



## Possible principles for breed association models in the genomics era, with reference to beef cattle and sheep breeds

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Beef cattle and sheep breeding in some countries is characterised by important roles for breed associations or societies, including delivery of multi-trait genetic evaluations. In parallel, research and development is typically predominantly funded by the public sector and/or the whole of industry. The breeding sector is therefore providing a genetic improvement service to the rest of industry, while engaging in competition for market share both between and within breeds.

The basis on which inputs to genetic improvement are funded can vary, but typically involves some investment by breeders themselves, usually to cover costs of providing database and data analysis services. In such situations, there is considerable scope for very low relationship between investment and return, at the individual breeder, the breed or the industry level.

This potential misalignment can be exacerbated in the genomics era, in which it is possible to completely decouple investment in performance recording from obtaining estimated breeding values (EBVs) and other genetic information, and from genetic improvement. At the same time, "genomics" offers scope for almost unlimited increase in scale in multiplication and hence harvesting of value.

These developments create conditions in which it is appropriate to consider carefully the nature of breeds and how they self-organise, with issues including:

- Should all input services (such as access to database and evaluation) be provided on a cost-recovery or cost-plus basis, or
- Should value-creation models be considered, where the value of data contributed, and the use to which EBVs are put, be recognised and in some way rewarded
- If it is possible to apply some form of value-creation model, what governance would be needed, and who across an industry and community could or should contribute?

The perspective of this paper is that genetic improvement, and contribution to generating and delivering it, are - at least in multi-enterprise industries - quite particular economic goods, and further, that current models of organisation and of technology delivery are poorly aligned with the overall goal of maximising genetic progress. In

### Abstract



very general terms, this is usually described as market failure, but this avoids the mental effort of diagnosing accurately what contributes to value and examining whether value-creation is prioritised.

Increasingly, genetic improvement in multi-agent organisations and industries will need to accommodate more nuanced thinking about externalities both within the breeding sector, and through the value chain, and whether and how to apply learnings from the literature on club or merit goods. Failure to do so will almost certainly lead to under-performance in terms of rate of genetic progress, likely coupled with hollowing-out of breed associations and loss of potentially valuable variation in decision-making.

There is real scope to evolve to new models of organisation and collaboration in this space, but very real changes in the "rules of engagement" in breed associations will be essential. This paper identifies some of the key challenges, and offers possible principles and approaches to addressing them.

*Keywords: breeds, organisational models, genomics.*

## Introduction

Genetic evaluation systems in beef cattle and sheep are typically delivered via or with breed associations, and to date have usually been on a within-breed basis. Submission of animals to the genetic evaluation is usually governed by some minimum criteria for data: for example, a date of birth, some pedigree data and at least one weight, might be required. There will usually be some charge for submission of animal records to the evaluation, although what such charges cover and how they are designed can vary. There will usually also be some cost for data collection on-farm (in the bull- or ram-breeding herd or flock), which may attract some support from the breed and/or government, and there may be some breed-level investment in special data collection herds, such as the Beef Information Nucleus herds developed in Australia (Banks, 2009).

Countries and breeds vary in their approaches to rules regarding what animals can be included in evaluation, and what traits can or must be recorded, but at least in Anglo-Saxon countries, access to genetic evaluation is relatively open, provided the animals meet some level of breed "purity", as defined on the basis of recorded pedigree. Extending this point, there is no automatic or necessarily close linkage between governance of the breed association and development and application of genetic evaluation.

A central economic fact of these systems is that data collection is tightly linked, or coupled, to evaluation: the breeder has to supply some performance and pedigree data in order to obtain estimates of genetic merit on his/her animals. This implies that the breeder anticipates receiving sufficient income from sales of genetic material (animals and/or semen, ova) to cover the cost of production of the animals, the cost of whatever recording is done, and any costs imposed for genetic evaluation.

As livestock evaluation makes increasing use of genomic methods, this tight coupling of data collection and genetic evaluation can be completely broken. Provided that a sufficiently large reference population is in place, animals can be evaluated on the basis of a genotype alone.

This decoupling generates additional complexity for breed associations, with the risk that they may not have the financial, managerial or technical resources to manage this complexity. Banks (2016) proposed a future role for breed associations, as R&D organisations, aiming to:

- maximise r. $\delta$ \$ per funds invested for some defined gene pool.
- maximise ir/L.

Achieving this will require new forms of association, likely new pricing and return models, and almost certainly include long-term partnerships with others in the value chain (either private and/or public). Van Eenannam and Drake (2012) expressed this similarly:

*"Breeds/groups that can organize themselves and technologically and structurally to seamlessly obtain and marry entire supply chain phenotypes and genotypes and take advantage of the rapidly-declining cost of genotyping to capture the cumulative value derived from using genomic information for multiple purposes (selection, parentage, genetic defects, marker-assisted management, product differentiation, traceability) will be ideally positioned to fully realize the nascent potential of genomic information."*

An additional dimension of challenge and opportunity arises from the fact that many breeds have populations in several countries. The opportunity arises from the potential to share reference data - genotypes and phenotypes - across countries, and thereby potentially increase the accuracy of genomic selection within each collaborating country (Berry, 20??).

The challenges include:

- Simply achieving collaboration.
- Ensuring that rules and procedures for including data (genotypes, phenotypes, pedigree) within- and across-countries are consistent, and ideally are equitable and efficient (in the sense of providing transparency in relation to incentives to collect phenotypic data), and minimise free-riding.
- Determining whether shared or coordinated design adds value and can be achieved, including options such as coordinated young sire sampling, designed phenotyping and genotyping .
- Managing collaborative R&D, which is essential to create the opportunities and overcome at least some of the challenges.

An obvious question that arises from these considerations is whether "breeds" need to work as global partnerships or networks to survive? The answer seems obvious in that there will almost certainly be advantage in doing so.

This paper explores some of the challenges that breed associations will face and have to overcome in order to survive and prosper in the genomics era, and suggests some principles that will be fundamental to success.

The decoupling of phenotyping and evaluation that is enabled with genomics generates major challenges and opportunities for groups of breeders working with a defined gene pool - a breed association. Assuming that they engage with genetic evaluation, such associations usually have some core costs associated with genetic evaluation, including database, staff, and analysis, but costs of phenotyping are dispersed across the members of the association. The members are usually diverse:

- They vary behaviours (recording, selection, marketing).
- They vary in contribution, measured as amount of genetic progress times number of animals generated.

## Breed associations and genomics



Incentives for member breeders include stud and herd bull sales. The system of data collection and evaluation generates externalities (Banks, 2014) only a small proportion of which are captured by the breeders (Banks, 2017). The scale of such externalities can be considerably greater with genomics, through the capacity to evaluate essentially infinite numbers of animals or animal-derived products from any point in the value chain.

To a large degree, breed associations have only very limited procedures and regulations relating to genetic evaluation and improvement technologies, and have restricted their regulatory systems to issues of breed purity. Accordingly, unless closely and strongly supported by technical resources, such associations face considerable organisational challenges in adopting and exploiting genomic technologies. These will include those around variation in the quality of phenotypic data, which animals are genotyped and phenotyped and so constitute the reference population, and the effectiveness of selection decisions. These 3 dimensions of investment and decision-making jointly determine the potential and actual value created and maintained by a breed.

In relation to breed associations and the breeds themselves, it is reasonable to ask "is there a reason to care?" How this question is addressed depends on the perspective of the questioner, will vary between countries, and involves consideration of both a technical and economic efficiency dimension, and a risk dimension (which could of course be included in economic efficiency) - is there any benefit from spreading investment and decision-making risk amongst multiple decision-makers, as opposed to some more corporate approach.

## A simple model

One aspect of the economic dimension of the challenge can be explored through a simple model. If we assume a breed that has arranged its affairs such that it has:

- A reference population ( $n = 1,000$  cows), where all recording takes place.
- A breeding nucleus ( $n = 10,000$  cows) which produces bulls, which breed commercial progeny ( $n = 360,000$  per year).

If the reference population costs \$1mAUD per year, a simple approach to recouping that investment is to impose a surcharge on the costs of genotyping nucleus bulls and heifers, and commercial progeny. It seems reasonable to charge more for tests on bulls and heifers because they have more expressions: approximately 45 expressions per nucleus bull or heifer, and 1 expression per commercial animal. Under the assumption of the reference population cost, and the numbers of animals in each category, this means surcharges of \$54 per nucleus animal and \$1 per commercial animal, on top of the cost of genotyping.

If this approach has merit, it will be essential to ensure transparency, and a satisfactory return on investment at both levels (nucleus and commercial): charging too much or too little will cause distortions in investment.

In real life, things will be more complicated: the reference population will likely include some defined collective investment in HTM traits, and some variable investment by individuals in other traits. It will be important to consider how to deal with the variable investment made by nucleus breeders, and how to return some share of the surcharge collected to those breeders.

Two "easy" solutions seem available for managing this coordination problem:

- Completely rule-defined, allowing no variation. This potentially more expensive, simply because of the imposition and monitoring of rules, and that additional cost must be met by someone. It also requires a very strong belief in the rules, and the ultimate success achieved by applying them. It also requires agreement on who sets the rules
- Completely market-based. Superficially this is very easy to implement ("the market decides"), and hence implementation risk and cost is minimised. At the same time, outcome risk is maximised

Neither is ideal.

Breed associations that survive and prosper in the genomics era will have to manage the following issues:

- Phenotypes vary in quality, or value - this needs to be recognised, ideally at the point or time of the recording (investment) decision.
- Variation in selection (direction, rate) affect both the individual and the breed, and ideally needs to be minimised.
- A mechanism for "payment" is needed - the individuals investing in reference phenotyping and genotyping must have confidence that their investment will be recouped. This will be challenging for most breed associations, in that financial payments are likely to be impossible for most organisations, and rewards or incentives must have limits (otherwise there is a redemption risk ie "payment" for phenotypes and genotypes could bankrupt the association). Any such incentives or rewards also have to be finely judged, since they are likely to reinforce any existing market rewards, and/or the risk of breeders leaving the association or ceasing to collect phenotypes. To avoid the problems of financial mechanisms, waiving genotyping surcharges, and/or providing technical advice may be more feasible options.
- Consideration should be given to developing point of decision apps help shift all decisions towards optima.

Breed associations that can devise and manage simple, transparent and equitable mechanisms for these issues, and hence solve what in economic terms are referred to as coordination problems, will prosper. Those that cannot will disappear.

## Principles

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