

Strategy for design and implementation of reference populations in beef and sheep breeding

R.G. Banks¹

¹ *Animal Genetics and Breeding Unit, University of New England, Armidale, 2351, Australia*
rbanks@une.edu.au (Corresponding Author)

Summary

The advent of genomic selection provides opportunities for increasing the rate and direction of genetic change in breeding programs, but depends critically on the existence and design of reference populations. Simultaneously, the scope for decoupling of recording from estimation, creates opportunities and challenges for multi-member organisations such as breed associations. These challenges are primarily economic and revolve around coordination and reward mechanisms. Significant change and innovation will be required for breed associations to survive and capitalise in the genomics era.

Keywords: genomic selection, breeds, organisation

Introduction

Systematic approaches for design and implementation of breeding programs for livestock have existed for many years (Cunningham, 1978; Harris and Newman, 1994). The steps in simple terms are to 1) define the breeding goal or objective; 2) estimate genetic parameters for the traits in the objective and/or criterion traits correlated with them; 3) implement recording and genetic evaluation to produce estimates of genetic merit for recorded individuals, followed by; 4) selection and subsequent mating of the individuals selected to be parents.

This framework or versions of it have provided a theoretical ideal, usually not precisely followed, at least in extensively managed species such as beef cattle and sheep.

In this perspective, the strategically most important decision is the definition of the breeding objective, and everything thereafter involves only operational efficiency questions. In practice, issues of cost and practicality of recording different traits, coupled with the flow of returns to breeders of bulls and rams, have meant that genetic evaluation systems can end up focussing on making the best use of the criterion traits that are actually collected, and developing approaches to resolving the fragmented and variable (in quality and trait coverage) nature of the data. In economic terms, this has two important elements: the total recording effort is not optimised; and the direction of genetic change will at best be reasonably correlated with the direction implicit in the vector of economic values.

Further, it is usually the case that in implementation of genetic evaluation, evaluation is restricted to individuals with performance records (although this does not have to be the case). With genomics, this is no longer necessarily true. In parallel, rapid developments in recording technologies (Brown et al, 2017) provide scope to revisit the questions around what data can be used in genetic evaluation. This paper examines the consequences of these two developments for the strategy and operations of breeds or breeding groups comprising multiple independent businesses.

Re-visiting the fundamental questions

Implementing genomic selection is here viewed as consisting of two core elements or processes: establishing and maintaining a reference population, and genotyping individuals to identify merit and determine allocation for breeding and/or production utilisation.

The reference population consists of individuals with phenotypes and genotypes. An extreme version of the model would therefore have complete separation between the reference as defined here, and all other individuals, none of which would be recorded for anything. In practice, breeds may have some herds or flocks dedicated to recording and genotyping, and/or recording both performance and pedigree, with some genotyping as well.

Given this perspective, there are 5 key issues that must be addressed by organisations such as breed associations and other multi-member breeding groups.

1. The breeding objective

This is unchanged under genomic selection: the organisation must decide which traits are important and their relative value. This should not be constrained by what is currently recorded, anywhere in the value chain, or by what is currently seen as important. Ideally, every direct source of income or cost anywhere in the value chain that has a genetic basis will be included in the objective, and careful strategic consideration given to traits which potentially will impact profit and market share in the future. Examples including methane output, health and immunity traits, product composition, and so on.

2. The cost of recording objective traits

For every trait impacting current or future income or cost, a method of recording that trait on a sufficient number of new animals each year should be identified, and costed. The aim is to determine the total cost of obtaining a specified number of quality or effective records for the objective traits or very closely correlated criteria, in order to optimise the investment in recording. In principle, the investment should be made according to the “economic recording efficiency” – how much objective accuracy is obtained per dollar invested in each trait. If recording is completely optimisable, then the aim should be to equalise the resulting accuracy of genomic selection across traits, meaning that selection can be perfectly aligned with the objective direction. Exploring this idea shows that in the extreme case of n completely uncorrelated objective traits, all investment should be in recording the trait with the highest accuracy per dollar, so clearly some form of optimisation algorithm across traits will be required. It is also worth noting that the heritability of the trait has only limited impact on this process – since while heritability of a record does influence genomic accuracy and how it varies with numbers in the reference population (Goddard and Hayes, 2009), it is the cost of achieving a specified level of accuracy that is most important.

Optimising investment in recording will almost certainly shift any collective investment away from traits recorded in breeding herds, and may require either specially contracted recording units and/or data-sharing partnerships with businesses through the value chain.

3. Funding the investment in recording

Traditionally, breeders have funded recording from sales of seedstock or other genetic

material, and breed associations have not invested in such activities. External investment, such as via government research programs and/or industry R&D funding, has contributed in a variety of ways in different countries.

Once there is some combination of breeder and/or association-funded recording, how to recoup that investment becomes a critical issue. One possible approach is to impose a levy or surcharge on genotyping. Essentially this would operate as a user fee.

Devising an appropriate mechanism and level for such a levy involves two steps. Firstly, estimating the number of genotypes submitted annually for genetic evaluation, drawing on the reference data set, and secondly, deciding whether to apply differential rates for the levy. It seems logical and equitable to link this to the potential value of the estimate of merit. For example, animals used as herd bulls or flock rams (sires of commercial progeny) typically generate approximately 45 expressions of their genes, whereas commercial animals themselves generate only one expression. Accordingly, herd bulls or rams genotyped prior to sale or distribution should attract a levy approximately 45 times that of commercial animals. Taking differential expressions into account would likely mean providing differing amounts of information from the genotype: a complete list of EBVs for objective traits for nucleus-born animals, and a single EBV for enterprise or chain profit for commercial animals, for example.

Maximising the size of the genotyped population is desirable, simply to spread this fixed cost of the reference over a larger number of genotyped animals. It is important to keep the cost of evaluation via genotyping alone cost-competitive with actual recording, otherwise the potential benefits from decoupling recording and evaluation are unlikely to be captured.

Implementing a system such as this to recoup the investment in recording is not without risk. If the total system – nucleus plus commercial – is too small, the levy may simply be uneconomic. This will also be the case if the rate of genetic progress is too low, since the annual increment in genetic progress captured by the commercial producer or the seedstock breeder must match or exceed the cost of recording per animal. Market rewards for genetic progress and superiority are an important parameter in this model, and in most situations considerable extension or marketing effort will need to be expended to ensure these rewards approach economically rational levels.

4. Paying for phenotypes

In a version of this system in which some nucleus animals, in stud herds or flocks (as opposed to any special reference recording herds or flocks) are genotyped and phenotyped, an important consideration is how to pay for such phenotyping. In the case of the special recording herds or flocks, this is straightforward. In the case of breeders who invest in phenotyping, there is a risk that if they are not recompensed in some way, the amount of such phenotyping will erode, and either the accuracy of genomic selection will decline, or the organisation will have to increase its investment in the special recording operations to maintain the level of accuracy.

This latter option points to a potential mechanism by which to maintain stud-based phenotyping: such phenotyping generates credit based on the equivalent objective accuracy achieved. For example, if a recording nucleus of 1,000 animals costs \$1m and achieves 50% objective accuracy, in simple terms 10% accuracy is costing \$200 per animal recorded. From this it is possible to estimate the annual equivalent value of stud-based phenotyping, add that to the cost of special recording herds or flocks, and then recoup that total reference cost via the levy mechanism proposed in 3.

5. Rewarding selection efficiency and direction

The most important difference between implementation of genetic improvement in vertically integrated or corporate breeders, and the breed-based systems typical of beef cattle and sheep, is that in the latter, the overall recording and selection effort is the result of a large number of heterogeneous decision-makers. Traditionally this variation has been accepted, and may have helped maintain some genetic variation. Within such a system it is technically simple to evaluate every decision relating to recording and selection, at both the nucleus and commercial levels. This raises the question of whether manipulating rewards would be desirable, and if so, how best to do it. Before that, it raises the question of whether the organisation wishes to have some amount of variation between breeders, and if so, how much and in what parameters. It is not obvious how to answer that, but having a transparent goal and mechanism will be critical.

Challenges for organisations

Incorporating the responses to these five questions into the operation of a breeding organisation will involve significantly more “central” direction and coordination than is currently the case. This alone is a risk, with likely more rules or guides than are currently imposed on breeders by their associations, and so will require significantly higher levels of understanding, including of how the different roles in such a model interact and contribute to total value.

There has always been risk inherent in breed associations, but to a large extent it has been dispersed across the individual members and thereby apparently reduced. The investment in reference populations required for genomic selection coupled with the evaluation of all individuals, nucleus or commercial, which makes quantifying the risk almost automatic, and transforms the clarity of description of the risk, in turn making management of it central to the role of the organisation.

What if an appropriate level of understanding and acceptance of this and the approaches required cannot be achieved? One obvious outcome is to fragment into a series of what are effectively closed nuclei selling genetic material – breeding companies. However, each such unit will still benefit from participation in a larger reference, no matter how large their own reference is, and so the same questions still have to be addressed. Essentially the risks arising from sub-optimal investment and coordination would be shifted from within an organisation to across organisations. Any breeding and production system can be modelled and optimised, and the challenge of achieving optimality in practice will remain.

Conclusions

Effective implementation of genomic selection by breeds will require levels of coordination and risk management greater than have traditionally been applied, except perhaps where governments have had a strong role. The most important roles of the organisation will be to invest in the reference population, coupled with supporting maximising the value of genetic gain for the objective, since that is what ultimately funds the reference population. Genetic

improvement will become an explicit “information business”, in which successful organisations will manage the collection of data, its conversion to information, and the extraction of value from that information.

List of References

Goddard, M. E. and Hayes, B.J. (2009) *Nature Reviews Genetics* 10: 381-391