The National Pig Improvement Program – update

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Introduction

1. National Pig Improvement Program

The National Pig Improvement Program (NPIP) is an across-herd genetic evaluation system for pigs in Australia. Michael Macbeth from the Queensland Department of Primary Industries initiated the NPIP in 1995 with technical support from the Animal Genetics and Breeding Unit (AGBU). Since 2001, the NPIP has been the responsibility of AGBU and the analytical system is now based on the PIGBLUP genetic evaluation system.

The NPIP web site at http://npip.une.edu.au provides general information about the NPIP along with estimated breeding values (EBVs) for AI boars, genetic trends, distributions of EBVs for young animals and lists of the top young animals. Detailed information about the NPIP was provided at the last workshop (Crump and Hermesch, 2003) and only a brief overview is provided here.

2. NPIP EBVs predict differences in performance

Persuading commercial producers of the benefits of using EBVs to select replacement boars or AI boars is an ongoing issue in the Australian industry.

Differences in EBVs between animals should predict differences in their performance on average. Progeny receive half of their genes from their sire. Therefore, half of the differences in EBVs between sires should be reflected in the average performance of their progeny. These differences can only be demonstrated reliably with large data sets. Glasshouse Mountain Country Farm (GCF) has used sires from multiple herds of the NPIP continuously. The relationship between NPIP EBVs of AI sires and average performance of progeny groups of these sires of GCF is presented later.

The study of GCF data was originally carried out for presentation at Australian Pork Limited's (APL) Uptake 2004 meeting. For a previous APL Uptake meeting, the design of trials that use AI boars in one or more commercial herds to demonstrate the predictive power of EBVs was considered. A simulation program to assess the probable outcome of trials based on available AI boars was written. This program is also outlined here.

National Pig Improvement Program - overview

1. Participation

The NPIP is open to all herds in Australia. Initially, genetic evaluations were developed for Large White, Landrace and Duroc purebred populations with no requirement to register animals for herd book registration.

The across-herd genetic evaluations of the NPIP can also be applied to any synthetic commercial population if there is a demand from seedstock providers or producers for such a genetic evaluation. However, classifying a synthetic line as the same population across herds may be problematic and the genetic background of a synthetic line has to be similar across herds. For these reasons, expansion to synthetic lines has not yet occurred.

2. Procedure

Submission of data is via e-mail. Participating herds are required to supply data in electronic format to the e-mail address of the NPIP (npip@une.edu.au). So far, only one of the PIGBLUP data formats (version 1.0) is accepted by the NPIP. Other PIGBLUP formats will be accepted in the near future.

Data require for genetic evaluations include pedigree information and performance records. The traits analysed by the NPIP include lifetime growth rate, backfat and litter size, which is defined as a separate in the first parity versus later parities. A trait that will be implemented in the near future is juvenile insulin-like growth factor-1 (IGF1), which provides information on feed conversion ratio (FCR).

Genetic evaluations of the NPIP system start automatically once new data have arrived via e-mail. Firstly, the submitted data are compared with historical data. If there are few inconsistencies between new and old data then the genetic evaluation starts for each breed that has new data available.

Information from the across-herd genetic evaluation is automatically returned via e-mail to the participant once the genetic evaluation has been completed. If the analysis starts automatically this is normally achieved within 15 to 30 minutes. Members receive their results in the form of a ZIP archive that contains a series of HTML files (files for the set-up of a web page). Once these files have been extracted into a separate directory on their home computers members are able to view results with their standard web browser. The content of the HTML and graphics files sent to members is different to those shown on the NPIP web page. Individual participants receive results for young animals from their herd and their parents, within- and across-herd genetic trends, within-herd distributions of EBVs compared to those of the whole population and information relating to genetic linkage.

The NPIP web pages reporting analysis results are automatically updated during each genetic evaluation. The analyses are run separately for each breed and results are available on the web for Large White, Landrace and Duroc including:

- Genetic trends for growth rate, backfat and litter size.

- Distribution of trait EBVs and both Terminal Sire and Maternal indexes in young boars and gilts. The cut-off points for 10% groupings of EBVs for young boars and gilts are displayed, which are calculated for each trait independently.

- The list of AI boars that are available from different AI centres is shown. Information is provided about EBVs of AI boars along with their Terminal Sire and Maternal indexes.

- Lists of top young animals (boars and gilts) on the basis of either the Terminal Sire Index or the Maternal Index. This list also includes the sire identification of the top young animals.

3. Genetic linkage between herds

Across-herd genetic evaluation requires genetic linkage between herds in order to separate herd effects from genetic effects. Genetic links between herds are obtained by recording progeny from AI boars in multiple herds. In order to maintain genetic links between herds it is important to utilise AI boars across herds continuously. Members of the NPIP are encouraged to use 10% of their matings with link boars. These are boars that have recorded progeny in multiple herds and include boars from other herds as well as boars bred within the herd. Kim Bunter presented detailed guidelines for establishing genetic connections between herds during the 1995 workshop (Bunter, 1995).

4. Outlook

New NPIP members. There are currently three potential new NPIP members. Two of these are almost ready for inclusion as Large White herds, having made use of AI boars over a period of time to create linkage with the other members. The third potential member is still getting to grips with their data management practices.

Juvenile insulin-like growth factor-1 (IGF1). The use of juvenile IGF1 as a predictor of the genetic merit for feed conversion ratio in the NPIP has been on hold until the quantity and quality of incoming data has increased. A number of NPIP members record IGF1 for at least one breed. However there have been some data management issues with the data which have prevented it being incorporated into the NPIP system to date. These issues include:

- Herd management systems creating false IGF1 records where none should exist.

- Time lag in data entry – the transfer of IGF1 data into herd management systems and therefore into the data submitted to the NPIP has been delayed in some member herds.

- Suspension of recording during times of financial difficulty. Predictions of the genetic merit for FCR of young animals would thus be based on correlations between FCR and other traits, along with old IGF1 records on ancestors, reducing the accuracy of prediction.

Web pages for AI stations. On the NPIP web pages tables of AI boars by within AI station (or AI marketer) are presented for each breed. Where AI suppliers provide details of NPIP EBVs on their web site, these values are always out of date. Therefore, a single web page for each AI station has been developed with tables of AI boar EBVs within breed. As well as information on EBVs, parentage of the AI boars is also reported. These pages are intended to be accessed via links from the AI station web pages, possibly to open in either a frame or a pop-up window so that AI station clients do not actually leave the AI station's web site. In this way visitors to AI station web sites can have access to the most up to date NPIP evaluation results, as these pages will be updated with each run of the NPIP.

Demonstrations of EBVs predicting progeny performance

It is hoped that through the provision of material based around analysis of pre-existing data, and through support of people attempting to set up their own EBV demonstration trials that the degree of trust in EBVs in general and the NPIP in particular will grow in the industry. This should result in an increased use of EBVs by commercial producers to select animals when they need replacement parents or AI semen.

However, there are a number of pitfalls associated with boar comparison trials. Sampling is a major one; the EBVs are only estimates of the genetic merit and offspring only receive a sample of half of the genes from the boar. When comparing AI boars in a commercial environment, it is also necessary to have valid comparisons between contemporary progeny available. That is, progeny of more than one boar must be assessed at the same time and managed in the same way. Further, preferential treatment must be avoided; this is a temptation if you have paid good money for AI boar semen, and more so if you paid a premium because of the boar's genetic merit. Non-random mating of AI boars may be an issue, and in this situation use of information on the dam would be required. In commercial herds identification of progeny and sire can also be an issue.

1. Analysis of pre-existing data

Glasshouse Mountain Country Farm (GCF) is not a member of the National Pig Improvement Program. However, they have used a lot of AI over recent years, mostly from NPIP members. They routinely record backfat and daily gain. It is therefore possible to compare the NPIP EBVs of the AI boars used with the performance of their progeny at GCF. Since GCF is not part of the NPIP, the data has not already influenced the EBVs of the AI boars.

Some data restrictions were put in place in order to keep the analyses required simple and robust. The fifteen AI boars analysed all had accuracys exceeding 90% for both backfat and daily gain EBVs and had more than 20 recorded progeny at GCF. Only data from progeny recorded between 120 and 180 days of age, with the animals weighing 50 to 140 kg, were used. Although information on dams was available at GCF, this was ignored since it is unlikely that it would be present on most commercial farms.

Progeny data for backfat and daily gain was corrected for sex and calendar month in which it was recorded. In addition, backfat was corrected for weight at recording. These corrected progeny data were then averaged for each AI boar. The regression of progeny mean on AI boar EBV was then performed for each trait. Since progeny receive half of their genes from the boar, a difference of one in boar EBV should result in a difference of 0.5 in average progeny performance. That is, the expected value of the regression coefficients from these analyses is one half.

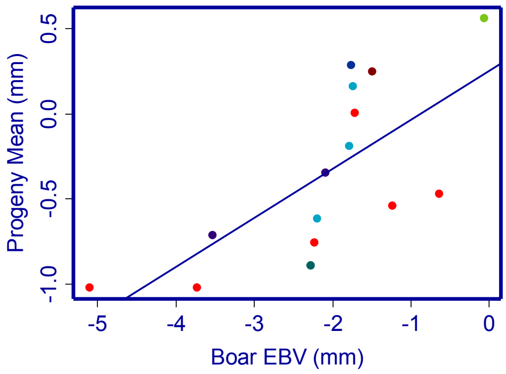

Figure 1 Mean of corrected progeny ultrasonic backfat performance against sire NPIP EBV for backfat .

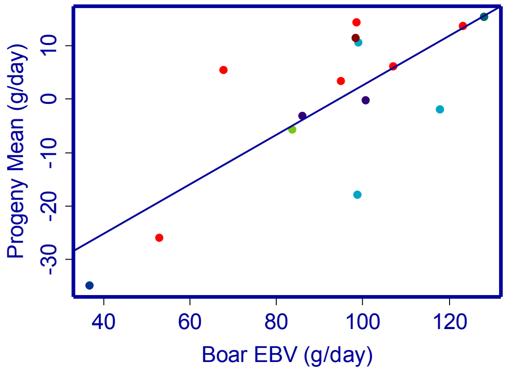

Figure 2 Mean of corrected progeny daily gain performance against sire NPIP EBV for daily gain.

Figures 1 and 2 contain plots of progeny average performance against AI boar EBVs for backfat and daily gain, respectively, with the estimated regression line superimposed upon it. The regression coefficient for backfat was 0.29 while that for daily gain was 0.46. Given the accuracy of the EBVs for both traits in this group of boars, it was hoped that both of the estimates would be close to one half. The reasons for the lower estimate of the regression line for backfat are not known, however it may be that the use of liquid feeding at GCF has had an impact (boars were evaluated using data from conventional dry feeding systems). In any case, the number of boars is relatively low, and chance cannot be discounted as the cause of the discrepancy.

The Gatton herd, which is a member of the NPIP, makes more use of link boars than any other member of the NPIP. The same type of analysis carried out for GCF is being performed for Gatton also, having run the NPIP evaluation excluding the Gatton data.

The results of the GCF and Gatton comparisons will be prepared as material that breeders can provide to their clients, in the form of handouts and as material on the NPIP web site.

2. Design of trials

When designing a trial to demonstrate the use of EBVs, it is important to remember the meaning of 'estimated' in EBV. EBVs for animals can change over time as additional information becomes available. The accuracy of an EBV is related to the variation associated with the estimate and subsequently changes as new data is added. Higher accuracy EBVs more likely to be close to the true genetic merit. The best results will be obtained with large groups of boars with accurate EBVs and with well compared progeny in the field. If a trial utilizes a group of boars with similar EBVs, their ranking for true genetic merit may differ from their current ranking on EBV. Boars in any demonstration trial must have EBVs available from the same evaluation (eg boars within breed from the NPIP), in order that they can be directly compared with one another. Selected AI boars can be used to produce contemporary offspring in the participating commercial herd(s) and analysis carried out to demonstrate that the regression of boar EBV on offspring performance is equal to a half (as above).

Field trials require a means of assessing the possible outcomes of the trial beforehand in order to avoid carrying out trials that have a high probability of failing to demonstrate the benefit of the use of EBVs. This may come about if, for example, there is not much variation in the genetic merit of the boars currently in the AI studs. This scenario has increased in recent years, since the AI boars made available by NPIP members tend to be of more uniform, relatively high genetic merit than in the past.

A computer simulation program (NPIPBTS) was developed to simulate the possible outcomes of any trial. This program requires the following data inputs for each boar that is a candidate for use in the trial: identifier, ADG EBV, ADG accuracy, BF EBV, BF accuracy. For any trial, the total number of matings and number of recorded offspring per mating must also be specified, these values being dependent upon the budget available for the study.

The simulation considers all possible combinations of sires having equal numbers of progeny per sire. For each combination of sires, a number of replicates of the simulation are performed. For each sire, in each replicate:

1. True breeding values are simulated for each trait as a random sample from the Normal distribution $a_i \sim N\left(\hat{a}_i, \sigma^2_{a_i}\left(1 - r_i^2\right)\right)$. Where for trait *i*, a_i is the true breeding value, $\hat{a}_i$ is the estimated breeding value, r_i^2 is the square of the accuracy and $\sigma^2_{a_i}$ is the additive genetic variance (as used in the NPIP evaluation to create the EBVs and accuracies being used).

2. The outcome of the matings is simulated as the offspring mean performance for each trait sampled from the Normal distribution $\bar{o}_i \sim N\left(\tfrac{1}{2}a_i, \left(\left(\tfrac{1}{4}\sigma^2_{a_i} + \sigma^2_{c_i}\right)/d\right) + \left(\left(1 - \tfrac{1}{2}\sigma^2_{a_i} - \sigma^2_{c_i}\right)/dn\right)\right)$. Here for trait i, $\bar{o}_i$ is the mean offspring performance, $\sigma^2_{c_i}$ is the common environmental variance (as used in the NPIP evaluation to create the EBVs and accuracies being used), *d* is the number of

dams being mated to this sire and *n* is the number of offspring being recorded from each mating of this sire.

3. Having simulated the outcome of the matings the regression $\overline{o}_i = b_i \hat{a}_i + e$ is calculated.

The expected value of b_i for each trait is one half. At the end of the simulation of a given sire combination, the proportion of b_i estimates between 0.4 and 0.6 is summed across traits. The sire combination that maximises this value is selected as the best for use in this trial. If there is a poor chance of success given the sires and funding available, other options should be considered.

Anybody wishing to take part in or organize this type of demonstration trial can obtain help in assessing the likely outcomes using the prepared simulation program. Contact AGBU (Ron Crump, ron.crump@une.edu.au) for further details.

References

Bunter, K.(1995). “Connectedness in Across Herd Genetic Evaluations.” *1995 Pig Genetics Workshop, Armidale.* pp 67-73.

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