Genetic evaluation systems for pigs used in Australia

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Development of genetic improvement systems for pigs

The development of PIGBLUP started in the late 80s and since then has been funded by Australian Pork Limited and its predecessors. Pig breeding companies require frequent genetic evaluations and it was decided to develop a system that would run on a microcomputer on farm and could be operated by breeders themselves. The initial version of PIGBLUP included three traits: average daily gain, backfat and number of piglets born alive and feed conversion ratio was added to the production module soon afterwards (Long et al., 1990). These traits were then combined using the $INDEX which was based on a profit function approach (Stewart et al., 1990). This module uses economic, production and marketing data supplied by the breeder to weigh estimated breeding values (EBVs) of traits and combine them into a single $Index.

The PIGBLUP v4.00 saw the transition from Fortran77 to Fortran90 (Crump and Henzell, 1998). More importantly for breeders, this version provided an additional trait; juvenile insulin-like growth factor 1 (IGF1) which had been shown to have genetic relationships with feed conversion ratio and lean meat growth (Bunter, 1996). Juvenile IGF1 is recorded in five weeks old piglets thus providing early information for selection decisions. The main addition to PIGBLUP 4.20 was a multi-trait analysis of five reproduction traits (Crump and Henzell, 2000). Litter size and 21-day litter weight are analysed as separate traits in the first and later parities. These four traits are analysed together with weaning to conception interval between the first and second parity. Modification of the reproduction module was based on results by Tholen et al. (1996).

PIGBLUP has had a fully functional Windows interface since version 5.00, which allows superior printing capabilities and higher resolution graphics. Three major additions are part of PIGBLUP version 5.10. Accuracies of estimated breeding values are calculated automatically. An alternative economic model has been added to derive the $Index. It is now possible to set up multiple $Indexes. An advanced selection and mate allocation module has been developed allowing breeders to optimise both, genetic merit of animals and relationships between animals in order to maintain genetic variation in the population. PIGBLUP version 5.20 due for release in 2005 includes a new module that allows incorporation of gene marker information in genetic evaluations.

The National Pig Improvement Program (NPIP) was initiated by the Queensland Department of Agriculture in 1995 and was transferred to AGBU in 2001. Genetic analyses are performed using the PIGBLUP software, which allows across-herd genetic evaluations. Breeders are able to send their data via e-mail to AGBU and information about estimated breeding values is returned automatically by the system. In addition, the web pages of the NPIP (http://npip.une.edu.au) are updated automatically showing genetic trends, EBVs for AI boars and mean EBVs for each 10-percentile class of young boars. Participating breeders are encouraged to use reference sires that are located in AI centres in order to achieve genetic linkage between herds. Participation in the NPIP is voluntary and individual breeders maintain their own independent breeding programs.

The PIGBLUP bureau service is being developed in 2005. The automated service allows individual pig producers to send data to AGBU via e-mail and EBVs are returned electronically. Producers who have an electronic herd recording system in place and select their own replacement stock will benefit from this service.

PIGBLUP analyses

Traits The list of traits available in PIGBLUP includes four production traits, three carcase traits, juvenile insulin-like growth factor 1 and five reproduction traits (Table 1). Estimated breeding values for these traits are obtained through two multiple trait analyses. The first analysis includes production and carcase traits along with juvenile IGF1 and the second analysis includes reproduction traits. **Please note**: Some breeding companies use alternative traits in place of the allocated default traits. These modifications require changes to the default genetic parameters.

Models. The management groups for these traits are formed automatically by the system accounting for sex, user-defined management groups and time period (or group size) in which the record was taken. These management groups are set up for each group of traits separately. Management groups are fitted as fixed effects. In addition, it is possible to fit genetic groups for introduced animals by defining the time period for each genetic group (in years).

Each of these traits can be pre-adjusted for weight or age. Breeders who are interested in analysing alternative traits to the specific PIGBLUP trait definitions may use this option. As mentioned above, these breeders also make changes to genetic parameters used in the analyses.

Parity of the sow is fitted for litter size and 21-day litter weight in later parities (NBA2 and LW2) in addition to the management group effects explained above. Both 21-day litter weight traits are adjusted for the number of piglets reared and the age of the litter at weighing. The trait weaning to conception (WCI) is adjusted for the number of piglets reared, the age at weighing, age at first farrowing and lactation length. Finally, herds using both AI and natural mating are able to correct reproduction traits for these types of matings. In addition, mating type accounts for differences between cross-bred versus purebred litters by using information about the breed of the service sire of the litter.

Table 1. Traits analysed in PIGBLUP

Trait Group	Trait Name	Trait Group	Trait Name
Production	Average daily gain Gain over test period Backfat Feed conversion ratio Live muscle depth	Reproduction	Number born alive in the first parity Number born alive in later parities 21-day litter weight in the first parity 21-day litter weight in later parities Weaning to conception interval between the first and second parity
Carcase	Carcase fat depth Carcase muscle depth Carcase lean meat %	IGF1	Juvenile insulin-like growth factor I

$Index. The $Index uses a profit function to weigh EBVs of individual traits and combine them into a single $EBV. Breeders are able to use their own economic, production and marketing information. The economic information is based on a payment grid for backfat and possibly muscle depth. A number of payment grids are available and breeders are able to generate payment grids that suit their own circumstances. Further input information includes price per kg, feed costs and non-feed costs per day. Production information includes performances in litter size, mortality rates, growth rate and backfat, target market carcase weight and dressing percentage. Marketing information defines the percentage of boars and gilts used as terminal sire or maternal line animals. This setting places different emphasis on production versus reproduction traits and allows breeders to distinguish between terminal sire,

maternal and dual-purpose lines. A number of $Indexes can be set up simultaneously.

Some breeding companies prefer to use their own economic weights and PIGBLUP allows this option. In addition, it is possible to normalise the $Index to a fixed mean and variance as is required in some countries.

Buyer's Own $Index. This separate module allows breeders to define profit functions and breeding objectives specifically for each individual client.

User-friendly program

The PIGBLUP program has been developed to be used on-farm by breeders themselves. In order to run PIGBLUP users only need to specify where the data file is located. PIGBLUP allows scanning of this file to determine start and end date of data available, breed codes and to infer data format. Once this information has been confirmed first-time users often run PIGBLUP with the default settings to see whether their data allows a genetic evaluation. Given a sufficient data quality, breeders then proceed to set up PIGBLUP for their breeding program by defining traits, models and the $Index.

Breeders are able to have separate set ups for each breed. Different breeds are installed in separate directories. Within each breed directory sub directories are created when a breeder defines different indices for individual customers. As a result the setup for individual breeds and customers is easy to monitor and used by the program 'Migrate', which has been developed in order to make the transition from one PIGBLUP version to the next as easy as possible for the user. This separate program determines the set up of the previous version and modifies the set up of the new version accordingly.
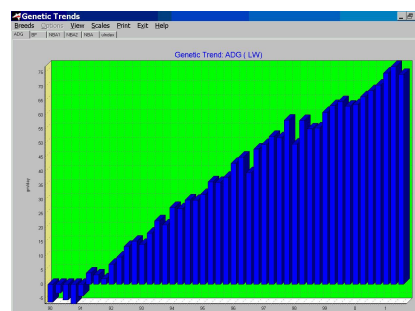
Display of EBVs

Estimated breeding values are only displayed for animals of interest. These include parents and young animals available for selection. Per default EBVs are shown for animals younger than 200 days of age. However, breeders are able to change this age for implicit flagging of animals. Animals that are older than the implicit flagging age and are not parents yet can be identified by the breeder as being active animals in order to obtain EBVs for these animals of interest.

Herd recording systems usually import the file containing EBVs of all animals of interest. However, it is possible to list EBVs separately for different sexes and to limit EBVs based on date of birth, $Index and days off test. The list of animals can be sorted on animal identification, date of birth, individual EBVs and accuracies allowing the user to efficiently evaluate the genetic merit of animals.

Graphs of genetic and environmental trends

The progress of the breeding program and changes in management procedures can be evaluated through genetic and environmental trends. Genetic trends are displayed for all analysed traits by showing the mean EBV of animals born in yearly quarters. It is possible to define the x-axis and y-axis specifically. The breed of interest needs to be defined in analyses with multiple breeds. Further information is available in the data window where the number of animals and mean EBV for each yearly quarter are shown.

Genetic Audit

The Genetic Audit module is used to monitor the progress of the breeding program

more closely. The Genetic Audit allows viewing average EBVs in a defined audit year and to compare these EBVs with the average of the previous five years. Information is provided about the number of litters, sows and boars tested and the proportion of these animals that was selected during each year. These selection intensities are then used to derive selection differentials that were possible for each trait. These selection differentials are based on the variance of EBVs and not the underlying genetic variances. Comparison of the possible and achieved selection differential for the $Index shows breeders how much of the gain in the breeding objective that was possible had actually been achieved.

Litters per boar, weeks at service and generation interval for boars (and sows) provides further information about the population structure. Together with average inbreeding levels over time in litters, sows and boars this information is of particular interest to balance genetic gain and inbreeding levels.

Selection and Mate Allocation

PIGBLUP has contained a mate allocation procedure since version 2.0 (released in 1992). This mate allocation procedure maximised the genetic merit of the offspring of matings while penalising inbreeding. Since then, dynamic selection and mate allocation procedures have been developed and PIGBLUP has a new system, which allows optimisation of selection and mating decisions. In both situations, at selection and at mating, a list of candidate animals is processed to find the best combination of animals based on a merit function. This function includes the genetic merit of animals and relationships among candidates as well as relationships of candidates with other animals that may join (they may not be born yet) or remain in the breeding herd. Other parameters of the merit function are inbreeding of offspring (for mate allocation only) and variance of genetic merit. The selection allocation provides a list of animals to be selected and the mate allocation lists candidate sows with first, second and third choice matings.

Across-herd and across-breed analyses

The within-herd analyses can be extended to across-herd analyses by defining different herds as different management groups. In addition, individual herds can be assigned a separate genetic group to take differences in the genetic base into account. An example for an across-herd evaluation is the Australian National Pig Improvement Program (http://npip.une.edu.au), which has been based on the PIGBLUP software since 2001.

Support of breeders

The PIGBLUP program is fully supported by the AGBU pig genetics team. Breeders can contact AGBU via e-mail, phone or fax when help is required. Various training sessions and workshops are conducted for breeders from time to time. In addition, pig genetics workshops are held every 18 months in Armidale to demonstrate new features of PIGBLUP and to discuss the latest research findings. These workshops provide the opportunity for users to exchange ideas and a number of international users have repeatedly attended these workshops. During these workshops users are asked to provide feedback and make suggestions for further developments of PIGBLUP. These suggestions are considered by the Pig Genetics Consultative Group, which determines further developments. This group consists of a number of breeders along with representatives of the industry and funding body who meet in six monthly intervals.

References

The list of references can be obtained from the first author.

Pig Genetics Info

Australian Pork

PIGBLUP –1

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