PROGRESS IN IMPLEMENTATION OF A BEEF INFORMATION NUCLEUS PORTFOLIO IN THE AUSTRALIAN BEEF INDUSTRY

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SUMMARY

This paper outlines the rationale behind development of a portfolio of Beef Information Nucleus projects in the Australian beef industry, and progress in establishing that portfolio. The projects are aimed at improving the quantity of data available on key hard-to-measure traits and simultaneously increasing the quantity of data available to support calibration of DNA tests. Five of the major commercially relevant breeds have established BIN projects, and the first cohort progeny tests are underway. Economic evaluation of the portfolio while not straightforward is promising. The portfolio seems likely to play an important role in stimulating acceleration of genetic progress, which will be extremely valuable for industry.

BACKGROUND

The Australian beef industry uses BREEDPLAN technology for genetic evaluation and to underpin genetic improvement. The industry investment in this technology is successful – economic analysis suggests a satisfactory return on investment (Farquharson *et al.* 2002), but at the same time recent analysis shows that Australian breeds are making progress at no more than average rates in comparison with the same breeds in other countries (McDonald 2008). Analysis also shows that there are large discrepancies in rates of progress between breeds in Australia (Johnston 2007), there are large "gaps" in performance recording, especially for hard-to-measure traits (Corrigan and Parnell 2006), and in the major breeds there is no strong evidence of acceleration in the rate of genetic progress since 1995 (McDonald 2008).

In addition, industry with R&D partners including the Commonwealth Government has over the period 1990 to 2008 invested heavily in gene marker discovery with the aim of utilising the discoveries and resulting technologies to both increase rates of gain and support more precise targeting of bulls for specific commercial applications. This investment has mirrored that in most major agricultural species (animal and plant) over that period, alongside a substantial effort in theoretical investigation via simulation studies. Three key messages are emerging from the studies of implementation of marker technologies (eg. SmartGene Report 2006):

- marker effects and frequencies must be estimated in the populations in which it is intended to use them (and both will *a priori*, vary between such populations);
- marker technologies of whatever form need some integration into or with existing methods – all sources of information need to be used together;
- there will be a continuing need for phenotyping especially for the hard to measure traits, with knowledge of effects such as breed, herd background etc, and with quite substantial numbers of animals needing to be recorded.

While not all details about how to apply marker data into evaluation and improvement programs have been examined or agreed, there is growing consensus around the three messages above, and in broad terms, a consensus is developing about analytical methods to use.

Together, these elements present the Australian beef industry with a significant challenge, which can be summarised simply:

- faster genetic progress is valuable, but the present infrastructure is either not able to deliver that, or will only do so in line with international (competitor) populations;

- genetic progress in hard-to-measure traits is considerably less than what is possible and desirable, but is almost certain not to be increased because there are almost no incentives for bull breeders to invest in such traits;
- utilisation of markers of whatever form, by anyone, will depend on having relevant Australian phenotype data with which to calibrate marker tools, whether they are individual markers or QTL, panels or whole genome screens.

IS THERE A SOLUTION?

Two responses seem to be available:

Continue as currently. Leave adoption of DNA technology to sellers and buyers to take whatever risks they are prepared to take in terms of what products are offered, with whatever description, and allow a relatively uninformed market to sort things out. Continue using BREEDPLAN at the present or slowly growing effectiveness.

This option would inevitably mean reliance on overseas data to back markers/panels with unknown relevance to Australian conditions, likely underinvestment in any traits specific to our production systems and markets, and would likely lead to reduced investment in genetic/genomic technologies and knowledge because importation would at least be supplying something.

This option would not stop genetic progress or choice, but it very unlikely that progress in these circumstances would be anywhere near what is possible, and would largely depend on a slowly emerging set of quasi-breeding companies – operations with the financial stability and resources to invest in at least some measurement of hard-to-measure traits. These could potentially be partnered with, or taken over by, multinationals seeking to reduce the risk of delivering marker and other technologies by bundling them into actual genetic materials.

Investment into an informed market-place to increase empowerment of all players. It is not being melodramatic to observe that Francis Bacon's "knowledge is power" applies quite precisely in animal breeding. Knowledge – of the genetic merit of animals, including the effects of individual genes or sets of genes, underpins all decisions made in this field, and there is good evidence that when at least breeders and producers have good information about genetic merit, their combined responses include faster genetic improvement for things that drive profit. Further, the services delivered to those buyers and sellers simply have to deliver value, so the market for services becomes more efficient as well.

Knowledge in breeding depends very simply on knowing phenotypes, pedigrees and genotypes, probably in that order. Collecting phenotypes on the right animals and genotyping them is the best approach – and animal breeding theory and economics allow us to optimise what data is collected on which animals.

So, we can work out which animals to measure for what things. What does a system that will do this and generate a well-informed market-place look like? Some thinking has been done about this and one version which has now been implemented is the Information Nucleus being run within the Sheep CRC in Australia (Banks et al., 2006). This is simply a well-constructed progeny test, with a few key elements:

- the sires chosen are young (so that the information generated is relevant for as long as possible), elite (so that they generate knowledge at or beyond the current limits of our knowledge of the genetics of the population), and diverse (so that the calibrations for markers are as robust as possible);

- the sires are progeny tested very evenly across a range of environments and for as many traits as can be afforded (both these features maximise the amount and value of the knowledge generated);
- the sires are genotyped for whatever markers, panels, whole genome screens etc are available, so that the most relevant and reliable estimates of marker effects are obtained – and by doing this on a rolling set of new young sires, the marker estimates are kept continually updated as the population's genetic makeup changes under selection. This means that sound information on the accuracy of marker tests is available to the market.

The Australian sheep and dairy industries are now using large progeny test datasets to calibrate marker tests (in the form of whole genome screens), which are now allowing evaluation and selection within sets of new candidate sires, thus adding information about hard-to-measure traits and/or reducing the need for progeny testing.

Based on this background, the Australian beef industry has moved over the last 3 years to implement Beef Information Nucleus projects (BINs).

PROGRESS IN IMPLEMENTATION

Meat and Livestock Australia has agreed to co-fund BINs for the major breeds through its Donor Company funding mechanism, and 5 projects are now in place with others under consideration.

Table 1. Beef Information Nucleus projects in place, 2011

	Charolais	Brahman	Limousin	Hereford	Angus
# Sire Intakes	3	3	3	3	5
# Sires per intake	10	10-12	10	10	40
# Progeny per Sire	15-20	10-15	16	48	30
Total progeny per year	250-300	125-150	240	480	1140

All 5 projects are in their first intake or cohort. All projects involve recording of a comprehensive set of growth, carcase, reproduction (male and female), eating quality, and docility traits. The Angus project has budgeted for recording of feed intake, and all other projects are keen to explore this. In addition, the breeds/projects are exploring partnering in recording more "research" traits, such as methane production. Use of other breed bulls as backups is encouraged, to generate data to enhance across-breed genetic evaluation.

In each project, technical guidance in selecting the sire intake has been provided by AGBU, and in each case the sire team average is approximately one objective standard deviation above current drop averages.

A condition of the funding is that during the life of this portfolio, the ongoing need for such phenotyping and new mechanisms for funding the activity be explored and developed.

EVALUATION OF POTENTIAL IMPACT

Economic evaluation of this co-investment is not straightforward but nevertheless essential. The approach that has been taken is to assume two scenarios:

- without BINs: the rate of progress for $index in each breed is assumed to continue rising at the rate observed over the last 15 years, which is 1.05x per year (ie the rate of progress in year n+1 is 1.05 x the rate in year n). This continues until the current rate has doubled.
- with BINs: the rate of progress for $index in each breed is assumed to rise at 1.07x each year (ie the rate of progress in year n+1 is 1.07x the rate in year n). This continues until the

present rate has doubled.

Table 2. Economic evaluation of the BIN portfolio

Total BIN investment $m to 2035	# Bulls pa recorded in BIN breeds*	Weighted average rate of gain at year 10 – without BINs ($ per cow joined)	Weighted average rate of gain at year 10 – with BINs ($ per cow joined)	BCR	NPV $m
49	92,750	$2.90 per cow joined	$3.43 per cow joined	16.6	211

* BREEDPLAN Report, 2010

The NPV is based on the number of bulls entering industry as shown, each breeding 100 progeny in their lifetime. The BIN investment is assumed to continue at present levels for 25 years, and the discount rate used is 7%. Note that the estimated investment in performance recording over the period to 2035 for these 5 breeds is $183m. As is typical for long-term investments in genetic improvement, the investment is very favourable. This should be treated as indicative only, since it is almost impossible to predict the continuing investment needed, and more importantly, to attribute the benefits to the BIN activity alone.

PROSPECTS

The BIN portfolio represents a significant organisational and financial challenge for breed associations, yet the major commercially relevant breeds have risen to this challenge. To a limited extent, this builds on earlier experience of two breeds (Angus and Shorthorn) which have conducted large-scale progeny tests during the last 10 years. These prior projects have already proven critical in generating data sets used in calibration of current DNA tests.

Over the coming years, industry will need to address the question of whether other breeds need to be evaluated in this way, and more importantly, how to fund continuing recording of hard-to-measure traits, if this proves (as expected) essential.

At the same time, these projects represent an invaluable nucleus for extension and for stimulating other genetic improvement initiatives. Industry is already showing clear signs of exploring these links and pushing to greatly accelerate genetic progress.

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