberian varieties

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Abstract

INGA FOOD, S. A. company has developed a crossbreeding scheme between two Iberian varieties (Retinto and Entrepelado) to generate a F_1 hybrid sow. A previous study has detected differences in the reproductive performance (litter size) across the two reciprocal crosses, suggesting the presence of imprinting effects. In this study, we developed a multivariate gametic model able to estimate the gametic correlations among the paternal and maternal effects generated from any of the two genetic origins. Gametic correlations significantly lower than one would explain the differences in performance across reciprocal crosses. The results indicated that, despite the small amount of available information, the estimates of the gametic correlation between paternal and maternal effects are smaller in the Entrepelado than in the Retinto populations. This would explain the differences in performance among the reciprocal crosses.

Introduction

The Iberian pig breed is recognized for their perfect adaptation to the "Dehesa" environment and the high quality of its products (Serra et al., 1998), Traditionally, the Iberian pig production was developed with purebred varieties and extensively. However, in recent decades, many traditional production systems have been replaced by intensive farms using crossbreeding with Duroc sires to improve growth and efficiency at final product (Serrano et al., 2008). Regulatory norms of Iberian pig production allow this cross, as long as the sow is Iberian. The reproductive performance of the Iberian sows is lower than in white pig populations (Silio et al., 2001). INGA FOOD, S. A. company developed a crossbreeding scheme between two Iberian varieties (Retinto and Entrepelado) to generate a F_1 hybrid sow associated with a relevant heterosis (Noguera et al., 2019). However, that study identified strong differences in performance between both reciprocal crosses (Entrepelado × Retinto –ER- vs Retinto × Entrepelado –RE-). Therefore, the aim of this study is to develop a multivariate gametic model able to estimate the paternal and maternal gametic contributions of the Retinto and Entrepelado varieties in the ER and RE crosses and the correlations among them.

Materials & Methods

Phenotypic and Genomic Data. The phenotypic data used in this study consisted of number of piglets born alive -NBA- from 206 Entrepelado × Retinto and 134 Retinto × Entrepelado sows. A summary of the data is presented in Table 1.

Table 1. Number of records (and sows between brackets), mean and standard deviation of the traits for Entrepelado × Retinto and Retinto × Entrepelado crosses.

	Entrepelado × Retinto	Retinto × Entrepelado
N[1] (NS)[2]	1,258 (206)	700 (134)
NBA[3]	8.77 ± 2.24	8.84 ± 2.37

[1] N: Number of records
[2] NS: Number of sows
[3] NBA: Number Born Alive

Genotypes for all sows were generated using the GeneSeek® GPP Porcine 70K HDchip (Illumina Inc., USA). The filtering consisted of excluding genotypes with a minor allele frequency lower than 0.05 and a SNP call rate less than 0.90 in the overall population. Subsequently, 33,875 SNP markers were used to calculate the paternal and maternal phases using the AlphaPhase software (Hickey et al., 2011).

Statistical Model. Data were analyzed with the following model:

$$\begin{bmatrix} \mathbf{y}_{ER} \\ \mathbf{y}_{RE} \end{bmatrix} = \begin{bmatrix} \mathbf{X}_{ER} & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_{RE} \end{bmatrix} \begin{bmatrix} \mathbf{b}_{ER} \\ \mathbf{b}_{RE} \end{bmatrix} + \begin{bmatrix} \mathbf{W}_{ER} & \mathbf{0} \\ \mathbf{0} & \mathbf{W}_{RE} \end{bmatrix} \begin{bmatrix} \mathbf{s}_{ER} \\ \mathbf{s}_{RE} \end{bmatrix} + \begin{bmatrix} \mathbf{Z1}_{ER} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z1}_{RE} \end{bmatrix} \begin{bmatrix} \mathbf{p}_{E} \\ \mathbf{p}_{R} \end{bmatrix} + \begin{bmatrix} \mathbf{Z2}_{ER} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z2}_{RE} \end{bmatrix} \begin{bmatrix} \mathbf{m}_{R} \\ \mathbf{m}_{R} \end{bmatrix} + \begin{bmatrix} \mathbf{e}_{ER} \\ \mathbf{e}_{RE} \end{bmatrix}$$

where $\mathbf{y}_{ER}$ and $\mathbf{y}_{RE}$ are the vectors of phenotypic records, $\mathbf{b}_{ER}$ and $\mathbf{b}_{RE}$ are systematic effects that include order of parity with 5 levels (first, second, third, fourth and five or more) and herd-year-season with 25 levels, $\mathbf{s}_{ER}$ and $\mathbf{s}_{RE}$ are the permanent sow environmental effects, $\mathbf{p}_E$ and $\mathbf{p}_R$ and $\mathbf{m}_E$ and $\mathbf{m}_R$ are the gametic paternal ($\mathbf{p}$) and maternal ($\mathbf{m}$) effects of Entrepelado and Retinto, respectively, and $\mathbf{e}$ are the vector of residuals. Further $\mathbf{X, W, Z1}$ and $\mathbf{Z2}$ are the corresponding incidence matrices. The prior distribution of the permanent sow environmental effects is:

$$\begin{bmatrix} \mathbf{s}_{ER} \\ \mathbf{s}_{RE} \end{bmatrix} = N(\mathbf{0}, \mathbf{I} \otimes \mathbf{H}) \text{ where } \mathbf{S} = \begin{bmatrix} \sigma^2_{sER} & 0 \\ 0 & \sigma^2_{sRE} \end{bmatrix}$$

and the prior distributions of the gametic effects are:

$$\begin{bmatrix} \mathbf{p}_{E} \\ \mathbf{m}_{E} \end{bmatrix} = N(\mathbf{0}, \mathbf{G}_{E} \otimes \mathbf{V}_{E}) \text{ and } \begin{bmatrix} \mathbf{p}_{R} \\ \mathbf{m}_{R} \end{bmatrix} = N(\mathbf{0}, \mathbf{G}_{R} \otimes \mathbf{V}_{R})$$

where $\mathbf{G}_E$ and $\mathbf{G}_R$ are the gametic relationship matrices of the Entrepelado and Retinto populations computed as defined by Nishio and Satoh (2015):

$$\mathbf{V}_{E} = \begin{bmatrix} \sigma^2_{pE} & \sigma_{pmE} \\ \sigma_{pmE} & \sigma^2_{mE} \end{bmatrix} \text{ and } \mathbf{V}_{R} = \begin{bmatrix} \sigma^2_{pR} & \sigma_{pmR} \\ \sigma_{pmR} & \sigma^2_{mR} \end{bmatrix}$$

where σ^2_{pX} and σ^2_{mX} are the paternal and maternal variances of the $\mathbf{X}=\{E,R\}$ population, and σ_{pmX} is the covariance between them. The analysis was performed using the *gibbsf90* software (Misztal et al., 2018) using a single chain of 5,000,000 iterations after discarding the first 1,000,000.

Results
The results of the posterior entail (and standard deviation) estimates of the variance components are presented in Table 2.

Table 2. Posterior mean (and standard deviation) estimates of variance components.

Variance Components	Population	
	Entrepelado × Retinto	Retinto × Entrepelado
σ_s^2	0.119 (0.086)	0.344 (0.185)
σ_p^2	0.218 (0.099)	0.229 (0.101)
σ_m^2	0.288 (0.145)	0.273 (0.133)
σ_e^2	4.270 (0.186)	4.660 (0.277)

σ_s^2 : sow permanent environmental variance
σ_p^2 : paternal gametic variance
σ_m^2 : maternal gametic variance
σ_e^2 residual variance

In addition, the posterior distribution of the genetic correlation between paternal and maternal effects in the Entrepelado and Retinto populations are presented in Figure 1.
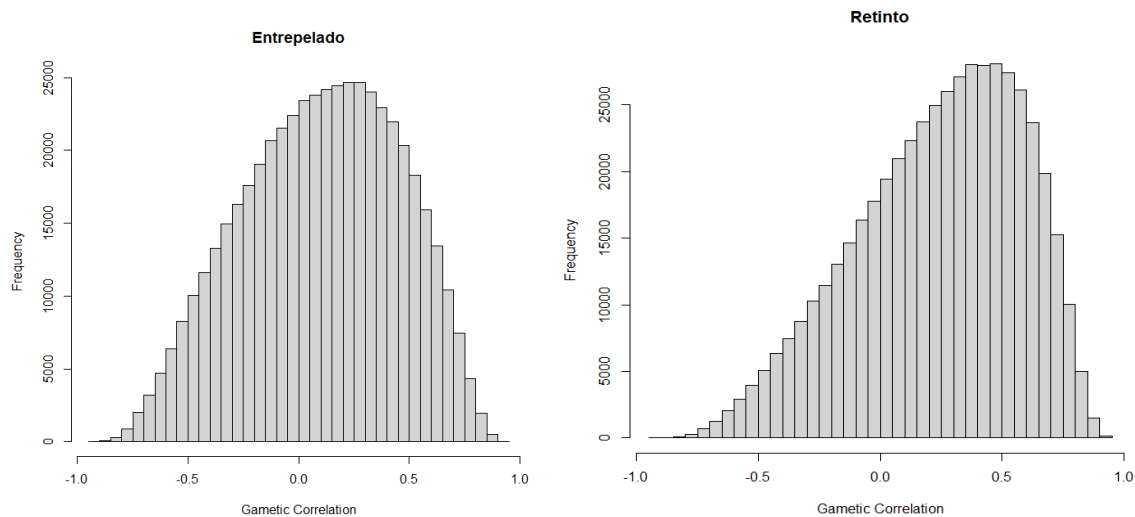

Figure 1. Posterior distributions of the correlations between paternal and maternal gametic effects in the Entrepelado and Retinto populations.

The posterior mean (and mode) was 0.101 (0.245) for Entrepelado and 0.239 (0.461) for Retinto, and the posterior probability of a positive gametic correlation was 0.613 and 0.755 for Entrepelado and Retinto, respectively.

Discussion

The proposed bivariate model allows to estimate the gametic effects of each founder population acting as paternal or maternal as well as their correlation. In absence of paternal or maternal imprinting, the correlation among them should be perfect (one). A significant deviation from this perfect correlation would indicate differences in the performance of crossbred individuals depending on each of the population is acting as paternal (or maternal).

The results of the study are very preliminary, as the amount of phenotypic and genotypic information is very low. Differences in the posterior distribution of the correlation between gametic effects in Retinto and the Entrepelado varieties can be observed. The posterior

distribution of the correlation in the Retinto variety is more positively skewed than the Entrepelado one. It suggests that the gametic contribution of Retinto individuals acting as boars or sows of the crossbred individuals are more similar, while the contribution of the Entrepelado individuals diverge greatly if they are used as boars or sows. This result may explain the differences in performance among the reciprocal crosses observed by Noguera et al. (2019) who propose using the Retinto variety as boar and the Entrepleado as sow providing a better performance that the opposite cross.

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