Livestock Genetics Investment Priorities - Industry Discussion Paper 2
October 2015
MOVING TO MULTI-BREED AND CROSSBRED BREEDPLAN ANALYSES

Purpose of this discussion paper

This is one of five discussion papers on key issues prepared to stimulate discussion of, and feedback on, the consultation draft of beef genetics research, development and extension (RD&E) investment priorities for the next 5 years.

This paper discusses the different approaches, issues and future requirements to be considered in delivering a multi-breed analysis or analyses to the Australian beef industry. It covers the likely technical and infrastructural investments that would need to be addressed for multi-breed analysis to be a reality.

The Genetics RD&E Steering Group is seeking feedback on its perception and assessment of these key issues and on the RD&E priorities in the industry consultation draft. Feedback can be emailed to livestockgenetics@mla.com.au by 31 January 2016.

Background

One of the core recommendations to raise the overall level of genetic gain in the Australian beef industry from the scoping workshop in May 2015 was to move away from predicting performance of purebred bulls and cows primarily within a single breed. This has also repeatedly been requested by some stakeholders and identified in industry surveys and market research[1]. Evaluation across breeds and also in crossbreds would allow for more selection based on breeding objectives and genetic merit, rather than on breed as a proxy for key traits.

Multi-breed (also known as across-breed) analysis uses data from more than one breed (and can also include data from their crosses), with 2 possible outputs:

a) Ranking of all animals for genetic merit on the same scale, regardless of their breed or breed composition (and providing an EBV for that genetic merit)
b) If crossbred data is included, EBVs could be produced that separately ranked animals for both purebred and crossbred matings.

Crossbred analysis refers to using some crossbred data in a genetic analysis to more accurately evaluate purebred cattle, or guide selection when grading up from other breeds. An EBV for predicting a bull's

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[1] Of 88 BREEDPLAN users responding to the survey, 57% suggested BREEDPLAN EBVs that allow comparison across breeds rather than within breed (57%) as a system improvement. MLA Report B.NBP.0753 "Barriers to adoption of genetic improvement technologies in northern Australia beef herds"(2015)

performance for crossbreeding based on crossbred information should be more accurate than an EBV based only on purebred information.

Greater use of these two types of analyses should provide greater relevance and value to commercial bull buyers by allowing them to select the best bull that meets their breeding/market objectives, including for use in cross-breeding or developing composites as an additional tool to take advantage of heterosis and complementarity across breeds. This is particularly valuable in northern Australia where only around 12% of the *Bos Indicus* bulls sold have BREEDPLAN EBVs[2] and cross breeding / composites are increasingly used to increase the productivity and marketability of offspring from tropically-adapted *Bos Indicus* derived cows.

The current situation

All the major beef breeds using BREEDPLAN in Australia currently have 'within-breed, across-herd' genetic evaluations that mainly use data collected in pure-bred herds. EBVs from within-breed evaluations describe the additive merit of each animal. While this does not allow pure-bred animals of different breeds to be compared against each other using common EBVs, it does allow cattle breeders to find the best animals within a breed for use in a crossbred program.

Some breeds include and use crossbred data in their evaluations. For example, the Angus evaluation now includes a range of crosses and breed combinations with the common element that they are all Angus-influenced animals that now receive EBVs, and these data improve the accuracy of the Angus sires used and their relatives. This analysis accounts for the estimated non-additive (ie hybrid vigour or heterosis) effects in crossbred data when calculating EBVs for purebred and crossbred animals.

1. Developing multi-breed EBVs – two alternatives

The work that AGBU did over 18 years ago with SARDI and Vic DPI[3] produced a "Multibreed Conversion" table, which consisted of estimating breed means for several traits, allowing for the ranking of all animals for genetic merit on the same scale.[4]

The Beef Improvement Federation in the USA regularly produces similar conversion tables, using records generated at the USDA Animal Research Centre at Clay Center, Nebraska.

An important question around the conversion factor approach and multi-breed EBVs in general, is the accuracy of the comparisons. The accuracy now has 2 components each with their own error: the within-breed part, and the across-breed part. The across-breed part of the accuracy is completely dependent on the strength of the head to head comparisons for each breed x trait combination. This means that determining

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[2] MLA Report B.EVA.0001/0002 "Evaluating the impact of genetics and genomics RD&E investment." (2014)

[3] Graham, J; Hygate, L; Cummins, L; Ponzoni, R; Goddard, M; Deland, M; Carrick, M "Developing multi breed estimated breeding values for beef cattle." Proc. Adv. Anim. Breed.Gen. (1997) 12

[4] Johnston, DJ; Graser, HU; Moore, KL; Graham, JF. "BREEDPLAN multi breed EBVs for growth traits in Angus, Hereford, Simmental and Limousin breeds." Proc. Adv. Anim. Breed.Gen. (2003) 15:

which accuracy to use in a multi-breed analysis with several breeds involved becomes more complicated than in a within-breed analysis.

AGBU has developed and trialled multi-breed genetic analyses for the European breeds (Charolais, Limousin and Simmental) and the British breeds (Angus, Hereford and Shorthorn), using BREEDPLAN software as an alternative to the conversion factor approach.

That research showed that multi-breed EBVs could be generated for the main growth traits, and to some extent scan traits in the Euro breeds, but severe data limitations exist for all other traits (reproduction, docility, eating quality, etc). This is due to the limited numbers of direct head to head comparisons of pure-bred animals from different breeds run in the same management groups. The low number of direct comparisons subsequently reduces the accuracy of multi-breed EBVs and their usefulness to industry.

2. Developing crossbred EBVs

To produce EBVs for specific crosses (or crossbred progeny in general), it is preferable to estimate the pure-bred x crossbred correlations for the key profit driver traits. This compares how the purebred progeny of bulls differ from their crossbred progeny, when run in the same management group. This allows EBVs to be expressed on a scale relevant to the crossbred population. There may also be a heterosis effect. So for example, when predicting the merit of Angus-Hereford cross calves sired by an Angus bull, they will get ½ the Angus sire EBV expressed on the crossbred scale, as well as the heterosis effect.

The opportunity - perceived advantages

1. Using all data for a breed, including from crossbreds, is no less accurate and may improve accuracy. This depends on how much data is available from crossbreds, but basically the more there is of it, the more benefit it will bring.
2. Using all data may be important to maximise accuracy of genomic breeding values. Given that large numbers of animals need to be phenotyped and genotyped to produce high accuracy genomic EBVs, it is logical to use all data available. In addition, knowing genomic composition of animals, especially crosses, may in theory allow more accurate use of crossbred data, for each parent breed, as it will more accurately account for breed content in crosses beyond F1.
3. Buyers of performance-recorded breeding stock will be able to select across breeds, using a common language to directly compare genetic merit, and be more confident in how those animals will perform in their own herds and breed combinations. For example, Sheep Genetics now provides multi-breed analyses, allowing breeders and producers to select rams most suited to their requirements using breeding values on the same scale across all meat breeds.
4. This transparency and comparability will drive competition between breeds to stimulate greater focus on genetic improvement and increasing rate of genetic gain, or it may promote greater incentives to clearly differentiated breed roles.
5. There are potential savings for ABRI and breed societies. Individual breed analyses currently take approximately 24 hours per breed, whereas a multi-breed analysis (say all Euro breeds combined) might take 30 hours. Other likely options are a single evaluation across all British breeds, and another across all tropical breeds.
6. Providing such analyses would maintain a single national evaluation system and common language, and minimise the need for disenfranchised breeders to seek similar services overseas.

Discussion points

1. *Will multi-breed and crossbred evaluations:*
    - a. *significantly improve the relevance and value of genetic information to commercial producers and thereby increase the demand for performance-tested bulls, regardless of breed?*
    - b. *increase competition and promote greater rates of genetic improvement?*
    - c. *reduce complexity by presenting EBVs from multiple breeds on the same scale?*
    - d. *stimulate greater clarity and/or change in breed roles?*
    - e. *provide value to purebred breeders or primarily benefit commercial buyers?*
    - f. *be a threat or an opportunity to current business models of breed societies, genetic evaluation delivery, or other roles?*
2. *Is there value in producing additional EBVs on a crossbred scale to be more relevant to producers interested in crossbreeding, or would crossbred EBVs create confusion?*
3. *Should future reference herds be structured and managed to capture comparative data to expand multi-breed information as a requirement for ongoing industry funding?*
4. *Will commercial breeders be encouraged to collect information on animals that could be of benefit to genetic evaluation and how will that data be integrated?*
5. *Will producers who exploit cross-breeding collect and share phenotypic data to expand multi-breed analysis capability?*
6. *Will moving to only 2 or 3 multi-breed analyses for breed groups significantly reduce overall costs of BREEDPLAN runs?*

What would be required to implement multi-breed analysis?

From the AGBU research in 2012, it was identified that there is some data held in separate breed society databases which comes from multi-breed management groups, but this needs collation and verification. There is also some additional coding work required from AGBU before the multi-breed version of BREEDPLAN could be transferred to ABRI.

There are also some potential datasets in industry as yet not put into any breed database, involving both seed-stock and commercial herds. This data could be put into the two experimental multi-breed databases already established at ABRI (one southern/Euro breeds, one tropical breeds) but would require careful checking to ensure that the data is genuine multi-breed ie head to head comparisons of animals of at least two pure breeds, with pedigree links back to those breeds, and with measurements recorded in the same management groups.

A significant industry investment would be needed to generate useful multi-breed data for maternal traits, and for different breed combinations - this would require daughters from 2 or more sires per breed, mated, managed and recorded in the same management group. At least 200 females would be needed for 2 breeds, to produce both pure and crossbred progeny.

Perceived disadvantages/challenges

1. Initial multi-breed analysis combinations would be limited in scope to the most common industry crosses, and only for growth and possibly carcase traits.
2. This data generation may need to be ongoing to capture the effects on breed differences of genetic change within breeds, but this depends on the genetic analysis model used. The cross breeding herds generated could contribute to industry reference data for hard-to-measure traits if the appropriate traits were being recorded.
3. ABRI would need the agreement of breed associations to run their data in a multi-breed analysis and establish a common base, and a source of funding if not supported by the breed societies.
4. ABRI would require a method of cross-referencing the animals that are common across the individual breed databases, such as a universal unique ID system, and a commitment to maintain and update this.
5. Changes would be required to re-calculate BREEDOBJECT selection indices which currently use breed-specific co-variances, though this is required of any significant change to the genetic evaluation models.
6. Hardware used for genetic evaluation would need to be upgraded, but this will need to occur anyway to handle the very large databases that include genomic data for use in next generation genomic evaluation.
7. Priorities would need to be agreed for developing and running Australian genetic evaluations with different combinations of multi-breed, multi-country and Single Step genomic analyses.
8. The initial introduction would be disruptive and require a transition period as multi-breed genetic evaluations are phased in, backed by a structured communication /education program to explain changes.

Discussion points

1. *What head to head comparisons of purebred and crossbred progeny already exist that allow an initial multi-breed analysis to be offered to the industry? Who should pay to source that data, and what restricts them being used now?*

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