



The National Pig Improvement Program (NPIP)

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Background

The National Pig Improvement Program (NPIP) was established by the Queensland Department of Primary Industries in 1995 under the initiative of Michael Macbeth as a means of evaluating and promoting genetic improvement in economically important traits.

In 2001 the NPIP service was transferred to the Animal Genetics and Breeding Unit (AGBU) in Armidale. Since 2001, the genetic evaluations for the NPIP have been performed using the PIGBLUP computer program, in order that both NPIP and PIGBLUP clients can benefit from the joint development of these systems

Information about the NPIP and results from genetic evaluations are displayed at the web site of the NPIP (<http://npip.une.edu.au>).

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 in the Australian purebred pig herd book. Please note, the across-herd genetic evaluations of the NPIP can be applied to any synthetic commercial population if seedstock providers or producers demand such an across-herd genetic evaluation.

Procedure

Data submission. Submission of data has been automated via an e-mail system. Participating herds are required to supply data in electronic format to the e-mail address of the NPIP. The data format used follows the PIGBLUP data format.

Data submitted. Data required 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 trait in the first parity versus later parities. The PIGBLUP data file contains a number of rows for each animal, which contain pedigree, production and reproduction information.

Pedigree information

- Unique identifiers for animals, sires and dams within herds.
- Identifiers of animals introduced from other herds should include the three-letter herd code and the unique identifier used within the herd of origin.

Production and reproduction information

- Information about performance includes weight of the animal and backfat at the P2 site
- Information about the sex of the animal, date of birth, weighing dates and management groups
- Information about litter size along with mating and farrowing dates, parity of the sow and management groups

Genetic evaluations of the NPIP system start automatically once new data have arrived via e-mail. The submitted data are then 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.

Return of results to members. Information from the across-herd genetic evaluation is automatically returned via e-mail to the member once the genetic evaluation has been completed. If the analysis starts automatically this is usually 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 setup 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. This format allows presentation of results in logical groupings instead of being part of a long e-mail. It is possible to present graphics and HTML files can be read by other applications (ie. Word or Excel), if members wish to organise results in a different manner.

Results returned to members

Estimated Breeding Values (EBVs). Following the PIGBLUP grouping of animals, EBVs are displayed for parents (boars, sows) and animals that are younger than 200 days of age (young boars, gilts). The list of parents is restricted to parents that were born during the last five years or, if the date of birth is not available, parents whose progeny were born during the last four years prior to the date of analysis.

Each list includes the animal identification, the number of herds that have recorded progeny of the animal, EBVs and their accuracies as well as the Terminal Sire Index and the Maternal Index. The ranking of each animal within its respective group is shown for both indexes. This ranking is also expressed in percentile groups for each trait and index for young animals. Animals are sorted on the Terminal Sire Index.

Genetic trends are displayed for all traits as well as both indexes. The within-herd genetic trend is shown in comparison to the overall genetic trend of all herds.

Distribution of EBVs. The distributions of EBVs are shown for young animals distinguishing between young animals that belong to the member and all young animals present in the across-herd genetic evaluation at the time of data submission.

Lists of AI boars. Estimated Breeding Values, accuracies and both indexes are shown for boars available from different AI centres. AI boars are sorted on the Terminal Sire Index within each AI centre.

Base parents. Animals that are parents but have no pedigree information available are defined as base parents. These animals are of interest since they may be animals that provide genetic linkage between herds but the linkage with the other herd has not been documented. The list of base parents shows the animal identification, its sex and the date of birth of first and last recorded progeny in the data. Members are asked to provide information about the herd of origin and identifier used in the herd of origin for these base parents.

Link animal usage. The across-herd genetic evaluations rely on sufficient linkage between herds in order to separate herd effects from genetic effects. Usage of boars across herds over time is summarised in the link animal lists. The number of recorded offspring born to sires with recorded offspring in multiple NPIP herds is listed. In addition, the number of recorded offspring of sires with recorded offspring in each of the other NPIP herds is reported. The number of recorded offspring from link sires is shown as a proportion of all offspring recorded in the herd of the member. This information is listed for each quarter since 1995.

Connectedness is indicated between all herd combinations in a graphical manner. The connectedness calculations relate to comparisons between the herds as far as they represent a source of parental genes. Herds that have low connectedness on this measure may still be connected via genes inherited from more distant relatives.

Web pages of the NPIP

The site of the NPIP can be accessed at <http://npip.une.edu.au>, which is hosted on an AGBU machine. The NPIP site includes a number of pages that display general information about the NPIP and pages that display results. The general pages provide information about the history of the NPIP, participation, a glossary and herd codes of individual herds.

The pages that display results from the NPIP analyses are updated automatically after each genetic evaluation. The analyses are run separately for each breed and results are displayed for Large White, Landrace and Duroc. Results from the genetic evaluations include genetic trends, distribution of EBVs and list of AI boars and top young animals.

Genetic trends show the genetic improvement that has been achieved over time. For each breed, the average EBV of animals born each year is shown for growth rate, backfat and litter size. The genetic trends for growth rate and backfat in Large White are shown as examples in Figure 1 and Figure 2.

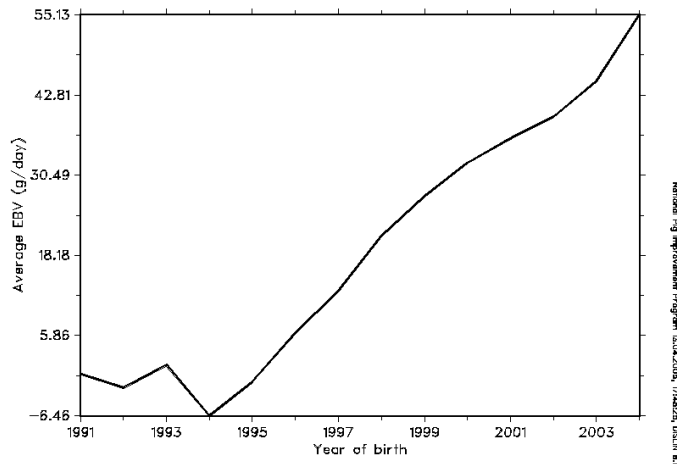


Figure 1. Genetic trend of the NPIP for growth rate in Large White (April 2005)

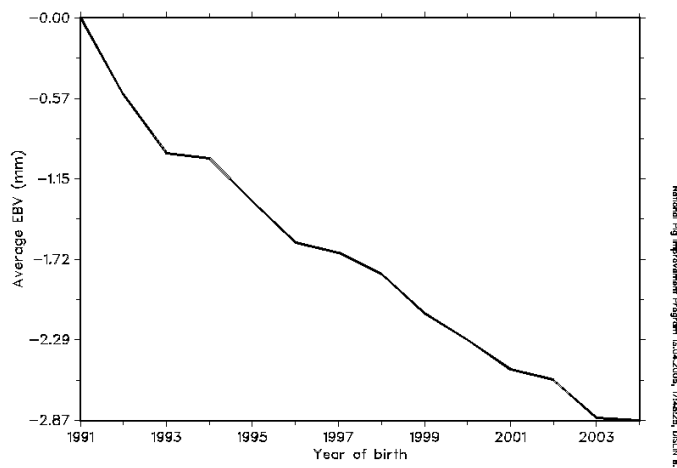


Figure 2. Genetic trend of the NPIP for backfat in Large White (April 2005)

Distribution of EBVs and both indexes in young boars and gilts younger than 200 days of age is displayed. The cut-off points for 10% groupings of EBVs for young boars and gilts are shown, which are calculated for each trait independently of the other traits.

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) are shown for each breed on the basis of the Terminal Sire Index or the Maternal Index. These lists also include the sire identification of the top young animals.

