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Additional Information

1 **Genetic parameters and direct, maternal and heterosis effects on litter size in a**

2 **diallel cross among three commercial varieties of Iberian pig**

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22 **ABSTRACT:** To be written….

23

24 *Keywords:* Prolificacy, Diallel Cross, Heritability, Crossbreeding, Iberian pig

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26

INTRODUCTION

The populations of Iberian pigs are recognized worldwide as some of the porcine populations with the best quality of meat. This is a key factor for their conservation, since they have lower growth and food efficiency (Barea et al., 2011) or prolificacy (Silió et al., 2001) than other commercial populations of pigs. However, the Iberian pork sector is affected by a profound transformation that has involved the disappearance of many traditional producers due to their replacement by intensive management farms. Under this new scenario, the improvement of the reproductive efficiency of the Iberian pig population has become a requirement for its future economic viability.

The numerical productivity (number of piglets live born per year) can be considered as one of the most important parameters in the profitability of pig farms and its most important component is litter size (Legault, 1985). The 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 the heterosis. Traditionally, genetic improvement for litter size in Iberian populations has been scarce (Fernández et al., 2008) and Iberian pig producers have not used crosses since they exclusively breed one of the varieties available in the Iberian breed (Martínez et al., 2000). This contrast markedly with other populations of commercial pigs, where the selection efforts in recent decades for prolificacy in maternal lines have been enormous and where crossbreeding is a standard procedure (Dekkers et al., 2011).

However, several studies have shown the existence of genetic variability for prolificacy within (Rodríguez et al., 1994, Fernández et al., 2008) and between (García-Casco et al., 2013) the Iberian varieties. Therefore, both strategies for improvement are

plausible, within line selection and implementation of a maternal crossbreeding scheme. However, to establish the most appropriate strategy, it is necessary to have reliable estimates of the heritability of prolificacy in each population and of the crossbreeding parameters defined by the Dickerson model (Dickerson, 1969).

Thus, the objective of this study was to carry out a full diallel experimental design (Hayman, 1954) between 3 contemporary commercial varieties of Iberian pig (Entrepelado, Retinto and Torbiscal), under intensive management conditions, as well as to estimate the additive genetic variation and the heritability and the crossbreeding effects (direct, maternal and heterosis) in prolificacy. The final objective of the results is to contribute to the definition of suitable genetic improvement strategies within a pyramidal breeding program in the Iberian pig population.

MATERIALS AND METHODS

Animals and experimental design.

The research ethics committee of Institute of Agrifood Research and Technology (IRTA) previously approved all the management and experimental procedures involving live animal and were carried out in accordance with the Spanish Policy of Animal Protection RD1201/05, which complies with the European Union Directive 86/609 about the protection of animals used in experimentation. The data sets used in this study consist of 18,193 records for TNB (Total Number Born) and NBA (Number Born Alive) from 3,800 sows that were obtained from a full diallelic experiment between three strains 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 three varieties are recognized in Spain's official Iberian herd-book (Spanish

4

Association of Iberian Purebred Pig Breeders [AECERIBER]). A more detailed

description of its characteristics is presented by Ibáñez-Escriche et al. (2016). The

purebred dams were located in two selection farms in intensive commercial management

(FARM 1 and 2), while the boars were kept in a center of artificial insemination. The

third group of sows is in a commercial production farm (FARM 3) were all sows,

purebred and crossed, were mated with boars from a Duroc population according to usual

commercial production system in Iberian pig. The distribution of data between farms and

breed of sire of service are presented in Table II. In addition, the pedigree of each animal

goes back up to 3 generations and it consist of 4,609 individuals. The number of founders

per population was 47 (EE), 80 (TT) and 107 (RR).

Statistical analyses.

Both traits, TNB and NBA, were analyzed under a multiple population repeatability

model following García-Cortés and Toro (2006), that it is able to divide the additive

genetic values into separate fractions depending on their genetic origin. Thus, the general

model of analysis was:

$$\mathbf{y} = \mathbf{Xb} + \sum_{i=E,R,T}^{3} \mathbf{Z_i a_i} + \mathbf{Wp} + \mathbf{e}$$

where $\mathbf{y}$ is the vector of phenotypic records (TNB and NBA), $\mathbf{b}$ is a vector of systematic

effects: order of parity (6 levels -1st, 2nd, 3rd, 4rd, 5th and 6th and beyond-), farm-year-

season (85 levels), genetic line of boar of mate (4 levels, EE, RR, TT and Duroc –DU-),

and the direct line (L_E, L_R, L_T), maternal (M_E, M_R, M_T) and heterosis (H_{ER}, H_{ET}, H_{RT})

effects following Dickerson (1969) model. In addition, $\mathbf{a_i}$ is the vector of random additive

genetic effects of *ith* line (4,609 levels), $\mathbf{p}$ is the vector of the permanent effect of the sow

98   (3,800 levels), and **e** is the residuals vector; **X**, **Z$_i$**, and **W** are known incidence matrices

99   that links fixed and random effects with the vector **y**. It should be noticed that this model

100 allows for different additive variance component for each genetic origin and the

101 permanent environmental coefficient **p** was assumed homogeneous between lines. The

102 model assumed uniform bounded prior for systematic effects and multivariate Gaussian

103 distributions for the additive (**a$_i$**), permanent environmental (**p**) and residual effects (**e**).

104 The permanent environmental effects and the residuals were assumed identical and

105 independently distributed, thus their prior distribution was:

106 $$\mathbf{p} \sim \mathbf{N}\left(\mathbf{0}, I\sigma_p^2\right) \qquad\qquad \mathbf{e} \sim \mathbf{N}\left(\mathbf{0}, I\sigma_e^2\right)$$

107 On the contrary, the assumed prior distribution for the additive effects were:

108 $$a_E \sim \mathbf{N}\left(\mathbf{0}, A_E \sigma_{a_E}^2\right) \qquad a_R \sim \mathbf{N}\left(\mathbf{0}, A_R \sigma_{a_R}^2\right) \qquad a_T \sim \mathbf{N}\left(\mathbf{0}, A_T \sigma_{a_T}^2\right)$$

109 Being A_E, A_R and A_T, the partial kindship matrices generated by the founders of

110 Entrepelado, Retinto and Torbiscal, respectively. The calculation of these matrices was

111 performed following the algorithm proposed by García-Cortés and Toro (2006).

112 From this general model (LMH), several models model were defined by fixing to zero

113 the direct (MH), maternal (LH), and heterosis effects (LM) and direct and maternal (H),

114 direct and heterosis (M) and maternal and heterosis effects (L). The analyses for all

115 models were carried out using a *Gibbs sampling* algorithm (Gelfand and Smith, 1990)

116 with a single long chain of 1,250,000 iterations, after a period of "burn in" of 250,000

117 iterations.

118 **Model Comparison**

119 The above described models were compared using the deviance information criteria –

120   DIC – (Spiegelhalter et al., 2002) and the logarithm of the conditional predictive ordinate

121   – LogCPO – (Gelfand, 1996).

122   *Deviance information criterion*

123   The DIC compares the global quality of two or more models accounting for model

124   complexity. For a particular model M, the DIC is defined as:

125
$$DIC_M = 2\overline{D}_M - D(\overline{\theta}_M),$$

126   where $\overline{D}_M$ is the posterior expectation of the deviance $D(\theta_M)$, and $D(\overline{\theta}_M) = -2\log\left(p\left(\mathbf{y}\right.\right.$

127    $\left.\left.|\overline{\theta}_M\right)\right)$ is the deviance evaluated at the posterior mean estimate of the parameter vector

128   (θ_M). The computation of DIC is composed by two terms, i.e., $\overline{D}_M$ is a measure of model

129   fit and $\overline{D}_M - D(\overline{\theta}_M)$ is related to the effective number of parameters. Models with smaller

130   DIC exhibit a better global fit after accounting for model complexity.

131   *Log-marginal probability (logCPO)*

132   If we consider the data vector $\mathbf{y} = (y_i, \mathbf{y}_{-i})$, where y_i is the *i*th datum and $\mathbf{y}_{-i}$ is the vector

133   of data with *i*th datum deleted, the conditional predictive distribution has a probability

134   density equal to:

135
$$p(y_i|\mathbf{y}_{-i}) = \int p(y_i, \theta|\mathbf{y}_{-i})\, p(\theta|\mathbf{y}_{-i})d\theta,$$

136   where θ is the vector of unknown parameters in the model. Therefore, $p(y_i|\mathbf{y}_{-i})$ can be

137   interpreted as the probability of each datum given the rest of the data, and it is known as

138   the conditional predictive ordinate (CPO) for the *i*th datum. The pseudo log-marginal

139   probability of the data is then:

140
$$\sum_i ln\, p(y_i|\mathbf{y}_{-i}),$$

141 A Monte Carlo approximation of the CPO suggested by Gelfand (1996) is

142 $\sum_i ln\, \hat{p}(y_i|\mathbf{y}_{-i})$, where $\hat{p}(y_i|\mathbf{y}_{-i}) = N\left[\sum_{j=1}^{N} \frac{1}{p(y_i|\theta^j)}\right]^{-1}$, and N is the number of Markov

143 chain Monte Carlo (MCMC) draws, and θ^j is the jth draw from the posterior distribution

144 of the corresponding parameter. The higher the value of the LogCPO, best fit of the model

145 to data.

146 **RESULTS**

147 The results of the model comparison procedures are presented in Table II. For both NBA

148 and TNB, the model with best fit with DIC and LogCPO was the complete LMH model,

149 followed by a group of models (LH, MH and H) whose differences with the best model

150 varied between 5.9 to 8.0 units for DIC and between 0.4 to 6.9 for LogCPO. Finally, the

151 LM, D and M models had a worse adjustment and their differences with the LMH model

152 ranged between 22.4 to 26.6 for DIC and between 19.8 to 23.3 for LogCPO.

153 The posterior mean (and posterior standard deviation) of the variance components,

154 heritabilities and the percentages of permanent environmental variation for model LMH

155 are presented in Table III for NBA and TNB, respectively. The posterior mean estimates

156 ($\pm$ posterior standard deviations) of the additive variance ranged between 0.371 ± 0.106

157 (TT) to 0.665 ± 0.123 (EE) and between 0.418 ± 0.115 (TT) to 0.717 ± 0.126 (EE) for

158 NBA and TNB, respectively, and the posterior mean estimates ($\pm$ posterior standard

159 deviations) of the permanent environmental and residual variances were 0.361 ± 0.051

160 and 4.020 ± 0.048 for NBA and 0.371 ± 0.053 and 4.029 ± 0.048 for TNB. As a

161 consequence of the figures described above, the posterior mean ($\pm$ posterior standard

162 deviations) estimates for the population specific heritabilities were 0.078 ± 0.021 (TT),

163 0.084 ± 0.017 (RR) and 0.131 ± 0.022 (EE) for NBA and 0.086 ± 0.022 (TT), 0.090 ±

164 0.017 (RR) and 0.140 ± 0.022 (EE). The results under models MH, LH, LM, L, M and H

165 were similar and they are presented in Supplementary Tables I and II for NBA and TNB,

166 respectively.

167 The results of contrast between direct line and maternal effects and the heterosis effects

168 under model LMH are presented in Table IV. The posterior mean ± standard deviation

169 estimates of the differences between EE and RR, EE and TT and RR and TT were -0.684

170 ± 0.317, 0.114 ± 0.324 and 0.798 ± 0.210 for NBA and -0.876 ± 0.327, -0.024 ± 0.334

171 and 0.852 ± 0.217 piglets for TNB. Moreover, the posterior mean ± standard deviation

172 estimates of the differences of the maternal effects of EE with RR and TT were 0.443 ±

173 0.123 and 0.450 ± 0.144 for NBA and 0.554 ± 0.117 and 0.533 ± 0.117 piglets for TNB,

174 whereas the differences between RR and TT were only 0.007 ± 0.104 and -0.021 ± 0.107.

175 These results of the maternal effects were confirmed with the comparison between

176 reciprocals. Thus, the posterior mean ± standard deviation estimates of differences

177 between ER vs RE and between ET and TE were -0.443 ± 0.123 and -0.554 ± 0.125 and

178 -0.450 ± 0.144 and -0.534 ± 0.147 for NBA and TNB, respectively, whereas the

179 differences between TR and RT were negligible (-0.007 ± 0.104 and 0.021 ± 0.107).

180 Moreover, the posterior mean (and standard deviation) estimates of the heterosis effects

181 ranged between 0.600 ± 0.129 (EE and TT) to 0.690 ± 0.092 (RR and TT) for NBA and

182 between 0.622 ± 0.131 (EE and TT) to 0.666 ± 0.093 (RR and TT) for TNB. The results

183 under the remaining models followed the same pattern and they are presented in

184 Supplementary Tables III and IV for NBA and TNB, respectively.

185 Finally, the posterior mean (and standard deviation) of the difference between each cross

186 with respect to the RE and the posterior probability of being the best cross with model

187 LMH are presented in Table V. As observed, the differences ranged between -0.443 (with

188 ER) to -1.566 piglets (with TT) piglets for NBA and between -0.464 (with TE) to -1.607

189 (with TT) for TNB and the posterior probability of being the best cross given the LMH

190 model were 0.985 and 0.991 for NBA and TNB, respectively.

191 **DISCUSSION**

192 The main advantage of the proposed approach (García-Cortés and Toro, 2006) is that it

193 provides specific estimates of the additive variance component (and heritabilities) for

194 each population of origin and, therefore, it is able to detect differences in their genetic

195 variation. The results of additive variance (and heritability) of the EE variety were

196 markedly higher than the other two populations (RR and TT) under all model of analysis.

197 In fact, in comparison with the estimates available in the literature, the results of the EE

198 population were higher than those obtained in previous studies (Pérez-Enciso and

199 Gianola, 1992; García-Casco et al., 2012) in Iberian pig populations. while the estimates

200 for RR and TT are closer to agreeing with them. However, estimates of heritability over

201 0.10 are frequent in white pig populations (Noguera et al., 2002; Bidanel, 2011). The

202 results of this study would have to be confirmed with a larger database, but in light of the

203 results, it seems plausible that the response to selection in the EE population under an

204 appropriate breeding scheme for improving litter size can be larger than in the other lines.

205 Therefore, the EE variety is a good candidate to be included in a pyramidal scheme for

206 the improvement of litter size.

207 The results of the comparison of models indicated the relevance of the direct line,

208 maternal and heterosis effects with both procedures (LogCPO and DIC) since the model

209 with the best fit was LMH. However, the magnitude of this relevance was heterogeneous.

210 For example, the best model was followed closely by a group of models that share in

211 common the presence of the effects of heterosis (LH, MH and H). This result is reinforced

by the posterior probability of a heterosis effect greater than zero that was greater than 0.999 for all models and traits. Therefore, we can affirm that there is clear evidence of heterosis between any of the three potential crosses and without notable differences between them. The presence of a relevant degree of heterosis was expected, as is observed regularly in crosses between porcine populations (Haley et al, 1995, Cassady et al., 2002; García-Casco et al., 2012). However, the results were relatively surprising, because previous studies (Fabuel et al., 2004) had suggested that the genetic distance between EE and RR is lower than between TT. Therefore, we expected a lower degree of heterosis between EE and RR than in crosses involving TT.

The superiority of model LMH with respect to MH and the posterior distribution of the contrast between direct line effects under the LMH model also confirm the differences between direct line effects in litter size. There are many references in the literature about differences in reproductive performance among swine populations (Bidanel, 2011). Therefore, it is not surprising that this variability also appears among the Iberian varieties since the genetic diversity of Iberian pig populations is as high as among white pig populations (Martinez et al., 2000; Fabuel et al., 2004). Moreover, the Iberian pig populations had evolved thanks to selection and adaptation processes that could be related with litter size. In general, the RR population had the best line effects and the EE and TT populations had a similar performance.

In addition, the best fit of LMH with respect to the LH model and the posterior distribution of maternal effects also provides evidence of its relevance. In fact, the results showed a clear superiority (posterior probability over 0.99) of the maternal effect of the EE population with respect to the RR and TT populations, confirmed by the highly relevant differences between reciprocals (RE versus ER and TE versus to ET). In quantitative genetics, the importance of maternal effects is deeply recognized (Wolf and Wade, 2009)

237 and they are typically found in growth traits in non-prolific species (Waldron et al., 1993)

238 where they act as an environmental variation in the performance progeny and disappear

239 after weaning. Therefore, the maternal effects are not expected in litter size as it is

240 understood as a trait of the sow. However, some studies have detected the presence of

241 significant maternal genetic variation (Southwood and Kennedy, 1990, Irgang et al.,

242 1994) and, more recently, the influence of maternal care on the reproductive performance

243 of adult females has been investigated in several species (Cameron, 2011). In addition,

244 the recent developments on the genetic determinism of prolificacy in pigs are picturing a

245 very complex panorama that can help to understand the presence of maternal effects in a

246 diallelic cross. In fact, there is recent evidence of the effects of DNA methylation (Hwang

247 et al., 2017) and the presence of imprinted genes (Coster et al., 2012) that affect the size

248 of the litter of pigs. In addition, it has been claimed that epistasis is a very important

249 source of genetic variation in litter size in mice (Peripato et al., 2004) and swine (Noguera

250 et al., 2009). Finally, another possibility that can not be ruled out is the effects of

251 mitochondrial DNA whose variation has recently been associated with the maturation of

252 oocytes in cattle (Srirattana et al., 2017) and the reproductive performance in pigs (Tsai

253 et al., 2016).

254 Despite the uncertainty about the biological basis of the observed results, the conclusion

255 of this study points out the clear advantage of crossbred individuals with respect to the

256 purebred ones in litter size traits in the Iberian breed. Therefore, the implementation of

257 pyramidal scheme to provide crossbred dams to the producers is strongly recommended.

258 Among the analyzed varieties, we have detected that the RR population has a greater

259 direct line effect, whereas the EE population has the greater maternal effect and provides

260 a clear advantage when used as maternal line. As a consequence, in light of the results,

261 the recommended cross for a practical implementation of a pyramidal scheme is RR as

262 paternal and EE as maternal lines, reinforced by posterior probability of being the best

263 cross for both NBA and TNB with the analyzed dataset.

264 **ACKNOWLEDGEMENTS**

265

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350

351 **Table I.** Distribution of phenotypic records by farm and breed of service sire and dam.

Dam (Number of Sows)	FARM 1 Sire			FARM2 Sire			FARM3 Sire
	EE	RR	TT	EE	RR	TT	DU
EE (707)	517	752	5	255	811	70	433
ER (527)	-	-	-	-	-	-	2336
ET (177)	-	-	-	-	-	-	942
RE (196)	-	-	-	-	-	-	806
RR (874)	1450	491	96	655	277	633	870
RT (488)	-	-	-	-	-	-	2450
TE (36)	-	-	-	-	-	-	192
TR (343)	-	-	-	-	-	-	1993
TT (452)	197	808	58	109	507	247	232
TOTAL	2164	2051	159	1019	1595	950	10255

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355 **Table II.** Results of the Deviance Information Criterion (DIC) and the Logarithm of the

356 conditional predictive ordinate (LogCPO) and the absolute value of the differences with

357 the best model (between brackets) for number born alive (NBA) and total number born

358 (TNB).

	NBA		TNB	
MODEL	DIC	LogCPO	DIC	LogCPO
LMH	112437.0 (0.0)	-56102.7 (0.0)	112417.2 (0.0)	-56062.4 (0.0)
MH	112443.3 (6.3)	-56103.6 (0.9)	112423.1 (5.9)	-56062.8 (0.4)
LH	112443.3 (6.3)	-56107.7 (5.0)	112422.9 (5.7)	-56065.3 (2.9)
LM	112460.8 (23.8)	-56122.5 (19.8)	112439.6 (22.4)	-56084.6 (20.2)
D	112463.3 (26.3)	-56125.0 (22.3)	112443.0 (25.8)	-56085.4 (23.0)
M	112463.6 (26.6)	-56123.6 (20.9)	112443.3 (26.1)	-56085.7 (23.3)
H	112444.5 (7.5)	-56109.6 (6.9)	112425.2 (8.0)	-56067.2 (4.8)

359

360 **Table III.** Posterior Mean (and Standard Deviation) estimates of heritabilities (h^2) and

361 additive, permanent environmental and residual variance components for number born

362 alive (NBA) and total number born (TNB) with model LMH.

363

	NBA	TNB
σ_{aE}^2	0.665 (0.123)	0.717 (0.126)
σ_{aR}^2	0.401 (0.088)	0.439 (0.091)
σ_{aT}^2	0.371 (0.106)	0.418 (0.115)
σ_p^2	0.361 (0.051)	0.371 (0.053)
σ_e^2	4.020 (0.048)	4.029 (0.048)
h_E^2	0.131 (0.022)	0.140 (0.022)
h_R^2	0.084 (0.017)	0.090 (0.017)
h_T^2	0.078 (0.021)	0.086 (0.022)

364

365

366 **Table IV.**Posterior Mean (and Standard Deviation) estimates of the contrast between

367 direct line and maternal effects and the heterosis effects for Number Born Alive (NBA)

368 and Total Number Born (TNB) under model LMH.

		NBA	TNB
Direct Line	EE vs. RR	-0.684 (0.317)	-0.876 (0.327)
	EE vs. TT	0.114 (0.324)	-0.024 (0.334)
	RR vs. TT	0.798 (0.210)	0.852 (0.217)
Maternal	EE vs. RR	0.443 (0.123)	0.554 (0.147)
	EE vs. TT	0.450 (0.144)	0.533 (0.117)
	RR vs. TT	0.007 (0.104)	-0.021 (0.107)
Heterosis	EE with RR	0.653 (0.098)	0.661 (0.099)
	EE with TT	0.600 (0.129)	0.622 (0.131)
	RR with TT	0.690 (0.092)	0.666 (0.093)

369

370

371 **Table V.** Posterior mean (and standard deviation) of the differences of the crosses with

372 the RE population and posterior probability of being the best cross under model LMH.

	NBA		TNB	
	Dif.	Prob.	Dif.	Prob.
EE	-0.995 (0.196)	0.000	-1.09 (0.202)	0.000
ER	-0.443 (0.123)	0.000	-0.554 (0.125)	0.000
ET	-0.902 (0.175)	0.000	-1.000 (0.178)	0.000
RE	-	0.985	-	0.991
RR	-0.754 (0.189)	0.000	-0.777 (0.193)	0.000
RT	-0.471 (0.178)	0.003	-0.516 (0.183)	0.002
TE	-0.452 (0.164)	0.003	-0.464 (0.169)	0.003
TR	-0.463 (0.198)	0.009	-0.536 (0.203)	0.004
TT	-1.560 (0.226)	0.000	-1.607 (0.232)	0.000

373 Dif: Posterior mean estimate (and standard deviation) for the difference with the RE
374 population.. Prob: Posterior probability of being the best cross.

375

377 **Supplementary Table I.** Posterior Mean (and Standard Deviation) estimates of heritabilities (h^2) and additive, permanent environmental and

378 residual variance components for Number Born Alive (NBA) with models MH, LH, LM, L, M, H.

	MH	LH	LM	L	M	H
σ^2_{aE}	0.673 (0.124)	0.693 (0.126)	0.658 (0.123)	0.674 (0.125)	0.660 (0.123)	0.711 (0.127)
σ^2_{aR}	0.466 (0.094)	0.390 (0.087)	0.393 (0.090)	0.387 (0.089)	0.442 (0.094)	0.469 (0.094)
σ^2_{aT}	0.423 (0.110)	0.362 (0.104)	0.382 (0.109)	0.385 (0.109)	0.430 (0.112)	0.454 (0.111)
σ^2_{p}	0.339 (0.051)	0.367 (0.052)	0.385 (0.053)	0.387 (0.052)	0.368 (0.052)	0.332 (0.051)
σ^2_{e}	4.019 (0.048)	4.020 (0.047)	4.022 (0.047)	4.022 (0.047)	4.022 (0.048)	4.020 (0.047)
h^2_{E}	0.133 (0.022)	0.136 (0.022)	0.130 (0.022)	0.132 (0.022)	0.130 (0.022)	0.140 (0.022)
h^2_{R}	0.096 (0.018)	0.081 (0.017)	0.082 (0.017)	0.080 (0.017)	0.091 (0.018)	0.097 (0.018)
h^2_{T}	0.088 (0.021)	0.076 (0.021)	0.080 (0.021)	0.080 (0.021)	0.089 (0.021)	0.094 (0.021)

379

380 **Supplementary Table II.** Posterior Mean (and Standard Deviation) estimates of heritabilities (h^2) and additive, permanent environmental and

381 residual variance components for Total Number Born (TNB) with models MH, LH, LM, L, M, H.

	MH	LH	LM	L	M	H
σ^2_{aE}	0.734 (0.128)	0.753 (0.130)	0.709 (0.126)	0.730 (0.128)	0.718 (0.127)	0.771 (0.132)
σ^2_{aR}	0.516 (0.097)	0.430 (0.090)	0.436 (0.093)	0.431 (0.092)	0.498 (0.098)	0.511 (0.097)
σ^2_{aT}	0.483 (0.119)	0.413 (0.115)	0.427 (0.117)	0.434 (0.118)	0.487 (0.121)	0.514 (0.121)
σ^2_p	0.343 (0.052)	0.376 (0.053)	0.395 (0.053)	0.396 (0.053)	0.372 (0.053)	0.339 (0.052)
σ^2_e	4.028 (0.047)	4.029 (0.047)	4.031 (0.047)	4.031 (0.048)	4.031 (0.048)	4.030 (0.048)
h^2_E	0.143 (0.022)	0.146 (0.022)	0.138 (0.022)	0.141 (0.022)	0.139 (0.022)	0.150 (0.022)
h^2_R	0.105 (0.018)	0.089 (0.017)	0.089 (0.018)	0.089 (0.018)	0.101 (0.019)	0.104 (0.018)
h^2_T	0.099 (0.022)	0.085 (0.022)	0.088 (0.022)	0.089 (0.022)	0.099 (0.023)	0.105 (0.022)

382

Supplementary Table III. Posterior Mean (and Standard Deviation) estimates of the contrast between direct line and maternal effects and the

heterosis effects for Number Born Alive (NBA) with models MH, LH, LM, L, M, H.

		MH	LH	LM	L	M	H
Direct Line	EE vs. RR	-	-0.241 (0.294)	-0.567 (0.311)	-0.250 (0.290)	-	-
	EE vs. TT	-	0.557 (0.295)	0.197 (0.318)	0.464 (0.290)	-	-
	RR vs. TT	-	0.798 (0.170)	0.761 (0.210)	0.715 (0.170)	-	-
Maternal	EE vs. RR	0.333 (0.115)	-	0.326 (0.119)	-	0.235 (0.111)	-
	EE vs. TT	0.564 (0.130)	-	0.294 (0.137)	-	0.409 (0.124)	-
	RR vs. TT	0.231 (0.088)	-	-0.032 (0.098)	-	0.174 (0.082)	-
Heterosis	EE with RR	0.629 (0.097)	0.579 (0.095)	-	-	-	0.598 (0.096)
	EE with TT	0.611 (0.129)	0.493 (0.123)	-	-	-	0.439 (0.123)
	RR with TT	0.693 (0.093)	0.674 (0.091)	-	-	-	0.629 (0.091)

386 **Supplementary Table IV.** Posterior Mean (and Standard Deviation) estimates of the contrast between direct line and maternal effects and the

387 heterosis effects for Total Number Born (TNB) with models MH, LH, LM, L, M, H.

		MH	LH	LM	L	M	H
Direct Line	EE vs. RR	-	-0.318 (0.305)	-0.733 (0.321)	-0.318 (0.300)	-	-
	EE vs. TT	-	0.499 (0.306)	0.089 (0.329)	0.418 (0.301)	-	-
	RR vs. TT	-	0.817 (0.178)	0.822 (0.217)	0.735 (0.176)	-	-
Maternal	EE vs. RR	0.417 (0.117)	-	0.427 (0.121)	-	0.314 (0.114)	-
	EE vs. TT	0.629 (0.133)	-	0.365 (0.140)	-	0.468 (0.127)	-
	RR vs. TT	0.212 (0.091)	-	-0.061 (0.100)	-	0.154 (0.084)	-
Heterosis	EE with RR	0.630 (0.099)	0.568 (0.097)	-	-	-	0.585 (0.097)
	EE with TT	0.628 (0.131)	0.501 (0.125)	-	-	-	0.448 (0.125)
	RR with TT	0.672 (0.094)	0.649 (0.092)	-	-	-	0.607 (0.092)

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