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

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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 (c²; 0.35, 0.28 and 0.27) and low maternal effects (m²; 0.11, 0.05 and 0.01) were obtained for WW, SW and GR, respectively. Both, c² and m² 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.
**Keywords:** genetic parameters, growth rate, slaughter weight, variability growth traits, weaning weight.

**Implications**

It is important to assess the effect on growth traits when selecting by ovulation rate and litter size since growth is one of the main objectives in rabbit selection programs. The increase of litter size at weaning and at slaughter time after two-stage selection by ovulation rate and litter size does not reduce weaning and commercial weight. The selection does not also modify variability growth traits. Therefore, two-stage selection by ovulation rate and litter size could be used as a selection criterion in maternal rabbit lines since no negative consequences on growth traits were observed.

**Introduction**

Growth rate and litter size are the most common selection criteria for commercial lines. Two-stage selection by ovulation rate and litter size has been proposed as a way to improve more efficiently litter size at birth, weaning and slaughter than direct selection for litter size at weaning in rabbits (Badawy et al., 2019). However, it is unknown the consequences of this kind of selection on growth traits (weaning weight, slaughter weight and growth rate) and their variability in rabbits. It is known that increasing the number of total kits born can reduce the weight at birth and increases the intra-litter weight variability, reducing the probability of postnatal survival in rabbits (Argente et al., 1999) and pigs (Damgaard et al., 2003; Wolf et al., 2008; Zhang et al., 2016). Genetic correlations between litter size and growth traits in rabbits are generally low, 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 (Ruiz-Flores and Johnson, 2001; Rosendo et al., 2007), weight at 125 and at 178 days (Ruiz-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
17, respectively. Details about breeding and feeding management were described by Badawy et al. (2019).

**Traits**

Weaning weight (WW, kg) and slaughter weight (SW, kg) of each young rabbit were measured individually at 28 and 63 days of age, respectively. Growth rate (GR, kg) was estimated as the difference between SW and WW. The variability of WW, SW and GR was calculated as the absolute value of the difference between the individual value and the mean value of its litter (DWW, DSW and DGR in kg, respectively)). Litter size (LS) was measured as the total number of kits born per litter up to five parities. Ovulation rate (OR), estimated as the number of corpora lutea, was measured at second and last gestation. More details about reproductive traits have been given by Badawy et al. (2019). Number of records for weaning weight (WW), slaughter weight (SW) and growth rate (GR) was 30,420, 29,075 and 29,057, respectively. The same number of data was also used to estimate the growth variability traits (Table 1). These data came from 1,317 dams with 4,027 litters. Data from 1,210 ovulation rates and 4,480 parities were analyzed. The number of animals in the pedigree was 30,666.

**Statistical Analysis**

Bayesian inference methods were used to analyze data from all generations of selection. Trivariate animal models were fitted to estimate genetic parameters and responses. Each trivariate analysis included the selected traits (LS and OR) and one of each growth traits (WW, SW, GR, DWW, DSW and DGR). The repeatability animal model used for analyzing OR and LS was described by Badawy et al. (2019).
The model used for analyzing WW, SW, GR, DWW, DSW and DGR was:

\[ y_{ijkl} = b \text{NBA}_{ijk} + \text{YS}_i + \text{PO}_j + m_k + c_{ijk} + a_{ijkl} + e_{ijkl} \]

in which, \( y_{ijkl} \) is the record of the trait of animal \( l \); \( \text{NBA}_{ijk} \) is the number of kits born alive in which the animal \( l \) was born and \( b \) is the regression coefficient on \( \text{NBA} \); \( \text{YS}_i \) is the effect of year season (three months per each year season; 46 levels); \( \text{PO}_j \) is the effect of the parity order in which the animal was born (4 levels: 1\textsuperscript{st}, 2\textsuperscript{nd}, 3\textsuperscript{rd} and >3\textsuperscript{rd}); \( m_k \) is the environmental maternal random effect of the overall parities of the dam of the animal \( l \); \( c_{ijk} \) is the random effect of the common litter in which the animal \( l \) was born; \( a_{ijkl} \) is the random additive value of animal \( l \), and \( e_{ijkl} \) is the residual effect.

Common litter effect ratio \((c^2)\) was defined as the ratio between the variance of common litter effects and the phenotypic variance, and maternal effect ratio \((m^2)\) was defined as the ratio between the variance of permanent environmental effects and the phenotypic variance. The joint prior distribution assumed for additive genetic effects was \( N(0, \textbf{A} \otimes \textbf{G}_a) \), where \( \textbf{G}_a \) was the genetic (co)variance matrix between the traits and \( \textbf{A} \) was the additive genetic relationship matrix. Environmental maternal effects \((m_k)\) of growth traits and permanent environmental effect of the doe \((p_k)\) on LS and OR are correlated. The joint prior distribution for the permanent environmental effect of the doe \((p_k)\) and the maternal effect on growth trait \((m_k)\) was \( N(0, \textbf{I} \otimes \textbf{G}_p) \), where \( \textbf{G}_p \) was the (co)variance matrix between these effects. There is a correlation between the residual term of the reproductive trait and the common litter effect \((c_{ijk})\) of the growth trait (García and Baselga, 2002; Mínguez \textit{et al.}, 2016), therefore an environmental covariance structure between growth traits and reproductive traits was established. The prior distribution for the common litter effect \((c_{ijk})\) of one of the growth traits and the residual term of the one of reproductive traits was \( N(0, \textbf{I} \otimes \textbf{G}_c) \), where \( \textbf{G}_c \) was the (co)variance
matrix between these effects. The residual prior distributions for all traits were $N(0, \sigma_i^2)$.

The order of the identity matrix $I$ was equal to the number of records measured in each case. Bounded uniform priors were used for the components of the (co)variance matrices. The program TM (Legarra et al., 2008) was used for Gibbs sampling procedures. Chains of 3,000,000 samples each were used, with a burn-in period of 750,000. One sample in each 100 was saved to avoid high autocorrelation between consecutive samples. Geweke's Z-score was estimated to test the chain convergence.

A heritability higher than 0.10 was considered relevant for growth traits. Selection on growth traits with heritability lower than 0.10 leads to low genetic responses per generation. Similarly to Badawy et al. (2019), the relevant value for correlation was 0.3 (in absolute value) considering the low percentage of the explained variance. The features of the marginal posterior distributions showed in Tables 2 and 3 were also described by Badawy et al. (2019).

**Results and discussion**

Means, standard deviations (SD) and coefficients of variation (CV) for growth traits and their variability are shown in Table 1. Values for growth traits were similar to those presented in several maternal lines selected for number of kits at weaning (García and Baselga, 2002; Mínguez et al., 2016). For example, Mínguez et al. (2016) obtained mean values of $0.57 \pm 0.13$ kg, $1.86 \pm 0.26$ kg and $36.70 \pm 5.70$ g/d for weaning and slaughter weights and growth rate, respectively, after analyzing a large set of data from four maternal lines. Up to now, there is no information about the individual variability of weights at weaning and slaughter in rabbits. The raw values for variability growth traits were low, ranging from 0.05 to 0.11 kg, and the coefficients of variation were
high. Argente et al. (1999) studied the standard deviation of weaning weight within litter obtaining a value close to 0.07 kg.

The effect of the covariate NBA for all growth traits was negative (-0.028±0.002 for WW, -0.041±0.003 for SW and -0.012±0.001 for GR; data not shown) and showed high accuracy. These results were in concordance with the correlated response on growth traits in selected maternal lines found by García and Baselga (2002) and Mínguez et al. (2016). Drummond et al. (2000) and Poigner et al. (2000) also observed that larger litters had a lower average birth weight and lower growth rate from birth to weaning than smaller litters. The effect of the covariate NBA for all growth variability traits was positive (0.0008±0.0001 for DWW, 0.0032±0.0001 for DSW, and 0.0021±0.0001 for DGR) and also showed high accuracy.

**Genetic parameters**

*Heritabilities.* The heritabilities for the selection criteria traits, OR and LS, were 0.25 (HPD$_{95\%}$=0.17-0.33) and 0.10 (HPD$_{95\%}$=0.05-0.14), respectively (Badawy et al.; 2019). Features of the marginal posterior distributions of the heritability for growth traits and their variability are shown in Table 2. Heritability estimates for growth traits were low. The probability of the heritability being higher than 0.10 was high for SW and GR, whereas the heritability of WW was likely to be lower than 0.10. Low to moderate heritabilities for growth traits depending on the rabbit populations or the methods of estimation have been reported (Argente et al., 1999; Drouilhet et al., 2013; Mínguez et al., 2016). Monte Carlo standard errors for all estimations were small, less than or equal to 0.008, and no lack of convergence was detected by Geweke test.
Genetic variation for growth variability traits was negligible. In rabbits, no previous estimations of heritabilities for growth variability traits were reported. In pigs, heritabilities for variability of weight at birth and at weaning, measured as intra-litter standard deviation were also low, ranged from 0.05 to 0.08 (Damgaard et al., 2003; Wolf et al., 2008; Zhang et al., 2016). The heritabilities of weight variability were lower than those for weight at birth and at weaning as in in our results (from 0.10 to 0.39).

Common litter ($c^2$) and maternal ($m^2$) effects ratio. Features of marginal posterior distributions of common litter and maternal effects ratio for growth traits are shown in Table 2. All estimations showed a high accuracy. Estimated values for common litter effect ratio were moderate for all growth traits being 0.35 for WW, 0.28 for SW and 0.27 for GR, and with high probability of being higher than 0.10. These results show that common litter effect ratio decreases over time, as expected. Maternal effect ratio was low for WW and SW and negligible for GR. Similar estimations for common litter effects ratio for WW, SW and GR were obtained in rabbit maternal lines by García and Baselga (2002) and for common litter and maternal effects ratio by Mínguez et al. (2016). However, higher estimations for maternal effects ratio (0.18, 0.21 and 0.26, respectively) were reported by García and Baselga (2002). In agreement with our results, relevant litter common and maternal effect ratios were also found in rabbit lines selected by growth rate and food efficiency traits (Drouilhet et al., 2013). Our results support the important influence of a pre-weaning environment provided by the female on growth at least until slaughter in rabbits. Regarding variability growth traits, common litter effect ratio for DWW, DWS, and DGR showed values closed to 0.10. However, 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
correlations at least 0.65. There are no studies about the genetic relationship between OR and growth traits in rabbits. In pigs, no consistent correlated responses between ovulation rate and weight from birth to the end of the fattening period were obtained, being most of them close to zero (Ruiz-Flores and Johnson, 2001; Rosendo et al., 2007; Hsu and Johnson, 2014). In agreement with our results, Bidanel et al. (1996) reported positive and low genetic correlations between ovulation rate and average daily gain, (0.20 ± 0.06). Finally, line OR_LS showed also positive genetic correlations between OR and growth variability traits, which are the first estimations in commercial prolific species. Phenotypic correlations between OR and growth traits and between OR and variability of growth traits were also positive

**Correlated response to selection**

Rabbit line OR_LS was obtained by selection of high ovulation rate for six generations (first period) and then by two-stage selection for ovulation rate and litter size for 11 generations (second period). Correlated responses to selection were estimated at the end of both selection periods as the difference of the average breeding values between the end and the beginning of each period. Both selection periods are shown in all figures. In the first period, selection for ovulation rate for six generations improved OR in 0.24 ova per generation (corresponding to an improvement of 1.5 % per generation) but showed a low correlated response on litter size (0.07 kits per generation, 0.8 % per generation) (Badawy et al., 2019). Correlated responses on WW, SW and GR were found (Figure 1) being 2.7, 11.3 and 8.5 grams per generation, respectively. The correlated response on WW corresponded to 0.5 % per generation which was estimated as the percentage of the response of selection by generation (0.016 / 6) respect to the raw mean (0.50). Similarly, the response on SW and GR corresponded
to 0.7 % and 0.7 % per generation respectively. However, correlated response on variability growth traits was close to zero (Figure 2). In pigs, selection by ovulation rate increased the weight at puberty, although no correlated response on weaning weight was found (Rosendo et al., 2007). In the selection experiment by ovulation rate performed by Cunningham et al. (1979), no correlated responses were obtained for litter birth weight and litter weaning weight.

In the second period of selection, Badawy et al. (2019) found a lower response in OR (0.17 ova; i.e., 1.0 % per generation) and a higher response in litter size (0.17 kits; i.e., 1.9 % per generation) than in the first period after 11 generations of two-stage selection. During this second period of selection, in agreement with a reduction of response on OR, the correlated response on growth traits was lower (Figure 1); 1.9, 8.0 and 5.4 grams, which means an improvement around 0.4 %, 0.5 % and 0.4 % per generation for WW, SW and GR, respectively. In addition, correlated responses on variability growth traits were not found (Figure 2). No substantial changes in weight variability are in agreement to the non-variation in postnatal survival from birth to slaughter previously described in this line by Badawy et al. (2019).

The moderate positive genetic correlation estimated between OR and growth traits could explain the differences in correlated response between the two selection periods. During the first period of selection, a higher increase of ovulation rate was achieved, which is associated to a higher correlated response on growth traits. The positive correlated response in growth traits was in concordance with the results obtained in a pig line selected by the same selection criterion, a first period by ovulation rate and thereafter by two-stage selection for ovulation rate and number of fully formed pigs
(Ruiz-Flores and Johnson, 2001). These authors showed a positive correlated response on weight at birth, at weaning and at 125 days. No information about correlated response on weight variability was provided in this two-stage experiment in pigs.

To sum up, selection for ovulation rate and for independent culling levels for ovulation rate and litter size resulted in a slight increase in weight at weaning and slaughter, whereas the variability of these weights did not increase. These results are in concordance with the no correlated responses on survivals at weaning and at slaughter found in rabbit line OR_LS (Badawy et al., 2019). No negative consequences on growth traits can be expected in current commercial maternal lines.

Acknowledgements

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Declaration of interest

The authors declare no conflict of interest in this article.

Ethic statement

All experimental procedures involving animals were approved by the Universitat Politècnica de València Research Ethics Committee.

Software and data repository resources
None of the data were deposited in an official repository.

References


Table 1 Descriptive statistics for weaning weight (WW, kg), slaughter weight (SW, kg), growth rate (GR, kg) and their variability (DWW, DSW and DGR) in OR_LS line.

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

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

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 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 \((DWW, DSW \text{ and } DGR)\) in OR_LS line\(^1\)

<table>
<thead>
<tr>
<th>Trait</th>
<th>Mean</th>
<th>HPD(_{95})%</th>
<th>(P_{0.10})</th>
<th>(Z)</th>
<th>MCse</th>
<th>Mean</th>
<th>HPD(_{95})%</th>
<th>(P_{0.10})</th>
<th>(Z)</th>
<th>MCse</th>
<th>Mean</th>
<th>HPD(_{95})%</th>
<th>(P_{0.10})</th>
<th>(Z)</th>
<th>MCse</th>
</tr>
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<tbody>
<tr>
<td>WW</td>
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<td>[0.05,0.12]</td>
<td>0.22</td>
<td>1.12</td>
<td>0.003</td>
<td>0.11</td>
<td>[0.09,0.13]</td>
<td>0.76</td>
<td>1.76</td>
<td>0.003</td>
<td>0.35</td>
<td>[0.33,0.37]</td>
<td>1.00</td>
<td>-0.78</td>
<td>0.008</td>
</tr>
<tr>
<td>SW</td>
<td>0.13</td>
<td>[0.09,0.17]</td>
<td>0.92</td>
<td>0.89</td>
<td>0.004</td>
<td>0.05</td>
<td>[0.03,0.06]</td>
<td>0.00</td>
<td>-1.14</td>
<td>0.002</td>
<td>0.28</td>
<td>[0.26,0.30]</td>
<td>1.00</td>
<td>0.32</td>
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<tr>
<td>GR</td>
<td>0.14</td>
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<td>0.97</td>
<td>0.08</td>
<td>0.003</td>
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<td>0.001</td>
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<td>0.08</td>
<td>-1.49</td>
<td>0.004</td>
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<tr>
<td>DSW</td>
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<td>[0.00,0.01]</td>
<td>0.00</td>
<td>0.94</td>
<td>0.0001</td>
<td>0.003</td>
<td>[0.00,0.01]</td>
<td>0.00</td>
<td>1.49</td>
<td>0.002</td>
<td>0.10</td>
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<td>0.87</td>
<td>0.001</td>
<td>0.01</td>
<td>[0.00,0.02]</td>
<td>0.00</td>
<td>0.65</td>
<td>0.001</td>
<td>0.14</td>
<td>[0.10,0.17]</td>
<td>0.93</td>
<td>-0.98</td>
<td>0.006</td>
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</table>

\(\text{HPD}_{95}\)% = 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

<table>
<thead>
<tr>
<th>Trait</th>
<th>$r_g$</th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th>$r_p$</th>
<th></th>
<th></th>
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</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>HPD$_{95%}$</td>
<td>P</td>
<td>Ps</td>
<td>$P_{30}$</td>
<td>Z</td>
<td>MCse</td>
<td>Mean</td>
<td>HPD$_{95%}$</td>
<td>Z</td>
</tr>
<tr>
<td>LS, WW</td>
<td>-0.11</td>
<td>[-0.43,0.23]</td>
<td>0.73</td>
<td>0.87</td>
<td>0.09</td>
<td>-1.35</td>
<td>0.004</td>
<td>0.02</td>
<td>[-0.04,0.09]</td>
<td>-0.61</td>
</tr>
<tr>
<td>LS, SW</td>
<td>0.03</td>
<td>[-0.27,0.34]</td>
<td>0.58</td>
<td>0.94</td>
<td>0.04</td>
<td>0.82</td>
<td>0.001</td>
<td>0.07</td>
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<td>0.18</td>
</tr>
<tr>
<td>LS, GR</td>
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<td>[-0.18,0.42]</td>
<td>0.76</td>
<td>0.89</td>
<td>0.11</td>
<td>1.69</td>
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<td>[-0.02,0.19]</td>
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<tr>
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<td>[-0.47,0.33]</td>
<td>0.58</td>
<td>0.80</td>
<td>0.16</td>
<td>1.15</td>
<td>0.002</td>
<td>0.01</td>
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<tr>
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<tr>
<td>OR, SW</td>
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<td>0.38</td>
<td>[0.21,0.51]</td>
<td>0.33</td>
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HPD_{95\%} = \text{High posterior density interval at 95 \%}; P = \text{Probability of the } r_g \text{ being higher than zero when the mean is positive or lower than zero when it is negative};

P_s = \text{Probability of similitude; probability of the } r_g \text{ being between -0.30 and 0.30}; P_{30} = \text{Probability of the } r_g \text{ being higher than 0.30 when } r_g > 0 \text{ or lower than } -0.30 \text{ when } r_g < 0; Z = \text{Geweke's Z-score; MCse = Monte Carlo standard error.}

\textit{\textsuperscript{1}}\text{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.}
Figure captions

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.