The National Pig Improvement Program

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Introduction

The National Pig Improvement Program (NPIP) was established in 1995 by the Queensland Department of Primary Industries (QDPI) as a means of encouraging genetic improvement in seedstock herds and the dissemination of this improvement to the commercial tier.

Michael Macbeth at QDPI was responsible for the development, maintenance and day-to-day running of the NPIP system until 2001 when responsibility for the NPIP was passed to the Animal Genetics and Breeding Unit (AGBU).

At AGBU, development of the NPIP will continue alongside that of PIGBLUP. Funding of development work is through Australian Pork Limited (formerly the Pig Research and Development Corporation). A Pig Genetics Consultative Group has been formed to guide and review the research and development work in this area. Those of you that remember the PIGBLUP Guidance Group will be familiar with this concept, although the Pig Genetics Consultative Group has a wider remit. The Consultative Group contains PIGBLUP and NPIP users.

What is the NPIP?

The NPIP is primarily an across-herd evaluation system. The benefits of such a system can only be realised when there are genetic links between the herds, eg through use of the same or related boars via artificial insemination. When genetic links exist, estimated breeding values (EBVs) can be compared between the linked herds. This allows for selection of animals to be introduced into your herd based on your breeding objectives. As a result, extra genetic progress can be made through importation as well as the reduction in inbreeding levels from introducing unrelated animals into your herd.

In 2000, a sire-referencing component was introduced to the NPIP, to try and foster acceptable levels of connectedness among the participants.

In addition to the analysis function of the NPIP, it also has a role in the promotion and extension of the use of genetic improvement in the pig industry. Through the newly created Pig Genetics Coordinator post, this role will continue to be developed to the benefit of both the purebred and commercial sectors of the industry.

How does it work?

The system was originally set-up to receive and handle data, in PIGBLUP format, via e-mail or floppy diskettes. In the case of data submitted by e-mail, the arrival of the data triggered the running of the system.

The NPIP runs on a computer at AGBU that uses the Linux operating system. This operating system is very robust, and hence highly suitable for use as a genetic evaluation server where constant monitoring/user intervention is not desired. The other benefit of using a Linux-based computer for this is the presence of many free software packages that form an important part of the software component o the system (eg mail servers, programming and scripting languages).

Originally, the NPIP was run using a genetic evaluation program called PEST (Groeneveld, 1998), which is free for non-commercial use. With the transfer of NPIP a number of changes have been implemented.

What has been changed?

There have been a number of changes to the NPIP system, both major (eg switching the analysis to use PIGBLUP) and cosmetic (eg web page redesign).

The e-mail address

The first obvious change is to the e-mail address that data should be submitted to. It is now `npip@une.edu.au,` along with this change of e-mail address comes a change of host computer, with a new, dedicated machine being housed at AGBU.

PIGBLUP is now the analysis engine

The analysis components of PIGBLUP have been compiled as a series of standalone programs to run on the Linux operating system. Some changes were necessary to remove Microsoft DOS/Windows operating system specificity – eg directory name separators are \ on Windows and / on Linux. These minor changes will not impact on PIGBLUP performance on Windows.

Various modifications were required to merge the within-herd data files into an across-herd PIGBLUP format (rather than PEST format) data-file, and to handle the PIGBLUP format output files.

As a result of the transfer to PIGBLUP, the analysis of number born alive is now carried out as a two-trait analysis of number born alive in the first parity and number born alive in subsequent parities.

Data used

The historical test-station data has been removed from the evaluations, as has data from farms that are not members of the NPIP. References to animals from non-NPIP herds still exist, and these animals will getEBVs as parents of NPIP member herd animals

where appropriate, but performance and pedigree data from the original non-member herd has been excluded.

While acknowledging the contribution of the test-station data to connectedness, via the direct comparison of the performance of animals in a single environment, the differences between the test-station environment and the commercial one reduces this influence and the historical nature of the data devalues it further. At QDPI, the test-station traits were treated as separate traits from the on farm traits.

Accuracy calculations

The programs used to calculate accuracy, originally provided by AGBU, were modified:

- To read data from interim PIGBLUP data files, thereby fitting them conveniently into the analysis.

- To calculate accuracies for number born alive in a bivariate fashion, to match the two-trait genetic evaluation model.

Results returned

PIGBLUP automatically treats all animals under a certain age (set to be 200 days old) as active. An NPIP member that has submitted data receives results for active animals, parental animals (sows and boars that are parents in that herd, irrespective of whether they originated in that herd or not) and the current list of publicly available artificial insemination animals.

The results include EBVs and accuracies for lifetime daily gain, backfat, number born alive in the first parity, number born alive in subsequent parities and combined number born alive. They also receive index EBVs.

At present, three indexes are being formed and returned to the member. The two indexes previously used at QDPI and a PIGBLUP $INDEX using the default PIGBLUP economic settings.

The web pages

The NPIP web pages have been redesigned. Most of the previous information presented has been retained – genetic trends, distributions, results for AI animals – but the presentation is slightly different.

For security reasons, it was not possible for the NPIP system to automatically update the information on the web pages at QDPI. As the NPIP analysis server is also the web server for the NPIP site this is no longer an issue and graphs of genetic trends, distributions of EBVs for active animals and AI boar results are updated each time an NPIP run is performed.

The NPIP web pages can be accessed at `http://npip.une.edu.au`. It is recommended that a recent version of any of the popular web browsers (eg Netscape 6.1, Internet Explorer 5.5 or above) is used to view the site.

What is in the pipeline?

There will be on going development of the NPIP system alongside PIGBLUP so that each service benefits from developments in the other, and clients get the best from both systems.

PIGBLUP clients will see features from the NPIP system included in future PIGBLUP releases, eg accuracy calculations.

There are also some NPIP-related areas that will see changes soon.

Increased activity

The Pig Genetics Coordinator will be actively encouraging NPIP members to increase the frequency that they submit data to be analysed, and some automated reminder system may be put in place.

The sire-referencing scheme will be re-launched and a system for monitoring it developed.

As part of the overall duties of the Pig Genetic Coordinator an operational plan including ways of increasing both the levels of participation in the NPIP and the use of high genetic merit parents in the commercial sector is under development.

Modifications to the software

Under consideration are:

- Changes to allow the NPIP system to use PIGBLUP data formats other than version 1.0.

- Revisiting the connectedness calculations.

- Consideration of additional traits (eg weaning weight, IGF1) and systems for analysing and reporting of traits that are only recorded by a subset of members.

- Investigation of re-ranking issues

    - Sire×Herd interactions – ie the boars rank differently between herds, the combination of genes that are best in one specific environment may not be the best in another environment (herd).

    - Within-herd (PIGBLUP) vs across-herd (NPIP) ranking changes.

- Investigation of heterogeneity of variance across herds, and if it is an issue, developing a strategy to overcome it. Heterogeneity of variance is when different herds are more or less variable for a trait. Herds that are more variable tend to have the best (and the worst) animals in the evaluation rankings.

There are many other changes possible, and the members have an opportunity to influence areas of development both at this meeting and through contact with AGBU staff and Pig Genetics Consultative Group members.