

The efficiency of using more than one record as the selection criteria for litter traits in pigs

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ABSTRACT

Repeatability estimates for litter size and weight, at birth and at day 21, are reported for three breeds of pigs. The estimates ranged from 0.122 to 0.185, averaging 0.149. The repeatabilities were used to maximize the genetic progress in litter traits per time unit, and a rough prediction of genetic progress in the sampled populations was provided. It was concluded that data from the first two litters should be used to obtain the maximum possible amount of genetic progress.

INTRODUCTION

Knowledge of the repeatability of a trait allows the evaluation of the contribution of temporary environment to phenotypic variance. One could also predict future records of an animal and choose the most appropriate number of records on which selection should be based. The evaluation of the genetic merit of an animal, based on its phenotype, is not very accurate in cases where the heritability of a trait is low. However, the accuracy of selection may be increased by using an average of several phenotypic records, since the variance of an average of n records decreases when n increases (Cardellino and Rovira, 1987). As a consequence, errors in ranking animals by their breeding values would be less frequent. It is

advantageous to use an average of several records in place of a single one, when the influence of the temporary environment is high. Traits with low repeatabilities fit perfectly in this situation.

Previous studies have shown that repeatability estimates for litter traits are low, ranging between 0.11 and 0.28 for litter size, and between 0.11 and 0.27 for litter weight (Strang and Smith, 1979; Ferguson *et al.*, 1985; Ferraz and Duarte, 1989; Siqueira, 1990; Severo, 1991). Thus, ranking of sows based on their first litter could lead to serious errors.

The genetic progress from one generation to another will increase in direct proportion to the number of records used, but the generation interval will also be increased. In pigs, about six months would be necessary for a female to farrow an additional litter; thus genetic progress will be weakened in time. An appropriate solution to this problem is to find the number of records which will maximize the genetic progress per unit of time.

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MATERIAL AND METHODS

The sample consisted of 2061 Large White (LW), 1236 Landrace (LR), and 787 Duroc (DC) sows, which farrowed, respectively, 7064, 4538, and 2400 litters. Litters were born in 69 commercial pig farms, in the state of Santa Catarina, southern Brazil. Data collection was supervised by Brazil's National Pig Farmers Association (Associação Brasileira de Criadores de Suínos).

The sows were the progeny of 326 (LW), 169 (LR), and 123 (DC) boars. For each breed, only the farms with progenies of at least four boars were included in the sample. The weight and the number of live piglets in each litter was recorded at birth (LWB, LIVB) and at day 21 (LW21, LIV21). The total number of piglets born (TOTB) was also studied, but mummified piglets were not included in TOTB. Piglets were kept with the sow at least up to 21 days of age. Litters in which crossfostering was practiced before piglets reached 21 days of age were excluded.

It was assumed that each combination of farm-year-month offered to sows similar conditions. Under typical commercial conditions in southern Brazil, pregnant sows are provided a diet containing about 13-14% of crude protein, 3400 kCal/kg of digestible energy and 0.45% lysine, *ad libitum*.

Pigs raised on commercial farms usually are originated from breeding companies, which emphasize selection for fast growth and reduced fat. It can be assumed that no selection for litter traits was practiced in the populations under consideration. Under the hypothesis of independent inheritance of reproductive, growth and carcass traits (Gu *et al.*, 1989; Kuhlert and Jungst, 1992, 1993), one could use methods of variance component estimation, such as Henderson III, that don't take into account selection biases.

An observation was described by the following linear model:

$$Y_{ijkm} = \mu + F_i + s_j + p_{jk} + W_{ijkm}$$

where

Y_{ijkm} are individual observations on TOTB, LIVB, LIV21, LWB, or LW21,

μ is a constant inherent to all observations,

F_i is the i th level of the fixed effects that affect the observations (farm, year, and month of litter's birth and sow's age at farrowing),

s_j is the random effect of the j th sire, $s_j \sim (0, \sigma_s^2)$,

p_{jk} is the random effect of the k th progeny (sow) of the j th sire, $p_{jk} \sim (0, \sigma_p^2)$, and

W_{ijkm} is the random effect of the m th observation (litter) in the k th progeny of the j th sire, $W_{ijkm} \sim (0, \sigma_w^2)$.

Variance components were estimated by the Henderson III method (Henderson, 1953), using LSMLMW & MIXMDL PC-2 software (Harvey, 1990). The variance components, σ_s^2 , σ_p^2 , and σ_w^2 were obtained by equating the observed to the expected mean squares (Table I). The genetic interpretation of the variance components is presented in Siewerdt (1993). The phenotypic variance was obtained by adding the three variance components. Adding the σ_s^2 and the σ_p^2 components, one would obtain a value that estimates all the genetic variance plus the general environmental variance. This value corresponds to the numerator of the repeatability expression (Falconer, 1989). The standard errors of the repeatability estimates were computed according to Becker (1985).

The maximization of annual genetic progress was worked out following the procedures described below. The annual genetic progress (ΔG_a) was defined (Cardellino and Rovira, 1987) as:

$$y = \Delta G_a = I_{AC} \cdot i \cdot \sigma_A \cdot I^{-1}$$

where I_{AC} is the accuracy of selection, i is the selection intensity, σ_A is the additive genetic standard deviation, and I is the generation interval, expressed in years. If selection is based on an average of n records collected for an animal, then the accuracy of selection is $I_{AC} = \sqrt{n/[1+(n-1) \cdot R]} \cdot h$, where R is the repeatability and h is the square root of the heritability of the trait (Cardellino and Rovira, 1987). The accuracy of selection is not the only term of the above equation that depends on the number of records used. The generation interval also depends on n , since it will increase as n increases. Generation interval may be redefined as $I = a + nb$, where $a + b$ is the generation interval when selection is performed only with one record per animal (the first record effectively used) and b is the increase caused in I when an additional record is used. Performing these substitutions in the above equation leads to:

$$y = \Delta G_a = \sqrt{\frac{n}{1+(n-1) \cdot R}} \cdot h \cdot i \cdot \sigma_A \cdot \frac{1}{a+nb}$$

The maximization of ΔG_a with regard to n is obtained by equating to zero the first derivative of the last equation, and solving the resulting expression for n . It leads to the following expression:

Table I - Variance components' and phenotypic variances of litter traits.

Trait ²	Breed	σ_s^2	σ_p^2	σ_w^2	V _P
TOTB	Large White	0.091	0.765	5.026	5.883
	Landrace	0.170	0.748	4.702	5.620
	Duroc	0.093	0.610	4.048	4.751
LIVB	Large White	0.086	0.738	4.898	5.722
	Landrace	0.156	0.688	4.424	5.268
	Duroc	0.084	0.597	3.937	4.618
LIV21	Large White	0.101	0.557	4.733	5.391
	Landrace	0.126	0.615	4.229	4.970
	Duroc	0.092	0.591	3.781	4.464
LWB	Large White	0.517	1.578	11.628	13.723
	Landrace	0.496	1.870	10.447	12.813
	Duroc	0.307	1.158	9.793	11.258
LW21	Large White	5.481	16.037	143.806	165.324
	Landrace	5.238	16.384	124.748	146.370
	Duroc	5.771	15.124	111.544	132.439

¹ σ_s^2 : sire component; σ_p^2 : progeny component; σ_w^2 : litter component; V_P phenotypic variance.

² TOTB: total number of piglets born, except mummified; LIVB: number of live piglets at birth; LIV21: number of live piglets at day 21; LWB: litter weight at birth; LW21: litter weight at day 21.

$$n = \frac{b(R-1) + \sqrt{b(1-R) \cdot [b(1-R) + 8aR]}}{4bR} \quad [1]$$

which solution provides the number of records to be obtained in each animal, in order to maximize ΔG_a . The corresponding demonstration is presented in the appendix.

RESULTS AND DISCUSSION

The structure of the data permitted the estimation of heritabilities and of genetic correlations among the traits. These genetic parameters are reported in Siewerdt *et al.* (1995). The standard errors were low, suggesting that the estimates do not differ greatly from the parameters in the population. Repeatability values suggest that the temporary environmental variance has a great effect on the reproductive performance of the sows. Therefore, evaluating the sows based on a single litter would not assure correct ranking by their corresponding additive genetic values.

Expression [1] stated in the previous section was applied to the present situation, using the repeatability scores reported in Table I. As the

generation interval was redefined as $a + nb$, the following criteria were used to establish the values of a and b : (1) the gilt litter is farrowed at the age of 12 months; (2) each female farrows two litters per year, leading to an interval of six months between two consecutive farrowings; (3) the replacement gilts will be chosen among those born in the last litter farrowed; (4) no evaluation is performed on boars; they are not selected and are mated at the age of ten months. At progeny birth, boars are 14 months old (1.167 years). The contribution of the sows to the enlargement of generation interval is $b = 0.5$ for each extra litter. However, boars are always 10 months old at mating, so their contribution to increase of generation interval is $b = 0$. The average value $b = 0.25$ is used to obtain n . An average value of 13 months ($a + b = 1.083$ years) is the age at the first production, resulting in $a = 0.833$ years. The results are presented in Table III, and were similar throughout breeds and traits. As the solutions are not exact numbers, they should be rounded to the nearest integer, namely 2, in all breeds and traits. The increase in the generation interval is compensated by a corresponding gain in genetic progress with the inclusion of a second record in the selection criterion, such that the genetic progress per time unit is increased. It can be concluded that using the average

of the data from the first two litters would be the most proper strategy for genetic improvement of litter traits.

The repeatabilities reported in Table II were used to predict the genetic progress that could be achieved, per generation and per year, for each trait, in situations where selection is based on data from one to four litters. These results are presented in Table IV. It can be observed that from the third litter on, the improvement of accuracy is not compensated by the consequent enlargement of the generation interval. As an example, the expected genetic progress in LWB, using the formation from a single litter is 0.558 kg/generation or 0.515 kg per year in the LW breed. The expected genetic progress in LWB increases 0.177 kg by adding data from a second litter. The generation interval increased from 1.083 to 1.333 years, and the corresponding annual genetic progress increased 0.036 kg. Using data from a third litter, the genetic progress increases 0.111 kg, but the corresponding annual genetic progress decreased 0.017 kg, since the generation interval reached 1.583 years. The use of a fourth litter would follow the same trend observed in the third one. Although the improvement per generation increased by an extra 0.078 kg, the corresponding improvement per year decreased another 0.030 kg. Therefore, using data from two litters is appropriate for maximizing the genetic progress in relation to time unit. The same trend can be observed in all the other traits and in the three breeds. This agrees with the results presented in Table III.

Genetic improvement of litter size, at birth, would be faster in the LR breed than in the other two breeds, since the predicted values for genetic improvement per generation are larger in TOTB (0.17 piglets) and in LIVB (0.16 piglets) than in the other two breeds. The advantage of the LR breed over the LW and DC breeds was smaller in the litter size at day 21. This trait had, in the LR breed, a predicted genetic progress of 0.07 piglets larger than the average of the LW and DC breeds. In both situations, the differences in predicted values are due to the higher genetic variability in the LR breed, demonstrated by the higher heritability values of the litter size traits (Siewerdt *et al.*, 1995). The expected progress in predicted litter size presented here could influence selection efforts on litter size for improvement of profit in pig farms.

The expected genetic progress, per generation, in litter weight at birth and at day 21 was equivalent in the LW and LR breeds, averaging 0.73 kg (LWB) and 2.28 kg (LW21). The DC breed had a lower predicted value for genetic progress in litter weight at birth, but a higher predicted value in litter weight at day 21. The differences are mainly due to different heritability values

Table II - Repeatabilities (\pm standard errors) of litter traits.

Trait ¹	Large White	Landrace	Duroc
TOTB	0.146 \pm 0.012	0.163 \pm 0.015	0.148 \pm 0.021
LIVB	0.144 \pm 0.012	0.160 \pm 0.015	0.148 \pm 0.021
LIV21	0.122 \pm 0.012	0.149 \pm 0.015	0.153 \pm 0.022
LWB	0.153 \pm 0.012	0.185 \pm 0.016	0.130 \pm 0.021
LW21	0.130 \pm 0.012	0.148 \pm 0.015	0.158 \pm 0.022

¹Abbreviations defined in Table I.

Table III - Number of records per sow that maximizes the annual genetic progress¹.

Trait ²	Large White	Landrace	Duroc
TOTB	1.985	1.910	1.976
LIVB	1.994	1.923	1.976
LIV21	2.103	1.971	1.953
LWB	1.953	1.823	2.062
LW21	2.062	1.976	1.932

¹Numerical solution of expression (1).

²Abbreviations defined in Table I.

(Siewerdt *et al.*, 1995), since the VP values are similar in the three breeds. The predicted correlated responses to selection have a favourable sign, since the genetic correlations between the five traits are positive. As found for litter size, selection for litter weight could result in economically useful genetic progress.

Ollivier (1982) stated that using repeatability models for selection purposes requires the assumption that the heritabilities of litter traits are equal for all parities, and that the genetic correlation between all records is equal to unity, since the genotype is constant. Johansson and Kennedy (1985) reported genetic correlations which ranged from 0.18 to 0.90, for litter size in the first and second litters. It seems that these two particular litters may have a weak genetic relationship, resulting in losses in accuracy of selection.

In summary, the ranking of sows based on the data of their first two litters leads to an average improvement of 32% in expected genetic progress, per generation, and of 7%, per year, when compared to the selection performed on a single litter. The behaviour of correlated responses should follow the same patterns of the trait used as the selection criterion. The same can be expected when a selection index that combines information from several traits is used. The low estimates of heritabilities of the litter traits (Siewerdt *et al.*, 1995) would lead to little genetic progress, although there is sufficient phenotypic variance to allow exploration by selection means.

Table IV - Predicted genetic progress for selection based on a varying number of litters per sow.

Selection criteria ¹	Number of litters	Genetic progress per generation			Genetic progress per year		
		LW ²	LR	DC	LW	LR	DC
TOTB (piglets)	1	0.151	0.286	0.171	0.139	0.264	0.158
	2	0.199	0.375	0.226	0.149	0.281	0.169
	3	0.230	0.430	0.260	0.145	0.272	0.164
	4	0.252	0.469	0.285	0.137	0.256	0.155
LIVB (piglets)	1	0.143	0.273	0.157	0.132	0.252	0.145
	2	0.189	0.358	0.207	0.142	0.269	0.155
	3	0.218	0.412	0.239	0.138	0.260	0.151
	4	0.239	0.449	0.261	0.130	0.245	0.143
LIV21 (piglets)	1	0.175	0.226	0.174	0.162	0.209	0.161
	2	0.234	0.298	0.229	0.175	0.224	0.172
	3	0.272	0.344	0.264	0.172	0.217	0.167
	4	0.299	0.376	0.288	0.163	0.205	0.157
LWB (kg)	1	0.558	0.554	0.366	0.515	0.512	0.338
	2	0.735	0.720	0.487	0.551	0.540	0.365
	3	0.846	0.820	0.565	0.534	0.518	0.357
	4	0.924	0.888	0.621	0.504	0.485	0.339
LW21 (kg)	1	1.705	1.732	2.006	1.574	1.599	1.852
	2	2.268	2.286	2.636	1.702	1.715	1.978
	3	2.631	2.635	3.029	1.662	1.665	1.913
	4	2.892	2.883	3.305	1.578	1.573	1.803

¹Abbreviations defined in Table I.²LW: Large White; LR: Landrace; DC: Duroc.

APPENDIX

We want to maximize ΔG_a with regard to n . We assume h , i , and σ_A constant and different from zero. The first derivative of y is equated to zero and the resulting equation is solved for n as shown below.

$$y = \Delta G_a = \sqrt{\frac{n}{1+(n-1) \cdot R}} \cdot h \cdot i \cdot \sigma_A \cdot \frac{1}{a+nb}$$

$$\frac{dy}{dn} = h \cdot i \cdot \sigma_A \left[\frac{1}{a+nb} \cdot d \left(\sqrt{\frac{n}{1+(n-1) \cdot R}} \right) / dn + d \left(\frac{1}{a+nb} \right) / dn \cdot \sqrt{\frac{n}{1+(n-1) \cdot R}} \right] = 0$$

Since $(h \cdot i \cdot \sigma_A)$ is different from zero, we may divide both sides of the equation by $(h \cdot i \cdot \sigma_A)$, resulting in:

$$\frac{1}{a+nb} \cdot d \left[\sqrt{\frac{n}{1+(n-1) \cdot R}} \right] / dn + d \left(\frac{1}{a+nb} \right) / dn \cdot \sqrt{\frac{n}{1+(n-1) \cdot R}} = 0 \quad (a)$$

The derivative of the first term in the left hand side of (a) is:

$$\begin{aligned} d \left[\sqrt{\frac{n}{1+(n-1) \cdot R}} \right] / dn &= \frac{1}{2 \sqrt{\frac{n}{1+(n-1) \cdot R}}} \cdot d \left(\frac{n}{1+(n-1) \cdot R} \right) / dn \\ &= \frac{1}{2 \sqrt{\frac{n}{1+(n-1) \cdot R}}} \cdot \frac{1 \cdot [1+(n-1) \cdot R] - n \cdot R}{[1+(n-1) \cdot R]^2} \\ &= \frac{1-R}{2 \sqrt{n} \cdot [1+(n-1) \cdot R]^{3/2}} \end{aligned} \quad (b)$$

and the derivative of the second term in the left hand side of (a) is:

$$\begin{aligned} d \left(\frac{1}{a+nb} \right) / dn &= \frac{-1 \cdot b}{(a+nb)^2} \\ &= \frac{-b}{(a+nb)^2} \end{aligned} \quad (c)$$

By providing the substitution of (b) and (c) into (a) and putting it into a second degree equation on n, we obtain the following expression:

$$\frac{1}{a+nb} \cdot \frac{1-R}{2 \sqrt{n} \cdot [1+(n-1) \cdot R]^{3/2}} + \frac{-b}{(a+nb)^2} \cdot \sqrt{\frac{n}{1+(n-1) \cdot R}} = 0$$

$$2bRn^2 + b(1-R) \cdot n - a(1-R) = 0$$

The resulting equation is of second order, and has two real roots. In strictly mathematical sense, n is obtained by:

$$n = \frac{b(R-1) \pm \sqrt{b(1-R) \cdot [b(1-R) + 8aR]}}{2 \cdot (2bR)} \quad (d)$$

However, $b(R-1)$ always has a non-positive value, since R is a value between 0 and 1. If one uses the root with the negative sign, a negative value for n, which has no biological interpretation, will be obtained. Using only the root obtained with the positive sign, the expression (d) reduces to:

$$n = \frac{b(R-1) + \sqrt{b(1-R) \cdot [b(1-R) + 8aR]}}{4bR}$$

RESUMO

Apresenta-se estimativas de repetibilidade do tamanho e peso de leitegada ao nascer e a 21 dias para três raças de suínos. As estimativas variaram entre 0,122 e 0,185, com valor médio de 0,149. As estimativas de repetibilidade foram utilizadas para maximizar o progresso genético dos caracteres de leitegada, por unidade de tempo. Estimou-se o progresso genético passível de ser obtido nas populações amostradas. Concluiu-se que a seleção deve basear-se na média dos dados de tamanho e de peso das duas primeiras leitegadas produzidas por cada fêmea.

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