

Livestock Genetics Investment Priorities - Industry Discussion Paper 1

October 2015

SIGNIFICANT CHANGES IN BOTH TECHNOLOGY AND TO THE BEEF BREEDING SECTOR THAT NEED TO BE CONSIDERED IN DEVELOPING LIVESTOCK GENETICS RD&E INVESTMENT PRIORITIES FOR THE NEXT FIVE YEARS

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 over the next 5 years.

This paper provides an overview of the guiding principles for developing the RD&E priorities and outlines areas where there will likely be significant technology and structural changes across the beef breeding sector that need to be considered in future investments.

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.

Current status of genetic improvement

The meat industry's long term investments in beef cattle genetic improvement since the 1980s, via both MRC and MLA project funding and through facilitating very significant co-investment from both breeders and research organisations, have been outstandingly successful. These investments have built world-class capacity and delivered arguably one of the best beef cattle genetic evaluation systems in the world.

A significant proportion of the investment has flowed into the functions of the BREEDPLAN Analytical Software developed by AGBU and jointly owned by MLA, UNE and NSW DPI. ABRI, as the licensee of the BREEDPLAN software, today provides genetic analyses to 23 Australian beef breeds and 48 international beef groups in 8 countries. This includes across-country analyses for Hereford (4 countries), Limousin (4 countries) and Australia/NZ (8 breeds), with similar analyses under development for Brahman (4 countries) and Wagyu (up to five countries).

Despite these technological and commercial successes, concerns remain that the overall rate of genetic progress in the Australia beef industry is about average on an international scale¹. This overall rate of improvement masks a very large variation between breeders and between breeds, and the average is significantly below the potential possible when compared to genetic gain achieved by competing industries.

¹ MLA Report B.COM.1080 "[Comparison of genetic improvement systems for beef cattle industries internationally](#)" 2008

The opportunities

Industry average annual genetic gain can be stimulated by several mechanisms, all of which compete for scarce R&D funding.

1. Increasing genetic gain in individual participating breeding herds by:
 - a. increasing the EBV accuracy and range of traits that determine commercial value
 - b. decreasing cost of participation²
 - c. decreasing complexity of participation
2. Increasing the number of herds participating by:
 - a. establishing compelling value proposition³
 - b. decreasing cost of participation
 - c. decreasing complexity of participation
3. Increasing the number of genetically improved bulls purchased for commercial production by:
 - a. establishing the compelling value proposition for purchasers
 - b. decreasing complexity for purchasers
 - c. increasing demand for improved genetics driven by feedlot and meat processor requirements.

Significant changes influencing future priorities

There are a variety of known and potential changes in both technology and industry structures and processes that will potentially affect what will be needed to meet the needs of stakeholders, and will alter what is technically possible in future genetic evaluation and improvement programs. These factors are listed below and for each factor, there is a list of possible impacts that have implications for the RD&E strategy.

1. Various technologies are increasing our ability to measure “hard-to-measure” traits, such as net feed intake and carcase traits. These will contribute to more complete estimates of the true commercial value of individual animals, but will also likely change the cost and complexity of phenotyping.
 - a. The industry will still require permanent reference herds, potentially with new designs and on a much larger scale than at present.
 - b. Different types of data from many sources will need to be integrated efficiently into EBV calculations and selection indexes.
 - c. This could generate a market value for phenotypes, determined by some measure of the quality, accuracy and scarcity of the phenotypes.
2. Data capture and communication technologies are creating new “Big Data” opportunities, particularly where large volumes of data that are traditionally captured and housed in independent

² 104 stud breeders of a total 227 surveyed reported not using BREEDPLAN, primarily due to a perceived lack of financial rewards for the sale of animals with EBVs (46% of respondents) followed by the perceived cost being too high (34%). MLA Report B.NBP.0753 “[Barriers to adoption of genetic improvement technologies in northern Australia beef herds](#)” 2015

³ 42% of northern stud breeder respondents do not record data for BREEDPLAN genetic analyses because they do not believe that it works. MLA Report B.NBP.0753 “[Barriers to adoption of genetic improvement technologies in northern Australia beef herds](#)” 2015

databases can be efficiently linked. This allows extraction of new information that can create potential benefits to all data owners. This may also allow data to be captured on many more relatives of animals that are currently being evaluated for genetic improvement, though the value of this approach is in proportion to how closely related these animals are to the next generation of breeding stock.

- a. There will be a need to efficiently connect industry databases, or create a virtual single data platform using a common language.
- b. There is a potential opportunity to link the genetic and genomic databases to the biosecurity (NLIS, LPA, NVD) and carcass feedback (Livestock Data Link, MSA) databases to capture new information, provided data sharing and privacy issues can be resolved.
- c. Diverse groups are likely to share information only if there are clear incentives and benefits delivered to all players, not just the breeding sector. Hence a “Big Data” future will require genetic improvement to be better integrated and aligned with the interests of other sectors of the beef value chain.

[Note: This topic is discussed in more detail in a separate discussion paper].

3. There is increasing interest in the application of international genetic evaluations to increase the size of genomic reference populations for individual breeds, as well as to facilitate the trading of germplasm (animals, semen, embryos) internationally.
 - a. There is a need for a single language to identify animals and describe traits to facilitate the exchange of information.
 - b. There is a need for more efficient ways of combining diverse databases on a routine basis, when data comes from different sources (countries, providers etc).
4. Demand from producers to have evaluation systems for crossbred and composite animals, as well as across-breed genetic evaluations (referred to as multi-breed evaluations) is increasing.⁴ This is to improve the profitability of crossbreeding through selection to maximise heterosis and breed complementarity, and also to increase rates of genetic gain by selecting across breeds. It could also simplify and consolidate a common selection currency by presenting EBVs from multiple breeds on a comparable scale. (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.)
 - a. There is a need to determine the requirements for multi-breed and crossbred genetic evaluations to be routinely run. A range of technical and operational issues will need to be resolved and evolved over time.
 - b. Incentives are needed to collect and share phenotypes from crossbred animals, and from purebred animals of different breeds run in the same contemporary groups.

[Note: This topic is discussed in more detail in a separate discussion paper on multi-breed analyses]

⁴ Of 88 BREEDPLAN users responding to the survey, 57% suggested BREEDPLAN EBVs that allow comparison across breeds rather than within breed as a system improvement. MLA Report B.NBP.0753 “[Barriers to adoption of genetic improvement technologies in northern Australia beef herds](#)” 2015

Discussion points

1. *Will multi-breed and crossbred evaluations:*
 - a. *increase competition and promote greater rates of genetic improvement?*
 - b. *reduce complexity by presenting EBVS from multiple breeds on the same scale?*
 - c. *stimulate greater clarity and/or change in breed roles?*
 - d. *provide value to purebred breeders or primarily benefit commercial buyers?*
 - e. *be a threat or an opportunity to current business models of breed societies, genetic evaluation delivery, or other roles?*
2. *Should future reference herds be structured and managed to capture comparative data to expand across-breed information?*
3. *Will commercial breeders be encouraged to collect information on animals that could be a benefit to genetic evaluation and how will that data be integrated?*
4. *Will producers who exploit cross-breeding collect and share phenotypic data to expand multi-breed analysis capability?*

5. The role of breed societies is changing. Some societies may become even more involved in facilitating genotype and phenotype data collection for their members, and/or fully embed BREEDPLAN evaluations into their services, while others may reduce or eliminate most of their current roles in data management, outside of pedigree registrations.
 - a. The industry may need a system that supports those breed societies that take on more active roles in data acquisition and breeding support services.
 - b. There will be a need to demonstrate the benefits achieved through better data sharing protocols and incentives, when more breeds work together.

Discussion points

1. *Will cheap DNA tests for parentage identification and genetic associations between animals reduce or replace the need for breed society pedigree databases?*
2. *Could medium to high density genotyping (required to produce genomic EBVs) become sufficiently cheap that virtually all breeding animals are genotyped?*
3. *Would this replace the current pedigree registration systems?*
4. *What impact will this have on the willingness of breeders to collect phenotypes?*

6. The increasing number of breed societies and individual breeders/companies actively embracing BREEDPLAN and related technologies is increasing the demand for greater expertise and flexibility in servicing from AGBU and ABRI to meet the demands of the increasing number and complexity of breed genetic evaluations, many of which are customised.
 - a. Substantial efficiencies are likely to be possible through consolidating analyses into across-breed analyses with similar objectives, rather than providing multiple individual breed-specific analyses. e.g. include British breeds together, European breeds together and tropical breeds together, so that only three analyses are then required compared to the 23 breed-specific analyses required today.

- b. It is expected that increasing industry resources will be required to maintain and service an increasingly powerful but complex system, with more diverse information being generated that increases the industry's ability to select for total value chain profitability.

[Note: This topic is discussed in more detail in a separate discussion paper on multi-breed analyses]

Discussion points

1. *What extra resources will be required and where will such resources come from to service the needs of an increasingly large set of genetic evaluations?*
2. *Should individual breeders be able to purchase GROUP BREEDPLAN analyses for their herds without having to go through a breed society? If so, what is an equitable basis for this transaction such that both parties benefit and who determines what GROUP BREEDPLAN runs are delivered?*
3. *With a large number of genetic evaluations each customised to individual client needs, and given the technical expertise and time required to service these analyses, what system would be able to continue to meet all the needs of individual clients in a timely manner at a reasonable cost in the future?*
4. *Alternatively, if the system cannot meet all client needs in a timely manner, how should the individual client/group needs be prioritised, and how should that prioritisation be communicated to all stakeholders so that this system is seen to be working transparently and appropriately?*

7. The Beef CRC no longer exists and Sheep CRC will terminate in 2019, but both have been the impetus for significant amounts of independent industry genomic R&D. Continued improvement of the accuracy of genomic EBV requires ongoing collection of phenotypes for key traits (including traits for which genomic EBV are not yet available) on large numbers of animals. Genotypes must also be collected on a sub-set of several thousand animals that have good phenotypes.

- a. With current genotyping technology and analytical methods, genomic EBVs maintain sufficient accuracy to be commercially useful only when the animals using the commercial test are closely related to the animals on which the genomic EBV methods are developed.⁵ This means that a large number of animals in each breed or population must have accurate phenotypes and genotypes each year, in order to maintain the accuracy of genomic EBVs offered commercially. For maximum cost-effectiveness, optimised designs will be required to gather such information. How much will it cost and who should pay still needs to be determined.

⁵ Various research indicates that a genomic EBV is sufficiently accurate for use in selection of animals when the animal being tested is less than two generations away from animals that have both phenotype and genotype information. If people stop recording phenotypes because they now have accurate genomic tests that they prefer to use instead of collecting phenotypes, then the genomic EBV rapidly become less accurate over time. Various models can be imagined for regular replenishment of phenotype and genotype data to keep genomic EBV accurate. But the least risky model is one where a sufficient number of animals that are representative of the whole breeding population are phenotyped and genotyped every year. With this model the accuracy of genomic EBV increases over time until it reaches a plateau and is then maintained at that level as long as the phenotyping and genotyping program is continued at the same level each year. Advances in genotyping and sequencing technology might in future allow development of genomic EBV that maintain accuracy over much longer periods of time, and potentially might work also across breeds. But if and when this will become feasible is unknown at present.

- b. Reference herds (also known as BINs) will likely play a key role in the generation of data for genomic and traditional EBVs, particularly for key traits. Designs may need to be modified to maximise efficiency and capture the full benefits of the various technologies.
- c. There is likely to be a point where price is sufficiently low and accuracy sufficiently high that genotyping will become practically viable in commercial herds. That could have significant impacts on commercial delivery systems and data flows.
- d. New technologies such as electronic ID, smart data acquisition applications, carcase scanning, objective measurements in processing plants, and others could reduce the cost of phenotype collection. That could impact on the design of traditional and genomic data collection for genetic evaluation systems.

Discussion points

1. *Angus Australia has genomic EBV accuracies up to 45% for some traits; Dairy Australia is working towards collecting genotypes and phenotypes on 50,000 related individuals to develop 90% accuracy for EBVs. Is there a point at which the accuracy of an genomic EBV for key traits becomes sufficiently high that breeders will no longer invest in phenotype recording? How will data acquisition then be maintained at sufficient levels to maintain genetic evaluation systems in the longer term?*
2. *Genomic EBVs are currently breed specific. This means that only breeds with large amounts of data and the resources to develop genomic EBVs and invest in BINs can use this technology effectively. Can multi-breed genomic EBVs be developed with sufficiently accuracy to be useful in several breeds, allowing smaller breeds to access the benefits of genomic evaluation?*

8. There could be increasing competition from alternative genetic evaluation systems. Some larger companies will undertake genetic evaluations and improvement entirely (or largely) in-house. Some breeders are already using overseas genetic evaluations services. A substantial movement to independent genetic evaluation systems could push up the costs of delivery to remaining clients on the BREEDPLAN system.
 - a. There will be need for an arm's length assessment of the advantages and disadvantages to breeders using alternative genetic evaluations services so that the breeders using these alternative services and also the BREEDPLAN system operators are properly aware of the drivers and difficulties of developing, using and maintaining different evaluation systems.
9. There is widespread adoption of genetic evaluations and genetic improvement in southern regions, but less penetration amongst the northern tropical breeds. Approximately 75% of *Bos taurus* bulls have BREEDPLAN EBVs, compared with only 12% of *Bos indicus* bulls⁶. Also the average rates of genetic progress in herds participating in BREEDPLAN in tropical breeds remains quite low (e.g. \$1.21 per year for the weighted average index for Brahman, Brangus, Belmont Red and Santa Gertrudis⁷) and is substantially higher in southern breeds (e.g. \$3.67 per year for the weighted average index

⁶ MLA Report B.EVA.0001/0002 "[Evaluating the impact of genetics and genomics RD&E investment.](#)" 2014

⁷ TBTS TECHNICAL OFFICER'S REPORT TO 18th ANNUAL MEETING, 4th August 2015

values of 10 British and European breeds⁸). 45% of studs nationally and 43% of northern commercial producers recently surveyed scored level of importance of BREEDPLAN information in selection decisions at 4 or less (ie little to no use) on a 1-9 scale.⁹

- a. There is a need to better understand the factors holding back rates of genetic improvement and adoption of genetic evaluations in all cattle populations, but particularly for the northern industry. Factors are likely to include location, social and economic drivers, in addition to differences in production systems and supply chain structures.
- b. These factors may require consideration of moving from the current range of breed-centric genetic services to supporting and integrating either different approaches to genetic evaluation or several versions of the current system to better meet the diverse needs of different users.

Discussion points

1. *Can new technology significantly reduce the cost and complexity of collecting performance measurements in extensive conditions?*
2. *To what extent will growing demand from the corporate pastoral operations, or the adoption of industry programs such as MSA, encourage adoption of genetic evaluation across a broader section of the northern industry?*
3. *To what extent will genotyping be valuable for reducing the need to record traits that are particularly difficult to measure in northern systems?*
4. *What are the most effective ways to demonstrate the value of buying bulls with EBVs to northern producers?*

Acknowledgements:

This paper has been prepared with input from Alex McDonald, Steven Skinner (ABRI), Robert Banks and David Johnston (AGBU), plus various MLA reports and feedback from a number of breeders and other stakeholders.

⁸ SBTS TECHNICAL OFFICER'S REPORT TO 9th ANNUAL MEETING, 18th February 2015

⁹ MLA Report B.NBP.0753 "[Barriers to adoption of genetic improvement technologies in northern Australia beef herds](#)" 2015