Livestock Genetics Investment Priorities - Industry Discussion Paper 4
October 2015
INCREASING THE RELEVANCE OF GENETIC RD&E FOR BULL BREEDERS

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 highlights some of the challenges in developing a single national evaluation system for a diverse range of breeders, production systems and environments, and suggests that genetic R&D in the future may need to consider producing management methods and tools that allow breeders to increase genetic gain through greater customisation of traits and indexes, greater focus on the EBVs of bull teams rather than of individual bulls, and through increased selection intensity and shortened generation interval.

The Genetics RD&E Steering Group is seeking feedback on its current 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

The Australian beef industry is both diverse and dynamic in terms of production systems and market end points, and therefore in the breeding objectives that are needed to produce the best product possible for each environment and market scenario. With a shift from a commodity-based industry to one that is now more consumer focussed, structural changes in the beef industry are occurring that may promote the demand and need for different systems of genetic evaluation.

The Australian beef genetic improvement system has evolved around BREEDPLAN genetic information to service a bull breeding market that has been strongly led by the seedstock sector of the industry and delivered through breed societies. This sector has a clearly identified hierarchy of registered herds breeding bulls in a nucleus population and then selling those bulls to commercial producers and other registered or non-registered bull breeders, who in many cases have widely different breeding objectives and goals. This system has focussed on the core principles of collecting pedigree and measurements to generate information with high accuracy, with the selection intensity almost exclusively occurring in the seedstock sector. The BREEDPLAN system has also ensured that there is a common language for describing genetic merit using estimated breeding values (EBVs) that are consistent across the seedstock sector to simplify understanding and adoption of EBVs as an aid in bull purchasing decisions.

However, current and future industry structural changes suggest that industry should review whether alternative systems that provide a different yet complementary approach to genetic evaluation would assist with the overall goal of increasing the rate of genetic improvement across the beef industry as a whole.

Technologies and tools to enhance the current genetic improvement system - not just EBVs

The major determinants of achieving increased rates of genetic gain are the selection differential (picking the best animals), the accuracy of selection (making sure they are the best animals), and the generation interval

(using the best animals as soon as possible). Genetic evaluation services such as BREEDPLAN primarily address only the first two of these drivers.

The current structure of BREEDPLAN provides data analysis services producing EBVs that allow bulls to be ranked on estimated genetic merit for multiple traits, delivered primarily to the seedstock sector. Rates of genetic improvement vary across breeds and individual herds and range from world class to ones that are clearly below expectations. Where outcomes are below those that are possible, it is usually due to a lack of engagement and adoption of clear management practices that are proven to enhance rates of genetic gain. In addition to EBVs, there are other practices that assist with improving accuracy (eg genomics; using new technologies to measure difficult or hard-to-measure traits) and selection intensity [greater use of existing and new reproductive technologies; young sire programs; linkage to reference herds, also known as beef improvement nucleus herds or "BINs"].

The overriding value proposition for the seedstock bull breeder is the sale price of bulls and therefore motivation to adopt practices and measurement will always be driven by the commercial returns from the bull sales. This at times may not be strongly linked with the goal of maximising genetic improvement as occurs when the genetic merit of an individual animal is not as important to the buyer as the physical appearance of the bull. Recent anecdotal data still shows that for many bull sales, the weight of the bull on the day has the strongest influence on price.

The ability to now use integrated genomic and genetic information in the form of "blended EBVs" in breeding programs offers significant benefits to bull breeders in Australia wishing to improve rates of genetic gain. Specifically, the ability to use genomic information to select animals in yearling selection programs on traits that are either expensive or hard to measure commercially at young ages and still achieve accuracies equivalent to direct measurement in later life will change the way that breeders select breeding animals. However these additions will require different information and new tools to enable bull breeders to take full advantage of these opportunities. As an example, identifying which animals will still require later life measurements, and what animals should also be genotyped are key decisions that need to be made.

Traits that are either expensive or too hard to measure can also be traits that are difficult to quantify in terms of economic value and commercial return, particularly for the bull breeder (eg carcase value and eating quality traits). Bull breeders will require better tools to estimate and balance the appropriate economic weighting of such traits. In situations where commercial value information is available from, for example, direct connection to supply chains and consumers, the value of using these traits in the breeding objective and in genetic evaluation will be clearer.

Selection of breeding animals at younger ages offers the ability to reduce the generation interval. However, for many bull breeders there is a risk that selection of young animals may mask traits such as physical structure, visual performance traits and fitness (reproduction) that could have a major impact on the commercial viability of their beef breeding operation. It will be critical that the population of selected young animals is genetically connected to a population of animals where these important traits are then expressed at older ages, to identify any potentially deleterious effects as they arise. Alternatively, further effort could be put into finding genomic predictions of the structural, fitness and visual traits. This would require further investment as generally the numbers of phenotypes for these traits are limited.

Tools that assist in selecting the right animals will be a critical requirement by breeders, as they integrate genomic information from DNA testing with performance measurements to achieve more accurate results.

Not only is the question of which animal to measure and genotype going to become more complex - the more strategic question will be which animals are selected as parents to manage inbreeding and balance genetic diversity and favourable allele frequencies. Mate selection tools such as MATESEL are already capable of doing this; however these tools will have to have a much higher adoption rate if industry is to successfully capture the most benefit from genomic integration.

These technology changes may also allow bull breeders to seek greater flexibility than the current "stud-oriented" system allows. As an example, bull breeders may wish to screen large numbers of animals that have been bred in their own environment with genomic tests to give them the capacity to achieve higher genetic gains than currently possible through buying bulls with EBVs from stud breeders, where those bulls are often bred and managed in more favourable environmental conditions.

The examples listed above show that any future genetic R&D program should not just focus on the delivery of more accurate breeding values, but also on a suite of tools that assist all bull breeders to make more informed decisions in selecting the right animals. This suite of tools is equally important to the seedstock sector as it is to bull breeders servicing a more vertically-integrated value chain sector.

Vertically-integrated industry value chains

As integration increases across the beef value chain, there are bull breeding entities in both the north and the south that have a much greater linkage to the beef value chain and to their end consumers through the sale of branded products. As a result, these bull breeders will have more options for, and a much different focus on, where and when data is collected to inform genetic selection. They are also likely to have different traits in their breeding objectives and data on more relevant traits eg carcase marbling not scanned IMF; pregnancy rate not days to calving; days on feed to a specification, not net feed intake. In these structures, the bull breeding entity is more likely to have clearer and more holistic breeding objectives aligned to maximising returns across the whole value chain, and therefore more incentive to achieve genetic improvement in the commercial herds that they supply. As a result, these value chains might require enhancements to the current evaluation system that would include the development of customised traits and indexes, maintaining heterosis, and cheaper phenotyping in commercial herds. They would likely be less motivated by factors such as breed-specific genetic parameters, indexes and having a common language or base, and place more emphasis on the collection of large volumes of data on many animals, rather than the intensive measurement on a few.

They are also likely to be less interested in the value of an individual bull compared to the value of a team of bulls; hence their genetic evaluation systems may require more customisation around prediction accuracy of the genetic merit of the group, than just the individual bull. A question that then arises is whether the current system that is optimised for an individual prediction would give the same optimal result for a group of animals. An example is the use of pedigree - it is extremely valuable for an individual to have the correct parentage, whereas for an integrated sector, it may be more important to have a greater focus on the genomic relationships between groups of animals.

When considering ways to increase average genetic gain across the diversity of the beef industry, the different motivations, incentives and needs of the entire bull breeding sector, and how this is developing within numerically-influential commercial value chains, need to be taken into account. Rather than relying solely on "trickle down" genetic improvement from a small stud sector at the top of the pyramid, changes

that allow the current genetic evaluation system to have more flexibility and better meet the needs of both stud and commercial breeders should be included in any prioritisation of R&D investment.

As discussed in this paper, these needs for larger commercial bull breeders might include:

1. Better tools to estimate the appropriate economic weighting of expensive or hard-to-measure traits in specific supply chains;
2. Genomic predictions of the structural, fitness and visual traits (and temperament?) valued by northern breeders – an ability to screen large numbers of animals at an earlier age for suitability to a specific environment;
3. A different analytical approach to estimating the breeding value of a cohort of bulls, rather than an individual bull;
4. The need for greater customisation of selection indices than is currently available for tropical breeds (to enable inclusion of saleable meat yield, eating quality, feed conversion efficiency, etc for integrated supply chains with grain finishing and specific market specs);
5. New reproductive technologies to allow increased selection differential and/or reduced generation interval;
6. Automated measurement technologies that enable key data for genetic improvement to be captured.
7. Optimisation of breeding program design including MATESEL for groups.
8. Prediction of GXE interactions ie estimating the reliability of an EBV measured in one environment (or production system) to be expressed in a different environment.
9. Novel techniques to reduce costs and simplify measurement of phenotypes in extensive environments, including development of proxy measurements.

Discussion points

1. *Should there more than one model of genetic evaluation to ensure that genetic delivery and gain is optimised in different sectors of industry?*
2. *In the current model phenotypic data collection and accuracy on the individual in the seedstock sector is a primary goal. Is this a primary goal in an integrated sector?*
3. *Should there be a greater focus on the tools to support selection decisions rather than continually improving the current genetic prediction model?*
4. *To what extent will growing demand from the corporate pastoral integrated programs change the requirements of the genetic evaluation system and will optimisation for this sector lead to different models and different R&D requirements?*
5. *Does a focus on individual animal EBVs in the current seedstock sector restrict genetic improvement for those integrated sectors that have a focus more on genetic merit of a whole bull cohort?*
6. *Are requirements for multi-breed and composites in the northern sectors indicating that more emphasis should be placed on increasing the commercial relevance and value of genetic information to beef producers and their supply chain customers?*
7. *Does the industry need to maintain a common language of genetic information to service all stakeholders or does it allow customisation across different models?*

Acknowledgements

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