

# Avenues for genetic improvement of litter size and litter mortality

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## Introduction

Maximising the number of piglets weaned per litter is a major goal for genetic improvement of reproductive performance of the sow. So far, breeding programs have mainly focussed on litter size to achieve this goal. However, selection experiments have shown that the number of piglets born dead increases with selection for litter size (see review by Blasco et al. 1995). In addition, selection for larger litter size has led to higher piglet mortality until weaning (Rydhmer, 2000) and breeding programs have to look beyond sole selection for litter size in order to achieve a higher number of piglets weaned per litter.

Litter size has been shown to have a negative genetic correlation with the average piglet weight at birth (for example see Rydhmer et al., 1992 and Crump et al., 1997) and light piglets are more likely to die from hyperthermia and/or malnutrition. On the phenotypic level, the within litter variation of piglet weights at birth has been discussed as a major cause for pre-weaning litter mortality (see review by Le Dividich, 1999). Any trait describing the within-litter variation of piglet weights require to measure every individual piglet within a litter, which is not done on a routine basis in nucleus herds. Therefore, genetic parameters between within-litter variation of piglet weights, pre-weaning mortality and further litter traits of the sow are limited. The aim of this paper is to present genetic parameters for additional litter traits of the sow and to evaluate their usefulness in breeding programs.

## Description of litter traits

The information available from the data on individual piglets described in the previous paper in this workshop was used to derive a number of litter traits of the sow. These traits included litter size, litter weight and the average piglet weight of the litter. These traits were recorded at birth and at 14 days after farrowing.

Variation of individual piglet weights within a litter was analysed using two definitions of this trait. The first description of this trait was the standard deviation of individual piglet weights within a litter. The second description was based on the coefficient of variation for the within-litter variation of individual piglet birth weight. This within-litter coefficient of variation was derived as the standard deviation of piglet weights within a litter divided by the average piglet weight of the litter. The harmonic mean was explored as a third trait to define the variation of piglet weights within a litter. This trait was genetically the same trait as the average piglet weight and did not provide any further information. For further info on this trait see Hermesch et al. (2001a).

A number of traits were also evaluated to analyse litter mortality. It is suggested to use the total number of piglets that died per litter including the number of stillbirths. An alternative definition of litter mortality was evaluated in Hermesch et al. (2001b).

Last but not least, gestation length was analysed to evaluate genetic relationships with these litter traits. Gestation length is easily derived from information that is already available in herd recording systems and is known to have a high heritability.

Only the main traits are presented in this paper to highlight the main findings. For a better overview, individual traits are listed again in Table 1 along with the number of records and the coefficients of variation for each trait. The number of records is reduced for litter traits recorded at 14 days after farrowing. Cross-fostering was practiced in this herd and analyses showed that during the first four months of the project the number of piglets recorded at 14 days after farrowing did not include piglets that were fostered onto a sow. Consequently, these litter records were not included in the analysis.

Table 1. Litter traits of the sow along with the number of records (N) and the coefficient of variation (CV) for each trait

| <b>Trait</b>   | <b>Abbreviation</b> | <b>Unit</b> | <b>N</b> | <b>CV</b> |
|--|---------------------|-------------|----------|-----------|
| Number born in total   | NBT                 |             | 2281     | 27        |
| Litter weight based on NBT                                       | LWBT                | kg          | 2278     | 26        |
| Average piglet weight at birth based on NBT                      | APWBT               | kg          | 2281     | 17        |
| Number of piglets nursed   | N14                 |             | 1664     | 20        |
| Litter weight  | LW14                | kg          | 1663     | 26        |
| Average piglet weight  | APW14               | kg          | 1663     | 16        |
| Within-litter standard deviation of piglet weight at birth       | SDPWB               | kg          | 2281     | 37        |
| Within-litter coefficient of variation of piglet weight at birth | CVPWB               | %           | 2278     | 38        |
| Number of piglets that died including stillbirths                | NDIEDT              |             | 2297     | -         |
| Gestation length   | GEST                | Days        | 2297     | 3         |

## Heritability estimates

The month of farrowing and line and parity of the sow were the main effects affecting litter traits of the sow. In addition, the line by parity interaction was a significant effect for the average piglet weight at birth. The number of piglets nursed at 14 days after farrowing were only affected by the month of farrowing which accounted for four per cent of the total variation (Table 2). This trait was strongly influenced by cross-fostering practices. The fixed effect model explained six per cent of the total variation for number of piglets born in total. More variation was explained by the fixed effect model for litter weight traits and coefficients of variation ranged from 0.13 to 0.21. The coefficient of variation was also larger for the standard deviation of piglet weights within a litter in comparison to the coefficient of variation of piglet weights within-litter. Litter mortality was defined as the number of piglets that died per litter. Similar to litter size, the model explained only a low proportion of the phenotypic variation for this trait ( $R^2$ : 0.05).

Litter size at birth was lowly heritable ( $h^2$ : 0.06). In comparison, the heritability estimates for total litter weight and average piglet weight at birth were 0.16 and 0.31, respectively. Roehe (1999) also found higher heritability estimates for litter weight adjusted for litter

size in comparison to the unadjusted litter weight. Heritabilities estimates for litter birth weights were higher than estimates obtained in these populations in an earlier study (Hermesch et al., 2000). Litter birth weight is influenced by the milk intake of the piglet after birth and an early measurement after birth is important (Rydhmer et al., 1992). Piglets were weighed within 12 hours after farrowing according to a consistent recording protocol, which may explain the higher heritability in this study in comparison to the earlier study. In summary, these results highlight the importance of consistently weighing pigs shortly after farrowing in order to use the average piglet weight at birth in breeding programs.

The heritability estimate for litter size at 14 days was not significantly different from zero. This trait is strongly influenced by cross-fostering practices, which limits the use of this trait under such management practice in genetic improvement program. The second trait that depends on the number of piglet nursed at 14 days, the average piglet weight at 14 days, also had a lower heritability estimate of 0.15 in comparison to the average piglet weight at birth. In contrast, the average piglet weight at three weeks had a heritability of 0.30 in the study by Högberg and Rydhmer (2000). Their study was based on data derived in a research herd at the Swedish University where no cross-fostering was practiced. These results highlight that cross-fostering should not be practiced in nucleus herds that would like to use information on litter traits recorded after farrowing.

Table 2. Coefficients of determination ( $R^2$ ), heritability estimates and permanent environment effect of the sow along with phenotypic standard deviation ( $\sigma_p^2$ ) for litter traits of the sow

| <b>Trait</b> | <b><math>R^2</math></b> | <b><math>h^2</math></b> | <b>(se)</b> | <b>pe<sub>sow</sub></b> | <b>(se)</b> | <b><math>\sigma_p^2</math></b> |
|--------------|-------------------------|-------------------------|-------------|-------------------------|-------------|--------------------------------|
| NBT          | 0.06                    | 0.06                    | (0.03)      | 0.11                    | (0.05)      | 7.88                           |
| LWBT         | 0.17                    | 0.16                    | (0.04)      | 0.14                    | (0.05)      | 14.1                           |
| APWBT        | 0.16                    | 0.31                    | (0.05)      | 0.14                    | (0.01)      | 0.0554                         |
| N14          | 0.04                    | 0.02                    | (0.03)      | 0.06                    | (0.06)      | 2.93                           |
| LW14         | 0.13                    | 0.13                    | (0.05)      | 0.06                    | (0.06)      | 89.3                           |
| APW14        | 0.21                    | 0.15                    | (0.05)      | 0.14                    | (0.06)      | 0.413                          |
| SDPWB        | 0.15                    | 0.15                    | (0.03)      | 0.00                    | -           | 0.00687                        |
| CVPWB        | 0.07                    | 0.11                    | (0.03)      | 0.00                    | -           | 37.8                           |
| NDIEDT       | 0.05                    | 0.05                    | (0.03)      | 0.05                    | (0.05)      | 3.27                           |
| GEST         | 0.15                    | 0.44                    | (0.05)      | 0.05                    | (0.05)      | 2.39                           |

for abbreviations see Table 1

Both traits describing within-litter variation were heritable traits. Estimates were 0.15 for the standard deviation of piglet weights within a litter and 0.11 for the coefficient of variation for piglet weights within a litter. Literature values were only found for the standard deviation of piglet weight within a litter in a few recent studies. Estimates presented by Högberg and Rydhmer (2000) and Knol et al. (2001) were 0.10 and 0.06, respectively.

The heritability for litter mortality was 0.05. The two recent studies by Högberg and Rydhmer (2000) and Knol et al. (2001) who both used exactly the same definition of litter mortality presented similar estimates of 0.09 and 0.07, respectively.

Gestation length is a trait that is a by-product of other data routinely recorded in herd recording systems. This trait has a high heritability 0.41 and may be used in breeding programs to provide information for other traits.

## Genetic correlations

### Litter traits recorded at birth and at 14 days

Litter size had a moderate genetic correlation with litter weight (0.54) reflecting the part-whole relationship of these two traits (Table 3). In contrast, litter size had no significant genetic correlation with the average piglet weight at birth. However, the higher magnitude of the phenotypic correlation between these two traits was based on the permanent environment of the sow (not shown in Table 3). Previous studies found stronger genetic correlations between litter size and the average piglet weight at birth (Crump et al, 1997; Hermesch et al., 2000) and the lower magnitude of the genetic correlation found in this study may be due to sampling effects. Overall, the unfavourable genetic relationship between litter size and the average piglet weight at birth should not be ignored.

Total litter weight at birth had a high genetic correlation with the average piglet weight at birth as well as both weight measurements recorded at 14 days after farrowing. Litter size at birth, however, had no genetic correlation with the average piglet weight at 14 days. Genetic parameters between this trait combination have rarely been presented. The recent study by Högberg and Rydhmer (2000) also found no significant genetic correlation between litter size and the average piglet weight at 21 days.

Table 3. Genetic (above diagonal) and phenotypic (below diagonal) correlations between litter traits recorded at birth and 14 days after farrowing

| Trait | NBT   | LWBT | (se)   | APWBT | (se)   | LW14 | (se)   | APW14 | (se)   |
|-------|-------|------|--------|-------|--------|------|--------|-------|--------|
| NBT   |       | 0.54 | (0.15) | -0.17 | (0.20) | 0.38 | (0.30) | 0.04  | (0.29) |
| LWBT  | 0.82  |      |        | 0.73  | (0.11) | 0.88 | (0.17) | 0.71  | (0.18) |
| APWBT | -0.47 | 0.08 |        |       |        | 0.75 | (0.10) | 0.62  | (0.14) |
| LW14  | 0.00  | 0.22 |        | 0.33  |        |      |        | 0.99  | (-)    |
| APW14 | -0.17 | 0.12 |        | 0.47  |        | 0.60 |        |       |        |

for abbreviations see Table 1

### Within-litter variation and litter mortality

Both traits describing within-litter variation had no significant genetic correlation with litter size (Table 4). In contrast, the standard deviation of piglet weights within a litter had a strong genetic correlation with litter weight trait (LWBT, APWBT, LW14, APW14). The coefficient of variation is defined as the standard deviation divided by the mean and as a result this definition of within-litter variation had no significant genetic correlations with litter weight traits. These two traits describing variation within a litter are genetically a different trait, which is reflected in different genetic correlations with further litter traits.

Litter mortality had the strongest genetic correlation with litter size (rg: 0.76) followed by a moderate genetic correlation with the average piglet weight at birth (rg: -0.46)

(Table 4). Placing selection emphasis solely on litter size, therefore, causes a genetic response in increased litter mortality. Both traits describing within litter variation of piglet weights had no significant genetic correlations with litter mortality which supports findings by Högberg and Rydhmer (2000). In contrast, Knol (2001) reported a non-significant genetic correlation between litter mortality and the average piglet weight at birth and a positive genetic correlation between litter mortality and within-litter variation.

Table 4. Genetic (first row) and phenotypic (second row) correlations between within-litter variation, litter mortality and gestation length and further litter traits of the sow (standard errors, se, in brackets).

| <b>Trait</b> | <b>SDPWB</b> | <b>(se)</b> | <b>CVPWB</b> | <b>(se)</b> | <b>NDIEDT</b> | <b>(se)</b> | <b>GEST</b> | <b>(se)</b> |
|--------------|--------------|-------------|--------------|-------------|---------------|-------------|-------------|-------------|
| NBT          | 0.03         | (0.22)      | 0.23         | (0.26)      | 0.76          | (0.20)      | -0.54       | (0.19)      |
|              | 0.20         |             | 0.36         |             | 0.50          |             | -0.13       |             |
| LWBT         | 0.52         | 0.13        | -0.08        | (0.18)      | 0.14          | (0.27)      | -0.34       | (0.13)      |
|              | 0.22         |             | 0.14         |             | 0.25          |             | -0.03       |             |
| APWBT        | 0.58         | (0.11)      | -0.27        | (0.13)      | -0.46         | (0.20)      | 0.04        | (0.11)      |
|              | -0.04        |             | -0.47        |             | -0.43         |             | 0.17        |             |
| LW14         | 0.63         | (0.18)      | 0.15         | (0.26)      | -0.13         | (0.27)      | 0.03        | (0.11)      |
|              | 0.07         |             | -0.07        |             | -0.21         |             | 0.16        |             |
| APW14        | 0.68         | (0.16)      | 0.05         | (0.24)      | -0.18         | (0.29)      | -0.19       | (0.16)      |
|              | 0.15         |             | -0.06        |             | -0.18         |             | 0.09        |             |
| SDPWB        |              |             | 0.41         | (0.11)      | -0.22         | (0.27)      | 0.02        | (0.11)      |
|              |              |             | 0.87         |             | 0.22          |             | 0.04        |             |
| CVPWB        |              |             |              |             | 0.16          | (0.30)      | -0.06       | (0.16)      |
|              |              |             |              |             | 0.40          |             | -0.02       |             |
| NDIEDT       |              |             |              |             |               |             | -0.53       | (0.25)      |
|              |              |             |              |             |               |             | -0.12       |             |

for abbreviations see Table 1

Gestation length had a genetic correlation of -0.54 with litter size and -0.53 with litter mortality. A shorter gestation length is genetically correlated with a larger litter size (desired) but also a higher litter mortality (undesired). The antagonistic interests of the sow and the litter may be reflected in these genetic correlations. It is of interest to the sow to have an early farrowing date when she is carrying a large litter. On the other hand, it is of interest to the litter to have a later farrowing date in order to have a higher birthweight and therefore better chances of survival.

## Evaluation of selection strategies

The direction of a breeding program is defined by the breeding objective. The breeding objective should include all economically important traits. For reproduction traits, many breeding companies base their breeding objective on litter size only. However, this selection strategy increases litter mortality which needs to be considered in order to maximise genetic improvement of number of piglets weaned.

The breeding objective for reproductive traits included number of piglets born alive (NBA) and litter mortality (NDIEDT) defined as the number of piglets that died until weaning. Litter traits are of high importance in maternal lines and an economic weight of A\$ 48 per litter was used for number born alive as derived through the PIGBLUP

profit function (Pig Genetics Workshop Notes, 1997). It is assumed that the economic weight for one piglet dying before weaning has the same magnitude (but opposite sign) as the economic weight for a piglet born alive. Consequently, the economic value for litter mortality was A\$ - 48. This economic weight is a conservative economic weight placing equal emphasis on litter size and litter mortality.

In addition, average piglet weight at birth (APWBT) and gestation length (GEST) were evaluated as selection criteria. These two traits do not have an economic value themselves but are highly correlated with traits in the breeding objective thus providing extra information. Benefits of using this extra information for genetic improvement are evaluated. No selection emphasis is placed on gestation length since it has a low variation and only a low selection response is achievable despite its high heritability. Secondly, it is assumed that this trait has a physiological optimum, which should not be altered through selection. Genetic parameters and economic weights are presented in Table 5. It was assumed that information was available from the dam and both grand-dams for the animal of interest. Implications of these genetic parameters for genetic improvement were evaluated through index calculations using the selection index program (SIP) developed by Wagenaar *et al.* (1995). It was assumed that the top five per cent of boars (equivalent to selection intensity ( $i$ ) = 2.063) and top 20 per cent of gilts ( $i$  = 1.40) were selected (average  $i$  = 1.7315). These selection intensities reflect the average selection intensity achieved in practice. In theory, higher selection intensities are possible since less than five per cent of boars are required for selection.

Table 5. Phenotypic standard deviations ( $\sigma_p$ ), economic weights (on a per litter basis), heritabilities ( $h^2$ ) and litter effect estimates ( $c^2$ ) along with genetic and phenotypic correlations used in index calculations for reproduction traits.

| Trait   | $\sigma_p$ | economic weight (A\$) | $h^2$ | $c^2$ | Correlations <sup>1</sup> |         |       |       |
|---------|------------|-----------------------|-------|-------|---------------------------|---------|-------|-------|
|         |            |                       |       |       | NBA                       | NDI EDT | ABWBT | GEST  |
| NBA     | 2.64       | 48                    | 0.05  | 0.10  | 0.76                      |         | -0.11 | -0.60 |
| NDI EDT | 1.80       | -48                   | 0.05  | 0.05  | 0.30                      |         | -0.46 | -0.53 |
| APWBT   | 0.235      |                       | 0.31  | 0.14  | -0.43                     | -0.40   |       | 0.03  |
| GEST    | 1.54       |                       | 0.44  | 0.05  | -0.12                     | -0.12   | 0.16  |       |

<sup>1</sup> Genetic correlations above diagonal and phenotypic correlations below diagonal

Abbreviations:

- NBA            Number of piglets born alive (used instead of NBT because NBA is used in breeding programs)
- NDI EDT       Number of piglet that died before weaning
- APWBT       Average piglet weight at birth
- GEST           Gestation length

The first index represents single trait selection for litter size (Table 6). This index is practiced in many breeding programs in Australia. Responses in individual traits were 0.139 and 0.071 for number of piglets born alive and mortality rate, respectively. Genetic gain achieved in number of piglets born alive is accompanied by an increase in the number of piglets that die per litter. Relative to each other the increase in litter mortality amounts to approximately half of the response obtained for litter size. The response in the breeding objective was \$A 3.20 per litter. This response in the breeding objective was set to 100 for the comparison with other indices.

The second index uses information on litter mortality in addition to index one. Using this extra information resulted in hardly any extra response in the breeding objective

(A\$ 3.24; =101). In contrast, gestation length provided extra information to the first index. A higher response was achieved in litter size, which was accompanied by a higher positive (undesired) response in litter mortality. The improvement in litter size was larger than the undesired response in litter mortality and the response in the breeding objective was increased to A\$ 5.19 equivalent to 162% in comparison to index one. Information about gestation length is available in nucleus herds without any additional costs for recording since this trait is derived from the farrowing date and the mating date. Gestation length is highly heritable and has moderate to high genetic correlations with litter size and litter mortality making it a useful selection criterion for genetic improvement of reproductive traits.

Index four uses information on the average piglet weight at birth. This index provides a response of 0.094 in litter size and - 0.031 in litter mortality. The response in the breeding objective is A\$ 5.96 per litter equivalent to 186 per cent in comparison to the first index. This index achieves an improvement (reduction) in litter mortality but does not maximise genetic response in the overall breeding objective. Maximum response is achieved by using information on all four traits (Index 5b). However, the extra response achieved by recording litter mortality is minimal (Index 5 versus Index 5b). Litter mortality is indirectly influenced by cross-fostering practices and it is suggested not to use information on litter mortality.

Table 6. Reproduction traits included in the selection index along with genetic response to selection in individual traits (selection intensity = 1.7315) after one generation along with financial change in the overall breeding objective ( $R_H$ ) and the correlation between the index and the breeding objective (accuracy,  $r_{IH}$ ) applying different indices.

| Trait                                      | Index 1 | Index 2 | Index 3 | Index 4 | Index 5 | Index 5b |
|--|---------|---------|---------|---------|---------|----------|
| Traits recorded                            |         |         |         |         |         |          |
| NBA  | ✓       | ✓       | ✓       | ✓       | ✓       | ✓        |
| NDIEDT                                     |         | ✓       |         |         |         | ✓        |
| AVNBT                                      |         |         |         | ✓       | ✓       | ✓        |
| GEST                                       |         |         | ✓       |         | ✓       | ✓        |
| Genetic response in individual traits      |         |         |         |         |         |          |
| NBA  | 0.139   | 0.126   | 0.256   | 0.094   | 0.210   | 0.215    |
| NDIEDT                                     | 0.071   | 0.059   | 0.149   | -0.031  | 0.052   | 0.057    |
| Response in breeding objective             |         |         |         |         |         |          |
| Absolute response in $R_H$<br>(A\$/litter) | 3.20    | 3.24    | 5.19    | 5.96    | 7.57    | 7.62     |
| Relative Response in $R_H$                 | 100     | 101     | 162     | 186     | 236     | 238      |
| $r_{IH}$                                   | 0.10    | 0.10    | 0.16    | 0.19    | 0.23    | 0.24     |

The current set up of PIGBLUP allows analysing three reproductive traits simultaneously, litter size, 21-day litter weight and weaning to conception interval. Ultimately, the reproductive module in PIGBLUP should be extended to include at least, the average piglet weight at birth and gestation length in addition to the traits currently available. Further, litter mortality should be included as a breeding objective trait. It is recommended to extend the number of traits available in the reproductive module in PIGBLUP.

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