BREEDPLAN IN A GENOMICS WORLD – OPPORTUNITIES AND CHALLENGES

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SUMMARY

The Agricultural Business Research Institute has been providing estimates of breeding values to cattle breeders for over 40 years. In that time, it has progressed from within herd, to BREEDPLAN, Group BREEDPLAN, and multi-country analyses. For most of that time, the data analysed was phenotypic, with genomic data only included fairly recently via blending.

In April 2017, ABRI released a production BREEDPLAN run to the Australian Brahman Breeders' Association using Single-Step methodology. This full multi-trait analysis, using pedigree, performance and genomic data simultaneously, was a world first for beef cattle.

The incorporation of genomic data into routine Single-Step BREEDPLAN runs opens many opportunities to cattle breeders around the world, including the potential to significantly enhance the accuracy of analyses, allow breeders to make more accurate selection decisions, and therefore increase the rate of genetic gain. However, there remain significant challenges to overcome before these opportunities can be fully realised.

INTRODUCTION

This presentation is intended to examine the practical implications, opportunities and challenges for cattle breeders resulting from the introduction of Single-Step BREEDPLAN analyses. It is not a scientific paper. There are other technical papers available detailing Single-Step BREEDPLAN methodology in these proceedings.

Hugh Nivison has been Managing Director of ABRI since October 2015. He is not a geneticist, coming from a background of sheep and cattle breeding in northern NSW. Hugh holds a Bachelor of Veterinary Science from the University of Sydney, and is an Adjunct Associate Professor at the School of Veterinary Medicine with the University of Queensland. His career has been spent working in agricultural production (primarily livestock) in Australia and overseas.

The Agricultural Business Research Institute (ABRI) is responsible for commercialising the BREEDPLAN suite of software, holding the exclusive licence from the owners of the software, Meat and Livestock Australia (MLA), University of New England (UNE) and New South Wales Department of Primary Industries (NSWDPI). The software is developed by the Animal Genetics and Breeding Unit (AGBU), a joint venture of UNE and NSWDPI, with funding from MLA.

ABRI provides genetic analyses for 84 discrete beef cattle breed associations or clients, many as part of combined multi-country analyses (Trans-Tasman Angus, Pan-American Hereford, Southern-African Brahman for example). ABRI and AGBU are collaborating in two MLA Donor Company funded projects to expand capacity to provide multi-country analyses, and to investigate the technical and data limitations on providing full multi-trait, multi-breed analyses.

DISCUSSION

The practical outcome for any genetic analysis system must be increased rate of genetic gain through more accurate and more timely selection decisions on farm. The key components of that desired outcome are:

    1.More accurate predictions

    2.Earlier predictions

    3.On-farm adoption

OPPORTUNITIES
- **Pedigree**
  - Provided animals have genomic data, Single-Step BREEDPLAN accurately assigns relationships based on the true genetic comparisons of the animals. Whereas relationships have traditionally been described as ½, ¼, 1/8 etc. they can now be described more accurately. Half-sibs can range from 0.16 to 0.34 (vs 0.25) allowing increased accuracy from the BLUP calculation
  - Single-Step BREEDPLAN identifies errors in existing pedigrees that have gone uncorrected previously. Significant improvements in accuracy result from correct parentage assignment, and elimination of previously unknown pedigree errors.
  - Single-Step BREEDPLAN can fill the blanks for some animals where there was no previously recorded pedigree if the parent/s and offspring have genomic information. Some breed societies already require DNA parent verification, but this process can add accuracy for those breeds where this does not currently occur.
  - Accurate assignment of genetic relationships is a key factor in producing accurate BLUP analyses. Single-Step BREEDPLAN allows for greater accuracy in pedigree than was previously available.
- **Hard to Measure (HTM) traits**
  - Many economically important traits are difficult to measure on animals retained as seedstock sires and dams. Carcase and long term fertility traits are obvious examples.
  - Animals that are related genomically, although perhaps not by pedigree, to animals that have the phenotypic records for HTM traits will be able to receive EBVs for those traits if the relationship and accuracy is high enough.
  - Early selection of replacement females using fertility traits generated by Single-Step BREEDPLAN can significantly increase the rate of genetic gain for those traits as opposed to waiting for the animal to generate phenotypic data.
- **Animals with no performance**
  - Animals with no phenotypic records can receive accurate EBVs for a wide variety of traits provided they have a genomic result, and are closely enough related to animals with phenotypic data in the analysis.
  - Dairy heifer selection is an excellent example of this practice, but its application in beef is likely to be less as there is not the dominance of small numbers of sires as in dairy herds.
- **Combining discrete data sets**
  - Data sets that currently have no linkage via pedigree may be used to inform a Single-Step BREEDPLAN analysis via their genomic linkage. Abattoir data combined with BREEDPLAN data holds an exciting prospect of better informing both seedstock and commercial cattle selection systems.
  - Highly accurate carcase EBVs for breeding animals, and highly accurate feed efficiency estimates for feedlot cattle are some of the possibilities.

CHALLENGES

As attractive as the opportunities are for cattle breeders, there remain some disincentives that may prevent uptake of the technology.

- (mis)Understanding
  o There will be some major EBV changes, and some of those will be for well-known and well used sires. While the changes will have justification (pedigree correction for example), some breeders will see this as an example of the analyses being unreliable.
  o Single-Step BREEDPLAN is currently designed to work for pure-bred animals. During the analysis, a Breed percentage is calculated based on an individual's relationship with a reference population representative of the various breeds existing in Australia. Animals less than a threshold (80% for example) are excluded as not being purebreds. Unfortunately, some breeders have seen this as meaning animals less than 100% are not "Pure" and are attempting to use this analysis procedure for political gain.
  o Managing expectations will remain a challenge. Some breeders expect that they will now be able to just pull a tail hair and receive full BREEDPLAN EBVs without any data collection irrespective of how closely they are related to other animals in the analysis.
  o Breed Societies and others charged with administration of the pedigree, performance and genomic databases will have an increased responsibility for ensuring the accuracy of these data sources. Potential errors in pedigree, or breed will need to be investigated, and if confirmed will need to be rectified. Telling a breeder the recorded pedigree for his well-used sire is incorrect will be an uncomfortable role for breed society staff. This is likely to be a short term issue until the various inconsistencies are resolved.

- Cost
  o SNP data is currently expensive to collect when considering the sample collection and testing charges together. As volume increases for laboratory testing, costs can be expected to decrease, but the on-farm cost will remain similar. While cattle prices remain buoyant, producers are likely to embrace the technology. However, if they are forced to prioritise discretionary expenditure in a downturn, they may reconsider their participation in genomics, particularly on a whole-herd scale.
  o There will need to be some consideration given to the differing influence of phenotypic and genomic data in the Single-Step BREEDPLAN analyses, including the option of differential pricing structures based on the value of the contribution from different data sources. Accurate collection of phenotypic data, particularly for HTM trait will need to be encouraged, potentially via financial incentives.

- Reduced phenotypic recording
  o The beef industry in general, and breed societies in particular will need to actively ensure sufficient, accurate and linked phenotypic performance data continues to be collected to enable the Single-Step BREEDPLAN analyses. Systems including Reference populations and BINs can provide this data, but are expensive to operate, and will likely require industry funding as they are usually beyond the financial abilities of individual breeds. Innovative alternative methods of collecting and generating this data in a more cost-effective manner should be investigated.

- o The education of seedstock and commercial breeders on the importance of phenotypic data, and possible financial incentives for collection will need to be a focus for both breed societies and the wider industry.
- No of tested animals
    - o Breeds with smaller populations may initially struggle to implement Single-Step BREEDPLAN due to their low numbers of total genomic results. The GBLUP method of Single-Step BREEDPLAN requires the generation of a Genomic Relationship Matrix (GRM) which may have stability issues at low level of results.
- Technical
    - o The sheer volume of extra data generated by combining genomic results with existing pedigree and performance datasets will lead to challenges in both storage and transmission. Breed societies and the BREEDPLAN service will need to develop innovative methods for ensuring efficient and cost effective data management during Single-Step BREEDPLAN runs.
    - o The technical complexity of combining datasets for multi-country or multi-breed analyses is further complicated by the addition of genomic data. Many of the current BREEDLAN analyses are conducted on a multi-country basis, and further expansion of this service is planned. BREEDPLAN is also exploring opportunities for robust multi-breed, multi-trait analyses and the associated complexity of merging the pedigree, performance and genomic datasets involved.
    - o The much greater computational requirements of Single-Step BREEDPLAN could have potentially slowed the speed of analysis down considerably. Innovative development by AGBU has ensured that the full multi-trait Single-Step BREEDPLAN analyses run in a time comparable with existing BREEDPLAN runs. Further enhancements in software and hardware are planned, and will be essential as many BREEDPLAN clients move to more frequent evaluations.

BREEDPLAN in a genomics world (Single-Step BREEDPLAN) will provide cattle breeders with more accurate analyses, leading to more accurate selection decisions, and resulting in increased rates of genetic gain. The challenges involved in achieving this outcome are not insignificant, but the rewards of adoption should ensure the opportunities will be realised.