

Strategies to support phenotyping for genomic selection R&D and implementation in beef and sheep industries

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Abstract

Phenotypic recording is central to all genetic improvement. In the pre-genomics era, such recording tended to be focussed on selection candidates, particularly in beef cattle and sheep. In the genomics era, recording and selection can be completely uncoupled. This in turn makes explicit the importance of the key decisions: what to breed for, which leads to what to record, which leads to how to invest in recording (what traits, when recorded, how many records per trait, and which individuals). In single integrated organisations these decisions are relatively straightforward, but in multi-owner or –stakeholder situations, new approaches and levels of investment planning and coordination will be required for optimal sustained genetic progress. Approaches for such planning and coordination have been used (e.g. simulation modelling) are under development (for business aspects of the problem), but organisations and industries will need new models and levels of management for success.

Introduction

A basic algorithm for genetic improvement has been described (Harris and Newman, 1994) and its successful implementation widely documented (e.g. Hill, 2010). The algorithm can be summarised as i) definition of the breeding objective, ii) recording appropriate traits, and iii) prediction of genetic merit, leading to iv) selection and mating. When carefully applied, rates of improvement in productivity of 3 to 5% are feasible and simultaneous improvement in productivity and product quality attributes can be achieved (MLA, 2021). Appropriate data collection, or phenotyping is critical.

Since the 1980s, the prediction step in most animal species has been via pedigree-BLUP procedures, enabling use of data that is often variable in terms of what traits are recorded – with recording predominantly for traits that are relatively easily recorded on-farm. This is particularly the case for extensive industries such as beef cattle and sheep, which in most countries are characterised by low levels of organisation or coordination in the sense of not having defined nucleus populations or systematic collection of off-farm data.

More recently, genomic selection (Goddard *et al.*, 2009) has become more widely used, with a key feature being the ability to estimate genetic merit in a population for which a genomic reference population exists. The value of the reference population in terms of accuracy of prediction of genetic merit is broadly understood and underpins an essential feature and opportunity of genomic selection, i.e., the decoupling of phenotype recording from selection. Under pedigree-BLUP, most recording has been conducted by individuals (or enterprises) who then make selection and subsequent marketing decisions on the recorded animals. Under

genomic selection, provided a suitable reference population exists, breeding enterprises can operate effectively without conducting any recording themselves. Another way of thinking about this is that it implies scope for explicit investment decisions on what to record, and how much to invest in recording, recognising that accuracy generally increases with level of investment, but with declining marginal return on investment (Goddard *et al.*, 2009). This paper considers some implications of this feature and opportunity, with particular focus on the beef and sheep industries of Australia.

Implementation of genomic selection for beef and sheep in Australia

The beef and sheep industries in Australia (and elsewhere, to varying degrees) are characterised in genetic terms by wide variation in: enterprise size in the breeding sector (MLA, 2019a); phenotype recording effort (e.g. Johnston, 2007); selection effort (expressed as i/L , selection intensity relative to generation length); and the role and effectiveness of breed associations. Within this context, there have been solid achievements, including development of reference populations through co-investment models; introduction of single-step genomic evaluation; expansion of traits under evaluation; and accelerating growth of genotyping for genomic prediction (MLA, 2021). This early phase implementation provides a basis for confidence in the technology and for continued and potentially increased investment. How best to invest is the challenge.

Challenges to investment in genomic selection

The starting point for considering investment for genetic improvement, at any level of organization, should be to define the breeding objective. Under genomic selection, this need not be constrained either by what is currently recorded or what is currently paid for by product markets or value chains. In this sense, genomic selection shifts genetic improvement towards being a design enterprise and, thus, managers of improvement programs should think broadly about both current and future attributes of their product (e.g. social license traits, see Miller and Retallick, *these proceedings*). Decision-making on breeding objectives needs to take account of all stakeholders in current value chains, including consumers, and to carefully assess what might seem likely to become important in the medium-term. If traits are prioritised that are not currently important, how to fund the data collection and how to report genetic merit for recorded traits in ways that do not distort current enterprise finances, become important challenges.

The practical and financial imperative of this “design perspective” is that it must be backed by investment in recording the appropriate traits in the reference population. Given that in highly dispersed (in the ownership sense) industries, breeders only capture a small share of total income generated from progeny of bulls or rams (typically 5 to 10% in beef and sheep in Australia), there is a risk of insufficient funds for recording at the required scale. Two broad responses seem possible: firstly, leave this to the market and hope that at least some breeders have sufficient scale to make more speculative investments; or actively invest at a breed or industry level, using whatever funds can be collected, including industry or government R&D funds and, potentially, royalties imposed on genomic testing. Under the more active strategy, two challenges remain: the need for investment in recording is ongoing, in that reference populations need to be “topped up” with new data so that prediction accuracy is maintained (Dekkers *et al.*, 2021); and secondly, some form of coordination of funding becomes essential. Such coordination is outside the traditional domains of both R&D funding agencies and breed associations, at least in Australia, although both groups have moved in this direction in the last

decade (through co-investment in designed recording projects). However, it is not clear to what extent the required permanency of the funding is appreciated. Indeed, the fact that data collection for genomic reference populations is essentially continuing or real-time R&D (with new knowledge being generated continuously) challenges existing definitions of, and funding approaches for, R&D.

The rationale for role of industry or government agencies in funding the R&D aspects of genetic improvement has been considered previously (e.g. Smith, 1981, Elsen *et al*, 1986), but no obvious long-term system or approach has been implemented anywhere, although sustained sequential R&D investment has occurred in several countries (e.g. US (USDA), France, Ireland, and Australia).

Investment questions – what to invest in, how to fund it, and how to make decisions

The challenge in the genomics era for all organisations (public or private) can be distilled to two questions – i) what to breed for and ii) how to fund the data collection that will enable high rates of progress towards that goal? The inherent goal is to maximise return on investment. Defining a breeding objective is in principle straightforward and tools are available to assist the process (Barwick *et al*, 2005). For multi-member organisations, or for whole industries, the challenge of obtaining “buy-in” is real and is likely facilitated by widespread extension and consultation, particularly around traits that are currently not recognised in market prices but which are expected to enhance value in the future. This is somewhat analogous to the challenge of developing and achieving acceptance of multiple goals within a breed, which is technically straightforward but can be very difficult for such organisations (P. Parnell, *pers. comm.*)

Defining a breeding objective directly defines the data collection strategy, which should aim at maximising prediction accuracy for breeding objective traits (Van der Werf *et al.*, 2018). In broad terms, this means recording as many animals as can be afforded (as an approximation, the number to record should be proportional to the size of the commercial or production population, M. Goddard, *pers. comm.*), although an attractive feature of genomic selection is that recording can be concentrated and optimised, rather than depending on “partial” recording of large numbers of animals across multiple enterprises across the population. Particularly if the objective includes hard-to-measure and/or social license traits, it is likely that these a) will not currently be recorded, b) require expensive equipment, and c) require consciously planned recording projects. This implies access to funds and sound management of those funds.

To a large extent, funds for such recording have to date been obtained via R&D grants and it may be that this avenue will always be available but this cannot be guaranteed, and mechanisms to collect funds from other avenues will likely be valuable. An efficient and equitable mechanism for sharing recording costs across recorders and users was outlined by Banks (2021). This approach can incorporate funding from diverse sources, such that if industry and (or) government is willing to assist with costs of hard-to-measure and (or) as yet unpriced traits. At an industry level, investment in recording phenotypes should incorporate breed comparisons where possible, both to facilitate across-breed genomic selection and reduce individual breed recording requirements, but also to inform sire-buying markets, thereby increasing focus on objective merit and likely stimulating faster genetic progress within breeds.

The more rigorously investment thinking is applied to these challenges, the more likely specialised recording operations will become. In this, beef and sheep breeding will become more like the more intensive livestock industries, where ownership and recording is more concentrated. This will bring challenges for the roles of individual enterprises, in particular for “seedstock breeders”, and for how data access is funded. It is plausible but not necessarily optimal that recording and selection would become completely uncoupled business strategies.

Conclusions - key features of possible solutions

Optimally designed and scaled phenotyping is the fundamental issue for all genetic improvement programs into the future and holds special challenges for extensive multi-agent industries such as the beef cattle and sheep industries. Sustained genetic improvement utilising genomic selection seems certain to include the following features:

- definition of breeding objectives that draw on multiple stakeholders’ perspectives,
- specialist phenotype recording operations that complement activities of individual breeders and that are optimised at the breed or industry level for scale and traits included,
- mechanisms for harvesting appropriate shares of the value created to maintain funding for optimal recording and that, accordingly, explicitly value and remunerate recording efforts,
- and sound investment management for organisations, including sustained co-investment partnerships with industry and/or government.

Genomic selection increases scope for extensive industries to design and achieve more valuable genetic improvement than hitherto possible, but this will require new models for multi-member organisations and levels of coordination. Ongoing R&D into optimal breeding program design and, in particular, into methods for coordinating investment in phenotypes, will be valuable.

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