

# The PIGBLUP reproduction module

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## Introduction

The purpose of this paper is to describe a major update of the genetic evaluation procedure for reproduction traits in PIGBLUP. Although these modifications are not available in version 4.0, they are worth discussing at this point in order that you are comfortable with the changes and can make any preparations required for using the new information when it becomes available next year.

## The existing analysis

In version 4.0, and earlier releases, of PIGBLUP the analysis of reproduction traits consists of the following major features.

- Single trait analyses of number born alive (NBA) and litter weight adjusted to 21 days of age (W21). Use of single trait analyses means that information on genetically correlated traits is not taken into account in the estimated breeding values (EBVs) of the trait being analysed.
- Records across parities are treated as repeated measures on the same trait (the *repeatability* model). Under this model it is assumed that the genetic correlation between a trait measured in any two parities is equal to one and that the heritability is constant across parities.
- Fixed environmental factors (different mean levels of performance) which are accounted for are:-
  - parity (or groups of parities defined when setting up the analysis);
  - mating type (eg natural mating or artificial insemination) x mating breed type (purebred or crossbred mating) interaction; and
  - farrowing group (defined from the data using user supplied parameters<sup>1</sup> and user recorded management groups where available).
- Prior to running the BLUP evaluation, W21 records can be pre-adjusted to account for the actual age at weighing and litter size at weighing by one of three methods.
  - Using US National Swine Improvement Federation adjustment tables.
  - Straight line adjustment using only values from the current record<sup>2</sup>.
  - Linear regression, using regression coefficients calculated from the current data set. This is the recommended method for making adjustments.

Alternatively, W21 can be left unadjusted.

Reproduction data is input into PIGBLUP via record type four. The format of this record is given in Table 1.

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<sup>1</sup> The maximum number of sows per group and the maximum number of weeks per group.

<sup>2</sup> See the PIGBLUP manual for details.

**Table 1. PIGBLUP record type four (reproduction data) format**

<b>Field contents</b>	<b>Format<sup>1</sup></b>	<b>Compulsory<sup>2</sup></b>	<b>Comments</b>
Record type identification	i1	x	(always 4)
Animal identification	a10	x	
Animal breed code	a2	x	
Parity number	i2	x	
Mating date	3i2		(ddmmyy)
Service sire identification	a10		
Service sire breed	a2		
Mating type	a1		
<b>Date of farrowing</b>	3i2	x	
Number of piglets born alive	i2	x	
Number of piglets born dead	i2		
User recorded management group	a1		(version 1.0)
	a2		(version 1.1) <sup>3</sup>
Number of piglets at transfer	i2		
Date of piglet transfer	3i2		(ddmmyy)
Total weight of piglets at transfer	i3		
Number of piglets at weighing	i2		
Date of weighing	3i2		(ddmmyy)
Total weight of piglets at weighing	i3		
Farrowing data valid flag	a1		(v if valid)
21-day litter weight valid flag	a1		(v if valid)

<sup>1</sup> Format *xyz* denotes *x* repeats of a variable of length *z* and type *y* (i indicates integer data, a indicates character string data). For example, '3i2' indicates 3 integer values of length 2. In the case of the date 'October 22, 1998' this would be represented as 221098 in '3i2' format.

<sup>2</sup> Marked fields must contain data.

<sup>3</sup> Two PIGBLUP data file formats currently exist. The use of these formats must be consistent across record types.

## Review of traits

### 16. *Components of pigs/sow/year*

Improving overall reproductive performance of a breeding enterprise can lead to substantial gains in profitability. If we consider the number of pigs produced per sow per year to be one measure of reproductive performance, then it is clear that we may increase this through:

- increasing the litter size;
- decreasing the time between litters, and hence increasing the number of litters per year.

The trait responsible for most of the variation in reproductive performance in pigs, and other litter bearing species, is litter size (Pérez-Enciso and Bidanel, 1997). In

PIGBLUP, litter size is represented through the trait NBA. The heritability of NBA has been reported to be around 0.1 across many published studies and different commercial populations (Haley *et al*, 1988; Hermes, 1996).

The interval between litters is:

$$\begin{aligned} \text{Farrowing interval} &= \text{lactation length} \\ &+ \text{weaning to conception interval} \\ &+ \text{gestation length} \end{aligned}$$

Reductions in the farrowing interval (FI) can be achieved either through selection on the trait itself or upon the constituent traits. Selection for decreased FI would automatically put downward selection pressure on all the constituent traits.

Crump *et al* (1997a) reported a heritability of around 0.2 for gestation length. However, because of the very low variation in this trait there is little scope for genetic improvement.

The point at which piglets are weaned is a management decision. This prevents lactation length from being a viable trait to select on, as its expression is limited by management practices.

This leaves selection on weaning to conception interval (WCI) as the best option for decreasing FI.

Tholen *et al* (1996a) reported heritability estimates of around 0.1 for the interval between weaning in the first parity and conception for the second parity (WCI<sub>12</sub>) and 0 for WCI in subsequent parities. These results were consistent across two large Australian breeding herds. This implies that:

- genetic progress could only be made for WCI<sub>12</sub>;
- WCI records later in a sows life would provide no information on other traits (where there is no genetic variation, there can not be any genetic covariation).

In their analyses, Tholen *et al* (1996a) observed that lactation length had an effect upon WCI<sub>12</sub>. Lactation lengths of less than 20 days or greater than 28 days resulted in significant increases in WCI<sub>12</sub>, when compared to lactation lengths in the range 21 to 23 days. This effect can be accounted for in the PIGBLUP evaluation.

### **17. Piglet performance.**

We select for improvement in the performance of individual pigs when we select for the production traits included in the production analyses of PIGBLUP. Selection for these traits selects on the individuals own genetic merit for those traits.

In addition to this we can select for the ability of the sow to give her piglets a good start in life. This ability is reflected in the trait W21, which is the weight of the litter nursed by a sow at 21-days of age.

## 18. Sow longevity.

Simulation studies (Dijkhuizen *et al*, 1989; De Vries, 1989) have shown considerable economic benefit from improving sow longevity from four to five parities. Tholen *et al* (1996a) reported heritabilities of between 0.06 and 0.09 for stayability from first parity to parities two, three or four.

## 19. Traits chosen for inclusion in the new PIGBLUP reproduction analysis.

There will be three traits available for multivariate analysis in the new PIGBLUP reproduction module. These are **number born alive, 21-day litter weight and weaning to conception interval between parities one and two.**

In order that the current reproduction record structure (see Table 1) can be utilised, WCI will only be available when the W21 weighing is a weaning weight. That is, WCI will be calculated as the interval between 'Date of weighing' (for parity 1) and 'Mating date' (for parity 2).

**Stayability** will be added as a univariate analysis after the multivariate analysis development has been completed. The reason for keeping this trait separate is that the analysis of survival data requires specialised statistical techniques.

## Multivariate analysis

Multivariate analysis of reproduction traits will give more accurate estimates of EBVs by taking into account information on correlated traits.

The new PIGBLUP reproduction analysis will be multivariate. However, it will not be linked with the production analysis. The literature estimates of the genetic correlations between reproduction and performance traits indicate that they are very low (Hermesch, 1996; Crump *et al*, 1997b), and that little would be gained in accuracy from combining the two analyses. However, there would be a considerable loss in computing efficiency since all the male animals recorded for performance test traits would be included in the reproduction analyses.

## The repeatability model

The use of a repeatability model for reproduction traits of pigs has been standard practice for a long time. The review of Haley *et al* (1988) considered the results of a number of studies in which multiple-parity data for litter size was regarded as multiple traits. From the results of these studies it was not possible to conclude that the genetic correlations among the parities differed from one and so Haley *et al* concluded that the repeatability model was suitable for the genetic analysis of litter size.

When we use the repeatability model in a multivariate analysis, we are making assumptions not just about the relationships between parities within a trait, but also about the relationships between traits across parities. For example, it assumes that NBA in gilts the same genetic correlation with  $WCI_{12}$  as NBA in parity 4.

The most extreme solution to this problem would be to treat each record on NBA and W21 as a different trait in each parity. The following difficulties restrict the use of this approach.

- You have  $n$  traits representing each of NBA and W21, where  $n$  is the number of parities with records present ie NBA in the first five parities would represent five traits. This leads to far longer computation times for EBVs. In a herd in which sows survived for up to four parities, that would give rise to nine traits (4xNBA, 4xW21 and  $WCI_{12}$ ).
- Genetic parameters are required for each trait in each parity. These parameter estimates will be less well known for the later parities, as a result of there being fewer records on these parities.

An alternative approach would be to treat gilt records as one trait and records on all subsequent parities as repeated records on a second trait (ie make use of the repeatability model for parities two and above). The advantage of this model is that it recognises that gilt litters are a special case, and reproduction records recorded in gilts are genetically not the same trait as those recorded in later parities. Evidence for this comes from Tholen *et al* (1996b) and the review of Hermesch (1996); both of these sources quote genetic correlations of less than one between first and subsequent parity records and very high genetic correlations between second and third parities. Using this model in a multivariate analysis of NBA, W21 and WCI in our hypothetical herd using sows for four parities would result in us analysing 5 traits (NBA in the first parity, NBA in parities 2 and above, W21 in the first parity, W21 in parities 2 and above and  $WCI_{12}$ ), rather than the 9 from the full multivariate analysis.

As a result of sows gradually being replaced by younger genetically superior breeding stock, there are fewer records on later parities than early parities. Estimates of genetic correlations between these parities from commercial populations are therefore subject to higher standard errors than estimates of genetic correlations between early parity traits. These errors make interpretation of genetic correlations at later parities more difficult. It is considered to be safer to make use of the model which considers gilt litter records to be a separate trait from subsequent litter records for each trait than the full multivariate model (fitting each parity as a separate trait).

## Other considerations

In discussing the revamped reproduction module, it is necessary to mention some other effects which have been considered for inclusion in the analyses.

### 1. *Maternal effects*

There is no evidence to support the inclusion of maternal effects (that is, genetic effects of the mother of the recorded sow) in analyses of reproduction traits (see, for example, Haley *et al*, 1988; Crump *et al*, 1997a).

### 2. *Service sire effects*

There are a number of hypothesised ways in which the boar to which a sow is mated may affect her reproductive performance. In this section, the discussion will focus on NBA, as this is the trait that studies have covered to date.

- *Service sire age*

Boars which are either very young or coming to the end of their reproductive lives are hypothesised to have a negative effect upon NBA compared to boars which are at their most fertile age.

In a study of a synthetic line from an Australian producer service sire age was found to have a significant effect upon NBA only in the first parity. The mean service sire age at mating for parities 1 to 5 were 218, 308, 371, 411 and 425 days, respectively. When this study was repeated for a Large White line from another Australian herd which routinely used older boars for mating across all parities, service sire age was not significant in any parity. Average service sire ages for parities 1 to 5 were 325, 379, 410, 457 and 477 days, respectively.

From the average ages of service sires given above, we can see that there is a tendency to use younger boars on young females. A factor will be included in the new PIGBLUP reproduction module to take account of young service sires being used on gilts. Whether or not this factor is fitted for a given population will be determined from the incidence of young service sires in the data. The importance of this effect for W21 and WCI will be investigated.

- *Service sire breed*

Service sires of different breeds may affect the NBA for a sow either through breed differences in boar fertility or through their contribution to the genotype of the litter.

Fitting of 'Mating Type' can be turned on or off in PIGBLUP. If the mating type is being fitted then whether or not the litter is crossbred is taken account of. The specific service sire breed is not fitted, just that it differs from the sow breed. In this way heterosis may be partially accounted for.

- *Individual service sire effects*

The genotype of the litter may be expected to contribute to the observed NBA for that parity of the sow. Half of that genotype is due to genes inherited from the service sire. The size of these effects can be estimated using the same technology as that used to estimate the heritability.

Woodward *et al* (1993) developed an animal model for the across-herd genetic evaluation of NBA in US swine breeds. The benefit of fitting service sire (in terms of the quality of evaluations) was based on the assumption that service sire variation was responsible for 0.05 of the phenotypic variance. Estimates of the proportion of the phenotypic variance of NBA which was explained by service sire effects were presented as 0.01 - 0.02 by See *et al* (1993) from within-breed analysis of US swine populations. There would be less benefit from including service sire in evaluations at these levels of service sire variation.

Estimates of service sire variation as a proportion of the phenotypic variation from two Australian populations (one synthetic line, and one Large White) line are in agreement with those of See *et al* (1993). For young boars (those born in 1994 and later and with only gilt records on their female offspring) in each

population the ranking of boars on their NBA EBVs did not change when service sire was either included or omitted from the genetic evaluations.

## Summary of features of new PIGBLUP reproduction analysis

- Multivariate analyses of:
  - number born alive in the first parity (NBA<sub>i</sub>),
  - number born alive in second and later parities (NBA<sub>2+</sub>);
  - 21-day litter weight in the first parity (W21<sub>i</sub>);
  - 21-day litter weight in second and later parities (W21<sub>2+</sub>), and weaning to conception interval between the first and second parities (WCI<sub>u</sub>).
- Repeated records for NBA<sub>i</sub>+ and W21<sub>i</sub>+ are treated as repeated measures on the same trait.
- Fixed environmental factors (different mean levels of performance) which are accounted for are:
  - parity (or groups of parities) for NBA<sub>2+</sub> and W21<sub>2+</sub>;
  - mating type (eg natural mating or artificial insemination) x mating breed type (purebred or crossbred mating) interaction;
  - lactation length for WCI<sub>12</sub>;
  - farrowing group (defined from the data using user supplied parameters and user recorded management groups where available).
- Pre-adjustment of W21<sub>i</sub> and W21<sub>2+</sub> is as in the existing analysis.

## References

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