Badawy Elmoghazy, AY.; Peiró Barber, RM.; Blasco Mateu, A.; Santacreu Jerez, MA. (03-2). Correlated responses on litter size traits and survival traits after two-stage selection for ovulation rate and litter size in rabbits. Animal. 13(3):453-459. https://doi.org/10.1017/S1751731118002033

The final publication is available at

https://doi.org/10.1017/S1751731118002033

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

A.Y. Badawy [1,a], R. Peiró [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: Animal Production Department, Faculty of Agriculture, 41522 Suez Canal University, Egypt.*

[b] *Present Address: Instituto de Conservación y Mejora de la Agrodiversidad Valenciana, Universitat Politècnica de València.*

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

Short title: Correlated response on reproductive traits

Abstract

This study was aiming to estimate direct and correlated response on litter size traits and peri- and postnatal survival traits in the OR_LS rabbit line selected first only for ovulation rate (first period) and then for ovulation rate and litter size using independent culling levels (second period). Farmer profit depends on the number of slaughter rabbits and it is important to asses the effect of selection on litter size and survival rate from birth to slaughter.

The studied traits were ovulation rate (OR), litter size (LS) measured as number of total born, number of kits born alive (NBA) and dead (NBD), and number of kits at weaning (NW) and young rabbits at slaughter (NS). Prenatal survival (LS/OR) and survival at birth (NBA/LS), at weaning (NW/NBA) and at slaughter (NS/NW) were also studied. Data were analysed using Bayesian inference methods. Heritability for litter size traits were low, 0.07 for NBA, NW and NS. Survival traits had low values of heritability 0.07, 0.03 and 0.03 for NBA/LS, NW/NBA and NS/NW, respectively. After six generations of selection by ovulation rate (first period), a small increase in NBD and a slight decrease in NBA/LS were found. However, no correlated responses on NW/NBA and NS/NW were observed. After 11 generations of two-stage selection for ovulation rate and litter size (second period), correlated responses on NBA, NW and NS were 0.12, 0.12 and 0.11 kits per generation respectively, whereas no substantial modifications on NBA/LS, NW/NBA and NS/NW were found. Two stage selection improve the number of young rabbits at slaughter without modifying survival from birth to slaughter.

Keywords: kits dead, prenatal survival, perinatal survival, pre-weaning survival, post-weaning survival.

Implications

Two-stage selection by ovulation rate and litter size could be a way to improve the number of commercial young rabbits more effectively than direct selection. This enhancement was due to an increase in prenatal survival and no changes in peri- and postnatal survivals in rabbits. These results could be explained by an improvement of uterine capacity.

Introduction

In rabbits, indirect selection for either uterine capacity or ovulation rate for increasing litter size has not been more effective than direct selection (Santacreu *et al.*, 2005; Laborda *et al.*, 2012). However, a higher response in litter size was found in a two-stage rabbit selection by ovulation rate and litter size (Ziadi *et al.*, 2013), in agreement with previous results in pigs (Ruiz-Flores and Johnson, 2001). These results are in accordance with the theory developed by Bennet and Leymaster (1989), which predicted that selecting both traits is more effective than selecting each of them separately.

In a two-stage selection experiment performed in pigs (Ruiz-Flores and Johnson, 2001), an increase in number of stillborn was found in a line previously selected by an index of ovulation rate and embryonic survival. In pigs, unfavourable genetic relationships between litter size and perinatal and preweaning survivals were found (Lund *et al.*, 2002; Rosendo *et al.*, 2007; Su *et al.*, 2007; Putz *et al.*, 2015), thus the improvement of litter size has usually led to a decrease in these survivals. In rabbits, this adverse genetic relationship has not been investigated, but it is known that high ovulation rate increases uterine overcrowding and therefore competition among foetuses (Laborda *et al.*, 2011, 2012). A reduction in the development of fetuses and their placentas was observed in rabbits when the number of implanted embryos increased (Argente *et al.*, 2006), which may affect perinatal and preweaning survivals.

The experiment of two-stage selection by ovulation rate and litter size in rabbits by Ziadi *et al.* (2013) did not estimated correlated responses for litter size traits and survival traits. This experiment has been continued four generations more, until generation 17. The aim of this work is to estimate direct and correlated responses on prenatal and postnatal survival and litter size traits in this line.

Materials and methods

Animals and experimental design

All experimental procedures involving animals were approved by the Universitat Politècnica de València Research Ethics Committee. Animals involved in this experiment came from a synthetic line (line OR_LS). Line OR_LS 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. More details of the experimental procedure can be found in Ziadi *et al.* (2013).

Breeding & feeding managment

The first mating of females was performed at 18 to 20 weeks of age, and then 11 to 12 days after each parity. Females that did not accept males were mated again seven days afterwards. Pregnancy was checked approximately 12 days after mating by abdominal palpation. Adult animals were housed at the farm of the Universitat Politècnica de València in individual cages (flat-deck) having extractable nest box with isolated plastic. Kits were housed in dam's cages up to weaning (28 days of age) and then were placed in flat-deck cages during fattening, until 63 days of age (eight-nine rabbits per cage). Selected rabbits were placed in individual flat-deck cages from 9 to 18 weeks of age. During fattening, rabbits were fed *ad libitum* with a commercial diet (crude protein, 15.0 %; crude fiber, 16.8 %; crude fat, 2.4 %; ash, 7.3 % as fed basis; NANTA, S.A.®, Valencia, Spain). From 63 days old, rabbits were fed with a commercial diet (crude protein, 16.5 %; crude fiber, 15.0 %; crude fat, 3.0 %; ash, 7.8 % as fed basis; NANTA, S.A.®). Animals were reared under a photoperiod of 16-hours light: 8-hours dark and controlled temperature and ventilation.

Traits measured

1. Litter traits recorded in up to five parities

a. Ovulation rate (OR): Estimated as the number of corpora lutea, it was measured by laparoscopy at day 12 of second gestation. A second measurement of OR was done postmortem in the last gestation.

b. Litter size (LS): Measured as number of total born at parturition.

c. Number of kits born alive (NBA): Number of kits born alive at parturition.

d. Number of kits born dead (NBD): Number of kits born dead at parturition.

e. Number of kits at weaning (NW): Number of kits at 28 days of age (weaning) per litter.

f. Number of young rabbits at slaughter (NS): Number of young rabbits at 63 days of age (slaughter) per litter.

2. Survival traits

a. Prenatal survival (LS/OR): Survival from ovulation to birth.

b. Survival from ovulation to slaughter (NS/OR) (a & b estimated from second gestation).

c. Perinatal survival (NBA/LS): Survival at birth.

d. Survival at weaning (NW/NBA): Survival from birth to weaning.

e. Survival at slaughter (NS/NW): Survival from weaning to slaughter.

f. Survival from birth to slaughter (NS/LS) (c, d, e & f estimated in up to five parities).

Data from 1210 laparoscopies and 4480 parities were analysed. Number of records for each trait is presented in Table 1 and were obtained from August of 2001 to January of 2014. The number of animals in the pedigree was 30 666.

Statistical Analysis

Data from 17 generations (six from the first selection period and 11 from the second one) were analysed using Bayesian inference methods. The model used to analyse the data for all traits, except for NBA/OR and NS/OR, was:

$$y_{ijkl} = YS_i + L_j + a_k + p_k + e_{ijkl}$$

in which, y_{ijkl} is the record of the trait, YS_i is the effect of year season (three months per each year season; 44 levels for OR and 49 levels for the other traits), L_j is the effect of lactation status at mating (four levels for OR; lactating primiparous, non-lactating primiparous, lactating multiparous and non-lactating multiparous; five levels for the other traits; nulliparous status was also included), a_k is the genetic additive value of the animal k, p_k is the permanent environmental effect of the female k, and e_{ijkl} is the residual of the model. Number of kits born dead (NBD) was analysed as a threshold trait, divided into three categories (zero; from one to three; more than three).

The model used to analyse survival from ovulation to birth (NBA/OR) and survival from ovulation to slaughter (NS/OR) had no permanent environmental effect, since there was only data from the second gestation. For both traits, the effect of year season had 38 levels and the effect of lactation status at mating had two levels, lactating and non-lactating primiparous females.

Heritabilities and correlations between OR and LS were estimated using a bivariate analysis. Heritabilities and correlations for the other traits were estimated using a trivariate analysis including the selection criteria (OR and LS) and one of the remaining traits.

Random effects were considered independent between them. The joint prior distribution assumed for additive genetic effects was $N(\mathbf{0},\mathbf{A}\otimes\mathbf{G_a})$, where $\mathbf{G_a}$ was the genetic (co)variance matrix between the additive effects of the traits and **A** was the additive genetic relationship matrix. The joint prior distribution assumed for permanent effects was $N(\mathbf{0},\mathbf{I}\otimes\mathbf{G_p})$, where $\mathbf{G_p}$ was the (co)variance matrix between the permanent effects of the traits. The residual prior distribution for all traits was $N(\mathbf{0},\mathbf{I}\boldsymbol{\sigma}^2_\mathbf{e})$. Bounded uniform priors were used for all fixed effects and the (co)variance matrices.

Gibbs sampling algorithm was used to estimate marginal posterior distributions of all unknowns. Data augmentation was done to obtain the same design matrices (Blasco, 2017). The program TM (Legarra *et al.*, 2008) was used for Gibbs sampling procedures. Markov chains of 3000000 iterations and a burn-in period of 750000 was used. In order to reduce autocorrelation between consecutive samples, one sample every 100th iterations was saved. Monte Carlo standard errors were estimated and convergence was tested using the Z criterion of Geweke.

We considered a heritability to be irrelevant when it was lower than 0.10. In the case of correlation, we considered to be an irrelevant value all correlations in absolute value lower than 0.30, since the percentage of the variance explained by the other trait (r^2) is less than 10 %. The features of the marginal posterior distributions used were: mean, high posterior density interval at 95 % ($HPD_{95\%}$), probability of the mean being higher (or lower) than zero (P), probability of relevance (P_r, probability of being higher (or lower) than the assumed relevant value), probability of similitude (P_s, probability of being in absolute value lower than the assumed relevant value) and the guaranteed value (k) at 80 % (value k of the interval [k, 1] containing the 80 % of the probability). All these features are described in Blasco (2017).

Results and discussion

Income in meat rabbit depends on the number of rabbits arriving at slaughter (Cartuche *et al.*, 2014). We know that two-stage selection for ovulation rate and litter size increase the number of total born (Ziadi *et al.*, 2013) and it is important to asses the effect on litter size and survival rate from birth to slaughter. Means, standard deviations (SD) and coefficients of variation (CV) for litter size traits and survival rates are shown in Table 1. These values are in the range of those published in maternal rabbit lines by García and Baselga (2002a) and Laborda *et al.* (2012). For NBD, the coefficient of variation was extremely high because approximately 50 % of data are zero. Survival from ovulation until slaughter were less than fifty per cent of the number of ova shed and the seventy five per cent of this loss occurs before birth. Postnatal survivals were high, close to 0.90.

Similar genetic parameters and response to selection by generation were found for OR, LS and prenatal survival by Ziadi *et al.* (2013) analyzing the same experiment with four generations less.

Heritability

Features of the marginal posterior distributions of the heritability are shown in Table 2. All Monte Carlo standard errors (MCse) were very small and lack of convergence was not detected by the Geweke test. Heritabilities were low and not relevant for NBA, NW and NS (0.07). These heritabilities for litter size from birth to slaughter were in agreement with other studies in rabbit maternal lines (García and Baselga, 2002a; Ragab and Baselga, 2011).

According to our knowledge, there are no heritability estimations for NBD and postnatal survival traits in rabbits. The heritability for NBD, analyzed as threshold trait, was relevant (0.14), $P_{0.10}$=0.92. In pigs, similar heritability was found by Arango *et al*. (2005) analyzing data from Large White sows using also a threshold model. However, Ruiz-Flores and Johnson (2001) found a higher heritability (0.29 ± 0.05) analyzing the number of stillborn as a linear trait. Heritabilities for postnatal survival traits were low and not relevant, ranging from 0.03 (NW/NBA) to 0.07 (NBA/LS). For survival from birth to weaning and from weaning to slaughter, heritabilities were close to zero. Regarding survival at birth, Lund *et al.* (2002) found the same heritability to our estimation in pigs, but slightly higher heritabilities were found by Damgaard *et al.*

(2003) and by Su *et al.* (2007), ranging from 0.10 to 0.13. In concordance to our results, Su *et al.* (2007) found that heritability of survival at birth was higher than survival after birth. When these authors evaluated survival at birth as a piglet trait, lower heritability was obtained (Su *et al.*, 2007; Kapell *et al.*, 2011). In general, heritabilities of litter size and peri- and postnatal survivals at different times were low, although for NBD, LS/OR and NS/OR were relevant.

Permanent environmental effect

Features of the marginal posterior distributions of the permanent environmental effect are also shown in Table 2. The permanent environmental effects on litter size traits and survival traits were of the same magnitude to the additive effects. Permanent effects for NBA, NW and NS were consistent with results obtained in rabbits, for example García and Baselga (2002a) and Ragab and Baselga (2011). To our knowledge, there is no information about permanent environmental effect of NBD analyzed with a threshold model in rabbits and pigs.

Regarding peri- and postnatal survival traits, survival at birth showed the highest permanent effect (0.07), decreasing at weaning and slaughter. No literature was found in relation to permanent environmental effects of peri- and postnatal survival traits in rabbits. In pigs, in general, Su *et al.* (2007), Kapell *et al.* (2011) and Putz *et al.* (2015) obtained similar permanent effect for survival at birth and they observed that permanent effect decreased from birth to weaning.

Correlations between litter size and other traits

Features of the marginal posterior distributions of the phenotypic and genetic correlations between litter size and other traits are shown in Table 3. We considered 0.30 as a relevant value because for a correlation of 0.30, the percentage of the variance explained by the other trait (r^2) is less than 10 %. Therefore, the probability of similitude was defined as the probability of correlation being in the interval [-0.30, 0.30].

All $HPD_{95\%}$ for genetic correlations between LS and other traits were large, except for NBA, NW and NS. Nevertheless, we can distinguish when a genetic correlation is null for practical purposes (high P_s), and when we do not have data enough to know whether the genetic correlation is null or not. The genetic correlation between LS and NBA was high and relevant, as expected. The guaranteed value (k) at 80 % of this genetic correlation was also very high, 0.85 (data not shown). High genetic correlations between LS with NW and with NS were also obtained. Positive and high values for these correlations were also found by García and Baselga (2002 a,b) in rabbits. These findings show that litter size from birth to slaughter is essentially determined by the same genes. Genetic correlation between LS and NBD was low, and we can say that it was null for practical purposes, since its probability of similitude was relatively high (0.83). In pigs, similar correlation between number of born alive and of stillborn was found by Arango *et al*. (2005). Besides, Ruiz-Flores and Johnson (2001) also found a low correlation (0.20) between total number of piglets born and number of stillborn pigs.

No information about the genetic correlation between litter size and peri- and postnatal survivals was previously published in rabbits and little is known in pigs. In our work, genetic correlations between LS and peri- and postnatal survivals were low, the $HPD_{95\%}$ were large and the probability of similitude ranging from 0.63 to 0.77. In pigs, all genetic correlations between number of total born and survival at birth were low and with low accuracy, from positive (Rosendo *et al.*, 2007; Kapell *et al.*, 2011) to negative values (Su *et al.*, 2007; Kapell *et al.*, 2011; Nielsen *et al.*, 2013). For survival from birth to weaning, we found a positive and low correlation with LS. Low to moderate negative correlations were found in pigs by Su *et al.* (2007), Rosendo *et al.* (2007) and Putz *et al.* (2015).

Correlations between ovulation rate and other traits

Features of the marginal posterior distributions of the phenotypic and genetic correlations between OR and other traits are shown in Table 4. These genetic correlations were estimated with low accuracy since it is difficult to have a large number of records of traits measured by laparoscopy. The genetic correlations for OR with NBA, NW and NS were irrelevant (Ps > 0.85); irrelevant correlation for OR with NBA was also found by Laborda *et al*. (2011). Low (positive and negative) genetic correlations between OR and litter size traits were found in pigs (Ruiz-Flores and Johnson, 2001; Johnson *et al.*, 1999). On the other hand, a relevant positive genetic correlation between OR and NBD was observed ($P_{0.30}$=0.97). Similar to our result, positive and moderate-high genetic correlations between ovulation rate and number of stillborn pigs were found by Johnson *et al.* (1999) and Ruiz-Flores and Johnson (2001).

A low and negative genetic correlation between OR and survival at birth was found. This result agrees closely with the relevant and positive genetic correlation between

OR and NBD. Similar genetic correlation between ovulation rate and survival at birth was found by Rosendo *et al.* (2007) in pigs. Low genetic correlations with low accuracy were obtained for OR and survival at weaning and also at slaughter. Genetic correlation between OR and survival from ovulation to slaughter was moderate (-0.48) and relevant ($P_{0.30}$= 0.90).

Features of the estimated marginal posterior distributions of the phenotypic correlations of LS and OR with the other traits are also showed in Tables 3 and 4. Phenotypic correlations had the same size and sign as their relative genetic correlations.

Response to selection

Genetic trends for litter size and survival traits are shown in Figures 1 and 2, respectively. Correlated responses to selection were estimated at the end of both periods of selection as the difference between the average breeding values at the end and beginning of each period. Both periods of selection were distinguished in all figures.

Selection only for ovulation rate

Selection for ovulation rate improved 1.44 ova after six generations of selection, although it did not cause the expected enhancement in LS (0.07 kits per generation) due to a decrease in prenatal survival as Ziadi *et al*. (2013) observed. No correlated response was observed for NBA while at the same time a slight increase in NBD (-0.04 kits per generation; Figure 1). At weaning, no correlated response was either observed whereas low correlated response on NS was found (0.04 young rabbits per generation). Similar results on NBA and NW were observed in a rabbit selection experiment for ovulation rate (Laborda *et al*., 2011, 2012) and also in pigs (Cunningham *et al.*, 1979; Rosendo *et al.*, 2007).

A slight decrease in survival at birth (NBA/LS; Figure 2) was observed due to an increase in NBD (Figure 1), whereas survival at weaning was not modified and survival at slaughter was slightly modified (Figure 2). Due to the negative correlated response on prenatal and perinatal survival, a decrease on NS/OR was observed. There is no information about postnatal survival traits in selection experiments for ovulation rate in rabbits. In pigs, no correlated responses in percentage of stillborn and of survival from birth to weaning were found after six generations of selection by ovulation rate by Rosendo *et al.* (2007).

Selection by independent culling levels for ovulation rate and litter size

As selection for ovulation rate did not increase litter size more than direct selection, a two-stage experiment selection for ovulation rate and litter size was proposed as another alternative way to improve litter size in rabbits (Ziadi *et al.*, 2013). Response per generation for LS, OR and prenatal survival after 11 generations of two-stage selection was similar to previous results published by Ziadi *et al*. (2013) analyzing seven generations. Correlated response for NBA (0.12 kit per generation; Figure 1) was similar to direct response for LS, in agreement to the high genetic correlation between them and to the lack of response for NBD. The improvement estimated during the second period of selection was 0.12 kits and 0.11 young rabbits per generation for NW and NS, respectively. In pigs, a higher response on the number of pigs born alive was obtained in two lines underwent of two-stage selection on ovulation rate and fully formed pigs at birth (0.21 and 0.24 piglets born alive; Ruiz-Flores and Johnson, 2001). Besides, these authors obtained a correlated response on number of stillborn (0.11 ± 0.03 per generation) in the line with higher ovulation rate and no correlated response, as in our experiment, in the other selected line. Similar to our results, a positive correlated response on number of weaned in both lines of the two-stage selection experiment were obtained (0.09 and 0.16 weaned piglets). Besides, Lamberson *et al.* (1991) observed a similar direct response on number of piglets at birth (0.13 piglets per generation) using a line selected for litter size during eight generations. This line had high ovulation rate due to previous selection for ovulation rate.

Different correlated responses on prenatal and perinatal survival were observed in the second period of selection compared to the first one. Prenatal survival decreased until generation six and then increased around 1 % per generation (data not shown) in the two-stage selection period in agreement with the results found by Ziadi *et al*. (2013). Perinatal survival also decreased until generation six and no correlated response was observed in the second period (Figure 2). Two-stage selection did not modify survival at weaning and slaughter. Besides, no correlated response was also observed on NS/LS and NS/OR. After two-stage selection by OR and LS, an improvement in uterine capacity might have been achieved, which could account for the changes in NBD and in prenatal and perinatal survivals. Experiments of selection for uterine capacity highlight that increasing uterine capacity can modify several biological processes like an increase in the length of uterine horns (Argente *et al.*, 2006 in rabbits; Lents *et al.*, 2014 in pigs), a higher placental efficiency (review in pigs by Foxcroft *et al.*, 2009) or changes in protein level expression (e.g.

progesterone receptor, Peiró *et al.*, 2010 in rabbits). Therefore, changes in the biological processes related to the uterine capacity improvement could explain the increase in prenatal survival and non-reduction of the peri- and postnatal survival found after two-stage selection by ovulation rate and litter size.

In summary, selection for ovulation rate resulted in an improvement in ova shed but with a lower correlated response on number of kits at birth, weaning and slaughter. However, a slight negative correlated response on survival at birth was observed, whereas survivals at weaning and slaughter were not modified. Selection using independent culling levels for OR and LS resulted in an improvement not only of both traits but also the number of kits at birth, weaning and slaughter. Survival at birth was not reduced, possibly due to an improvement of uterine capacity. Besides, survival at weaning and slaughter were also unchanged.

Acknowledgements

This study was supported by the Ministerio de Economía y Competitividad (AGL2014-55921-C2-1-P) and by funds from Generalitat Valenciana research programme (Prometeo 2009/125). A.Y. Badawy was supported by a grant of the Egyptian Ministry of Higher Education. The authors declare no conflict of interest in this article. None of the data were deposited in an official repository.

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Table 1. Descriptive analysis for ovulation rate (OR, ova), litter size (LS), number of kits born alive (NBA), number of kits born dead (NBD), number of kits at weaning (NW), number of rabbits at slaughter (NS), prenatal survival (LS/OR), survival at birth (NBA/LS), survival at weaning (NW/NBA), survival at slaughter (NS/NW), survival from birth to slaughter (NS/LS) and survival from ovulation rate to slaughter (NS/OR) in OR_LS line.

Trait	N	Mean	SD	CV (%)	Min.	Max.
OR	2013	16.04	2.63	16.4	8	26
LS	4480	9.09	3.18	35.0	1	19
NBA	4480	8.13	3.42	42.1	0	18
NBD	4480	0.96	1.85	192.8	0	16
NW	4474	7.10	3.23	45.5	0	16
NS	4439	6.76	3.23	47.7	0	16
LS/OR	1211	0.589	0.200	34.0	0.05	1.00
NBA/LS	4480	0.886	0.221	25.0	0.00	1.00
NW/NBA	4474	0.844	0.259	30.7	0.00	1.00
NS/NW	4439	0.890	0.262	29.4	0.00	1.00
NS/LS	4439	0.743	0.281	37.8	0.00	1.00
NS/OR	1121	0.457	0.209	45.8	0.00	1.00

N= Number of data, SD= Standard deviation, CV= Coefficient of variation, Min. = Minimum, Max. = Maximum.

OR_LS line is 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 the marginal posterior distributions of the heritability (h^2) and permanent effect (p) of ovulation rate (OR), litter size (LS), number of kits born alive (NBA), number of kits born dead (NBD), number of kits at weaning (NW), number of rabbits at slaughter (NS), prenatal survival (LS/OR), survival at birth (NBA/LS), survival at weaning (NW/NBA), survival at slaughter (NS/NW), survival from birth to slaughter (NS/LS) and survival from ovulation rate to slaughter (NS/OR) in OR_LS line.

	h^2			**p**	
Trait	**Mean**	**$HPD_{95\%}$**	**$P_{0.10}$**	**Mean**	**$HPD_{95\%}$**
OR	0.25	[0.17 , 0.33]	1.00	0.05	[0.01 , 0.11]
LS	0.10	[0.05 , 0.14]	0.43	0.07	[0.03 , 0.10]
NBA	0.07	[0.04 , 0.11]	0.08	0.09	[0.06 , 0.12]
NBD	0.14	[0.08 , 0.21]	0.92	0.10	[0.05 , 0.16]
NW	0.07	[0.04 , 0.12]	0.15	0.07	[0.04 , 0.10]
NS	0.07	[0.04 , 0.11]	0.09	0.06	[0.03 , 0.09]
LS/OR	0.14	[0.10 , 0.19]	0.98	-	-
NBA/LS	0.07	[0.03 , 0.10]	0.05	0.07	[0.04 , 0.11]
NW/NBA	0.03	[0.01 , 0.06]	0.00	0.04	[0.01 , 0.06]
NS/NW	0.03	[0.01 , 0.04]	0.00	0.02	[0.00 , 0.04]
NS/LS	0.06	[0.03 , 0.10]	0.03	0.07	[0.04 , 0.10]
NS/OR	0.17	[0.08 , 0.25]	0.91	-	-

$HPD_{95\%}$= High posterior density interval at 95 %; $P_{0.10}$ = Probability of the heritability being higher than 0.10.

OR_LS line is 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 the marginal posterior distributions of the genetic (**r_g**) and phenotypic (**r_p**) correlation between litter size (LS) and ovulation rate (OR), number of kits born alive (NBA), number of kits born dead (NBD), number of kits at weaning (NW), number of rabbits at slaughter (NS), prenatal survival (LS/OR), survival at birth (NBA/LS), survival at weaning (NW/NBA), survival at slaughter (NS/NW), survival from birth to slaughter (NS/LS) and survival from ovulation rate to slaughter (NS/OR) in OR_LS line.

	r_g					**r_p**	
Trait	**Mean**	**$\text{HPD}_{95\%}$**	**P**	**Ps**	**$P_{0.30}$**	**Mean**	**$\text{HPD}_{95\%}$**
OR	0.37	[0.07 , 0.66]	0.99	0.32	0.68	0.20	[0.14 , 0.25]
NBA	0.89	[0.80 , 0.96]	1.00	0.00	1.00	0.85	[0.84 , 0.86]
NBD	0.01	[-0.39 , 0.41]	0.51	0.83	0.09	0.15	[0.11 , 0.19]
NW	0.81	[0.64 , 0.97]	1.00	0.00	1.00	0.71	[0.69 , 0.72]
NS	0.78	[0.62 , 0.93]	1.00	0.00	1.00	0.67	[0.65 , 0.69]
LS/OR	0.81	[0.73 , 0.89]	1.00	0.00	1.00	0.89	[0.88 , 0.90]
NBA/LS	0.12	[-0.30 , 0.58]	0.68	0.72	0.25	0.12	[0.09 , 0.16]
NW/NBA	0.15	[-0.31 , 0.61]	0.75	0.67	0.29	0.05	[0.01 , 0.08]
NS/NW	0.14	[-0.44 , 0.66]	0.71	0.63	0.30	0.16	[0.13 , 0.19]
NS/LS	0.10	[-0.33 , 0.51]	0.67	0.77	0.19	0.01	[-0.03 , 0.04]
NS/OR	0.41	[0.09 , 0.73]	0.99	0.32	0.68	0.58	[0.55 , 0.62]

$\text{HPD}_{95\%}$ = High posterior density interval at 95 %; P = Probability of the correlation being higher than zero; Ps= Probability of similitude; probability of the correlation being between -0.30 and 0.30; $P_{0.30}$= Probability of the correlation being higher than 0.30 when correlation is higher than zero or lower than -0.30 when correlation is lower than zero.

OR_LS line is 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 4. Features of the marginal posterior distributions of the genetic (**r_g**) and phenotypic (**r_p**) correlation between ovulation rate (OR) and number of kits born alive (NBA), number of kits born dead (NBD), number of kits at weaning (NW), number of rabbits at slaughter (NS), prenatal survival (LS/OR), survival at birth (NBA/LS), survival at weaning (NW/NBA), survival at slaughter (NS/NW), survival from birth to slaughter (NS/LS) and survival from ovulation rate to slaughter (NS/OR) in OR_LS line.

	r_g					**r_p**	
Trait	**Mean**	**$HPD_{95\%}$**	**P**	**Ps**	**$P_{0.30}$**	**Mean**	**$HPD_{95\%}$**
NBA	0.12	[-0.18 , 0.43]	0.78	0.85	0.14	0.11	[0.06 , 0.17]
NBD	0.55	[0.30 , 0.81]	1.00	0.03	0.97	0.18	[0.11 , 0.24]
NW	0.02	[-0.31 , 0.35]	0.53	0.92	0.05	0.06	[0.00 , 0.12]
NS	0.06	[-0.26 , 0.36]	0.64	0.93	0.06	0.06	[0.00 , 0.12]
LS/OR	-0.28	[-0.47 , -0.07]	0.99	0.58	0.42	-0.25	[-0.30 , -0.20]
NBA/LS	-0.34	[-0.69 , -0.01]	0.97	0.42	0.58	-0.08	[-0.15 , -0.02]
NW/NBA	-0.16	[-0.57 , 0.24]	0.78	0.74	0.25	-0.08	[-0.15 , -0.02]
NS/NW	0.09	[-0.33 , 0.52]	0.67	0.79	0.17	-0.04	[-0.11 , 0.03]
NS/LS	-0.24	[-0.58 , 0.11]	0.92	0.62	0.38	-0.10	[-0.17 , -0.04]
NS/OR	-0.48	[-0.75 , -0.19]	0.99	0.10	0.90	-0.27	[-0.33 , -0.22]

$HPD_{95\%}$ = High posterior density interval at 95 %; P = Probability of the correlation being higher than zero; Ps= Probability of similitude; probability of the correlation being between -0.30 and 0.30; $P_{0.30}$= Probability of the correlation being higher than 0.30 when correlation is higher than zero or lower than -0.30 when correlation is lower than zero.

OR_LS line is 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.

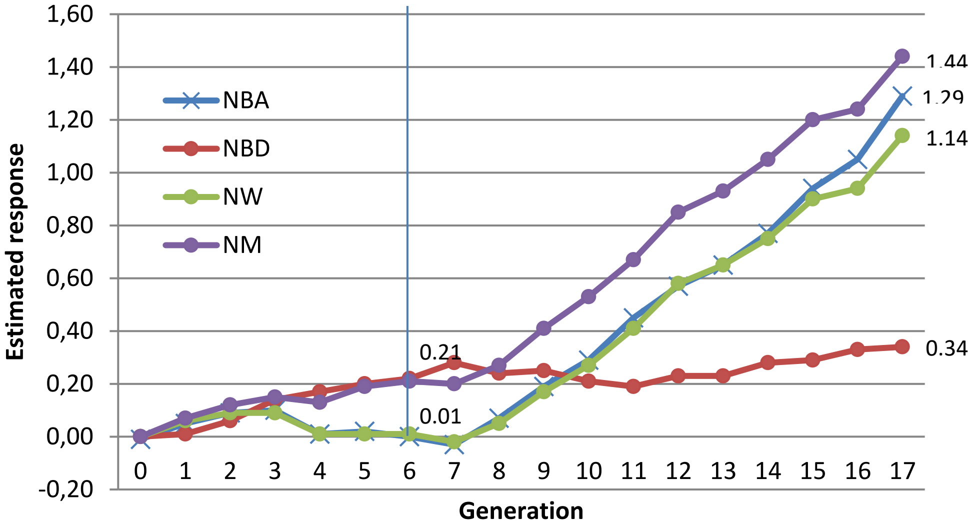

Figure 1. Genetic trends for number of kits born alive (NBA), number of kits born dead (NBD), number of kits at weaning (NW) and number of rabbits at slaughter (NS) of OR_LS line, initially selected for ovulation rate at second gestation from generation 0 to 6 and later for ovulation rate at second gestation 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.

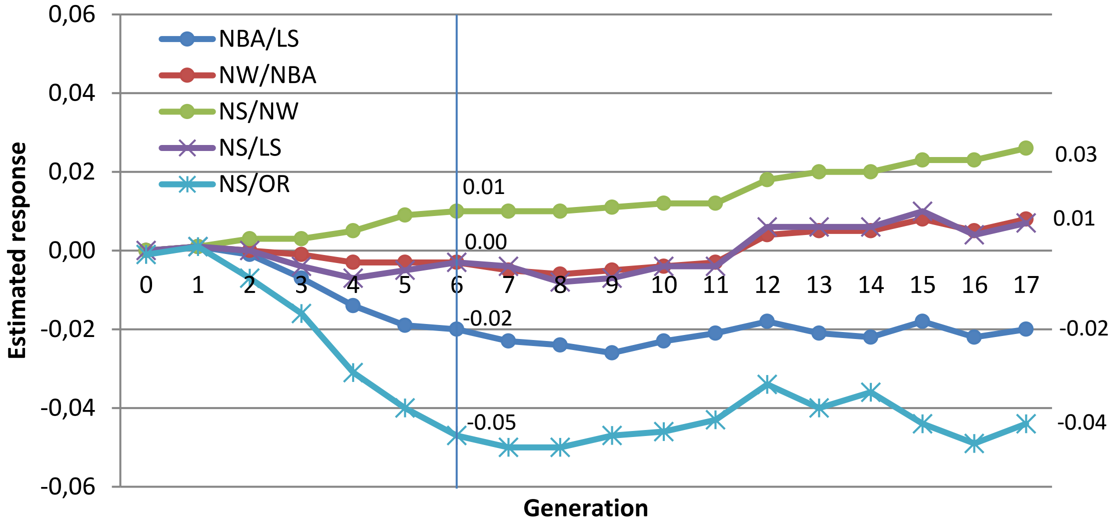

Figure 2. Genetic trends for survival at birth (NBA/LS), survival at weaning (NW/NBA), survival at slaughter (NS/NW), survival from birth to slaughter (NS/LS) and survival from ovulation rate to slaughter (NS/OR) of OR_LS line, initially selected for ovulation rate at second gestation from generation 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.