Correlated responses on growth traits after two-stage selection for ovulation rate and litter size in rabbits

R. Peiró [1,a], A.Y. Badawy [1,b], A. Blasco [1] and M.A. Santacreu [1]

[1] Instituto de Ciencia y Tecnología Animal, Universitat Politècnica de València, P.O. Box 22012, 46071, Valencia, Spain

[a] Present Address: Instituto de Conservación y Mejora de la Agrodiversidad Valenciana, Universitat Politècnica de València, P.O. Box 22012, 46071, Valencia, Spain

[b] Present Address: Animal Production Department, Faculty of Agriculture, 41522 Suez Canal University, Egypt.

Corresponding author: María Antonia Santacreu. E-mail: msantacr@dca.upv.es.

Short title: Correlated responses on growth traits

Abstract

Rabbit commercial maternal lines are usually selected for litter size and paternal lines for growth rate. Line OR_LS was selected by ovulation rate and litter size to improve litter size more efficiently. In this study, growth traits of line OR_LS were evaluated by estimating the correlated response on weaning weight (**WW**), slaughter weight (**SW**) and growth rate (**GR**) during fattening period as well as their variability (**DWW**, **DSW** and **DGR**, respectively). Data were analyzed using Bayesian inference methods. Heritability estimates were low for growth traits (0.09, 0.13 and 0.14, for WW, SW and GR, respectively) and negligible for variability growth traits (0.01, 0.004 and 0.01, for DWW, DSW and DGR, respectively). Moderate common litter effects (c^2; 0.35, 0.28 and 0.27) and low maternal effects (m^2; 0.11, 0.05 and 0.01) were obtained for WW, SW and GR, respectively. Both, c^2 and m^2 were lower at slaughter than at weaning. In addition, low common litter effect and negligible maternal effect were observed for variability growth traits. Genetic correlations between litter size and both growth traits and its variability were close to zero. Positive genetic correlations were observed between ovulation rate and growth traits (0.19, 0.38 and 0.36 for WW, SW and GR, respectively) as well as between ovulation rate and variability growth traits (0.35, 0.62 and 0.20 for DWW, DSW and DGR, respectively). Positive correlated responses in both periods were obtained for growth traits, WW, SW and GR (0.037, 0.156 and 0.110 kg, respectively). The correlated response found in growth traits might be due to the positive genetic correlations between ovulation rate and these traits. However, selection for ovulation rate and litter size using independent culling levels did not modify the variability growth traits. Therefore, no negative consequences on growth traits can be expected in current commercial maternal lines.

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Implications

45   It is important to assess the effect on growth traits when selecting by ovulation rate and

46   litter size since growth is one of the main objectives in rabbit selection programs. The

47   increase of litter size at weaning and at slaughter time after two-stage selection by

48   ovulation rate and litter size does not reduce weaning and commercial weight. The

49   selection does not also modify variability growth traits. Therefore, two-stage selection

50   by ovulation rate and litter size could be used as a selection criterion in maternal rabbit

51   lines since no negative consequences on growth traits were observed.

52

Introduction

54   Growth rate and litter size are the most common selection criteria for commercial lines.

55   Two-stage selection by ovulation rate and litter size has been proposed as a way to

56   improve more efficiently litter size at birth, weaning and slaughter than direct selection

57   for litter size at weaning in rabbits (Badawy *et al.*, 2019). However, it is unknown the

58   consequences of this kind of selection on growth traits (weaning weight, slaughter

59   weight and growth rate) and their variability in rabbits. It is known that increasing the

60   number of total kits born can reduce the weight at birth and increases the intra-litter

61   weight variability, reducing the probability of postnatal survival in rabbits (Argente *et*

62   *al.*, 1999) and pigs (Damgaard *et al.*, 2003; Wolf *et al.*, 2008; Zhang *et al.*, 2016).

63   Genetic correlations between litter size and growth traits in rabbits are generally low,

64   showing a high standard error (see review by Mocé and Santacreu, 2010). These low

genetic estimations are in agreement with the low or null correlated responses on growth traits obtained in maternal lines selected by litter size (Mínguez *et al.*, 2016).

For ovulation rate, there is no information in rabbits whereas few genetic correlations between ovulation rate and growth traits were found in pigs; low positive or null genetic correlations of ovulation rate with birth weight (Hsu and Johnson, 2014), weaning weight (Ruíz-Flores and Johnson, 2001; Rosendo *et al.*, 2007), weight at 125 and at 178 days (Ruíz-Flores and Johnson, 2001) and growth rate (Bidanel *et al.*, 1996; Rosendo *et al.*, 2007). Under our knowledge, genetic parameters of weight variability at weaning and at slaughter and their relationship with litter size or ovulation rate was never studied in rabbit.

Growth traits are economically important traits in commercial rabbit selection programs. The increase of litter size by selection could modify growth traits and its variability. The aim of this study is to estimate the correlated responses on weaning and slaughter weight, growth rate and their variability from a two-stage selection experiment for ovulation rate and litter size in rabbits.

Materials and methods

Animals and experimental design

Animals involved in this experiment came from a synthetic line (line OR_LS), which underwent 17 generations of selection. From base generation to generation six (first selection period), females were selected only for ovulation rate. From generation seven to 17 (second selection period), a two-stage selection for ovulation rate and litter size was performed. The average number of females and males per generation was 74 and

4

90   17, respectively. Details about breeding and feeding management were described by

91   Badawy *et al.* (2019).

92

93   *Traits*

94   Weaning weight (**WW**, kg) and slaughter weight (**SW**, kg) of each young rabbit were

95   measured individually at 28 and 63 days of age, respectively. Growth rate (**GR**, kg)

96   was estimated as the difference between SW and WW. The variability of WW, SW and

97   GR was calculated as the absolute value of the difference between the individual value

98   and the mean value of its litter (**DWW**, **DSW and DGR** in kg, respectively)). Litter size

99   (**LS**) was measured as the total number of kits born per litter up to five parities.

100   Ovulation rate (**OR**), estimated as the number of corpora lutea, was measured at

101   second and last gestation. More details about reproductive traits have been given by

102   Badawy *et al.* (2019). Number of records for weaning weight (WW), slaughter weight

103   (SW) and growth rate (GR) was 30,420, 29,075 and 29,057, respectively. The same

104   number of data was also used to estimate the growth variability traits (Table 1). These

105   data came from 1,317 dams with 4,027 litters. Data from 1,210 ovulation rates and

106   4,480 parities were analyzed. The number of animals in the pedigree was 30,666.

107

108   *Statistical Analysis*

109   Bayesian inference methods were used to analyze data from all generations of

110   selection. Trivariate animal models were fitted to estimate genetic parameters and

111   responses. Each trivariate analysis included the selected traits (LS and OR) and one

112   of each growth traits (WW, SW, GR, DWW, DSW and DGR). The repeatability animal

113   model used for analyzing OR and LS was described by Badawy *et al.* (2019).

114

115   The model used for analyzing WW, SW, GR, DWW, DSW and DGR was:

116    $y_{ijkl} = b\,NBA_{ijk} + YS_i + PO_j + m_k + c_{ijk} + a_{ijkl} + e_{ijkl}$

117   in which, y_{ijkl} is the record of the trait of animal l; NBA_{ijk} is the number of kits born alive

118   in which the animal l was born and b is the regression coefficient on NBA; YS_i is the

119   effect of year season (three months per each year season; 46 levels); PO_j is the effect

120   of the parity order in which the animal was born (4 levels: 1st, 2nd, 3rd and $>3^{th}$); m_k is

121   the environmental maternal random effect of the overall parities of the dam of the

122   animal l; c_{ijk} is the random effect of the common litter in which the animal l was born;

123   a_{ijkl} is the random additive value of animal l, and e_{ijkl} is the residual effect.

124

125   Common litter effect ratio (c^2) was defined as the ratio between the variance of

126   common litter effects and the phenotypic variance, and maternal effect ratio (m^2) was

127   defined as the ratio between the variance of permanent environmental effects and the

128   phenotypic variance. The joint prior distribution assumed for additive genetic effects

129   was $N(\mathbf{0}, \mathbf{A} \otimes \mathbf{G_a})$, where $\mathbf{G_a}$ was the genetic (co)variance matrix between the traits and

130    $\mathbf{A}$ was the additive genetic relationship matrix. Environmental maternal effects (m_k) of

131   growth traits and permanent environmental effect of the doe (p_k) on LS and OR are

132   correlated. The joint prior distribution for the permanent environmental effect of the doe

133   (p_k) and the maternal effect on growth trait (m_k) was $N(\mathbf{0}, \mathbf{I} \otimes \mathbf{G_p})$, where $\mathbf{G_p}$ was the

134   (co)variance matrix between these effects. There is a correlation between the residual

135   term of the reproductive trait and the common litter effect (c_{ijk}) of the growth trait (García

136   and Baselga, 2002; Mínguez *et al.*, 2016), therefore an environmental covariance

137   structure between growth traits and reproductive traits was established. The prior

138   distribution for the common litter effect (c_{ijk}) of one of the growth traits and the residual

139   term of the one of reproductive traits was $N(\mathbf{0}, \mathbf{I} \otimes \mathbf{G_c})$, where $\mathbf{G_c}$ was the (co)variance

140 matrix between these effects. The residual prior distributions for all traits were $N(\mathbf{0}, \mathbf{I}\sigma_e^2)$

141 . The order of the identity matrix $\mathbf{I}$ was equal to the number of records measured in

142 each case. Bounded uniform priors were used for the components of the (co)variance

143 matrices. The program TM (Legarra *et al.*, 2008) was used for Gibbs sampling

144 procedures. Chains of 3,000,000 samples each were used, with a burn-in period of

145 750,000. One sample in each 100 was saved to avoid high autocorrelation between

146 consecutive samples. Geweke's Z-score was estimated to test the chain convergence.

147

148 A heritability higher than 0.10 was considered relevant for growth traits. Selection on

149 growth traits with heritability lower than 0.10 leads to low genetic responses per

150 generation. Similarly to Badawy *et al.* (2019), the relevant value for correlation was 0.3

151 (in absolute value) considering the low percentage of the explained variance. The

152 features of the marginal posterior distributions showed in Tables 2 and 3 were also

153 described by Badawy *et al.* (2019).

154

155 **Results and discussion**

156 Means, standard deviations (SD) and coefficients of variation (CV) for growth traits and

157 their variability are shown in Table 1. Values for growth traits were similar to those

158 presented in several maternal lines selected for number of kits at weaning (García and

159 Baselga, 2002; Mínguez *et al.*, 2016). For example, Mínguez *et al.* (2016) obtained

160 mean values of 0.57 ± 0.13 kg, 1.86 ± 0.26 kg and 36.70 ± 5.70 g/d for weaning and

161 slaughter weights and growth rate, respectively, after analyzing a large set of data from

162 four maternal lines. Up to now, there is no information about the individual variability

163 of weights at weaning and slaughter in rabbits. The raw values for variability growth

164 traits were low, ranging from 0.05 to 0.11 kg, and the coefficients of variation were

165 high. Argente *et al.* (1999) studied the standard deviation of weaning weight within litter

166 obtaining a value close to 0.07 kg.

167

168 The effect of the covariate NBA for all growth traits was negative (-0.028±0.002 for

169 WW, -0.041±0.003 for SW and -0.012±0.001 for GR; data not shown) and showed high

170 accuracy. These results were in concordance with the correlated response on growth

171 traits in selected maternal lines found by García and Baselga (2002) and Mínguez *et*

172 *al.* (2016). Drummond *et al.* (2000) and Poigner *et al.* (2000) also observed that larger

173 litters had a lower average birth weight and lower growth rate from birth to weaning

174 than smaller litters. The effect of the covariate NBA for all growth variability traits was

175 positive (0.0008±0.0001 for DWW, 0.0032±0.0001 for DSW, and 0.0021±0.0001 for

176 DGR) and also showed high accuracy.

177

178 *Genetic parameters*

179 *Heritabilities.* The heretabilities for the selection criteria traits, OR and LS, were 0.25

180 (HPD$_{95\%}$=0.17-0.33) and 0.10 (HPD$_{95\%}$=0.05-0.14), respectively (Badawy et al.; 2019).

181 Features of the marginal posterior distributions of the heritability for growth traits and

182 their variability are shown in Table 2. Heritability estimates for growth traits were low.

183 The probability of the heritability being higher than 0.10 was high for SW and GR,

184 whereas the heritability of WW was likely to be lower than 0.10. Low to moderate

185 heritabilities for growth traits depending on the rabbit populations or the methods of

186 estimation have been reported (Argente *et al.*, 1999; Drouilhet *et al.*, 2013; Mínguez *et*

187 *al.*, 2016). Monte Carlo standard errors for all estimations were small, less than or

188 equal to 0.008, and no lack of convergence was detected by Geweke test.

189   Genetic variation for growth variability traits was negligible. In rabbits, no previous

190   estimations of heritabilities for growth variability traits were reported. In pigs,

191   heritabilities for variability of weight at birth and at weaning, measured as intra-litter

192   standard deviation were also low, ranged from 0.05 to 0.08 (Damgaard *et al.*, 2003;

193   Wolf *et al.*, 2008; Zhang *et al.*, 2016). The heritabilities of weight variability were lower

194   than those for weight at birth and at weaning as in in our results (from 0.10 to 0.39).

195

196   *Common litter (c^2) and maternal (m^2) effects ratio.* Features of marginal posterior

197   distributions of common litter and maternal effects ratio for growth traits are shown in

198   Table 2. All estimations showed a high accuracy. Estimated values for common litter

199   effect ratio were moderate for all growth traits being 0.35 for WW, 0.28 for SW and

200   0.27 for GR, and with high probability of being higher than 0.10. These results show

201   that common litter effect ratio decreases over time, as expected. Maternal effect ratio

202   was low for WW and SW and negligible for GR. Similar estimations for common litter

203   effects ratio for WW, SW and GR were obtained in rabbit maternal lines by García and

204   Baselga (2002) and for common litter and maternal effects ratio by Mínguez *et al.*

205   (2016). However, higher estimations for maternal effects ratio (0.18, 0.21 and 0.26,

206   respectively) were reported by García and Baselga (2002). In agreement with our

207   results, relevant litter common and maternal effect ratios were also found in rabbit lines

208   selected by growth rate and food efficiency traits (Drouilhet *et al.*, 2013). Our results

209   support the important influence of a pre-weaning environment provided by the female

210   on growth at least until slaughter in rabbits. Regarding variability growth traits, common

211   litter effect ratio for DWW, DWS, and DGR showed values closed to 0.10. However,

212   maternal effect ratio showed very low values for these traits. No literature values were

found for common litter and maternal effect ratios neither in rabbits or pigs for variability
growth traits.

Correlations between reproductive traits and growth traits. Features of the marginal
posterior distributions of the genetic and phenotypic correlation between the studied
traits are shown in Table 3. All genetic correlation values were estimated with a high
posterior density interval at 95 % probability. We considered 0.30 as a relevant value
as it represents less than 10% of the variance of one trait explained by the other one.
We also considered the probability of similitude, P_s, as the probability of a correlation
being in absolute value lower than 0.30. No relevant genetic correlations were
observed between LS and growth traits and also between LS and variability growth
traits, since values were close to zero and P_s were high. Likewise, phenotypic
correlations were also null between LS and growth traits and also with variability growth
traits. There are only few estimates of genetic correlations between litter size and
growth traits in rabbits with no clear pattern. Also, most correlations were low with high
standard errors (Mocé and Santacreu, 2010; Mínguez *et al.*, 2016). In pigs, a broad
range of correlation estimates between litter size at birth and litter weaning weight were
found using different models (Damgaard *et al.*, 2003; Wolf *et al.*, 2008; Zhang *et al.*,
2016) and no clear pattern was found.

In rabbit line OR_LS, low positive genetic correlation was found between OR and SW
and also between OR and GR, both with a probability of relevance (P_{30}) higher than
0.70. However, the probability of relevance for the correlation between OR and WW
was low, 0.19. Low and moderate positive genetic correlations between OR and DWW
and between OR and DSW were also found, with a probability of relevance for both

238   correlations at least 0.65.There are no studies about the genetic relationship between

239   OR and growth traits in rabbits. In pigs, no consistent correlated responses between

240   ovulation rate and weight from birth to the end of the fattening period were obtained,

241   being most of them close to zero (Ruíz-Flores and Johnson, 2001; Rosendo *et al.*,

242   2007; Hsu and Johnson, 2014). In agreement with our results, Bidanel *et al.* (1996)

243   reported positive and low genetic correlations between ovulation rate and average

244   daily gain, (0.20 ± 0.06). Finally, line OR_LS showed also positive genetic correlations

245   between OR and growth variability traits, which are the first estimations in commercial

246   prolific species. Phenotypic correlations between OR and growth traits and between

247   OR and variability of growth traits were also positive

248

249   *Correlated response to selection*

250   Rabbit line OR_LS was obtained by selection of high ovulation rate for six generations

251   (first period) and then by two-stage selection for ovulation rate and litter size for 11

252   generations (second period). Correlated responses to selection were estimated at the

253   end of both selection periods as the difference of the average breeding values between

254   the end and the beginning of each period. Both selection periods are shown in all

255   figures. In the first period, selection for ovulation rate for six generations improved OR

256   in 0.24 ova per generation (corresponding to an improvement of 1.5 % per generation)

257   but showed a low correlated response on litter size (0.07 kits per generation, 0.8 % per

258   generation) (Badawy *et al.*, 2019). Correlated responses on WW, SW and GR were

259   found (Figure 1) being 2.7, 11.3 and 8.5 grams per generation, respectively. The

260   correlated response on WW corresponded to 0.5 % per generation which was

261   estimated as the percentage of the response of selection by generation (0.016 / 6)

262   respect to the raw mean (0.50). Similarly, the response on SW and GR corresponded

263 to 0.7 % and 0.7 % per generation respectively. However, correlated response on

264 variability growth traits was close to zero (Figure 2). In pigs, selection by ovulation rate

265 increased the weight at puberty, although no correlated response on weaning weight

266 was found (Rosendo *et al.*, 2007). In the selection experiment by ovulation rate

267 performed by Cunningham *et al.* (1979), no correlated responses were obtained for

268 litter birth weight and litter weaning weight.

269

270 In the second period of selection, Badawy *et al.* (2019) found a lower response in OR

271 (0.17 ova; i.e., 1.0 % per generation) and a higher response in litter size (0.17 kits; i.e.,

272 1.9 % per generation) than in the first period after 11 generations of two-stage

273 selection. During this second period of selection, in agreement with a reduction of

274 response on OR, the correlated response on growth traits was lower (Figure 1); 1.9,

275 8.0 and 5.4 grams, which means an improvement around 0.4 %, 0.5 % and 0.4 % per

276 generation for WW, SW and GR, respectively. In addition, correlated responses on

277 variability growth traits were not found (Figure 2). No substantial changes in weight

278 variability are in agreement to the non-variation in postnatal survival from birth to

279 slaughter previously described in this line by Badawy *et al.* (2019).

280

281 The moderate positive genetic correlation estimated between OR and growth traits

282 could explain the differences in correlated response between the two selection periods.

283 During the first period of selection, a higher increase of ovulation rate was achieved,

284 which is associated to a higher correlated response on growth traits. The positive

285 correlated response in growth traits was in concordance with the results obtained in a

286 pig line selected by the same selection criterion, a first period by ovulation rate and

287 thereafter by two-stage selection for ovulation rate and number of fully formed pigs

288 (Ruíz-Flores and Johnson, 2001). These authors showed a positive correlated

289 response on weight at birth, at weaning and at 125 days. No information about

290 correlated response on weight variability was provided in this two-stage experiment in

291 pigs.

292

293 To sum up, selection for ovulation rate and for independent culling levels for ovulation

294 rate and litter size resulted in a slight increase in weight at weaning and slaughter,

295 whereas the variability of these weights did not increase. These results are in

296 concordance with the no correlated responses on survivals at weaning and at slaughter

297 found in rabbit line OR_LS (Badawy *et al.*, 2019). No negative consequences on

298 growth traits can be expected in current commercial maternal lines.

299

304

305 **Declaration of interest**

306 The authors declare no *conflict of interest* in this article.

307

308 **Ethic statement**

309 All experimental procedures involving animals were approved by the Universitat

310 Politècnica de València Research Ethics Committee.

311

312 **Software and data repository resources**

313   None of the data were deposited in an official repository.

314

315   **References**

316   Argente MJ, Santacreu MA, Climent A and Blasco A 1999. Phenotypic and genetic parameters

317   of birth weight and weaning weight of rabbits born from unilaterally ovariectomized and

318   intact does. Livestock Production Science 57, 159–167.

319   Badawy AY, Peiró R, Blasco A and Santacreu MA 2019. Correlated responses on litter traits

320   and survival traits after two-stage selection for ovulation rate and litter size in rabbits.

321   Animal. Animal 13 (3), 453-459.

322   Bidanel JP, Gruand J and Legault C 1996. Genetic variability of age and weight at puberty,

323   ovulation rate and embryo survival in gilts and relationship with production traits.

324   Genetics Selection Evolution 28, 103–115.

325   Cunningham PJ, England ME, Young LD and Zimmerman DR 1979. Selection for ovulation

326   rate in swine: correlated response in litter size and weight. Journal of Animal Science 48,

327   509–516.

328   Damgaard LH, Rydhmer L, Løvendahl P and Grandinson K 2003. Genetic parameters for

329   within-litter variation in piglet birth weight and change in within-litter variation during

330   suckling. Journal of Animal Science 80, 604–610.

331   Drummond H, Vázquez E, Sánchez-Colón S, Martínez-Gómez M and Hudson R 2000.

332   Competition for milk in the domestic rabbit: survivors benefit from littermate deaths.

333   Ethology 106, 511–526.

334   Drouilhet L, Gilbert H, Balmisse E, Ruesche J, Tircazes A, Larzul C and Garreau H 2013.

335   Genetic parameters for two selection criteria for feed efficiency in rabbits. Journal of

336   Animal Science 91, 3121–3128.

337   García ML and Baselga M 2002. Estimation of correlated response on growth traits to selection

338   in litter size of rabbits using cryopreserved control population and genetic trends.

339   Livestock Production Science 78, 91–98.

340   Hsu WL and Johnson RK 2014. Analysis of 28 generations of selection for reproduction,

341   growth, and carcass traits in swine. Journal of Animal Science 92, 4806–4822.

342   Legarra A, Varona L and López de Maturana E 2008. Program TM. Retrieves on 28 September

343   2017, from http://snp.toulouse.inra.fr/~alegarra/

344   Mínguez C, Sánchez JP, el Nagar AG, Ragab M and Baselga M 2016. Growth traits of four

345   maternal lines of rabbits founded on different criteria: comparisons at foundation and at

346   last periods after selection. Journal of Animal Breeding and Genetics 133, 303–315.

347   Mocé ML and Santacreu MA 2010. Genetic improvement of litter size in rabbits: a review. CD

348   In Proceeding of the 9th World Congress on Genetics Applied to Livestock Production, 1-

349   6 August 2010, Leipzig, Germany, communication 25.

350   Piles M, Gómez EA, Rafel O, Ramon J and Blasco A 2004. Elliptical selection experiment for

351   the estimation of genetic parameters of the growth rate and feed conversion ratio in

352   rabbits. Journal of Animal Science 82, 654–660.

353   Rosendo A, Canario L, Druet T, Gogue J and Bidanel JP 2007. Correlated responses of pre-

354   and postweaning growth and backfat thickness to six generations of selection for

355   ovulation rate or prenatal survival in French Large White pigs. Journal of Animal Science

356   85, 3209–3217.

357   Ruíz-Flores A and Johnson RK 2001. Direct and correlated responses to two-stage selection

358   for ovulation rate and number of fully formed pigs at birth in swine. Journal of Animal

359   Science 79, 2286–2297.

360   Wolf J, Záková E and Groeneveld E 2008. Within-litter variation of birth weight in hyperprolific

361   Czech Large White sows and its relation to litter size traits, stillborn piglets and losses

362   until weaning. Livestock Science 115, 195–205.

363   Zhang T, Wang LG, Shi HB, Yan H, Zhang LC, Liu X, Pu L, Liang J, Zhang YB, Zhao KB and

364   Wang LX 2016. Heritabilities and genetic and phenotypic correlations of litter uniformity

365   and litter size in Large White sows. Journal of Integrative Agriculture 15, 848–854.

366   Ziadi C, Mocé ML, Laborda P, Blasco A and Santacreu MA 2013. Genetic selection for

367   ovulation rate and litter size in rabbits: estimation of genetic parameters, direct and

368   correlated responses. Journal of Animal Science 91, 3113–3120.

369 **Table 1** *Descriptive statistics for weaning weight (WW, kg), slaughter weight (SW, kg),*

370 *growth rate (GR, kg) and their variability (DWW, DSW and DGR) in OR_LS line[1]*

Trait	N	Mean	SD	CV (%)
WW	30,420	0.50	0.12	23.9
SW	29,075	1.74	0.24	13.8
GR	29,057	1.24	0.17	13.7
DWW	30,420	0.05	0.04	82.7
DSW	29,075	0.11	0.10	90.5
DGR	29,057	0.08	0.08	97.8

371 N= Number of records; SD= Standard deviation; CV= Coefficient of variation.

372 [1] OR_LS line is a rabbit line selected for ovulation rate at second gestation from generation 0 to 6 and

373 later for ovulation rate at second gestation and litter size of the first two parities from generation 7 to 17.

Table 2 *Features of marginal posterior distributions of the heritability (h^2), proportion of the common litter effect variance respect to phenotypic variance (c^2) and proportion of the maternal effect variance respect to phenotypic variance (m^2) for weaning weight (WW), slaughter weight (SW), growth rate (GR) and their variability (DWW, DSW and DGR) in OR_LS line[1]*

	h^2					m^2					c^2				
Trait	Mean	HPD$_{95\%}$	P$_{0.10}$	Z	MCse	Mean	HPD$_{95\%}$	P$_{0.10}$	Z	MCse	Mean	HPD$_{95\%}$	P$_{0.10}$	Z	MCse
WW	0.09	[0.05,0.12]	0.22	1.12	0.003	0.11	[0.09,0.13]	0.76	1.76	0.003	0.35	[0.33,0.37]	1.00	-0.78	0.008
SW	0.13	[0.09,0.17]	0.92	0.89	0.004	0.05	[0.03,0.06]	0.00	-1.14	0.002	0.28	[0.26,0.30]	1.00	0.32	0.007
GR	0.14	[0.10,0.18]	0.97	0.08	0.003	0.01	[0.00,0.02]	0.00	-0.25	0.001	0.27	[0.25,0.29]	1.00	-0.12	0.008
DWW	0.01	[0.00,0.03]	0.00	0.59	0.001	0.01	[0.00,0.01]	0.00	0.36	0.001	0.07	[0.05,0.10]	0.08	-1.49	0.004
DSW	0.004	[0.00,0.01]	0.00	0.94	0.0001	0.003	[0.00,0.01]	0.00	1.49	0.002	0.10	[0.07,0.14]	0.55	1.67	0.004
DGR	0.01	[0.00,0.03]	0.00	0.87	0.001	0.01	[0.00,0.02]	0.00	0.65	0.001	0.14	[0.10,0.17]	0.93	-0.98	0.006

HPD$_{95\%}$= High posterior density interval at 95 %; P$_{0.10}$= Probability of the proportion being higher than 0.10; Z= Geweke's Z-score; MCse= Monte Carlo standard error.

[1] OR_LS line is a rabbit line selected for ovulation rate at second gestation from generation 0 to 6 and later for ovulation rate at second gestation and litter size of the first two parities from generation 7 to 17.

Table 3 *Features of marginal posterior distributions of the genetic (r_g) and phenotypic (r_p) correlation of litter size (LS) and ovulation rate (OR) with weaning weight (WW), slaughter weight (SW), growth rate (GR) and their variability (DWW, DSW and DGR) in OR_LS line[1]*

	r_g								r_p			
Trait	Mean	HPD$_{95\%}$	P	Ps	P$_{30}$	Z	MCse	Mean	HPD$_{95\%}$	Z	MCse
LS, WW	-0.11	[-0.43,0.23]	0.73	0.87	0.09	-1.35	0.004	0.02	[-0.04,0.09]	-0.61	0.001
LS, SW	0.03	[-0.27,0.34]	0.58	0.94	0.04	0.82	0.001	0.07	[-0.03,0.16]	0.18	0.003
LS, GR	0.11	[-0.18,0.42]	0.76	0.89	0.11	1.69	0.003	0.09	[-0.02,0.19]	0.96	0.004
LS, DWW	-0.06	[-0.47,0.33]	0.58	0.80	0.16	1.15	0.002	0.01	[-0.07,0.09]	1.59	0.001
LS, DSW	-0.16	[-0.56,0.18]	0.63	0.70	0.30	-0.29	0.004	-0.12	[-0.19,0.-05]	-1.75	0.002
LS, DGR	-0.20	[-0.62,0.21]	0.77	0.66	0.34	-0.35	0.005	-0.15	[-0.21,0.-07]	1.29	0.002
OR, WW	0.19	[-0.07,0.45]	0.92	0.81	0.19	-1.78	0.004	0.29	[0.04,0.50]	0.09	0.004
OR, SW	0.38	[0.16,0.60]	1.00	0.23	0.77	1.02	0.005	0.33	[0.04,0.58]	0.67	0.005
OR, GR	0.36	[0.14,0.58]	1.00	0.29	0.71	0.85	0.006	0.30	[-0.02,0.57]	0.55	0.004
OR, DWW	0.35	[-0.02,0.70]	0.91	0.35	0.65	1.36	0.006	0.10	[-0.04,0.25]	-0.48	0.002
OR, DSW	0.62	[0.24, 0.90]	1.00	0.07	0.93	-0.91	0.007	0.32	[0.16,0.42]	-0.95	0.006
OR, DGR	0.20	[-0.18,0.53]	0.78	0.62	0.38	-0.74	0.006	0.38	[0.21,0.51]	0.33	0.006

384   HPD$_{95\%}$ = High posterior density interval at 95 %; P = Probability of the r_g being higher than zero when the mean is positive or lower than zero when it is negative;

385   Ps= Probability of similitude; probability of the r_g being between -0.30 and 0.30; P$_{30}$= Probability of the r_g being higher than 0.30 when r_g>0 or lower than -0.30

386   when r_g<0; Z= Geweke's Z-score; MCse= Monte Carlo standard error.

387   [1]OR_LS line is a rabbit line selected for ovulation rate at second gestation from generation 0 to 6 and later for ovulation rate at second gestation and litter size

388   of the first two parities from generation 7 to 17.

Figure 1. Genetic trends for weaning weight (WW), slaughter weight (SW) and growth rate (GR) of OR_LS line. OR_LS line is a rabbit line selected for ovulation rate at second gestation from generation 0 to 6 and later for ovulation rate at second gestation and litter size of the first two parities from generation 7 to 17. Values represent the mean of the estimated breeding value of the trait at the end of both selection periods.

Figure 2. Genetic trends for weaning weight variability (DWW), slaughter weight variability (DSW) and growth rate variability (DGR) of OR_LS line. OR_LS line is a rabbit line selected for ovulation rate at second gestation from generation 0 to 6 and later for ovulation rate at second gestation and litter size of the first two parities from generation 7 to 17. Values represent the mean of the estimated breeding value of the trait at the end of both selection periods.