# The Genetic Foundation of Fitness and Reproduction Traits in Australian Pig Populations

## II. Relationships between weaning to conception interval, arrowing interval, stayability and other common reproduction and production traits

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## 1. Introduction

The economic importance of reproduction and fitness traits in pig production is undisputed. With electronic herd management systems, a tool is provided to record these traits under production conditions accurately. However, reliable and specific population parameters are essential in developing an efficient, long term improvement schemes for these traits. Currently, the reproductive module of PIGBLUP (LONG *et al.* 1992), the most frequently used software to estimate breeding values in the Australian pig population, includes the traits number of piglets born alive and 21-day litter weight of the piglets. Additional traits influencing sow reproductive efficiency are weaning to conception interval and sow longevity. THOLEN *et al.* (1995) estimated heritabilities of approximately 0.1 for the traits weaning to conception interval of gilts and stayability of sows from the first to the third or fourth parity. Although low, the heritability estimates suggest, that including weaning to conception interval or stayability into the breeding objective of pigs would increase the lifetime productivity of sows.

The major objective of this study was to verify genetic parameters for production and reproduction traits used in PIGBLUP, and to estimate the relationships between these traits and the 'new' reproductive traits weaning to conception interval, farrowing interval and stayability of sows from first to later parities.

## 2. Material

The data used in this study included reproductive and performance records of sows from two Australian piggeries. The first data set (Herd A) included records from 3942 sows of a synthetic line derived from the founder breeds Large White (LW) and Landrace (LR), and performance tested during the years 1983 to 1995. Data from the second herd (Herd B) included records from 3776 LW and 2274 LR sows, recorded from 1991 to 1995.

The following traits were available in the data:

- age at first farrowing (FA)

- number of piglets born alive in the first, second and third litter ($NBA_{1,2,3}$)

- average birthweight of piglets born alive in the first, second and third litter ($BW_{1,2,3}$)

- 21 - day litter weight of the piglets nursed in the first, second and third litter ($W21_{1,2,3}$)

- interval between weaning and conception following the first farrowing ($WCI_{1,2}$)

- interval between the first and second farrowing ($FI_{12}$)

- growth rate from birth to end of performance test (ADG)

- ultrasound backfat thickness following performance testing (BF)

- true stayability of the sow from the first to the second, first to third and first to fourth parity (STAY$_{12,13,14}$)
- functional stayability (STAY$_{13,14}$) was defined as the true stayability corrected for the average NBA calculated from previous litters (NL)

## 3. Data Characteristics

The number of records and standard deviations of performance and reproductive traits analysed are presented in Table 1. Differences between farms in their management strategies provided the most important explanations for differences between herd means. Gilts were performance tested for growth rate and ultrasound backfat to the age of approximately 140 days in Herd A and 160 days in Herd B. In Herd B, no information about the W21 were available. A more detailed description of the traits STAY, WCI and FI, and their characteristics, is given by THOLEN *et al.* (1995).

Table 1: Number of records, mean values (Mean) and standard deviations (SD) for the analysed traits

| Trait [units] Parity | Herd A | | Herd B | |
|---|---|---|---|---|
| | N | SD | N | SD |
| NBA [piglets/litter]  1 | 3943 | 2.69 | 6050 | 2.53 |
| 2 | 3212 | 2.90 | 4222 | 2.54 |
| 3 | 2441 | 2.84 | 3025 | 2.52 |
| BW [kg]       1 | 3943 | 0.25 | 4437 | 0.42 |
| 2 | 3211 | 0.25 | 2535 | 0.46 |
| 3 | 2436 | 0.24 | 1430 | 0.39 |
| W21 [kg]      1 | 3943 | 12.92 | — | — |
| 2 | 3042 | 15.14 | — | — |
| 3 | 2289 | 15.67 | — | — |
| WCI [days]   1-2 | 3164 | 13.11 | — | — |
| FI [days]      1-2 | 3165 | 14.11 | 4183 | 9.66 |
| ADG [g/day] | 3943 | 51.19 | 6050 | 54.73 |
| BF[mm] | 3943 | 2.18 | 6050 | 2.53 |

## 4. Statistical Analysis

Genetic and environmental parameters were estimated using REML (Restricted Maximum Likelihood) analysis based on an animal model as described by THOLEN *et al.* (1995). Traits recorded in each parity were treated as separate traits of the sow. Traits with the same expression, but recorded in parities one to three were analysed by means of a trivariate model. A bivariate trait model was used to estimate the correlations between different traits. Possible different design matrices for different traits and/or missing values for traits were taken into account.

A likelihood ratio test was performed to test the deviation of the genetic correlation between traits measured in different parities from unity. The genetic correlation of traits which have an expectation of unity (same trait, but measured in different parities) was fixed to one. Twice the difference in log-likelihood between models with and without

fixation was referred to a Chi-square distribution with one degree of freedom. This is an asymptotic, rather than an exact test.

No residual correlation existed between $STAY_{li}$ and traits measured in parity i and possible subsequent parities. This is because only sows which survived had a record in these parities. The REML algorithm of SCHAEFFER *et al.* (1978) based on a sire model allows for this special case of missing error co variances. This algorithm is a form of Fisher's scoring method based on a sire model, which does not guarantee that the parameter estimates are within parameter space. The relationship matrix between the sires multiplied by the corresponding matrix of genetic (co-)variances provides the tool to estimate the genetic correlation. However, the h2 estimates of $STAY_{li}$ were of a low magnitude. In this situation, it could be expected that the correlation between STAY and traits measured in later parities were imprecise. Therefore no REML correlations were estimated between $STAY_{li}$ and performance records in parity i and possible subsequent parities. Fixed effects included into the models for STAY, FI and WCI were given by THOLEN *et al.* (1995). Fixed effects included in the model of analysis for the remaining traits are presented in Table 2.

Table 2: Fixed effects (and $R^2$ resulting from the fixed model analysis), included in the model of analysis used for the different traits recorded in Herds A and B

| Traits | Herd | Fixed effects[b] | | | | | | $R^2$ [%], Parity: | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | FA | AI | BS | Y*S | WD | NW | 1 | 2 | 3 |
| NBA | A | 12[a] | | | 123 | | | 3.1 | 3.6 | 2.7 |
| | B | 12[a] | 12 | 1 | 123 | | | 1.6 | 2.1 | 1.8 |
| BW | A | 1 | | | 123 | | | 8.4 | 6.2 | 7.8 |
| | B | | 12 | 23 | 123 | | | 30.8 | 45.9 | 48.6 |
| W21 | A | 1 | | | 123 | 123 | 123 | 72.7 | 74.2 | 78.7 |
| ADG | A | | | | | | | 32.5 | | |
| | B | | | | | | | 11.1 | | |
| BF | A | | | | | | | 32.0 | | |
| | B | | | | | | | 23.1 | | |

[a]   Factor used for analysing trait recorded in the first, second and third parity or factor used for analysing STAY and STAYc from first to second, third or fourth parity

[b]   Fixed effects included into the model of analysis:

   FA:     Age of the sow at the first farrowing (linear co variable)

   AI:     Artificial Insemination (class: 2 levels; yes or no)

   BS:     Breed of the sow (class: 2 levels; LW or LR)

   Y*S:    Year*season (class: 46 levels in Herd A; 20 levels in Herd B)

   WD:     Age of the litter at weight date (linear covariable)

   NW:     Number of weaned piglets weighed (linear and quadratic covariable)

The models in this study did not contain random litter or random maternal effects, because they were not found to be significant effects in preliminary univariate REML analyses. However, in both data sets only 27 % (Herd A) or 19 % (Herd B) of the sows with a record had at least one full-sister in the data, so any estimates of litter effects would have been uncertain (GERSTMAYR, 1992).

# 5. Results and discussion

## 5.1 Estimates of heritability

Estimates of trait heritabilities along with standard errors and additive genetic variances are presented in Table 3.

Table 3: Heritabilities ($h^2$) with standard error (SE) and genetic variance ($\sigma^2_g$) of production and reproduction traits

| Trait | Parity | Herd A $h^2$ | SE | ($\sigma^2_g$) | Herd B $h^2$ | SE | ($\sigma^2_g$) |
|---|---|---|---|---|---|---|---|
| NBA | 1 | .12 | .03 | 0.88 | .10 | .02 | 0.60 |
|  | 2 | .13 | .03 | 1.04 | .11 | .03 | 0.62 |
|  | 3 | .16 | .04 | 1.28 | .09 | .03 | 0.40 |
| BW | 1 | .30 | .03 | 0.017 | .15 | .03 | 0.019 |
|  | 2 | .28 | .03 | 0.017 | .11 | .03 | 0.013 |
|  | 3 | .35 | .04 | 0.019 | .14 | .06 | 0.012 |
| W21 | 1 | .17 | .03 | 7.37 |  |  |  |
|  | 2 | .12 | .03 | 5.69 | — | — | — |
|  | 3 | .23 | .04 | 10.45 | — | — | — |
| WCI | 1-2 | .10 | .03 | 17.48 | .08 | .07 | 6.45 |
| FI | 1-2 | .09 | .03 | 16.66 | .00 | — | 1.82 |
| STAY | 1-2 | .05 | .03 | 0.0060 | .02 | .02 | 0.0034 |
|  | 1-3 | .08 | .03 | 0.0165 | .06 | .02 | 0.0142 |
|  | 1-4 | .08 | .03 | 0.0181 | .09 | .02 | 0.0160 |
| STAYc | 1-3 | .09 | .03 | 0.0201 | .07 | .02 | 0.0146 |
|  | 1-4 | .06 | .02 | 0.0241 | .09 | .02 | 0.0168 |
| ADG |  | .37 | .03 | 709.3 | .35 | .03 | 953.2 |
| BF |  | .36 | .03 | 1.23 | .45 | .03 | 2.32 |

Heritability estimates for **NBA** recorded in the first two parities were between 0.09 and 0.16 in both herds. With the exception of NBA$_3$ in Herd B, $h^2$ tended to increase from parity one to three. The lower $h^2$ for NBA$_3$ in Herd B is mainly caused by a reduced additive genetic variance.

Recent estimates of $h^2$ reported for litter size at birth were in the range of 0.09 to 0.14 (MERCER and CRUMP, 1990; SOUTHWOOD and KENNEDY, 1991; FERRAZ and JOHNSON, 1993; SEE *et al.* 1993). Marginally higher $h^2$ estimates (0.19 to 0.21) were found by IRGANG *et al.* (1994) for Duroc and Landrace gilts and for second parity Large White and Landrace sows.

Heritability estimates for NBA and the corresponding genetic correlations between NBA from different parities resulted from a multitrait animal model including records from the first to third parity. This trivariate analysis diminishes possible bias caused by culling of

sows with low prolificacy. The improved $h^2$ with increased parity number is in accordance with the results from VANGEN (1986) and IRGANG *et al.* (1994), who analysed data from LW and LR sows. In contrast, no improvement in $h^2$ estimates with parity were found by HALEY *et al.* (1988) and IRGANG *et al.* (1994) for Duroc sows.

Maternal effects were not included into the model of analysis, because this effect was not significant in the corresponding single trait analysis. This is in accordance with the results of MERCER and CRUMP (1990), PEREZ-ENCISO and GIANOLA (1992) and IRGANG *et al.* (1994), who found no significant maternal effects for NBA. Negative effects of being born in a large litter (large fraternity size) may persist to influence the reproductive performance of sows (VAN DER STEEN, 1985). It could therefore be argued that the presence of a negative maternal effect may have led to an underestimation of the h2 for litter size. However, in both herds it was common that gilts which perform well as piglets are chosen as replacements. In this situation RYDHMER *et al.* (1989) found that a large fraternity size does not necessarily have an unfavourable influence on the litter of the gilt.

The widely defined breeding goal in swine is to maximise the number of healthy piglets weaned. Piglet mortality is, however, highly influenced by management and subsequently has a heritability close to zero (LAMBERSON and JOHNSON 1984). An alternative trait is **mean piglet weight at birth** (BW), which is a trait positively correlated with the chance of piglets surviving during the first weeks, and production in later life (RYDHMER *et al.*, 1989). In Herd A, the heritability for BW was approximately 0.3 in all parities. These relatively high estimates are in agreement with the results of WEBB and KING (1976) and RYDHMER *et al.* (1992). Heritability ofBW recorded in Herd B was considerably lower. However, in Herd B the recording system for BW was changed in the fourth quarter of 1993. After this time litter weight was not recorded at farrowing, but after cross fostering approximately three days later, thus including the weights of the sows own and cross fostered piglets. This change in the recording system is likely to be responsible for this result.

Among the reproductive traits, **21-day litter weight** or weaning litter weight are also used as selection criteria. These two traits are used as indirect measures for milk production in the sow. In our study we found very different $h^2$ estimates between herds and parities, which ranged from 0.12 to 0.23. Heritability estimates reviewed by LAMBERSON (1990) were on average 0.15, with extremes of 0.07 (STRANG and SMITH, 1979) and 0.38 (YOUNG *et al.*, 1978). Most of the variation of W21 in our study could be explained by differences in the number of piglets nursed by the sow and the age of the litter at weighing. The inability to correct appropriately for these effects may be responsible for the considerable differences in $h^2$ between different parities.

The estimates of $h^2$ for **ADG**, approximately 0.35 in both herds, were larger than those found in other studies of pigs tested on-farm, which vary from 0.12 to 0.16 in some studies (e.g. MERKS, 1989; HOFER *et al.*, 1992). However, they were close to the results of LONG *et al.* (1990). The $h^2$ for **BF** were similar in magnitude and varied from 0.36 (Herd A) to 0.45 (Herd B). These estimates agree with those from several studies (e.g. SAVOIE and MINVIELLE, 1988; LONG *et al.*, 1990).

## 5.2 Estimates of phenotypic and genetic correlations

Phenotypic ($r_p$) and genetic correlations ($r_g$) estimated from the two data sets are summarised in Tables 4a and 4b. Correlations between $STAY_{li}$ and traits measured in parity (i) and subsequent parities were not estimated due to the presence of non-estimable error covariances for these trait combinations. The $h^2$ of $FI_{12}$ recorded in Herd B was not significantly different from zero. In addition, only a relatively small number of records for $WCI_{12}$ were recorded in Herd B (Table 1). Therefore, the estimated correlations between WCI, FI and other traits in Herd B are not presented due to a general lack of precision.

Correlations between weaning to conception interval, farrowing interval and other
reproduction and production traits

The traits $WCI_{12}$ and $FI_{12}$ were both negatively correlated with NBA recorded in the first and third litters, whereas the genetic correlations with $NBA_2$ were positive. RYDHMER et al. (1995) estimated negative genetic correlations of -0.03 and -0.10 between NBA measured in first and second parity and farrowing interval in each subsequent parity. This result is in agreement with the negative genetic correlation between NBA in the first litter and the first weaning to conception or farrowing interval found in our study. Nevertheless, second parity sows with a genetic disposition for a long $WCI_{12}$ or $FI_{12}$ tend to have a larger second litter. Young growing gilts with a large first litter probably need a longer period to recover than older sows. This recovery is certainly supported by a long weaning to conception interval after the first parity. In consequence, sows with a genetic disposition for a short $WCI_{12}$ (and high $NBA_1$) tend to produce a smaller second litter. The genetic correlations between $WCI_{12}$ or $FI_{12}$ and NBA recorded in the third litter were again favourable. This could be the result of planned culling of sows with a genetic disposition for a long $WCI_{12}$ or unplanned culling of sows with a high $NBA_2$.

The genetic correlations between **BW** measured in the first three parities and $WCI_{12}$ were consistently unfavourable. Hence, selecting sows for high BW per piglet leads to a prolonged $WCI_{12}$. A high BW of the piglets probably aggravates stress during pregnancy, birth and subsequent lactation with the consequence of a prolonged WCI. Relative to the WCI, the antagonism between FI and BW was reduced. Length of gestation and BW showed a negative genetic correlation (not shown). Hence, gestation length as an additional component of the FI diminished the antagonism between BW and FI.

A strong negative genetic correlation was found between $WCI_{12}$ or $FI_{12}$ and **W21** recorded in the second litter. Sows with a genetic disposition for long WCI in the first reproduction cycle are obviously not able to nurse a large litter in the second parity.

SHURSON and IRVIN (1992) described a selection experiment based on a 'sow production index' including litter size and adjusted 21-day litter weight. Sows selected for a high production index showed an increased body weight loss, with a subsequent delay in return to oestrus after weaning. In this study the genetic correlations between $WCI_{12}$, $FI_{12}$ and W21 or NBA recorded in the first parity were both favourable. Consequently, selection based on a $NBA_1$ and $W21_1$ would probably not lead to a longer $WCI_{12}$. In the second and third parities the genetic correlations between $WCI_{12}$, $FI_{12}$ and W21 or NBA were opposite in sign. This refected both the negative genetic relationship between NBA and W21 in all parities, as well as the change in relationship between WCI and NBA between the second and third parities. In particular, in the second parity favourable genetic correlations between W21 and $WCI_{12}$ or $FI_{12}$ were of greater magnitude than the unfavourable genetic correlations between NBA and $WCI_{12}$ or $FI_{12}$. This result also disagrees with the findings of SHURSON and IRVIN (1992). However, as pointed out previously, the genetic analysis of W21 measurements was uncertain because of the large phenotypic variation in this trait resulting from differences in the numbers of piglets nursed and the deviations in the age of the litter at weighing.

Table 4a: Multiple-trait estimates of phenotypic correlations (below diagonal) and genetic correlations (above diagonals), Herd A

| Trait | Parity | NBA 1 | NBA 2 | NBA 3 | BW 1 | BW 2 | BW 3 | W21 1 | W21 2 | W21 3 | STAY 1-2 | STAY 1-3 | STAY 1-4 | WCI 1-2 | FI 1-2 | ADG | BF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NBA | 1 |  | .74 | .74 | -.40 | -.24 | -.31 | -.12 | -.29 | .04 | -.04 | -.25 | -.10 | -.20 | -.16 | .07 | -.06 |
|  | 2 | .17 |  | 1.0 | -.38 | -.36 | -.44 | -.45 | -.39 | -.31 | — | .42 | .45 | .19 | .38 | -.10 | -.02 |
|  | 3 | .19 | .23 |  | -.62 | -.57 | -.53 | -.30 | -.38 | -.25 | — | — | .31 | -.28 | -.11 | -.11 | .11 |
| BW | 1 | -.46 | -.13 | -.17 |  | .89 | .91 | .41 | .53 | .40 | -.02 | .07 | -.02 | .20 | .12 | .18 | -.10 |
|  | 2 | -.03 | -.44 | -.13 | .33 |  | 1.0 | .43 | .55 | .53 | — | -.25 | -.36 | .13 | -.08 | .22 | -.08 |
|  | 3 | -.03 | -.12 | -.50 | .35 | .43 |  | .25 | .46 | .35 | — | — | -.31 | .32 | .05 | .27 | -.09 |
| W21 | 1 | -.11 | -.04 | -.03 | .23 | .09 | .12 |  | .85 | .66 | -.15 | -.07 | -.09 | -.09 | -.24 | .06 | -.14 |
|  | 2 | .02 | -.13 | -.01 | .10 | .20 | .08 | .21 |  | .95 | — | .06 | -.23 | -.46 | -.50 | .28 | -.09 |
|  | 3 | .04 | -.01 | -.09 | .11 | .15 | .24 | .20 | .26 |  | — | — | .38 | .23 | .05 | .05 | -.06 |
| STAY | 1-2 | .05 | — | — | -.01 | — | — | .05 | — | — |  | .83 | .75 | — | — | -.16 | -.03 |
|  | 1-3 | .09 | .16 | — | -.01 | .00 | — | .03 | .09 | — | .58 |  | .99 | -.45 | -.33 | -.15 | .06 |
|  | 1-4 | .09 | .13 | .23 | -.03 | -.04 | -.12 | .03 | .05 | .05 | .39 | .65 |  | -.22 | -.10 | .02 | .06 |
| WCI | 1-2 | -.02 | .15 | -.09 | .03 | -.03 | .07 | -.04 | -.04 | .02 | — | -.05 | -.05 |  | .97 | -.09 | -.24 |
| FI | 1-2 | -.01 | .17 | -.07 | .01 | -.05 | .02 | -.06 | .01 | -.02 | — | .06 | .01 | .93 |  | -.03 | -.15 |
| ADG |  | .01 | .04 | -.01 | .02 | .00 | .04 | .02 | .05 | .01 | -.06 | -.09 | -.08 | .02 | .00 |  | .45 |
| BF |  | -.01 | -.01 | .04 | -.03 | -.02 | -.05 | -.04 | -.05 | -.03 | .04 | .05 | .03 | -.02 | .01 | .31 |  |

Table 4b: Multiple-trait estimates of phenotypic correlations (below diagonal) and genetic correlations (above diagonals), Herd B

| Trait | Parity | NBA 1 | NBA 2 | NBA 3 | BW 1 | BW 2 | BW 3 | STAY 1-2 | STAY 1-3 | STAY 1-4 | ADG | BF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NBA | 1 | | .56 | .57 | -.79 | -.34 | -.25 | .35 | .04 | .12 | -.11 | .22 |
| | 2 | .17 | | 1.0 | -.39 | -.58 | -.32 | — | .25 | .29 | .12 | .26 |
| | 3 | .14 | .22 | | -.51 | -.49 | -.30 | — | — | .32 | .10 | .27 |
| BW | 1 | -.67 | -.12 | -.08 | | .85 | .59 | -.38 | -.31 | -.15 | .21 | -.05 |
| | 2 | -.09 | -.67 | -.15 | .18 | | .73 | — | -.24 | -.18 | .20 | -.09 |
| | 3 | -.07 | -.12 | -.55 | .13 | .28 | | — | — | -.33 | .41 | -.31 |
| STAY | 1-2 | .05 | — | — | -.05 | — | — | | .99 | .99 | -.31 | .36 |
| | 1-3 | .03 | .08 | — | -.04 | -.04 | — | .68 | | .97 | -.31 | .22 |
| | 1-4 | .03 | .05 | .05 | -.03 | -.05 | .01 | .30 | .49 | | -.23 | .07 |
| ADG | | .04 | .03 | .01 | .01 | -.01 | .01 | -.02 | .04 | -.06 | | .06 |
| BF | | .03 | .02 | .02 | -.03 | .00 | -.03 | .02 | -.07 | .05 | .04 | |

The genetic correlation between **ADG** and $WCI_{12}$ is close to zero, but sows with a genetic disposition for a short WCIu tend to have thicker **BF**, as indicated by the negative genetic correlations between $WCI_{12}$, $FI_{12}$ and BF. Three explanations were given for these antagonistic relationships in the review of TEN NAPEL *et al.* (1995):

1)  Genetic selection for minimal backfat is partially selection of animals with a low voluntary feed intake, at least during growth (FOWLER *et al.*, 1976; VANGEN, 1980; KANIS, 1988). Sows from these strains may have reduced lactational feed intake capacity, which causes severe losses in body weight during lactation, and subsequently a prolonged interval between weaning and oestrus. A genetically reduced appetite has also been suggested by COLE (1990) and MULLAN (1991).

2)  Furthermore, it has been suggested that primiparous sows of genetically improved strains of lean pigs have low body fat reserves at parturition, and therefore reach detrimental depletion earlier than older sows (MULLAN and WILLIAMS, 1989; COLE, 1990).

3)  Selection against backfat at market weight may favour late maturing animals (ELIASSON, 1991). These animals reach puberty at a later age (ELIASSON, 1991; RYDHMER *et al.*, 1992), but were generally mated at the same age as their earlier maturing contemporaries. At the time of first lactation, the former animals need more energy and protein for growth of their own body. Consequently, they may reach harmful depletion sooner than earlier maturing sows.

5.2.2.    Correlations between stay ability and other reproduction and production traits

In Herd A, all defined stayability traits were unfavourably correlated to **NBA** recorded in the first parity. This holds in particular for $NBA_1$ and $STAY_{13,14}$. Sows with a high genetic disposition for NBA in the first parity tend to be culled earlier than sows with a lower $NBA_1$. This relationship became even more unfavourable after fitting the factor 'average number of piglets of the sow from first to last parity' (NL) into the model of analysis for STAY (Table 5). However, in Herd B these unfavourable genetic correlations could not be found as the genetic correlations between $NBA_1$ and $STAY_{13,14}$ were slightly positive. Fitting the correction factor NL did not affect the magnitude of these genetic correlations in this herd.

Table 5:    Phenotypic ($r_p$) and genetic ($r_g$) correlations between STAYc and NBA

| Trait | Herd | $NBA_1$ | | $NBA_2$ | | $NBA_3$ | |
|---|---|---|---|---|---|---|---|
| | | $r_p$ | $r_g$ | $r_p$ | $r_g$ | $r_p$ | $r_g$ |
| STAYcis | A | -.04 | -.41 | .13 | .39 | - | - |
| | B | .04 | .10 | .13 | .24 | - | - |
| STAYcu | A | -.07 | -.32 | .08 | .34 | .20 | .25 |
| | B | .03 | .14 | .04 | .27 | .05 | .27 |

An increased number of sows will probably be selected on the basis of their NBA performance in parities two and three. In consequence, high genetic correlations between $NBA_{2,3}$ and $STAY_{13,14}$ were found in both herds. After correcting for NL, the genetic correlations between $STAY_{13,14}$ and NBA recorded in parity two and three remained positive. These results suggest that sows with a high NBA in the second or third parity were no more susceptible to unplanned culling than their lower performing contemporaries.

With the exception of the genetic correlation between $BW_1$ and $STAY_{13}$, all genetic relationships between stayability and average birth weight were unfavourable. As pointed out before, NBA plays an important role in the planned selection of third and fourth parity

sows. Because of the antagonistic relationship between BW and NBA, the negative genetic correlation between BW and STAY could be expected.

**W21** recorded in the first parity was also consistently correlated unfavourably to all STAY traits. Similar to NBA, sows which are able to wean a heavy litter in the first parity probably have a higher risk of being culled in subsequent parities. The favourable genetic correlations between $W2l_2$ and $STAY_{13}$ or $W21_3$ and $STAY_{14}$ were probably the consequence of planned selection of sows on the basis of their W21 in later parities.

The genetic correlations between STAY and the production traits **ADG** and **BF** were mostly unfavourable. As described in the previous chapter, a high ADG could have negative consequences on fertility (WCI) traits. Moreover, SORENSEN and SORENSEN (1992) showed that sows with a high growth rate had an increased susceptibility to leg weakness and a reduced longevity. Hence, selection for sows with a high ADG might increase both fertility and leg weakness problems. This could be a problem in the first and second parities particularly, as indicated by the strong negative genetic correlations between $STAY_{12,13}$ and ADG for sows in both herds.

Also unfavourable were the genetic correlations between BF and all stayability traits. Similar to ADG, this could be explained by increased fertility (WCI) problems with decreased BF thickness as described in previous chapter. This result agrees with the findings of GAUGHAN *et al.* (1995), who reported a significant phenotypic difference of approximately 0.8 litters/lifetime between sows with a BF depth of 13 mm and those with > 13 mm. However, in Herd A, the antagonism between stayability and BF was hardly significant. This result suggested that management factors could overcome the antagonistic relationship between BF and longevity to a certain extent.

5.2.3    Correlations between no. of piglets born alive and other reproduction and production traits

The genetic correlations between $NBA_1$ and $NBA_{2,3}$ were high but significantly different from one. The findings of STRANG and SMITH (1979), BOLET and FELGINES (1982), IRGANG *et al.* (1994) and ALFONSO *et al.* (1994) were similar. In contrast HALEY *et al.* (1988) concluded from his review, that there is no strong evidence for the hypothesis that the genetic correlation between adjacent litters is substantially less than one. However, in order to reflect the selection process properly, it is necessary to include all available parities into a multi trait model. This prerequisite was only fulfilled in the study of ALFONSO *et al.* (1994) who analysed NBA recorded in the first five parities simultaneously. Based on the results of ALFONSO *et al.* (1994) and the findings in this study, the hypothesis of non genetic identity between parities seems more credible than a unity genetic correlation.

Of considerable magnitude was the negative phenotypic correlation between NBA and BW, particularly when measured in the same parity. The genetic correlations between NBA and BW were also unfavourable, averaging -0.30. Selecting sows with a genetic disposition for high BW per piglet will reduce the NBA. This is in accordance with the results of RYDHMER *et al.* (1992) who analysed data from purebred Swedish Yorkshire pigs. The positive relationship between birth weight and piglet survival till weaning (RYDHMER *et al.*, 1992), complicates selection aimed at increasing litter size.

Genetic correlations between **W21** and NBA (Herd A) were similar in magnitude and sign to the genetic correlations between NBA and BW. This result indicated an apparently unfavourable association between a sow's breeding value for litter size and her genotype for successfully nursing a large litter. This agrees with the negative genetic correlation between NBA and average 21-day piglet weight (rg= -0.33) found by FERGUSON et al. (1985).

The genetic correlations estimated between NBA and the production traits **BF** and **ADG** were not consistent in magnitude or direction across the two herds. In Herd B the relationship between BF and $NBA_{1,2,3}$ was consistently unfavourable. However, with

the exception of the genetic correlation between BF and $NBA_3$ these genetic correlations were slightly favourable in Herd A. Inconsistent results found in the literature reflect this discrepancy between the herds. JOHANSSON and KENNEDY (1983) found an antagonistic relationship between NBA and BF. In contrast RYDHMER et al. (1992) and RYDHMER et al. (1995) found a favourable genetic correlation between NBA and estimated lean percent or BF in Yorkshire sows. Also the results of MCKAY's (1993) study showed an increase in litter size of gilts selected for leanness.

Also conflicting were the genetic correlations between ADG and NBA recorded in different parities. In Herd A, this relationship was positive in the first parity, but negative in parities two and three. In Herd B, the genetic correlations in successive parities were reversed in sign. RYDHMER et al. (1995) found no relationship between growth rate and litter size. In contrast, JOHANSSON and KENNEDY (1983) reported a favourable relationship between growth rate and litter size. KUHLERS and JUNGST (1993) reported a small but significant increase in litter size at birth when selecting Landrace pigs for a high 200-day weight. The same selection criteria for Duroc pigs resulted however, in a decreased litter size (KUHLERS and JUNGST, 1992). RYDHMER et al. (1995) concluded from these results that the relationship between growth rate and litter size at first parity probably varies with age and oestrus number at mating. Relative to Herd B, sows were on average 16 days younger at first mating in Herd A. Thus, the conclusion of RYDHMER et al. (1995) may also serve as an explanation for the conflicting results in our study.

### 5.2.4 Correlations between average birth weight per piglet, 21-day litter weight and production traits

With the exception of the genetic correlations between $BW_{1,3}$ and $W21_1$ and $W2l_3$, genetic correlations between BW and W21 measured in subsequent parities were not different from unity. This result indicates that the expression of BW and W21 recorded in different parities is influenced by the same set of genes. Because of a part whole relationship, high positive correlations were apparent between BW and W21 in Herd A, particularly when measured in the same parity.

BW was consistently favourably correlated with ADG, and to a lesser extent with BF. This result is in accordance with the finding of VANGEN (1980) who found that selection for a high production index including BF and growth rate resulted in larger piglets. A positive genetic correlation between BW and growth rate of individuals was reported by YOUNG et al. (1978) and RYDHMER et al. (1992). Selection for large litters in combination with high growth rate could perhaps keep the birth weight at an optimal level.

### 5.2.5 Correlations between average daily gain and backfat

Growth rate was estimated to have a low (Herd B) to moderate (Herd A) unfavourable phenotypic and genetic relationship with scanned backfat. Several studies (e.g. MCPHEE et al. 1979, BERESKIN and STEELE, 1988) have demonstrated an undesirable genetic relationship between growth rate and backfat thickness.

## 6. Summary and Conclusions

Data sets of two Australian piggeries were used to estimate the genetic parameters for the weaning to conception interval (WCI), farrowing interval (FI), number of piglets born alive (NBA), average birthweight of the piglets born alive (BW), 21-day litter weight of piglets (W21), stayability of sows from first to the fourth parities (STAY), growth rate from birth to end of performance test (ADG) and ultrasound backfat thickness following performance testing (BF). The data was recorded during the years 1982 to 1995 (Herd A) and 1990 to 1995 (Herd B).

The $h^2$ estimate of WCI was approximately 0.10 in the first parity, which is in the normal range of h2 estimates for reproductive traits in pigs. Although low, this $h^2$ suggests that including $WCI_{12}$ in the breeding objective of pigs could lead to a reduction of unproductive days. In addition, selecting for a short $WCI_{12}$ would have favourable consequences for the longevity of sows as indicated by the genetic correlations between $STAY_{13,14}$ and $WCI_{12}$. An incorporation of the WCI would have conflicting consequences for NBA recorded in different parities. NBA recorded in parities one and three would benefit from a selection for short $WCI_{12}$ (rg: -0.20, -0.28), whereas unfavourable consequences could be expected for $NBA_2$ (rg: 0.19).

$WCI_{12}$ is unfavourably correlated with BF (rg: -0.24), whereas the genetic correlation between $WCI_{12}$ and ADG does not differ significantly from zero. In selection schemes with a high emphasis on reducing BF, negative consequences for the $WCI_{12}$ can be expected. Hence, inclusion ofWCIi^ in the breeding object should be considered.

The $h^2$ estimates for the defined STAY from first to second parity was very low, with estimates from 0.02 (Herd B) to 0.05 (Herd A). Slightly higher estimates were found for $STAY_{13,14}$, which averaged 0.08 in both herds. Similar to $WCI_{12}$, the magnitude of the $h^2$ suggests that selection for stay ability of sows is not impossible. However, response to selection for stayability would be expected to be slow.

In our study, a strong negative genetic correlation between $STAY_{13,14}$ and $NBA_1$ was found in Herd A. This indicates that sows with a high first litter performance have reduced longevity within the herd. In addition, non-unity genetic correlations were apparent between NBA recorded in the first parity, and NBA recorded in the second and third parities in both herds. In many breeding programs a repeatability model is used to evaluate litter size, under the assumption that the genetic correlations between NBA recorded in subsequent parities is 1, or approximately 1. A genetic correlation of 1also means that genetic gains in first-parity sows would assure genetic gains in later parities, with the benefits of a reduced generation interval. Under the condition of a negative genetic correlation between STAY and $NBA_1$, such a selection scheme would lead to a decrease in the stayability of sows. Therefore, the inclusion of longevity traits in the breeding objective, or at least less selection emphasis placed on $NBA_1$ relative to NBA recorded in subsequent parities, should be considered.

Also unfavourable were the genetic relationships between $STAY_{13,14}$ and the production traits ADG and BF. The incorporation of STAY in the breeding objective may prevent a further decrease of the stayability of sows, caused by the selection for ADG and BF. However, STAY is a fairly complex trait which reflects different health problems. More specific traits like WCI or separate traits for legs and claws, which are related to the pig's locomotory abilities (VAN STEENBERGEN *et al.* 1990), could avoid a decrease in longevity more efficiently.

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