INTRODUCING THE SECOND GENERATION OF PIGBLUP

T. LONG1, H. BRANDT2, B. TIER3 and W. FUCHS3

Animal Genetics and Breeding Unit1
University of New England
Armidale, NSW 2351.

2University of Göttingen
Göttingen, Germany

3Markt Neubau
Kirchberg, Austria

INTRODUCTION

PIGBLUP is a production-mode genetic evaluation system for pigs. It uses a multiple trait animal model and has been developed to run on microcomputers with a user-friendly interface so pig breeders can do their own genetic evaluations on-farm. The initial version (V1.0) was described by Brandt et al. (1988) and was released to the Industry in 1989. This version calculated Estimated Breeding Values (EBVs) using Best Linear Unbiased Prediction (BLUP) for lifetime average daily gain (ADG) and backfat (BF). A modification of a multiple-trait reduced animal model (Quasas and Pollak, 1980) was used where pigs just coming off test were not absorbed into the parent equations. EBVs for number born alive (NBA) were calculated in a separate module using a single trait repeatability model. An upgraded version, (V1.1) was released in late 1990 which included analysis of two additional traits in the multiple trait model: feed conversion ratio (FCR) and average daily gain over a test period (TADG). Details of this system were reported by Long et al. (1990). Both these versions are currently being used by breeders in the Industry.

The second generation of PIGBLUP (V2.0) is to be implemented in 1992. This new version will contain enhanced flexibility of traits analysed, inclusion of three additional carcase traits and will use a new computing algorithm to predict breeding values (Tier and Graser, 1991). The new version will also contain two new modules: 1) The Genetic Audit, to aid breeders in assessing the effectiveness of the breeding programs, and 2) The Mate Selection Module, to give breeders suggested matings to enhance genetic gain and control inbreeding. The purpose of this paper is to briefly describe this new version.

ADDITIONAL TRAITS AND MODELS

Version 2.0 of PIGBLUP will enable three additional traits to be included in the analysis of production traits: lean meat yield (LMY), carcase fat depth (CF) and carcase muscle depth (CM). The user will have the option of choosing two of these three for analysis along with those traits already available in V1.0 and V1.1. The user can also specify within the menu which traits are being recorded, and this will determine the model as well as the appropriate variance-covariance matrices to be used in the analysis. Table 1 summarises the traits being analysed in the various versions of PIGBLUP. V2.0 will give breeders greater flexibility in customising the evaluation system for their particular recording scheme.

* AGBU is a joint institute of NSW Agriculture and The University.
Table 1. Traits analysed in PIGBLUP

<table>
<thead>
<tr>
<th>Module</th>
<th>V1.0</th>
<th>V1.1</th>
<th>V2.0</th>
</tr>
</thead>
<tbody>
<tr>
<td>Production</td>
<td>ADG, BF</td>
<td>ADG, TADG,</td>
<td>ADG, TADG,</td>
</tr>
<tr>
<td></td>
<td></td>
<td>BF, FRC</td>
<td>BF, FRC, LMY, CF, CM</td>
</tr>
<tr>
<td>Reproduction</td>
<td>NBA</td>
<td>NBA</td>
<td>NBA</td>
</tr>
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In multiple trait animal models the demand for computing resources (time, I/O and memory) increases with the square of the number of traits in the analysis. This can cause problems when working in a microcomputer environment. To limit the amount of memory and input required by PIGBLUP in V2.0 an implicit representation of the mixed model equations (MME) has been used (Tier and Graser, 1991). A reduction in the computational burden is accomplished by factoring out many common terms, achieved primarily by using a transformation of the MME (Tier and Graser, 1992). Table 2 gives the memory requirements and run times of the reduced animal model (RAM) algorithm of V1.1 of PIGBLUP and the Implicit Animal Model (IAM) algorithm of V2.0 for a data set of 8366 animals and 4 traits being analysed. Note that by using V2.0, the analysis of these data required 5% more time but only 14% of the memory used by V1.1. Although inclusion of the IAM in V2.0 will be essentially transparent to the user relative to earlier versions, it will greatly reduce memory requirements, thereby allowing analysis of a greater number of traits or animals in the microcomputer environment.

Table 2. Comparison of Memory Requirements and Run Times for the Reduced Animal Model vs Implicit Animal Model in PIGBLUP

<table>
<thead>
<tr>
<th></th>
<th>RAM</th>
<th>IAM</th>
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<tbody>
<tr>
<td>LHS</td>
<td>683k</td>
<td>7.2k</td>
</tr>
<tr>
<td>Solutions + RHS + Updates</td>
<td>117k</td>
<td>107k</td>
</tr>
<tr>
<td>Total</td>
<td>800k</td>
<td>114.2k</td>
</tr>
<tr>
<td>Run time (seconds)</td>
<td>1093</td>
<td>1143</td>
</tr>
</tbody>
</table>

THE GENETIC AUDIT

Genetic evaluation not only entails assessing individual animals for genetic merit but also involves evaluating the breeding program as a whole. One of the features of PIGBLUP is the graphical representation of both genetic and environmental trends. This feature allows breeders to assess the progress.
of their breeding programs over time. With V2.0, additional diagnostic tools will be provided that will give breeders the ability to better ascertain why their genetic trends are as they are.

The equation below gives various elements which contribute to genetic gain/year.

\[
\text{Genetic gain per year} = \frac{\text{Selection intensity} \times \text{selection accuracy}}{\text{Generation interval}} - \frac{\text{Inbreeding depression}}{\text{Generation interval}}
\]

The Genetic Audit of PIGBLUP provides the breeder with summary output which gives insight into various components in the above equation. The percentage of animals selected vs animals tested is given for the current audit year and relative to the previous 5 years of the breeding program. If all animals are being tested, this will be a measure of how intense selection has been. Selection differentials are also provided for the various traits in the analysis. The breeder can then assess the relative selection emphasis and intensity placed on traits in the analysis and whether changes need to be made in this area. In addition, average generation intervals for boars and sows are provided by the Genetic Audit. This will give an indication to the breeder of how fast animals are being turned over. Inbreeding is also reported as an annual average so the breeder can assess whether rates of inbreeding may be a problem in the herd. Each of these diagnostics will provide breeders with additional information on how they can improve their breeding operations.

THE MATE SELECTION MODULE

Currently, the majority of pig breeders are mating animals randomly, or assortatively (best to best) while avoiding the mating of close relatives (to control inbreeding). Following these types of mating policies, however, may not adequately address the problem of maximizing genetic gain while enabling control of inbreeding (Bunter and Long, 1991). To address this the 1st generation Mate Selection Module has been developed to provide practical mating options to breeders. This module identifies the sows and boars available for a week’s mating and uses linear programming techniques to provide suggested matings that will maximize the average EBVs of progeny and minimize their average inbreeding coefficients depending on the breeder’s concern about inbreeding. The emphasis a breeder may wish to place on minimizing inbreeding can be varied, recognizing that increasing emphasis on the minimization of inbreeding can reduce short term genetic gain thereby potentially reducing cumulative long-term gains. Details of the basic approach are given in Bunter et al. 1992. This module gives pig breeders a tool they’ve never had before which has the potential to manage inbreeding while retaining the advantages of using BLUP in a selection program.

FUTURE ISSUES

Version 2.0 of PIGBLUP is the most advanced genetic evaluation system for pig breeders currently available, and research and development work on the system is continuing. In the short term, enhancements to the reproductive analytical module are underway. The current system analyses only NBA, and additional traits will be added to give a better genetic assessment of mothering ability of candidates for selection. SINDEX, the current breeding objective module of PIGBLUP, will be refined to give breeders greater flexibility in defining and implementing their breeding objectives. Further refinements of the Mate Selection Module are also planned to enhance the balance between rate of genetic gain and inbreeding.
The current system is designed to analyse data on a within-herd basis, but a more comprehensive genetic evaluation would be to analyse data across herds with appropriate genetic ties. Ways to facilitate this and potentially incorporate data from central testing facilities will be investigated.

Finally, other traits (e.g., carcass quality measures) need to be evaluated for inclusion into the analytical system, the breeding objective module or both. Knowledge of the genetic relationships between these traits and traits in the current system will aid in incorporating them into the genetic evaluation system.

The PIGBLUP genetic evaluation system has the potential to provide the focus for planned breeding in the Pig Industry. By developing and refining modules to accommodate each area of breeding decisions, this system gives breeders a powerful tool they've never had before. The current system and future versions will aid breeders in enhancing the efficiency of their breeding operations to remain competitive in the marketplace.

REFERENCES