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Beef Genetics Pipeline Consultation and Green Paper

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Strategic questions related to RD&E genetics and genomics investment for the beef industry

Aims:

- To inform beef industry genetics and genomics RDE investment into the medium term, through consideration of
    - possible ratios of investment into strategic (longer-term), applied, and extension and implementation R&D
    - clarifying the need for resource populations (aka Beef Information Nucleus), their required size, genetic composition, and sources of co-investment
- To provide the results of this analysis to beef genetics and genomics RDE stakeholders (including industry players) at an Industry Forum likely to be held in November 2011

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Table of Contents

1. What shares of returns are captured by breeders, producers and processors?

Lead investigator: B Lindner, support from P Amer and J van der Werf

Synopsis

- Beef RDE investments can target different sectors along the beef production and marketing chain, including on-farm productivity, or can have off-farm targets such as improving efficiency in feedlots, abattoirs, or in the domestic or export marketing sectors.
- Impacts of any such investments will eventually flow through to the whole value chain of the industry because all sectors are related through demand and supply interrelationships.
- A comprehensive model of the Australian beef industry exists that disaggregates the supply chain horizontally into streams producing, grain and grass finished beef for domestic and export markets, as well as vertically into cattle breeding, backgrounding, finishing on grass, or finishing on grain in feedlots, processing, domestic or export marketing, and final consumption.
- The model has been used to analyse the share of returns from alternative RDE investments in farm production, feedlot nutrition, meat processing and meat marketing in both the grass and grain finished sectors, as well as from beef promotion in both domestic and export markets.
- Beef producers and consumers are estimated to be the major beneficiaries for all such investment scenarios.
- Investment in beef genetics and genomics RDE is most likely to shift down the supply curve of weaner producers, and to a lesser extent grass finishers and backgrounders.
- The model results can not estimate how much of the 33.7% of the benefits accruing to farmers from a shift in the weaner production supply curve is captured by beef breeders.
- The ultimate incidence of a sector specific levy to fund research that raises beef producers supply curve by 1% will closely mirror the incidence of benefits from that RDE.
- A levy on beef producers should continue to be a significant source of funding for beef genetics and genomics RDE.

Literature Review

Successful investment in agricultural R&D leads to the creation of technology which, when adopted, increases productivity in the sense that more output can be produced for a given cost, or lower costs need to be incurred to produce a given quantity of output.

Beef RDE investments can target different sectors along the beef production and marketing chain. For instance, such investments can target on-farm productivity, or can have off-farm targets such as improving efficiency in feedlots, abattoirs, or in the domestic or export marketing sectors. Furthermore, certain types of R&D, such as research on eating quality, can enhance the image of a product in the minds of potential consumers, and can increase the quantity demanded at a given level of price.

However, while research investment may be targeted to a particular sector of the industry, this impact will eventually flow through the whole value chain of the industry because all sectors are related through demand and supply interrelationships. Even if all markets are perfectly competitive, they are linked because the price of an output for a prior stage in the supply chain also is the price of an input in a subsequent stage in the supply chain. So long as the supply curves at each stage are less than perfectly elastic, then some of the benefits from genetic improvement that (say) shifts the weaner supply curve will be distributed through the various sectors in the supply chain. Similarly, adoption of productivity enhancing technology in the beef processing sector will not only be of benefit to abattoirs, but ultimately is likely to also benefit cattle producers, feedlots and domestic and overseas consumers.

Knowledge about the returns from alternative R&D investments targeting different sectors of the beef production and marketing chain is useful input to decisions about the efficient allocation of funds. Furthermore, information about the distribution of gross returns across various industry groups, including producers, feedlotters, processors, exporters, retailers, and domestic and export consumers, may guide decisions about who should fund these investments.

Equilibrium Displacement Modelling (EDM) is generally accepted to be the most suitable analytical framework to evaluate the magnitude and distribution of returns along all stages of the supply chain from RDE investments[1]. In these models, the industry is represented with a system of demand and supply relationships in upstream and downstream markets. Impacts of exogenous changes, such as faster weaner growth rates from genetic improvement, or more customer demand due to promotion campaigns, are modelled respectively as shifts in supply or demand curves from an initial equilibrium. Changes in prices and quantities that arise in all markets when the system equilibrium is displaced due to these exogenous shifts are estimated, as are the consequent changes in producer and consumer surplus reflecting welfare changes to various industry groups[2].

Zhao (1999) developed a comprehensive and elaborate EDM model of the Australian beef industry. Since beef is not an homogenous product, she extended the basic single market EDM model by disaggregating the supply chain horizontally into four streams producing, grain and grass finished beef for domestic and export markets. Also, production is disaggregated vertically into cattle breeding, backgrounding, finishing on grass, or finishing on grain in feedlots, processing, domestic or export marketing, and final consumption. In all sectors, inputs other than cattle and feedgrain (in feedlot sector) are combined as ‘other inputs’[3].

Inter alia, the model enables analysis of returns from R&D investments in technologies applicable in traditional farm production, feedlot nutrition, meat processing and meat marketing in both the grass and grain finished sectors, as well as from beef promotion in both domestic and export markets, and how producers and the community might benefit from the many alternative investment options.
In Zhao et. al. (2000), this EDM model was used to evaluate and compare broad categories of research-induced technological changes and promotions. Specifically, the focus was on the impact of a 1% shift in the relevant supply or demand curves induced by twelve scenarios involving either research investment in individual sectors, or promotion in export or domestic markets.

A subset of these twelve scenarios that are particularly relevant in the context of genetic improvement of beef cattle are as follows:

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[1] See Alston et. al. (1995).

[2] See appendix below for more detailed description of how vertical linkages between markets in the vertical supply chain distribute benefits up and down the chain.

[3] The supply of weaners for all four product categories is assumed homogenous in quality. While differences in breeds make some more suitable than others for grain- or grass-finishing, price differences at this level were not observable. Other features of the model include competitive behaviour at all production stages, constant returns to scale production technology with some substitutability between the farm input and the non-farm inputs, and a rising farm supply function.

1. Weaner Production Research: - research on any breeding or farm technologies that reduce the cost of producing weaners by 1%.
2. Grass-Finishing Research:- research on any farm technologies or new management strategies, including nutritional technologies in grain supplementing cattle, that increase the productivity of 'other inputs' and reduce costs in the grass-finishing sector by 1%.
3. Backgrounding Research: - research on any other technologies that reduce backgrounding costs by 1%.

Table 1 reproduces estimates of total returns for the same 1% exogenous shift in supply for these three scenarios, as well as their distribution among cattle producers, feedlotters, processors, exporters, retailers and domestic and overseas consumers. The size of this change in total welfare from each scenario is predominantly determined by the gross revenue of (or the value added by) the market where the exogenous shift occurs. Note that while the comparison of impacts is between 1% reductions in per unit costs in various production sectors, no attempt was made to estimate the R&D costs required to bring about these 1% shifts.

With regard to the share of benefits, a general result is that each sector captures a larger share of the benefits from new technologies or promotion that occur within their sector than they do from that in other sectors. This occurs because input substitution and product transformation causes "leakage" of benefits associated with differences in supply elasticities in different sectors. Note that because of the symmetrical nature of incremental shifts in supply and demand curves, these results also indicate the ultimate incidence of a sector specific levy to fund research that raises that sector's supply curve by 1%.

Table 1 Economic Surplus Changes ($million) and Percentage Shares to Industry Groups from Selected Investment Scenarios

	Scenario 1 Weaner Research		**Scenario 2 Grass-Finishing Research**		**Scenario 3 Backgrounding Research**	
	$m	**%**	**$m**	**%**	**$m**	**%**
weaner producers	6.00	30.6	2.98	22.3	0.41	23.3
grass-finishers	0.54	2.7	0.65	4.9	0.06	3.3
backgrounders	0.07	0.4	0.06	0.4	0.04	2.2
farmers subtotal	6.61	33.7	3.69	27.6	0.51	28.8
feedgrain growers	0.34	1.8	0.27	2.0	0.02	1.0
feedlotters	0.05	0.2	0.04	0.3	0.002	0.1
processors	0.19	1.0	0.14	1.1	0.02	1.1
exporters	0.09	0.5	0.07	0.5	0.01	0.5
domestic retailers	0.74	3.8	0.55	4.1	0.07	4.1
ROW Consumers	1.62	8.3	1.20	9.0	0.16	9.0
domestic consumers	9.97	50.8	7.38	55.4	0.97	55.4
Total Surplus	19.60	100	13.32	100	1.74	100

Zhao et. al. (2000) also evaluated the impacts of the following additional nine scenarios:

4. Feedgrain Industry Research: - research on any technologies in the grain industry that reduce feedgrain production costs by 1%.
5. Feedlot Research: - research on any technologies in the feedlot sector, such as feedlot nutrition and management that reduce feedlot costs by 1%.
6. Processing Research:- research on any new technologies or management strategies in the processing sector that reduce beef processing costs by 1%
7. Domestic Marketing Research:- research on any new technologies or improved management strategies in the domestic marketing and retailing sector that reduce costs by 1%

8. Export Marketing Research:- research on any new technologies or improved management strategies in export marketing that that increase export marketing efficiency and reduce costs by 1%
9. Export Grain-fed Beef Promotion: - research or promotion that changes tastes in overseas markets and increases consumers demand for export-grain-fed beef by 1%.
10. Export Grass-fed Beef Promotion: - research or promotion that changes tastes in overseas markets and increases consumers demand for export- grass-fed beef by 1%.
11. Domestic Grain-fed Beef Promotion: - research or promotion that changes tastes in domestic markets and increases consumers demand for Domestic Grain-fed beef by 1%.
12. Domestic Grass-fed Beef Promotion: - research or promotion that changes tastes in domestic markets and increases consumers demand for Domestic Grass-fed beef by 1%.

The impacts estimated by Zhao et. al. (2000) for these extra scenarios are not reported here because the specific findings may no longer be applicable, and because the estimated share of benefits going to consumers is counter-intuitive for some scenarios.

In general though, for all 12 scenarios, producers capture larger benefit shares from on-farm research than from off-farm research. Furthermore, apart from consumers, other sectors in the supply chain capture a very small share of the benefits from all scenarios. This reflects the fact that businesses that are intermediate in the value chain, such as grass finishers, backgrounders, feedlot owners, processors, exporters, face competition in their markets for both inputs and outputs. Hence, an average shift in technology across the sector (e.g. all feedlotter's or all processors) would mean that they could now afford to pay more for purchased stock, and/or be bid down in their selling price to the next step in the chain. However, if the supply curve is upward sloping in these sectors (due to some fixed factor of production, such as expertise, location, etc.), then a slightly larger part of total benefits might still accrue to these sectors. Also, if these businesses are able to adopt new research that is exclusive to their own business, then they can get a competitive edge against rival businesses competing in the same sector.[4]

In a subsequent paper, Farquharson et. al. (2003) undertook an evaluation of returns to beef cattle genetics and genomics research and development, defined to include all breed manipulation, including selection, crossbreeding and grading up or breed substitution including imported genetics. They found that net social benefits to producers and others in the beef industry, as well as to consumers of beef products, from investment in genetic selection and southern crossbreeding realised a net present value (NPV) of $861 million (and a benefit cost ratio (BCR) of 3.6 and an internal rate of return (IRR) of 19 per cent). Evaluation of these primary benefits was based on estimated genetic trends for progeny liveweight and cow weight derived from BREEDPLAN estimated breeding values (EBV) information for seedstock animals within breeds, which was then translated into seedstock EBVs for commercial herd traits using BreedObject software. Tacitly, Farquharson et. al. (2003) assumed that the only impact of uptake of results from beef cattle genetics and genomics RDE would be to shift down the supply curve for weaner production. In addition, they found in separate evaluations that the benefits from infusing Bos indicus cattle into the northern Australian herd resulted in net benefits of $8.1 billion, while changing herd breed composition in southern Australia showed a net benefit of $62 million.

For beef cattle genetics and genomics RDE, the shares of returns that are captured by breeders, producers and processors will depend first on the type of RDE outputs generated; and second, which supply curves (or demand curves) will shift, and by how much, if and when there is uptake of such outputs. It is conceivable that several supply curves in the beef supply chain, and even demand

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[4] Arguably, this has important implications, in that feedlotting and meat processing sectors are not highly motivated to engage collectively in activities that will result in industry wide efficiency improvements. Instead, they are motivated to work independently to gain an edge on their competitors.

curves, might shift as a direct result of uptake of results from beef cattle genetics and genomics research and development.

Improvements to beef cattle genetic traits, such as direct and maternal calving ease, direct and maternal 200 day weight, calving day and mature cow weight will mainly reduce average costs of weaner production, and hence initially shift down the supply curve for this sector. However, some growth traits also may lead to some reductions in costs at the backgrounder, feedlot and/or grass finishing levels. In addition, improved EBV's for net feed intake post weaning would impact on the costs of both grass-finishing and backgrounding, and so will shift down the supply curves for these sectors as well.

Less clear is whether improvements in such traits as carcase yield will have any impact on processing costs and supply. Last, there are some meat quality traits that are susceptible to genetic improvement, such as intra-muscular fat that affects marbling. To the extent to which domestic and/or ROW consumers are willing to pay a premium for better marbled beef, genetic improvement in this trait will shift domestic and/or export demand for grain-finished beef.[5]
Hence, the most relevant results from the Zhao study are the shares of benefits for scenarios 1 to 3 for traits that reduce on-farm costs. Domestic consumers are estimated to capture more than 50% of all benefits for these scenarios. Weaner producers are the next biggest beneficiary for all scenarios, and capture about 30% of the benefits from scenario one, and more than 20% for scenarios two and three.

Note also that the EDM model developed by Zhao does not disaggregate the farm production sector into separate sub-sectors of breeders vis-a-vis commercial weaner producers, grass-finishers, and backgrounders. Hence, the results from the model provide no estimate of how much of the 33.7% of the benefits accruing to farmers in general from a downward shift in the weaner production supply curve are captured by breeders. A priori, it seems unlikely that breeders (i.e. bull sellers) as an aggregate group would capture any significant share of benefits from genetic improvement because competitive forces screw down the price of breeding animals so that there are few if any opportunities for extra profits. At best, they might be expected to get back their investment in measurements, so performance recorded animals might fetch a higher price.

One caveat is that not all markets clear in this classic text book manner - in the sense that the price adjusts so that supply equals demand. Stiglitz (2001) argues that examples include labour markets, and in particular labour markets in some developing countries, as well as many financial investment markets, and in particular credit markets. These markets have the following characteristics in common. First, they hinge on considerable uncertainty about future outcomes, so imperfect information is unusually large. Second, the price is struck before buyers/sellers know what they will get in return, so there are significant information asymmetries between buyers and sellers about whether the contract price will be revealed ex post to be too high or too low. The market for bulls seems to share these characteristics, so it is possible that competitive forces might be impeded by market failure, and at least some breeders may be able to capture at least part of the benefits from genetic improvement on a sustained basis.

Moreover, there is the question of whether any share of the benefits might be captured by other organisations, such as breed societies. This is unlikely, because although they have some elements of monopoly power, they are clubs set up to promote the collective benefit of members.
Finally, there is the more controversial issue of intellectual property rights in animal genetic resources, and the possibility that owners of intellectual property rights might use their market

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[5] Some feedlotters prefer certain cattle breeds because of a link to high marbling, but do not pay a premium for better cattle within a breed because of the problem of ascertaining marbling prior to slaughter.

power to extort monopoly profits. To date, most sources of genetic improvement have not been patentable, but this may change as more genomic technologies are developed. Also, while there are no direct equivalents to plant breeders' rights available to animal breeders, there may be limited scope for beef breeders to use trademarks, contract law, and/or trade secrets to appropriate some benefits from genetic improvement on a sustained basis.

Notwithstanding some uncertainty about the shares of returns from beef genetic and genomic RDE that are captured by breeders, producers and processors; and in particular by domestic consumers, this is not a cause for major concern about how to fund genetic improvement RDE. Irrespective of the size of benefits captured by domestic consumers or ROW consumers, there is no practical means of financing RDE for beef genetic improvement by specifically taxing either group. Moreover, Australian taxpayers, who overlap Australian consumers to a considerable degree, are already the largest funder of RDE for beef genetic improvement. Furthermore, so long as the primary source of RDE funding is a levy initially imposed on beef producers, the ultimate incidence of such a levy will get sheeted back to beef producers and consumers in similar proportions to the benefits from genetic improvement that accrues to producers and consumers. This suggests that funding levies should target the weaner sector.

Conclusion

Irrespective of the sector targeted by investments in beef genetics and genomics RDE, the benefits will eventually flow through to the whole value chain of the industry because all sectors are related through demand and supply interrelationships. A comprehensive model of the Australian beef industry that disaggregates the supply chain horizontally into streams producing grain and grass finished beef for domestic and export markets, as well as vertically into cattle breeding, backgrounding, finishing on grass, or finishing on grain in feedlots, processing, domestic or export marketing, and final consumption has been used to analyse the share of returns from alternative RDE investments.

Investment in beef genetics and genomics RDE is most likely to shift down the supply curve of weaner producers, and to a lesser extent grass finishers and backgrounders. Beef producers and consumers are the major beneficiaries for these investment scenarios. However, the model results do not estimate how much of the 33.7% of the benefits accruing to farmers from a downward shift in the weaner production supply curve is captured by beef breeders.

Because the ultimate incidence of a sector specific levy to fund research that raises that sector's supply curve by 1% will closely mirror the incidence of benefits from that RDE, this is not a cause for major concern about how to fund genetic improvement RDE notwithstanding some uncertainty about the shares of returns from beef genetic and genomic RDE that are captured by breeders, producers, processors, and consumers. So long as the primary source of RDE funding is a levy initially imposed on beef producers, the ultimate incidence of such a levy will get sheeted back to beef producers and consumers in similar proportions to the benefits from genetic improvement that accrues to producers and consumers. This suggests that funding levies should target the weaner sector.

Possible future work

Modify the Zhao model so that it better emulates the current structure of the beef genetic RDE pipeline, and update the results using most recent available data.
An empirical study of the market for performance recorded bulls, and an assessment of the extent to which individual beef breeders, and breeders collectively, capture the gains from beef genetics and genomics RDE.

A study of the market for private sector beef genomic innovations, and the advantages and disadvantages of private sector investment in beef genomics RDE.

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Appendix ***Description of Changes in Value Chain due to Uptake of New Technology for Weaner Production (Scenario 1) (Adapted from Zhao et. al. 2000 pp. 72-74)***

In Scenario 1, the sole exogenous change simulated is technical change from genetic research that increases the calving percentage, and hence increases the efficiency of weaner production. This reduces the cost of producing weaner cattle, and assumed to result in a 1% downward shift of the supply curve for weaner cattle.

Because weaner cattle are inputs into the grass-finishing chain and/or the grain-finishing chain; the supply curves of all cattle and beef products in these downstream sectors are shifted down due to the reduced cost in weaner production. In turn, this will decrease prices and increase quantities of backgrounded cattle, grass-finished live cattle, feedlot-finished live cattle, processed grain-fed beef carcass for export markets, processed grass-fed beef carcass for export markets, processed grain-fed beef carcass for domestic markets, processed grass-fed beef carcass for domestic markets, export grain-fed beef, export grass-fed beef, domestic grain-fed retail beef cuts, and domestic grass-fed retail beef cuts.

On the other hand, the increased final beef consumption, resulting from the lower beef prices, also shifts the demand curves for all the cattle and intermediate beef products to the right. Additionally, the supply and demand curves for all cattle and beef products (other than the demand curves of export grain-fed beef and export grass-fed beef) are also shifted due to the substitution relationships among different types of cattle and beef from both the demand and supply sides. As the end result of all these displacements, the downward supply shifts dominate and all cattle and beef prices decrease and quantities increase.

While the supply curves of other inputs in all sectors (i.e. the backgrounding sector, the grass finishing sector, feedgrain inputs and other feedlot inputs, the processing sector, and the domestic and export marketing sectors) do not shift, the demand curves for these other inputs are shifted by two opposing forces. Increased beef consumption leads to increases in the demand for all other inputs, but the reduced cattle and beef input prices also decrease the demand for other inputs due to the input substitution effect. As only small substitution elasticities between cattle/beef inputs and other inputs were assumed, the substitution effect is smaller than the scale effect due to the increased consumption. Hence, demand for these inputs increases.

Using these changes in prices and quantities, the changes in economic surpluses for the various industry groups are calculated. Based on beef industry gross revenue of $4,000 million per year at the farm gate, the total economic surplus gain for this scenario is estimated as $19.60 million per year. All industry groups involved enjoy increased economic surpluses.

Farmers, including breeders, backgrounders and grass-finishers, share 33.7%, of the total benefits. Due to limited substitution possibilities between the weaner input and other inputs in the backgrounding and grass-finishing sectors, it is possible to use more of the relatively cheaper weaner input to substitute for the use of some other inputs. Thus, farmers receive a larger share of total benefits. The other major beneficiaries are domestic consumers, gaining 50.8% of total benefits. This is because of the high value of the domestic retail beef sector, and the much smaller domestic demand elasticities in comparison to export demand. Although having a higher volume at the carcass level than domestic beef, exported beef has a much lower price than domestic retail beef and thus a much lower sector value. The feedlotters, grain producers, processors, exporters and domestic retailers (supermarkets and butchers) only benefit by small amounts, sharing 7.2% of the total benefits among them, due to the assumption of elastic supply of other inputs in these sectors.

Predicted benefits from genomic selection in beef

(Julius van der Werf, Steve Barwick, version 28 Nov. 11)

Summary

This report attempts to estimate the potential effect of genomic selection on beef cattle selection indexes used in Australia. Based on a typical scenario of trait measurement, we predict the potential rate of genetic gain per year. The effect of genomic selection is modelled using selection index theory. The accuracy of genomic information to predict breeding value is assumed to be either low, moderate or high, and the use of genomic information will lead to an increase in selection accuracy that varies per trait, depending on phenotypic information available at the time of selection. Optimizing selection across age classes will also lead to shorter generation intervals.
The results show that for a moderate genomic selection accuracy the rate of genetic gain per year can be increased for various Angus indexes: +50 % for Domestic Self Replacing (-SR) , 40 % for Domestic Terminal (-T), +99 % for Japanese-SR and +95 % for Japanese-T. The predicted increase in gain for Brahman indexes is +59 %. However, these figures assume that all objective traits are measured in the reference population. When only selection criterion trails are measured in the reference, additional responses are considerably lower: : +9 % for Domestic -SR , 10 % for Domestic -T, +10 % for Japanese-SR, +5 % for Japanese-T and +7% for Brahman.

Introduction

To evaluate the potential cost benefit of investments in genomic information, it is important to prediction the effect of genomic selection on potential rates of genetic improvement in beef cattle. These predictions can be derived using selection index theory, where the effect of genomic information on selection accuracy for individual traits is specified, and translated into predictions of the rate of genetic progress in overall profit from an optimised selection scheme. The increase in selection accuracy for overall profit will depend on the accuracy of genomic prediction and on the phenotypic information typically already available at the moment of selection. Genomic information will lead to higher accuracies of EBVs in the younger age classes, and his will make it more optimal to select more breeding animals from the younger age classes.   Hence, an estimate can be made of the proportional increase in rates of gain for the various indexes used by industry.

Methods

Breeding objectives, selection criteria, and index derivation

Breeding objectives for a temperate breed (ANGUS) for commercial production systems targeting two diverse markets, a domestic Australian (DOM) and a high value export (JAP) market, were examined considering both self-replacing (maternal) and terminal (no animals kept for breeding) herds. The traits that were included in the breeding objective (Table 1a) and associated economic values (AU$ profit/cow exposed) were derived using the BreedObject software (Barwick, 1993; Barwick and Henzell, 1999). Because a gene flow method was used to derive discounted gene expressions in this study, the economic values (S. A. Barwick, personal communication) were derived without any discounting of future returns. The only discounting applied was to scale the rev of each trait to being expressed in the first year by a progeny. Similarly, two breeding objectives were considered for a tropical breed (Brahman) (Table 1b)

Table 1a. Economic value of traits for four Angus breeding objectives.

			Self Replacem. Indexes		Terminal Indexes	
	Abbrev	Units	Jap Self Repl	Dom Self Repl	Jap Term Sire	Dom Term Sire
Sale Liveweight Dir.	**SW-d**	kg	0.83[1]	0.86	0.54[1]	0.78
Sale Liveweight Mat.	**SW-m**	kg	0.42	0.60	0.00	0.00
Dressing percentage	**DP**	%	9.69	7.46	5.79	6.52
Saleable Meat	**SMP**	%	8.08	5.96	4.79	5.20
P8 Fat Depth	**Rump**	mm	0.00	0.72	0.00	0.49
Cow Weaning Rate	**CoWR**	%	1.37	0.99	0.00	0.00
Marbling Score	**MS**	Score	49.38	0.00	29.60	0.00
Cow Survival Rate	**CoSR**	%	3.82	3.67	0.00	0.00
Cow Weight	**CoW**	kg	-0.16	-0.12	0.00	0.00
Calving Ease Direct	**CED**	%	2.11	1.82	1.90	1.68
Calving Ease Maternal	**CE Dtrs**	%	0.84	0.73	0.00	0.00

Values increased by a factor sqrt(705/377) and sqrt(634/377) to apply same genetic variance for SW_d for all indexes.

Table 1a. Discounted economic value of traits for a Brahman breeding objective.

	Abbrev	Units	Self Repl
Sale Liveweight Dir.	**LW-d**	kg	0.34
Sale Liveweight Mat.	**LW-m**	kg	0.23
Dressing percentage	**D%**	%	4.12
Saleable Meat	**SM%**	%	3.29
P8 Fat Depth	**FatD**	mm	2.63
Cow Weaning Rate	**CoWR**	%	3.42
Marbling Score	**Marb**	Score	0.00
Cow Survival Rate	**CoSR**	%	3.36
Cow Weight	**CoWt**	kg	0.15

Multiple-trait selection index theory was used to predict the potential benefit of including DNA information in selection decisions (Hazel, 1943). The selection index methodology determines the selection criterion coefficients that maximize the response in a given breeding objective on the basis of available information. The base phenotypic records available for use as selection criteria in indexes were assumed to be those that are routinely recorded by breeders and which are used in BREEDPLAN, the national genetic evaluation system for beef cattle in Australia (Graser et al., 2005; Johnston et al., 1999). Details of these selection criteria including which animals they were recorded on are given in Table 2ab. Genetic and phenotypic variances and covariances (Table 4) were based on estimates detailed in Archer et al. (2004) for the temperate breed (mainly Angus) and via S. Barwick (personal communication 2011) for the Brahman breed. Note that none of the objective traits were measured directly in either of the breeds. This is because the objective traits are defined as traits as expressed in the commercial production sector whereas the selection criteria are traits as expressed in the studs.

Table 2a. Traits in the breeding objective and selection criteria for Angus, parameters and trait measurement information[1]

	Name	Units	phenSD	h2	TMC	AFM
Sale Live weight Dir.	SW-d	kg	34.6	0.31	0	0
Sale Live weight Mat.	SW-m	kg	34.6	0.04	0	0
Dressing percentage	DP	%	1.80	0.33	0	0
Saleable Meat	SMP	%	2.00	0.56	0	0
P8 Fat Depth	Rump	mm	1.98	0.41	0	0
Cow Weaning Rate	CoWR	%	32.5	0.05	0	0
Marbling Score	MS	Score	0.71	0.38	0	0
Cow Survival Rate	CoSR	%	10.0	0.03	0	0
Cow Weight	CoW	kg	46.9	0.41	0	0
Calving Ease Direct	CED	%	20.3	0.1	0	0
Calving Ease Maternal	CE Dtrs	%	20.3	0.1	0	0
Birth weight	BWT	kg/d	3.81	0.39	2	0
200 Day Growth	200d	kg	22.4	0.18	2	0.55
400 Day Weight	400d	kg	30.9	0.25	2	1.1
600 Day weight	600d	kg	34.6	0.31	2	1.65
P8 Heifers	PHh	mm	1.98	0.41	1	1.1
P8 bulls	Phb	mm	1.58	0.28	3	1.65
RIB heifers	RIBh	mm	1.38	0.34	1	1.1
RIB bulls	RIBb	mm	1.05	0.23	3	1.65
Eye Muscle Area Heifers	EMAh	cm2	5.25	0.26	1	1.1
Eye Muscle Area Bulls	EMAb	cm2	6.67	0.27	3	1.65
Intramuscular Fat Heifers	IMFh	%	1.00	0.25	1	1.1
Intramuscular Fat Bulls	IMFb	%	0.89	0.12	3	1.65
Scrotal Size	SS	cm	2.05	0.39	3	1.65
Days to Calving	DTC	days	23.5	0.07	11	3
Mature Cow Weight	MCW	kg	46.9	0.41	11	2.5

TMC= Trait Measurement Code: 1= Females only, 2 is both M+F, 3=Males only; 11 s repeated measurement. . AFM = Age at first measurement (years). Measurements available on 20 half sibs (10 if sex limited) and 20 progeny were added each year after first drop (2 years).

Table 2b. Traits in the breeding objective and selection criteria for Brahman, parameters and trait measurement information[1]

Trait	Abbrev	Units	phenSD	h2	TMC	AFM
Sale Live weight Dir.	SW-d	kg	65.55	0.31	0	0
Sale Live weight Mat.	SW-m	kg	27.25	0.04	0	0
Dressing percentage	DP	%	1.80	0.33	0	0
Saleable Meat	SMP	%	1.98	0.56	0	0
P8 Fat Depth	Rump	mm	2.10	0.41	0	0
Cow Weaning Rate	CoWR	%	46.48	0.05	0	0
Cow Survival Rate	CoSR	%	17.06	0.03	0	0
Cow Weight	CoWt	kg	46.10	0.41	0	0
200 Day Growth	200d	kg/d	22.25	0.19	2	0.55
600 Day weight	600d	kg	29.51	0.48	2	1.65
Days to Calving	DTC	kg	38.52	0.08	1	4
Scrotal Size	SS	mm	2.41	0.44	3	1.1
Mature Cow Weight	MCW	cm2	44.00	0.45	1	3

TMC= Trait Measurement Code: 1= Females only, 2 is both M+F, 3=Males only; 11 s repeated measurement. . AFM = Age at first measurement (years). Measurements available on 20 half sibs (10 if sex limited) and 20 progeny were added each year after first drop (3 years).

The information for each trait was used to construct selection indices for each sex and each age class, and selection was optimized across age class. Genomic information accuracy depends on the size and type of reference population. A reference population can be based on animals that are both genotyped and phenotyped (progeny reference population). Alternatively it can be based on progeny tested sires that are genotyped (sire reference population). The latter model is common in dairy and effectively uses fewer genotyping but many more phenotypes. It is a good model if phenotypes are abundantly available.

The accuracy of genomic selection was assumed to be known with accuracy equal to the square root of some specified fraction of heritability for each trait, the fraction depending on the size of the reference population. This is a good approximation under a progeny reference population. When the reference population gets bigger, it can be predicted using quantitative genetic theory that genomic selection accuracy will become a higher fraction of the square root of trait heritability. When using a sire reference population, the accuracy is more similar for different trait heritabilities.

The estimated size of the reference population to achieve the accuracy also, depends on the effective population size of the breed (bottom of the following table). Less diverse breeds have a lower effective population size and require smaller reference populations. The following table shows the genomic selection accuracy for individual traits of three different GS selecting accuracies, and the size of the reference population needed to achieve this accuracy.

Relationship between size of reference population and genomic selection accuracy when measuring and genotyping individuals

	GS Selection Scenario		
	Low	Moderate	High
h2	Accuracy of GS		
0.1	0.15	0.26	0.32
0.3	0.23	0.38	0.47
0.5	0.36	0.55	0.64
	Required size of reference population (individuals)		
Ne = 100	800	2000	5200
Ne= 200	1600	3600	8000
Ne = 500	3200	7600	20000

[1] Ne = effective population size

Relationship between size of reference population and genomic selection accuracy when genotyping progeny tested sires (40 progeny)

	GS Selection Scenario		
	Low	Moderate	High
h2	Accuracy of GS		
0.1	0.21	0.30	0.46
0.3	0.25	0.36	0.53
0.5	0.26	0.38	0.55
	Required size of reference population (sires)		
Ne = 100	300	700	1900
Ne = 200	500	1100	3600
Ne = 500	1100	2800	7200

The cost of maintaining the reference population depends not only on the size but also on the traits measured. We will compare various scenarios, with complete sets of traits as well as subsets of traits measured. Scenarios are:

Beef Information nucleus (**BIN**): All breeding objective traits are measured on progeny of an information nucleus, specifically bred for this purpose and measured under commercial environments. Under this scenario we also assume that all selection criteria are measured via the reference population, e.g. via genotyping progeny tested sires from previous years.

Stud Reference Population (**SRP**): Only selection criterion traits are measured for the reference population, e.g. via genotyping progeny tested sires from previous years.

Minimal Stud Reference Population (**MSRP**): Only a limited set of selection criterion traits are measured for the reference population. (YET TO BE DONE)

Herd structure

	Angus	Brahman
Nr of breeding females	400	400
Mating ratio (females/male)	50	50
Nr of males used per year	8	8
Weaning rate	80%	65%
Nr progeny born per year	320	260
mortality rate (%)	10	10
Earliest possible age of first drop males	1	2
Earliest possible age of first drop females	2	3
Max age class (years)	10	10

Results

Table 3: Comparison of accuracy and response with MODERATE GS accuracy using a BIN[1]

	Domestic SR	Domestic TS	Japanese SR	Japanese TS	Brahman
SDBrObj	22.93	19.20	33.42	20.43	39.15
No Genomic Selection					
acc	0.379	0.461	0.273	0.265	0.34
Lm	3.88	3.66	5.04	4.58	5.27
Lf	3.62	3.62	3.62	3.59	5.20
dG/yr	3.59	3.73	3.46	2.13	3.64
Genomic Selection					
acc	0.524	0.605	0.457	0.450	0.48
Lm	2.74	2.77	2.63	2.62	4.18
Lf	3.58	3.58	3.57	3.56	5.23
dG/yr	5.40	5.22	6.89	4.16	5.37
% Gain	50.4%	40.2%	98.9%	95.2%	47.4%

[1] Beef Information Nucleus

Table 4: Comparison of accuracy and response with LOW GS accuracy using a BIN[1]

		Domestic SR	Domestic TS	Japanese SR	Japanese TS	Brahman
	SDBrObj	22.93	19.20	33.42	20.43	39.15
No Genomic Selection						
	acc	0.379	0.461	0.273	0.265	0.34
	Lm	3.88	3.66	5.04	4.58	5.27
	Lf	3.62	3.62	3.62	3.59	5.20
	dG/yr	3.59	3.73	3.46	2.13	3.64
Genomic Selection						
	acc	0.459	0.540	0.365	0.360	0.45
	Lm	3.01	3.01	2.98	2.92	4.33
	Lf	3.60	3.59	3.60	3.58	5.23
	dG/yr	4.62	4.57	5.35	3.25	4.96
% Gain		28.9%	22.8%	54.3%	52.4%	36.4%

[1] Beef Information Nucleus

Notes:

- Accuracies are generally low without genomic selection
- None of the objective traits is measured; however genomic selection assumes them to be measured in a reference population (BIN scenario)
- We might need to think of some scenarios where 'cheaper reference populations' measured fewer traits (SRP scenario, see tables 5)
- The extra rates of gain are partly caused by higher accuracies achieved at a younger age. So higher accuracies as well as lower generation intervals will lead to increase dG.
- In various indexes males have high optimal generation intervals. In these cases, they have generally very low index accuracies and this increases only slowly as the animal gets older.

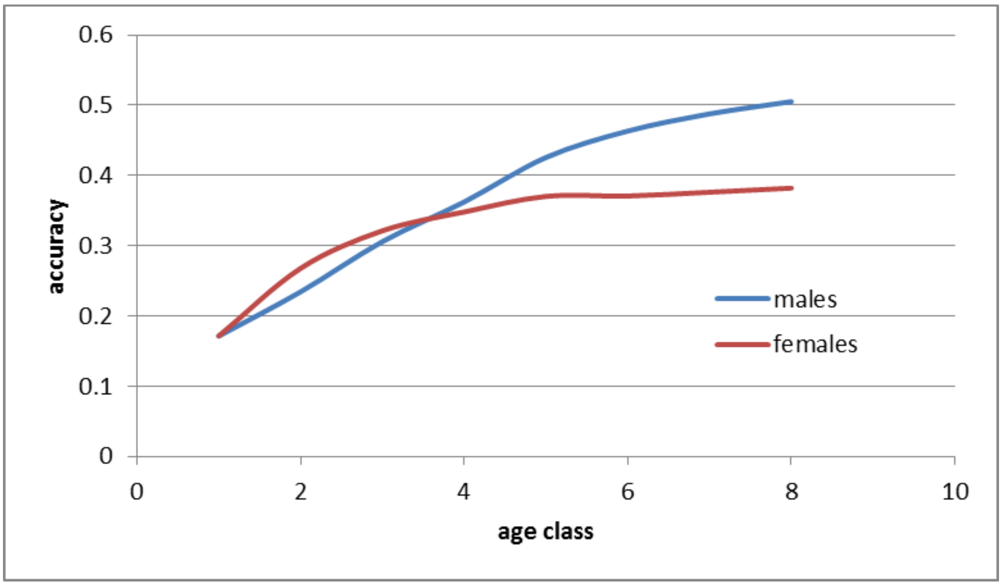


Fig 1 Accuracy per age class for the Domestic SR index with no genomic selection.

Details of accuracy and response per trait are given in the appendix. The following Table gives the dollar response per objective trait for the Japanese SR Index, showing that much of the extra benefit is due to one trait: Marbling Score, and nearly all benefit is in genetic gain for carcass traits.

Dollar response per year for breeding objective traits for MODERATE accuracy scenario and using a BIN

	JAP SR	
	GS	No GS
SW-d	0.92	0.83
SW-m	0.01	0.00
DP	0.81	0.36
SMP	0.92	0.52
CoWR	0.22	0.28
MS	3.85	1.55
CoSR	0.04	0.00
CoWt	0.04	0.00
CEd	0.04	-0.13
CEm	0.04	0.05
Index	6.89	3.46

When only selection criteria trait are measured in the reference population, the benefits from genomic selecting are significantly lower (Table 5)

Table 5: Comparison of accuracy and response with MODERATE GS accuracy using a SRP[1]

	Domestic SR	Domestic TS	Japanese SR	Japanese TS	Brahman
SDBrObj	22.93	19.20	33.42	20.43	39.15
No Genomic Selection					
acc	0.379	0.461	0.273	0.265	0.34
Lm	3.88	3.66	5.04	4.58	5.27
Lf	3.62	3.62	3.62	3.59	5.20
dG/yr	3.59	3.73	3.46	2.13	3.64
Genomic Selection					
acc	0.394	0.493	0.278	0.268	0.36
Lm	3.27	3.26	3.94	4.06	4.98
Lf	3.61	3.60	3.63	3.59	5.21
dG/yr	3.91	4.11	3.81	2.24	3.91
% Gain	9.1%	10.3%	10.1%	5.1%	7.3%

[1] Stud Reference Population

Discussion

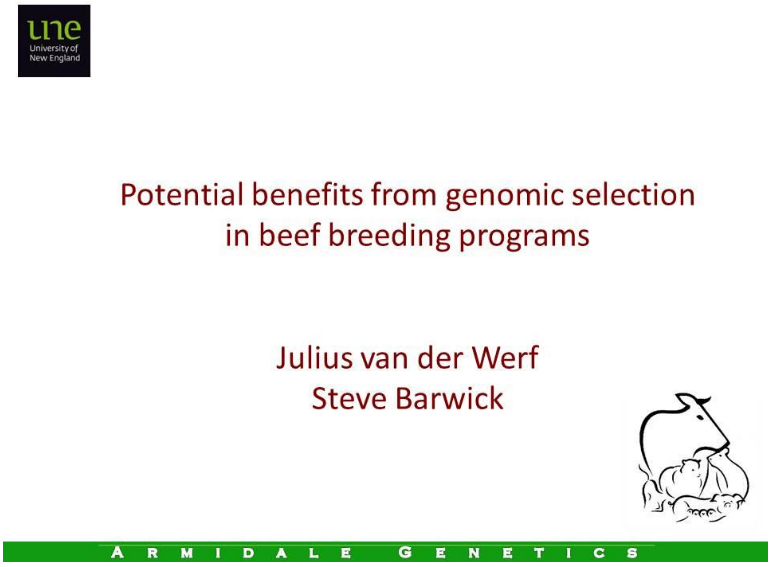
The same indexes and the same assumptions are used as in van Eenennaam et al. (2011). However, their paper looked at the value of bull selection, where accuracy was derived for young bulls. In the approach here, we look at optimal selection where he elected bulls are a mix of old and young bulls. This is more reflective of the actual effect on rate of genetic improvement.

Appendix 1: Response per year (trait units) and accuracy for individual trait in breeding objective and index for LOW accuracy genomic selection scenario and using a BIN.

		DOM Self Repl LOW GS accuracy				JAP SR 25% LOW GS accuracy			
		Genomic Selection		No Genomic Selection		Genomic Selection		No Genomic Selection	
	units	Response	Acc	Response	Acc	Response	Acc	Response	Acc
SW-d	kg	3.31	0.67	3.49	0.66	-0.32	0.68	-0.49	0.69
SW-m	kg	0.02	0.10	0.00	0.00	0.01	0.10	0.00	0.00
DP	%	0.04	0.35	0.00	0.21	0.06	0.34	0.03	0.22
SMP	%	0.28	0.74	0.15	0.54	0.06	0.72	0.05	0.59
Rump	mm	-0.08	0.66	-0.04	0.62	0.40	0.25	0.51	0.28
CoWR	%	0.29	0.25	0.34	0.25	0.06	0.59	0.03	0.46
CoSR	%	0.01	0.09	0.00	0.02	0.01	0.09	0.00	0.02
CoW	kg	3.36	0.63	3.89	0.59	-1.55	0.63	-1.49	0.64
CED	%	-0.07	0.34	-0.14	0.32	0.09	0.34	0.09	0.34
CE Dtrs	%	0.05	0.22	0.05	0.16	0.10	0.22	0.11	0.17
BWT	kg/d	0.21	0.79	0.21	0.78	0.00	0.79	-0.02	0.80
200	kg	1.18	0.69	1.28	0.71	0.00	0.69	0.02	0.74
400	kg	2.59	0.72	2.82	0.73	-0.18	0.72	-0.12	0.76
600	kg	3.49	0.73	3.85	0.73	-0.49	0.73	-0.41	0.77
PHh	mm	-0.08	0.73	-0.06	0.73	0.02	0.75	0.02	0.79
Phb	mm	-0.06	0.64	-0.05	0.64	-0.01	0.65	-0.01	0.70
RIBh	mm	-0.05	0.70	-0.03	0.70	0.02	0.71	0.02	0.75
RIBb	mm	-0.03	0.61	-0.02	0.61	0.00	0.62	0.00	0.67
EMAh	cm2	0.48	0.67	0.44	0.67	0.15	0.67	0.20	0.72
EMAb	cm2	0.63	0.64	0.57	0.63	0.16	0.64	0.22	0.68
IMFh	%	-0.04	0.62	-0.04	0.62	0.07	0.69	0.06	0.68
IMFb	%	-0.01	0.48	-0.02	0.50	0.04	0.53	0.04	0.56
SS	cm	0.07	0.56	0.09	0.53	0.08	0.56	0.09	0.59
DTC	days	-0.33	0.35	-0.43	0.37	-0.47	0.36	-0.65	0.42
MCW	kg	3.15	0.65	3.63	0.62	-0.83	0.66	-1.10	0.67
Index	SD	0.43	0.401	0.40	0.343	0.42	0.345	0.37	0.29

2. What are the estimated returns to the sectors from investment in information nucleus/reference populations?

Lead investigators: J van der Werf and P Amer



University of New England

Potential benefits from genomic selection in beef breeding programs

Julius van der Werf
Steve Barwick

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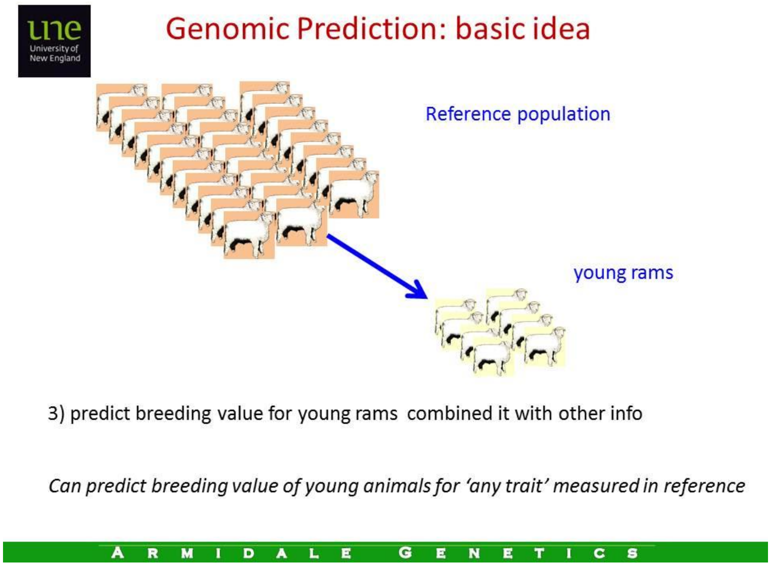

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Genomic Prediction: basic idea

Reference population

young rams

3) predict breeding value for young rams combined it with other info

Can predict breeding value of young animals for 'any trait' measured in reference

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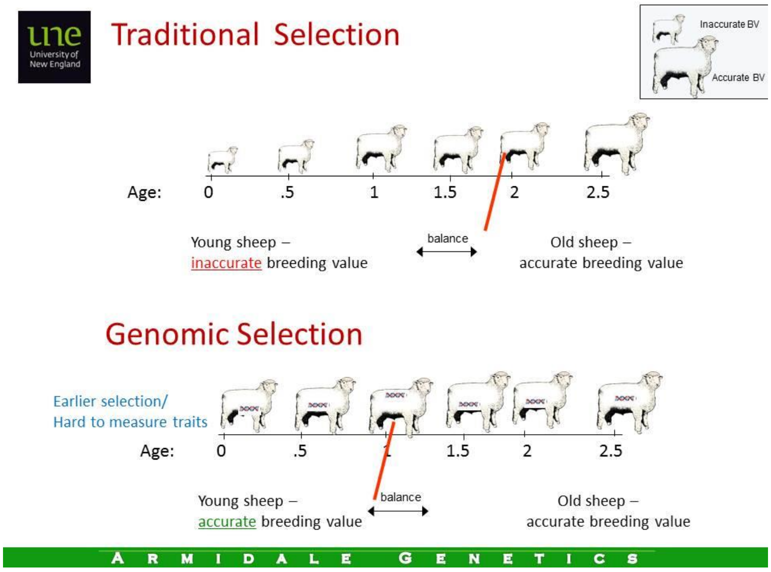

Traditional Selection

Young sheep –
inaccurate breeding value

Old sheep –
accurate breeding value

Genomic Selection

Earlier selection/
Hard to measure traits

Young sheep –
accurate breeding value

Old sheep –
accurate breeding value

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Genomic Selection: Benefit

Overall:
More accurate prediction of genetic merit for breeding objective

Specific:
Traits that are usually difficult to improve
- difficult or expensive to measure
- can not be measured early
- low heritability

Beef Specific:
- Carcass traits
- Reproductive rate
- Mature Weights
- Feed Intake

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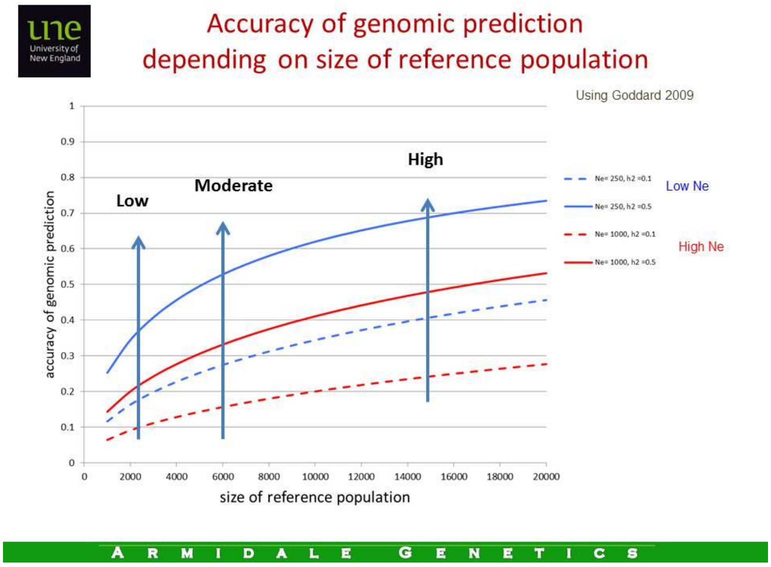
Accuracy of genomic prediction depending on size of reference population



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Aim of Study

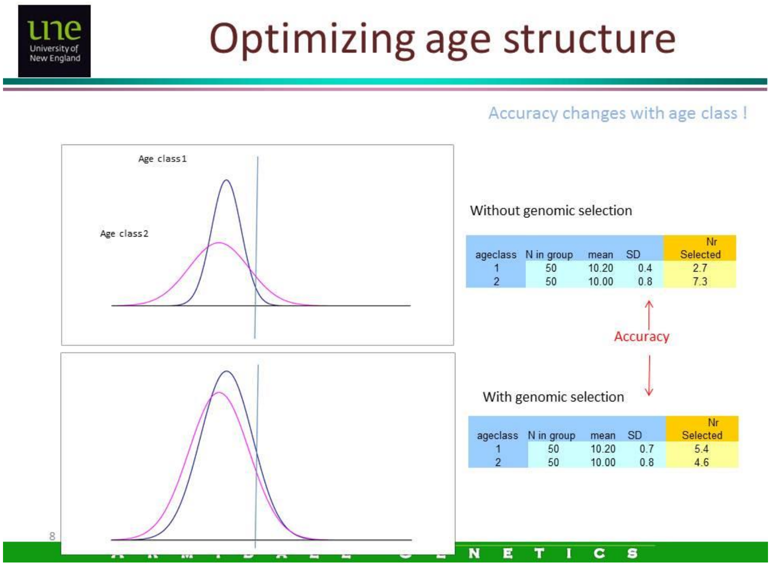
Estimate potential benefits of Genomic Selection
for sheep breeding programs

- increased selection accuracy
- decreased generation interval
- multiple trait selection scenario

Methods

- Modeling genomic selection in breeding programs

1. Selection index approach: multiple information, multiple traits
   Accuracy component
2. Optimizing selection across age classes
   Generation Interval component
3. Using industry scenarios for breeding objectives



Optimizing age structure

Accuracy changes with age class !

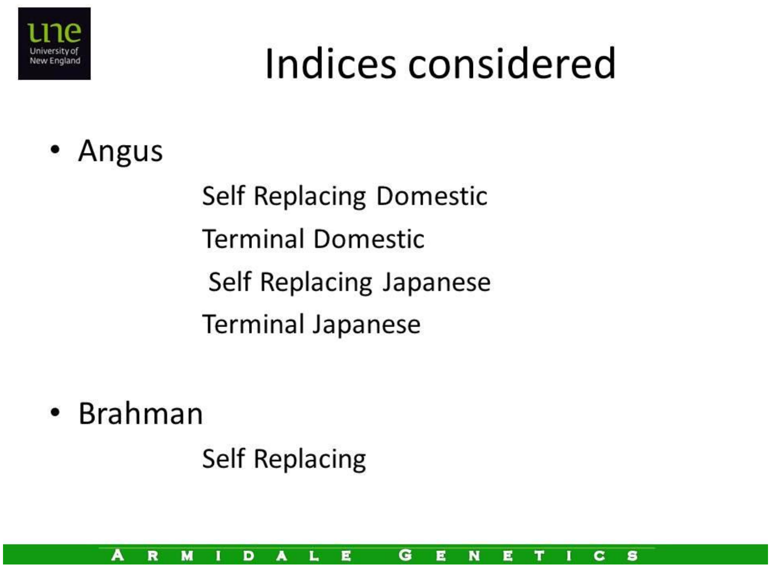
Without genomic selection

ageclass	N in group	mean	SD	Nr Selected
1	50	10.20	0.4	2.7
2	50	10.00	0.8	7.3

↑ Accuracy ↓

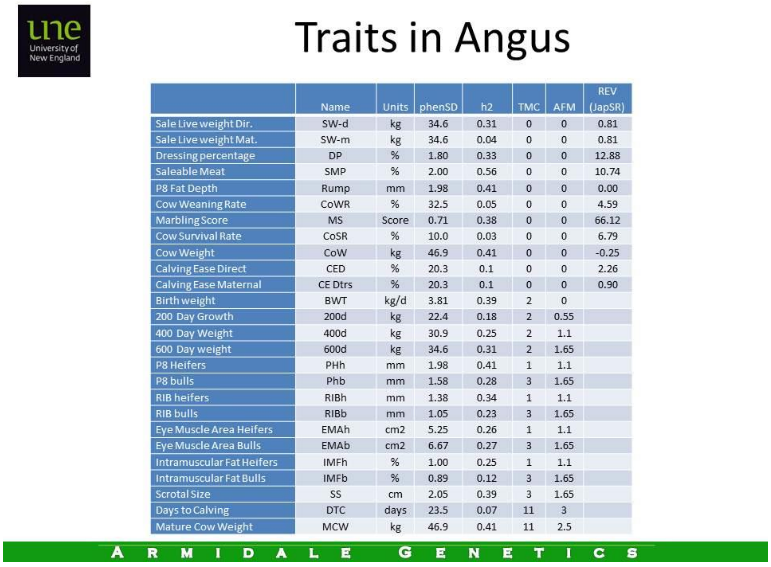
With genomic selection

ageclass	N in group	mean	SD	Nr Selected
1	50	10.20	0.7	5.4
2	50	10.00	0.8	4.6



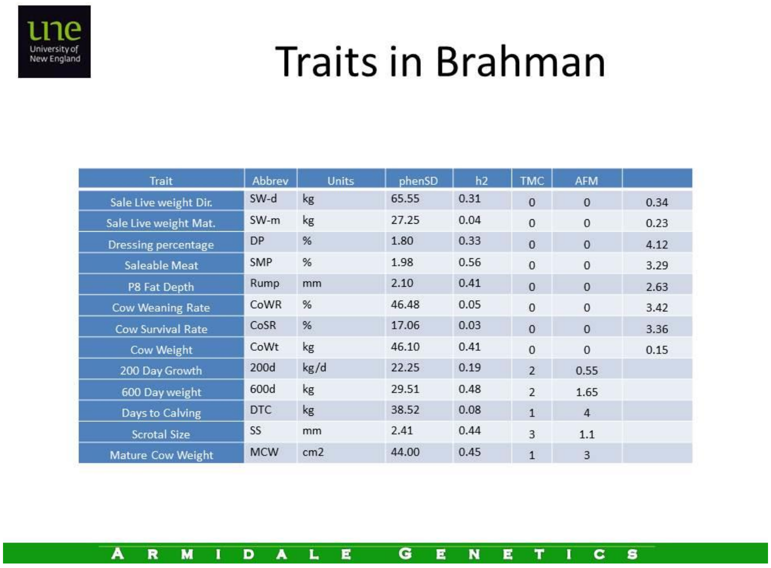
Indices considered

- Angus
  - Self Replacing Domestic
  - Terminal Domestic
  - Self Replacing Japanese
  - Terminal Japanese
- Brahman
  - Self Replacing



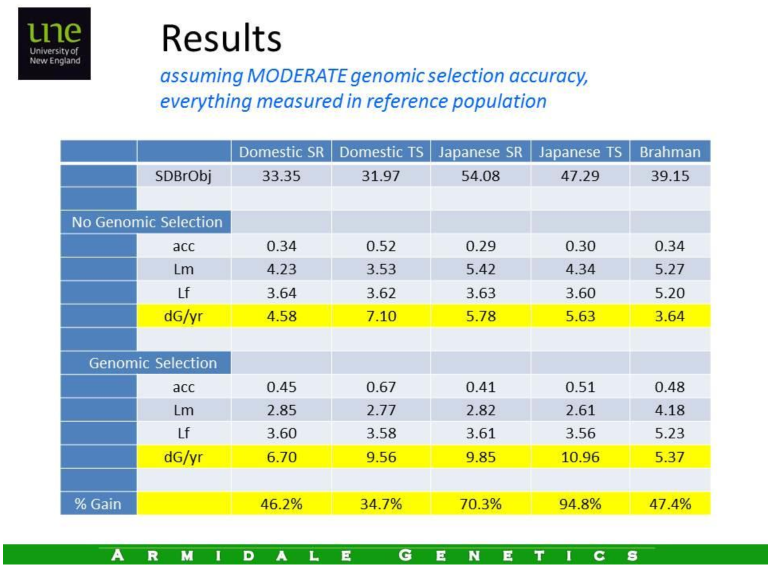
Traits in Angus

	Name	Units	phenSD	h2	TMC	AFM	REV (JapSR)
Sale Live weight Dir.	SW-d	kg	34.6	0.31	0	0	0.81
Sale Live weight Mat.	SW-m	kg	34.6	0.04	0	0	0.81
Dressing percentage	DP	%	1.80	0.33	0	0	12.88
Saleable Meat	SMP	%	2.00	0.56	0	0	10.74
P8 Fat Depth	Rump	mm	1.98	0.41	0	0	0.00
Cow Weaning Rate	CoWR	%	32.5	0.05	0	0	4.59
Marbling Score	MS	Score	0.71	0.38	0	0	66.12
Cow Survival Rate	CoSR	%	10.0	0.03	0	0	6.79
Cow Weight	CoW	kg	46.9	0.41	0	0	-0.25
Calving Ease Direct	CED	%	20.3	0.1	0	0	2.26
Calving Ease Maternal	CE Dtrs	%	20.3	0.1	0	0	0.90
Birth weight	BWT	kg/d	3.81	0.39	2	0	
200 Day Growth	200d	kg	22.4	0.18	2	0.55	
400 Day Weight	400d	kg	30.9	0.25	2	1.1	
600 Day weight	600d	kg	34.6	0.31	2	1.65	
P8 Heifers	PHh	mm	1.98	0.41	1	1.1	
P8 bulls	Phb	mm	1.58	0.28	3	1.65	
RIB heifers	RIBh	mm	1.38	0.34	1	1.1	
RIB bulls	RIBb	mm	1.05	0.23	3	1.65	
Eye Muscle Area Heifers	EMAh	cm2	5.25	0.26	1	1.1	
Eye Muscle Area Bulls	EMAb	cm2	6.67	0.27	3	1.65	
Intramuscular Fat Heifers	IMFh	%	1.00	0.25	1	1.1	
Intramuscular Fat Bulls	IMFb	%	0.89	0.12	3	1.65	
Scrotal Size	SS	cm	2.05	0.39	3	1.65	
Days to Calving	DTC	days	23.5	0.07	11	3	
Mature Cow Weight	MCW	kg	46.9	0.41	11	2.5	



Traits in Brahman

Trait	Abbrev	Units	phenSD	h2	TMC	AFM	
Sale Live weight Dir.	SW-d	kg	65.55	0.31	0	0	0.34
Sale Live weight Mat.	SW-m	kg	27.25	0.04	0	0	0.23
Dressing percentage	DP	%	1.80	0.33	0	0	4.12
Saleable Meat	SMP	%	1.98	0.56	0	0	3.29
P8 Fat Depth	Rump	mm	2.10	0.41	0	0	2.63
Cow Weaning Rate	CoWR	%	46.48	0.05	0	0	3.42
Cow Survival Rate	CoSR	%	17.06	0.03	0	0	3.36
Cow Weight	CoWt	kg	46.10	0.41	0	0	0.15
200 Day Growth	200d	kg/d	22.25	0.19	2	0.55	
600 Day weight	600d	kg	29.51	0.48	2	1.65	
Days to Calving	DTC	kg	38.52	0.08	1	4	
Scrotal Size	SS	mm	2.41	0.44	3	1.1	
Mature Cow Weight	MCW	cm2	44.00	0.45	1	3	



Results

assuming MODERATE genomic selection accuracy, everything measured in reference population

		Domestic SR	Domestic TS	Japanese SR	Japanese TS	Brahman
	SDBrObj	33.35	31.97	54.08	47.29	39.15
No Genomic Selection						
	acc	0.34	0.52	0.29	0.30	0.34
	Lm	4.23	3.53	5.42	4.34	5.27
	Lf	3.64	3.62	3.63	3.60	5.20
	dG/yr	4.58	7.10	5.78	5.63	3.64
Genomic Selection						
	acc	0.45	0.67	0.41	0.51	0.48
	Lm	2.85	2.77	2.82	2.61	4.18
	Lf	3.60	3.58	3.61	3.56	5.23
	dG/yr	6.70	9.56	9.85	10.96	5.37
% Gain		46.2%	34.7%	70.3%	94.8%	47.4%

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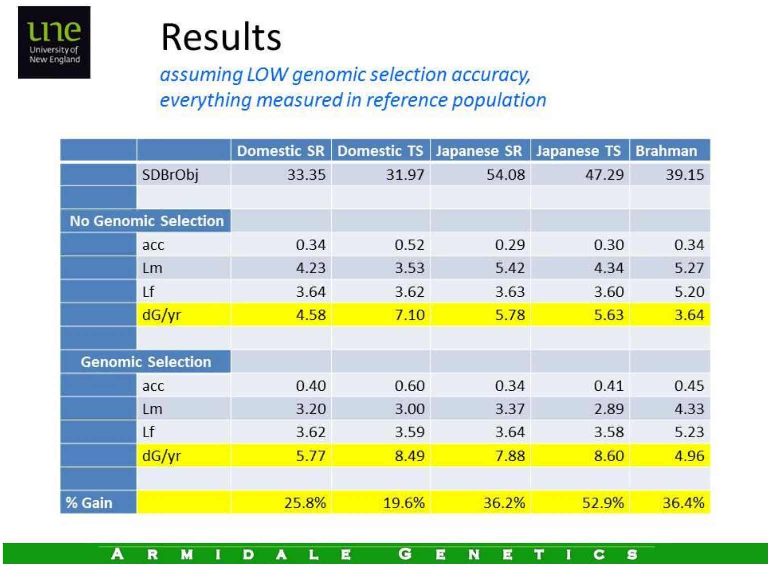

Results

assuming LOW genomic selection accuracy, everything measured in reference population

		Domestic SR	Domestic TS	Japanese SR	Japanese TS	Brahman
	SDBrObj	33.35	31.97	54.08	47.29	39.15
No Genomic Selection						
	acc	0.34	0.52	0.29	0.30	0.34
	Lm	4.23	3.53	5.42	4.34	5.27
	Lf	3.64	3.62	3.63	3.60	5.20
	dG/yr	4.58	7.10	5.78	5.63	3.64
Genomic Selection						
	acc	0.40	0.60	0.34	0.41	0.45
	Lm	3.20	3.00	3.37	2.89	4.33
	Lf	3.62	3.59	3.64	3.58	5.23
	dG/yr	5.77	8.49	7.88	8.60	4.96
% Gain		25.8%	19.6%	36.2%	52.9%	36.4%

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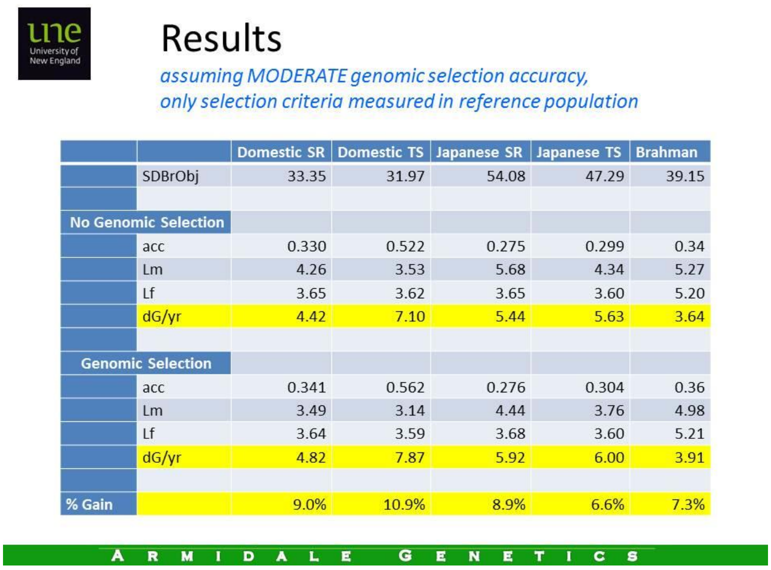
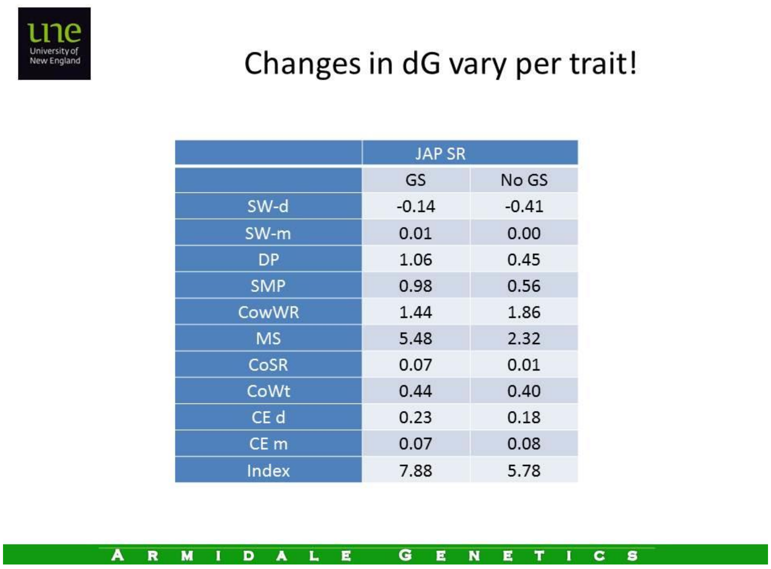


Results

assuming MODERATE genomic selection accuracy, only selection criteria measured in reference population

		Domestic SR	Domestic TS	Japanese SR	Japanese TS	Brahman
	SDBrObj	33.35	31.97	54.08	47.29	39.15
No Genomic Selection						
	acc	0.330	0.522	0.275	0.299	0.34
	Lm	4.26	3.53	5.68	4.34	5.27
	Lf	3.65	3.62	3.65	3.60	5.20
	dG/yr	4.42	7.10	5.44	5.63	3.64
Genomic Selection						
	acc	0.341	0.562	0.276	0.304	0.36
	Lm	3.49	3.14	4.44	3.76	4.98
	Lf	3.64	3.59	3.68	3.60	5.21
	dG/yr	4.82	7.87	5.92	6.00	3.91
% Gain		9.0%	10.9%	8.9%	6.6%	7.3%

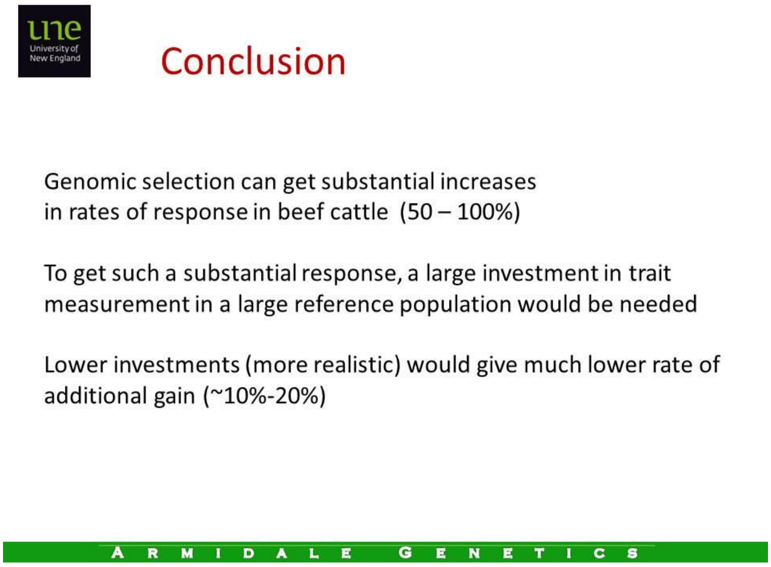
ARMIDALE GENETICS



Changes in dG vary per trait!

	JAP SR	
	GS	No GS
SW-d	-0.14	-0.41
SW-m	0.01	0.00
DP	1.06	0.45
SMP	0.98	0.56
CowWR	1.44	1.86
MS	5.48	2.32
CoSR	0.07	0.01
CoWt	0.44	0.40
CE d	0.23	0.18
CE m	0.07	0.08
Index	7.88	5.78

ARMIDALE GENETICS



Conclusion

Genomic selection can get substantial increases in rates of response in beef cattle (50 – 100%)

To get such a substantial response, a large investment in trait measurement in a large reference population would be needed

Lower investments (more realistic) would give much lower rate of additional gain (~10%-20%)

ARMIDALE GENETICS

3. What size of investment (animals, traits) is optimal for whole of chain returns?

4. What are the requirements for “information nucleus” populations to maintain accuracy of genomic predictions

Lead investigators: J van der Werf and P Amer

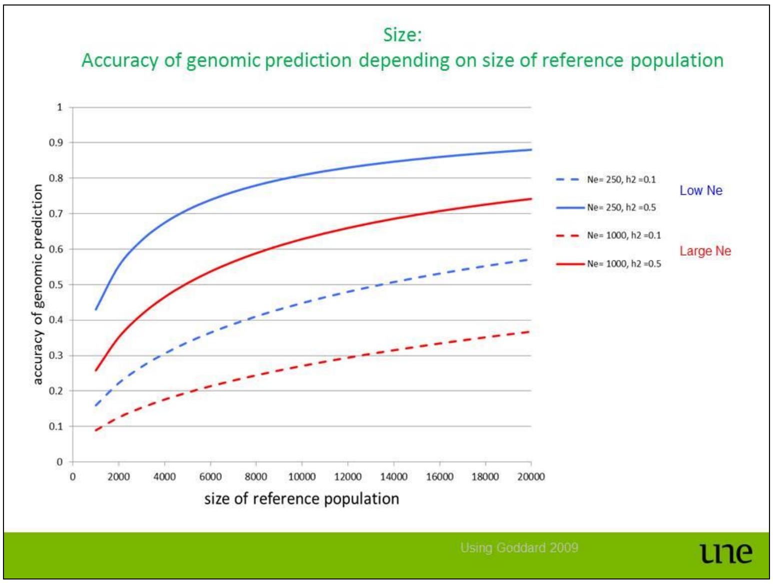
University of New England

What investments are needed
to enable genomic selection?

- size and type of reference population

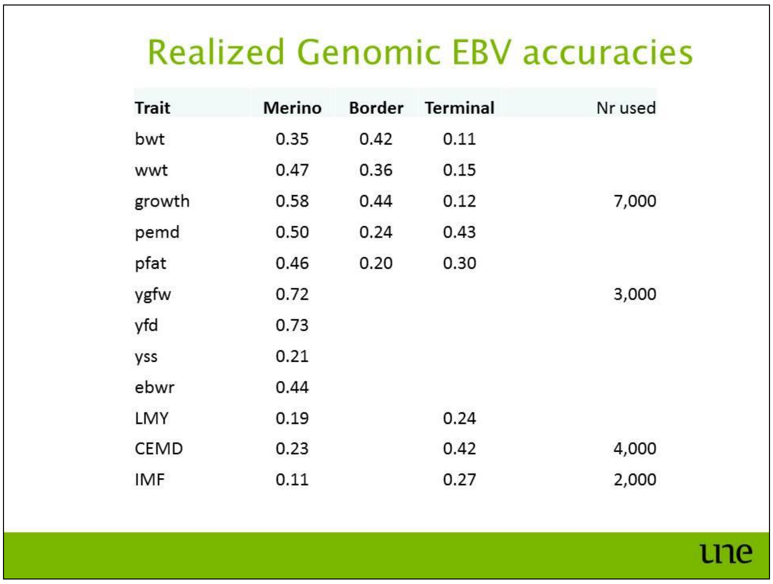
Julius van der Werf
Peter Amer

une



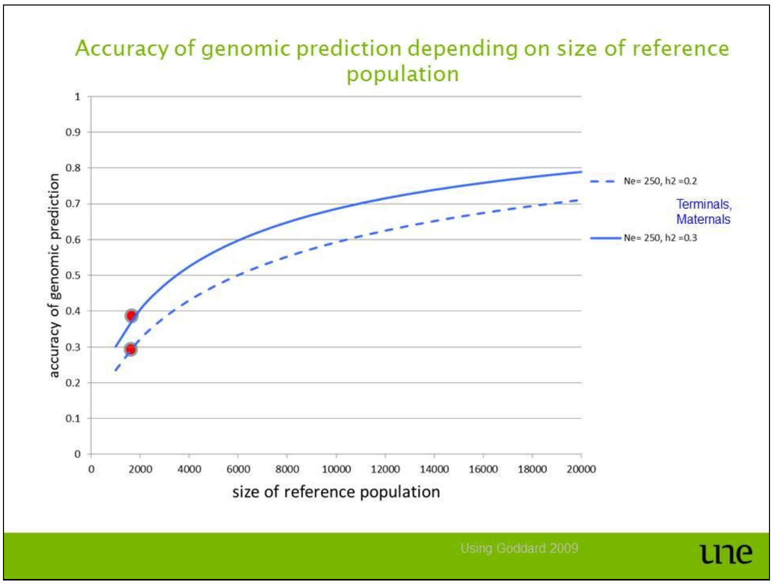
Size:
Accuracy of genomic prediction depending on size of reference population

Using Goddard 2009



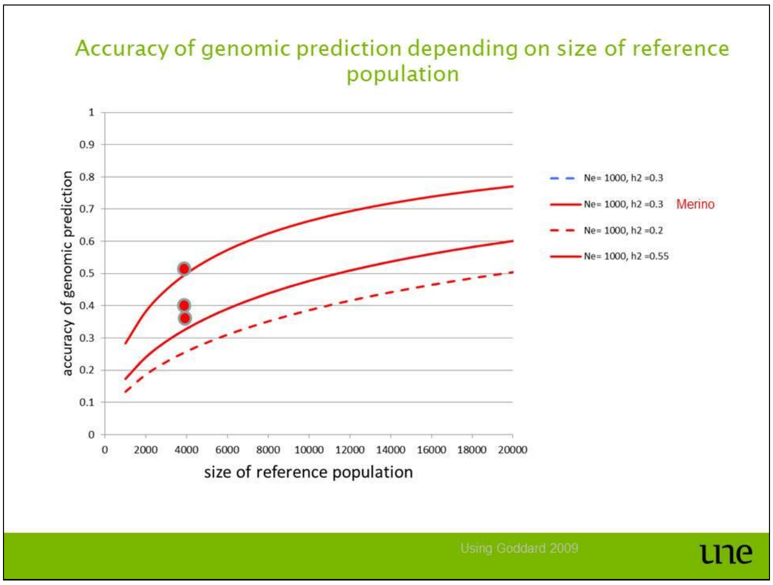
Realized Genomic EBV accuracies

Trait	Merino	Border	Terminal	Nr used
bwt	0.35	0.42	0.11	
wwt	0.47	0.36	0.15	
growth	0.58	0.44	0.12	7,000
pemd	0.50	0.24	0.43	
pfat	0.46	0.20	0.30	
ygfw	0.72			3,000
yfd	0.73			
yss	0.21			
ebwr	0.44			
LMY	0.19		0.24	
CEMD	0.23		0.42	4,000
IMF	0.11		0.27	2,000



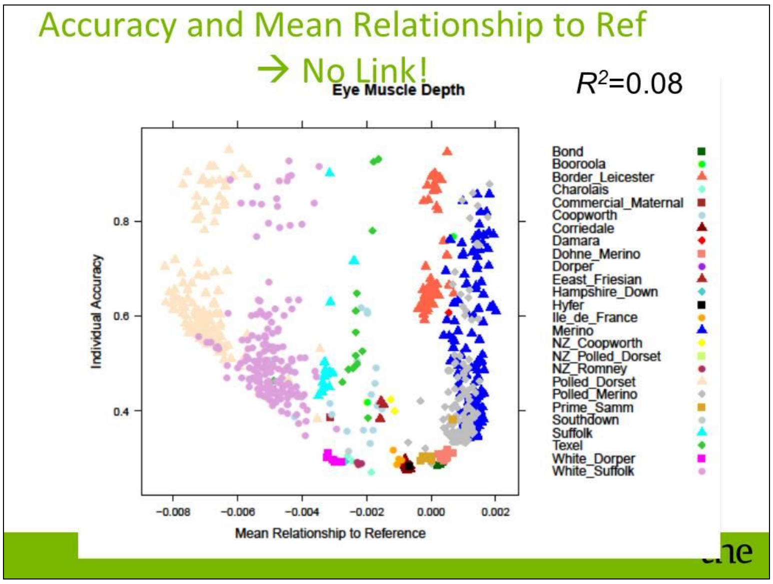
Accuracy of genomic prediction depending on size of reference population

Using Goddard 2009



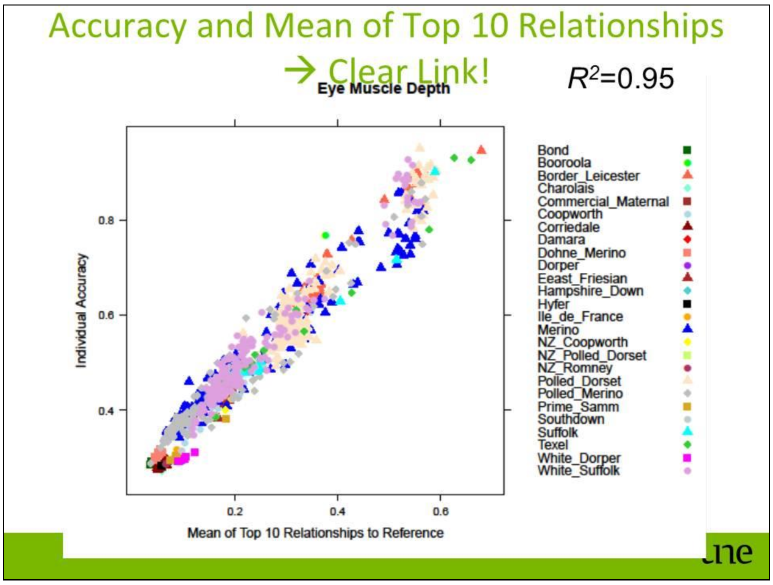
Accuracy of genomic prediction depending on size of reference population

Using Goddard 2009



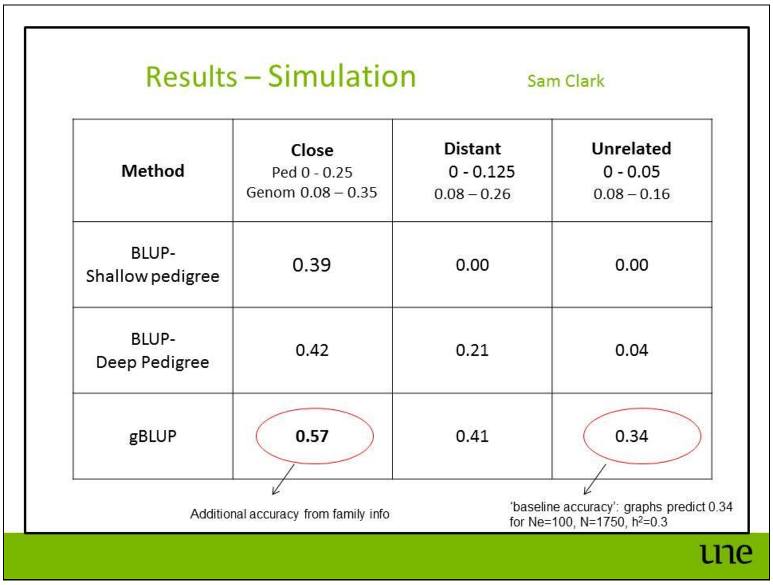
Accuracy and Mean Relationship to Ref → No Link!

R^2=0.08



Accuracy and Mean of Top 10 Relationships → Clear Link!

R^2=0.95



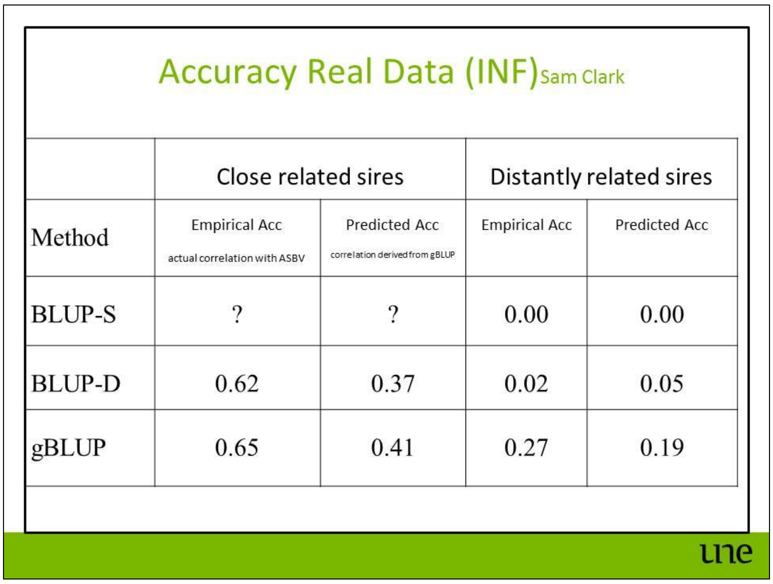
Results – Simulation

Sam Clark

Method	Close Ped 0 - 0.25 Genom 0.08 – 0.35	Distant 0 - 0.125 0.08 – 0.26	Unrelated 0 - 0.05 0.08 – 0.16
BLUP- Shallow pedigree	0.39	0.00	0.00
BLUP- Deep Pedigree	0.42	0.21	0.04
gBLUP	**0.57**	0.41	0.34

Additional accuracy from family info

'baseline accuracy': graphs predict 0.34 for Ne=100, N=1750, h^2=0.3



Accuracy Real Data (INF)Sam Clark

	Close related sires		Distantly related sires	
Method	Empirical Acc actual correlation with ASBV	Predicted Acc correlation derived from gBLUP	Empirical Acc	Predicted Acc
BLUP-S	?	?	0.00	0.00
BLUP-D	0.62	0.37	0.02	0.05
gBLUP	0.65	0.41	0.27	0.19

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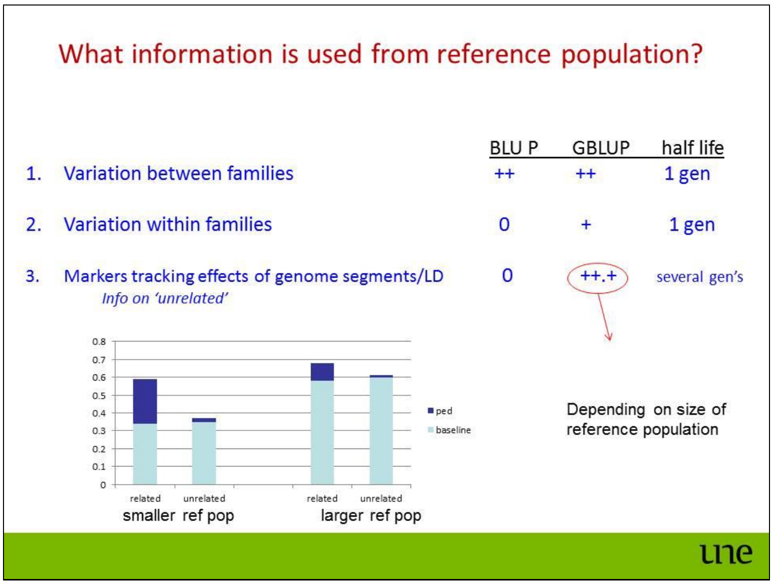

What information is used from reference population?

	BLU P	GBLUP	half life
1. Variation between families	++	++	1 gen
2. Variation within families	0	+	1 gen
3. Markers tracking effects of genome segments/LD *Info on 'unrelated'*	0	++.+	several gen's

Depending on size of reference population

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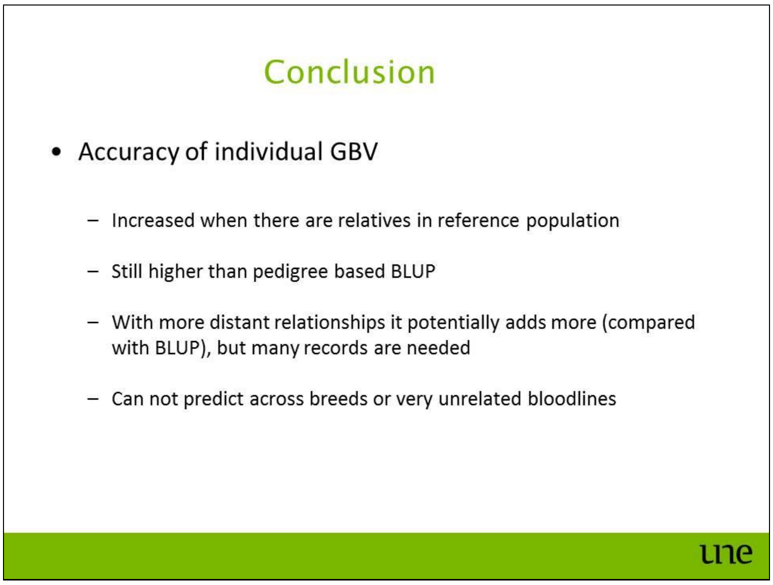


Conclusion

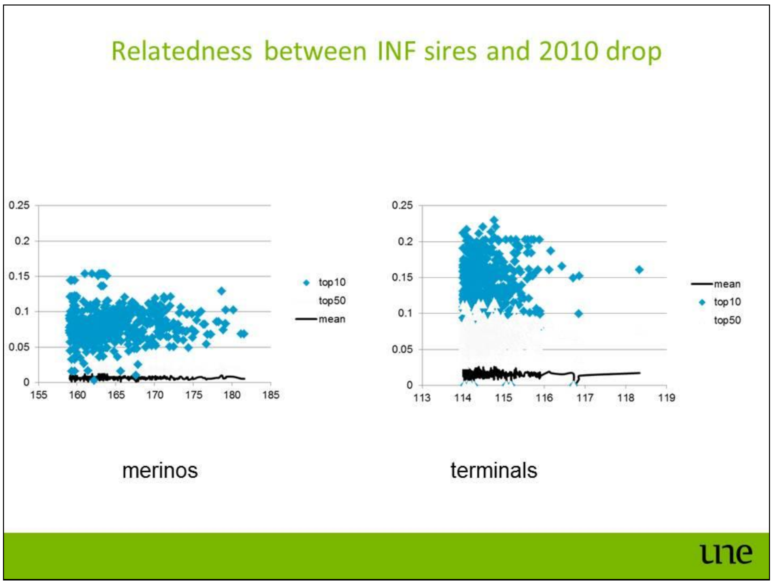
- Accuracy of individual GBV
  - Increased when there are relatives in reference population
  - Still higher than pedigree based BLUP
  - With more distant relationships it potentially adds more (compared with BLUP), but many records are needed
  - Can not predict across breeds or very unrelated bloodlines

une

Implication

- To predict a selection candidate
  - It needs to have 'relatives' in reference populations
  - We can afford a lower degree of relationship than with BLUP
    - » Can predict several generations away
  - Need large reference population

Relatedness between INF sires and 2010 drop

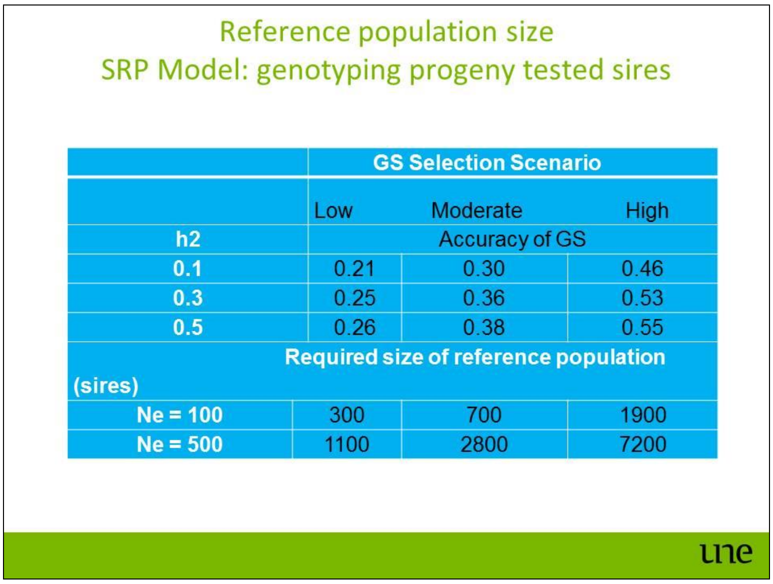


merinos

terminals

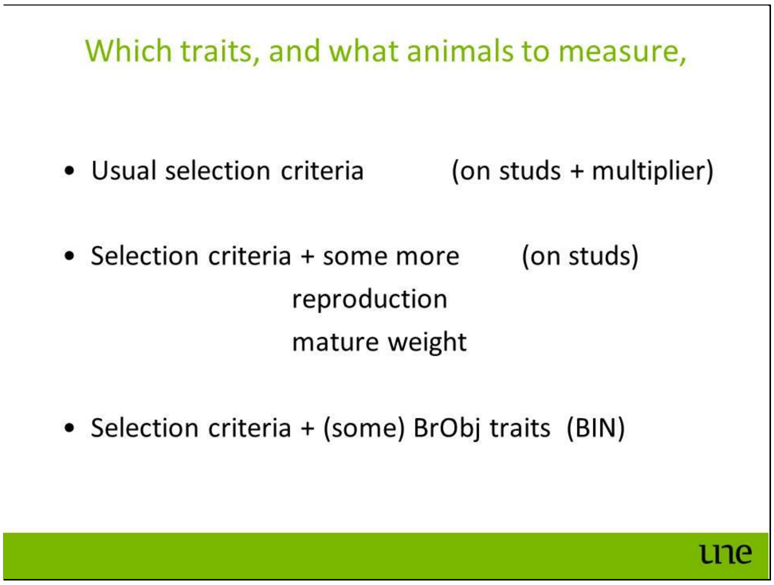
Reference population size
BIN Model: measuring and genotyping individuals

	GS Selection Scenario		
	Low	Moderate	High
h2	Accuracy of GS		
0.1	0.15	0.26	0.32
0.3	0.23	0.38	0.47
0.5	0.36	0.55	0.64
Required size of reference population (individuals)			
Ne = 100	800	2000	5200
Ne = 500	3200	7600	20000



Reference population size
SRP Model: genotyping progeny tested sires

	GS Selection Scenario		
	Low	Moderate	High
h2	Accuracy of GS		
0.1	0.21	0.30	0.46
0.3	0.25	0.36	0.53
0.5	0.26	0.38	0.55
Required size of reference population (sires)			
Ne = 100	300	700	1900
Ne = 500	1100	2800	7200



Which traits, and what animals to measure,

- Usual selection criteria (on studs + multiplier)
- Selection criteria + some more (on studs)
  reproduction
  mature weight
- Selection criteria + (some) BrObj traits (BIN)

5. How do the share of benefits (from #1) correspond to shares of investment in recording, evaluation, and R&D?

Lead investigators: R Woolaston and R Banks

Investors in recording, evaluation and RDE for genetic improvement essentially fall into four categories:

- Breeders (directly and collectively through breed associations)
- Levy payers (cattle producers and feedlotters)
- State and Federal governments (taxpayers/consumers)
- Service providers

Breeders

Breeders potentially invest in genetic improvement in six separate ways:

- Through the direct costs of measuring or assessing their stock on-farm. This involves the costs of labour, equipment, on-farm data processing and possibly outsourced testing services such as scanning, DNA pedigreeing or genomic profiling. A survey by Archer (2004) estimated the total direct costs to be about $25 per cow
- Through membership of BREEDPLAN and charges incurred for data processing and obtaining breeding value estimates
- By contributing to the costs of running Beef Information Nucleus herds, either through their breed society or individually
- By investing in extension, either through co-funding SBTS/TBTS via their breed societies, or possibly through hosting events such as “Closer to your Client” workshops[6].
- Through the transaction levy on cattle sold, currently set at $5 per head, which is allocated to MLA, Animal Health Australia and the National Residue Survey. This levy applies equally to all beef cattle sales, not just to breeders. Of the $5, MLA receives $4.58 per head, of which $0.92 is designated for RDE and $3.66 for marketing[7]. The RDE component is matched dollar for dollar by the Commonwealth. MLA’s annual expenditure for beef genetics and genomics is currently around $2.3m, so that the actual levy component is about $1.15m pa.
- As taxpayers, with a proportion of Federal and State budgets allocated to government RDE agencies and also to matching the RDE component of the transaction levy (described above) and also to matching MLA Donor Company investments (described below).

Producers and feedlotters

Beef producers and feedlotters pay taxes and transaction levies at the same rates as breeders and thus invest in RDE through MLA. As there are many more sales of commercial cattle than of seedstock cattle, the majority of the levy funds are derived from the producing sector rather than the breeding sector, though of course most breeders also run commercial herds as well. The Australian Lot Feeders Association (ALFA) has invested in genetics RDE through the Beef CRC via a $120k pa cash contribution, half of which is Commonwealth matching funds.

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[6] http://sbts.une.edu.au/pdfs/Closer.pdf

[7] http://www.agforceqld.org.au/index.php?tgtPage=&page_id=52

Processors

The Australian Meat Processor Corp Ltd (AMPC) is comprised of 123 members operating 154 meat processing establishments, representing over 96% of Australia's meat processing capacity. Prior to 2007 contributions were voluntary, but in 2007 the Commonwealth Government introduced a statutory levy on processors, with the funds collected being forwarded to AMPC. 75% of their funds come from beef[8] ($0.006 per kg of carcase weight[9]), with the balance from sheep, lambs and goats. AMPC's income in 2010/11 was budgeted at almost $15m, with just over half allocated to growing demand, maximising market access and product standards. None of this was invested directly in beef genetics RDE. Processors also pay company tax.

State and Federal governments (taxpayers/consumers)

As described previously, taxpayer funds are used directly for RDE through government instrumentalities such as CSIRO and State primary industry departments as well as through universities. They are also used to match transaction levy funds, as well as for special programs such as the MLA Donor Company program[10], which provides matching Commonwealth funds for RDE initiated by commercial entities. This latter funding stream is in addition to the general MLA budget for RDE. The rationale behind using taxpayer money for agricultural RDE is related to the need for governments to: encourage industry innovation; help meet the community need for education; help redress market failure where individual businesses cannot recoup the full benefits from their RDE investments; assist rural development; and through DAFF, specifically to assist primary industries[11]. Economic analyses of such investments often attribute benefits to the national economy through a multiplier effect of gains in production, income and value-add, typically of the order of 3x for beef cattle[12]. However, this is not necessarily valid, as summing the claimed multiplied effects across industries can lead to national benefits that are several multiples of GDP (B. Lindner, *pers. Comm*.). The largest single injection of government funds specifically for beef RDE is through the CRC for Beef Genetic Technologies ($30m over 7 years), which is due to terminate in June 2012.

Service providers

With very few exceptions, service providers invest in pipeline RDE because of a fairly straightforward business case i.e. they invest to make a profit. ABRI, a major participant in the pipeline, is a notable exception in that it is a not-for-profit organisation, so it only aims to break even. Other service providers, such as Pfizer Animal Health, have invested significant amounts into genomics RDE in Australia, but for the sole purpose of making a profit for its shareholders through the sale of products and services here and abroad. In order to offer a convincing business proposition to their prospective clients, service providers must provide a product or service to breeders that should, on average, return a profit to their client (in this case the breeder, farmer or feedlot operator), either through reduced costs or enhanced returns.

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[8] http://www.ampc.com.au/pdfs/uauu0flgbueofjatky0oopnxsoq1aabv.pdf

[9] http://www.daff.gov.au/__data/assets/pdf_file/0006/383982/71beef-production-notice.pdf

[10] http://www.mla.com.au/files/df8e21c6-c2a1-4984-8476-9d610081d43e/MLA-Partners-in-innovation-program.pdf

[11] According to http://www.daff.gov.au/about/what-we-do, one of DAFF's two planned outcomes is for:" More sustainable, productive, internationally competitive and profitable Australian agricultural, food and fibre industries through policies and initiatives that promote better resource management practices, innovation, self-reliance and improved access to international markets."

[12] E.g. http://www.agric.wa.gov.au/objtwr/imported_assets/content/amt/agec/multipliers_nislam.pdf

If the breeder purchases a service or product that reduces their costs but has no impact on their rates of genetic gain, then the increased wealth will be captured jointly by the service provider (through sales) and the breeder (through reduced costs), with little benefit spilling over to the breeders' clients and the industry as whole.

If, however, the product does indeed lead to improved rates of gain, either because the breeder measures more animals than previously, or because it enables them to measure economically important traits that they hitherto couldn't measure at all[13], then rates of gain in the aggregate breeding objective should improve. Under this circumstance, the breeder will be able to assess his/her animals' $index value more accurately and the breeder's clients can also benefit directly, because their bull-buying decisions will be better informed and their bull supplier will be making faster genetic gain in the $index. Market imperfections mean that the additional value of the bulls will probably not be fully incorporated into their sale price[14], so there may be whole-of-chain benefits from service provider investments. However, it is difficult to ascribe a value to this.

Finally, government agencies (including universities) that provide services which compete with (or potentially compete with) private sector service providers are generally required to adhere to competitive neutrality guidelines, so that the net cost to the taxpayer for such investments is (or should be) close to zero.

Share of investment

Tables 5.1 and 5.2 indicate the estimated investments in recording, evaluation and R&D for the beef pipeline at present and after the Beef CRC terminates, respectively. It is difficult to predict how RDE agencies will respond to reduction in Commonwealth funds when the CRC terminates, but the figures in Table 5.2 are based on the assumption that the current CRC partners will reduce their total expenditure in this area by 40%, by reallocation of resources to other priorities and some net reductions. Under this assumption, the total government (taxpayer) funds for beef genetic improvement approximately halve and current breeder contributions to CRC cease, while levy investments remain unchanged. As a proportion of the total (smaller) investment, levy contributions almost double while the share paid by breeders increases from 22% to 33%.

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[13] Provision of a cheap but effective method of measuring net feed intake would be an example

[14] Exceptions to this can occur if a breeder's marketing strategy distorts the imperfection in their favour; or in other words, it leads their clients to perceive a greater value in the resulting genetic improvement than what it is actually worth.

Table 5.1. Estimated investment in beef genetics and genomics according to funding source (2011)

Investment	**Estimated pa ($m)**			**Funding source (%)**			**Funding source ($m pa)**		
	Cash	**In-kind**	**Total**	**Breeders**	**Levies**[15]	**Govts**	**Breeders**	**Levies**	**Govts**[16]
Beef CRC	$7.3	$11.4	$18.7	1%	3%	95%	$0.27	$0.65	$17.80
AGBU	$0.7		$0.7		50%	50%		$0.35	$0.35
BINs	$2.5		$2.5	50%		50%	$1.25		$1.25
ABRI	$0.6		$0.6	100%			$0.60		
SBTS/TBTS	$0.5		$0.5	42%		58%	$0.21		$0.29
Sundry MLA	$0.3		$0.3		50%	50%		$0.15	$0.15
Other Govt RDE[17]			$1.0			100%			$1.00
On-farm recording[18]	$3.8		$3.8	100%			$3.75		
Totals	**$15.7**	**$11.4**	**$28.1**				**$6.08**	**$1.15**	**$20.84**
							22%	4%	74%

Table 5.2. Estimated investment in beef genetics and genomics according to funding source (post-CRC).

Investment	**Estimated pa ($m)**			**Funding source (%)**			**Funding source ($m pa)**		
	Cash	**In-kind**	**Total**	**Breeders**	**Levies**	**Govts**	**Breeders**	**Levies**	**Govts**
Ex-CRC partners	$1.5	$6.8	$8.3		7%	93%		$0.65	$7.69
AGBU	$0.7		$0.7		50%	50%		$0.35	$0.35
BINs	$2.5		$2.5	50%		50%	$1.25		$1.25
ABRI	$0.6		$0.6	100%			$0.60		
SBTS/TBTS	$0.5		$0.5	42%		58%	$0.21		$0.29
Sundry MLA	$0.3		$0.3		50%	50%		$0.15	$0.15
Other Govt RDE			$1.0			100%			$1.00
On-farm recording	$3.8		$3.8	100%			$3.75		
Totals	**$9.8**	**$6.8**	**$17.7**				**$5.81**	**$1.15**	**$10.74**
							33%	7%	61%

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[15] Transaction levy funds. Matching government funds included under “Governments”

[16] Includes Federal, State governments and Universities

[17] Possibly an under-estimate

[18] Based on 150,000 cows at $25 pa

6. What mechanisms could be implemented to improve whole-of-chain:
- **Planning**
- **Monitoring**
- **Coordination of effort**

Lead investigator: R Woolaston with support from P Amer

Synopsis

This topic was identified in 2006 as a key issue following extensive industry consultations and a working part was established to formulate recommendations.

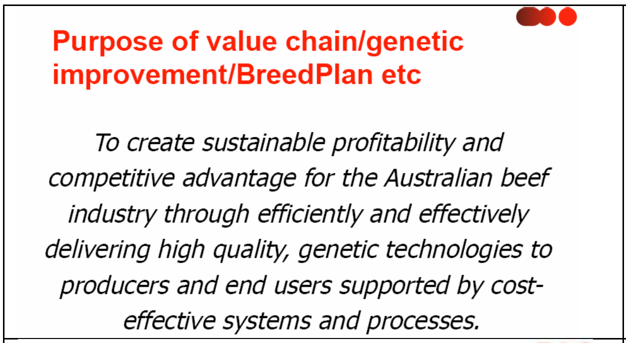
Commercialisation models, lines of communication and accountability for resolving issues and the need for a regular national forum were some matters raised by stakeholders. The working group recommended the formation of a high level body to have oversight of all beef genetic-related activities. The following responsibilities of that body were proposed:
Help shape long-term strategy for beef genetics;
Creating and overseeing implementation of national beef genetics strategic plan;
Debate issues and recommends policy;
Informs industry about decisions on a regular basis, perhaps through an annual forum;
Sets quality standards, and assessed products against these standards."

The preferred structure of the oversight body was not resolved, but suggestions included that it:
- Be constituted as a Board of an incorporated entity with Directors chosen for their skills.
- Be formed by senior representatives of the major entities involved in beef genetics;
- Be responsible for creating and overseeing implementation of national beef genetics strategic plan;
- Debates issues and is entrusted to make policy decisions that are binding through yet to be defined mechanisms;
- Requires a professional chairman with appropriate skills who is appropriately remunerated;
- Sets quality standards, and formally accredits products in relation to these standards.

The current AGBU Consultative Committee, formed after the last round of strategic planning, fulfils some, but not all, of these functions. More recent stakeholder feedback indicates that there is still support for a wider range of responsibilities as described above. The model that was described by the 2006 working group appears to have relatively widespread support, but has not yet been fully implemented. Reconstituting the AGBU Consultative Committee as recommended by the 2006 working group would seem to be the most logical mechanism for achieving the required whole-of-chain planning, monitoring and co-ordination of effort.

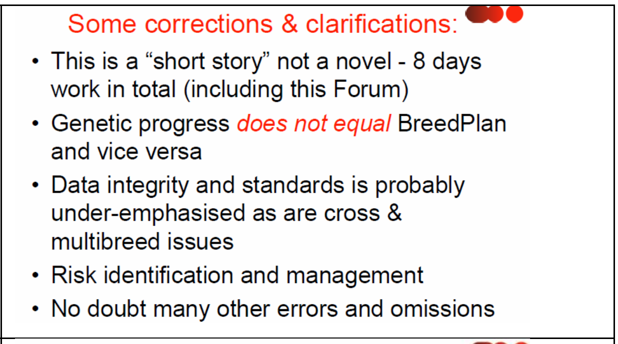
Background

This topic was the focus of one of the several stakeholder working parties formed during the previous round of strategic planning carried out in 2006. These working groups were established following a wider industry workshop which was held after Philip Pogson (of The Leading Partnership) was commissioned to conduct a series of confidential interviews with key stakeholders as a disinterested party. Some his observations remain highly relevant to this strategic question and are repeated here in the form of selected slides taken from his report:



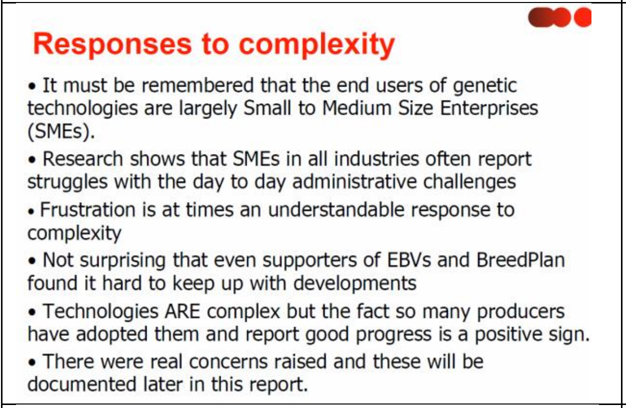
Purpose of value chain/genetic improvement/BreedPlan etc

To create sustainable profitability and competitive advantage for the Australian beef industry through efficiently and effectively delivering high quality, genetic technologies to producers and end users supported by cost-effective systems and processes.



Some corrections & clarifications:

- This is a "short story" not a novel - 8 days work in total (including this Forum)
- Genetic progress *does not equal* BreedPlan and vice versa
- Data integrity and standards is probably under-emphasised as are cross & multibreed issues
- Risk identification and management
- No doubt many other errors and omissions

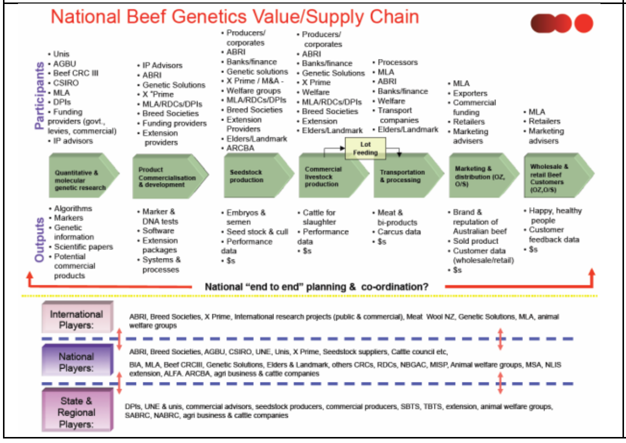


Responses to complexity

- It must be remembered that the end users of genetic technologies are largely Small to Medium Size Enterprises (SMEs).
- Research shows that SMEs in all industries often report struggles with the day to day administrative challenges
- Frustration is at times an understandable response to complexity
- Not surprising that even supporters of EBVs and BreedPlan found it hard to keep up with developments
- Technologies ARE complex but the fact so many producers have adopted them and report good progress is a positive sign.
- There were real concerns raised and these will be documented later in this report.

Technology complexity + value chain complexity + organisational complexity/ multiplicity

- This is not a critique but an observation…
- The purpose of this next slide is to help me to understand, it may also help others…
- There are many organisations in play, some operate at several points in the value chain and across more than one jurisdiction (state & regional, national, international)
- MLA works in partnership across the value chain, it has multiple roles to play
- The risk being that its role and function is not always transparent to all parties – even though its actions are within its charter



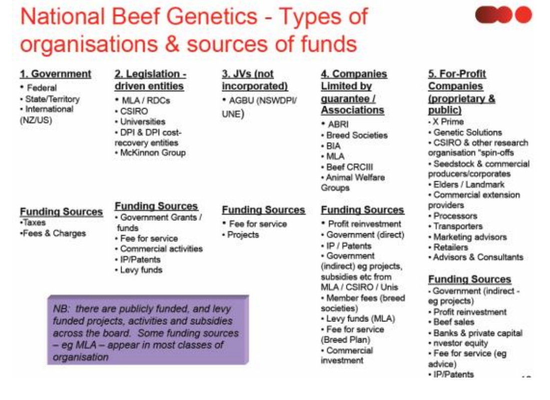
National Beef Genetics Value/Supply Chain

International Players: ABRI, Breed Societies, X Prime, International research projects (public & commercial), Meat Wool NZ, Genetic Solutions, MLA, animal welfare groups

National Players: ABRI, Breed Societies, AGBU, CSIRO, UNE, Unis, X Prime, Seedstock suppliers, Cattle council etc,

BIA, MLA, Beef CRCIII, Genetic Solutions, Elders & Landmark, others CRCs, RDCs, NBGAC, MISP, Animal welfare groups, MSA, NLIS extension, ALFA. ARCBA, agri business & cattle companies

State & Regional Players: DPIs, UNE & unis, commercial advisors, seedstock producers, commercial producers, SBTS, TBTS, extension, animal welfare groups, SABRC, NABRC, agri business & cattle companies



National Beef Genetics - Types of organisations & sources of funds

1. Government
- Federal
- State/Territory
- International (NZ/US)

Funding Sources
- Taxes
- Fees & Charges

2. Legislation - driven entities
- MLA / RDCs
- CSIRO
- Universities
- DPI & DPI cost-recovery entities
- McKinnon Group

Funding Sources
- Government Grants / funds
- Fee for service
- Commercial activities
- IP/Patents
- Levy funds

3. JVs (not incorporated)
- AGBU (NSWDPI/ UNE)

Funding Sources
- Fee for service
- Projects

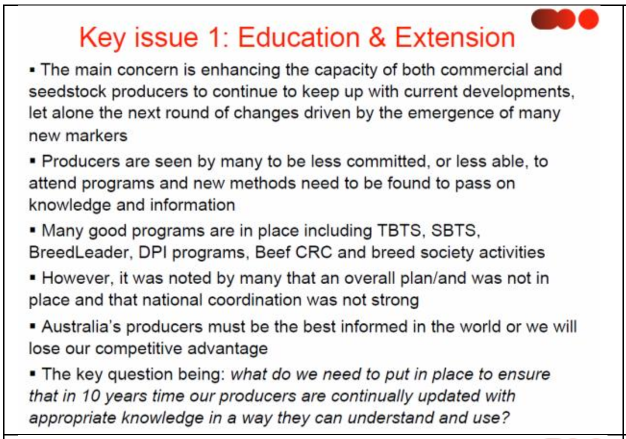
4. Companies Limited by guarantee / Associations
- ABRI
- Breed Societies
- BIA
- MLA
- Beef CRCIII
- Animal Welfare Groups

Funding Sources
- Profit reinvestment
- Government (direct)
- IP / Patents
- Government (indirect) eg projects, subsidies etc from MLA / CSIRO / Unis
- Member fees (breed societies)
- Levy funds (MLA)
- Fee for service (Breed Plan)
- Commercial investment

5. For-Profit Companies (proprietary & public)
- X Prime
- Genetic Solutions
- CSIRO & other research organisation "spin-offs
- Seedstock & commercial producers/corporates
- Elders / Landmark
- Commercial extension providers
- Processors
- Transporters
- Marketing advisors
- Retailers
- Advisors & Consultants

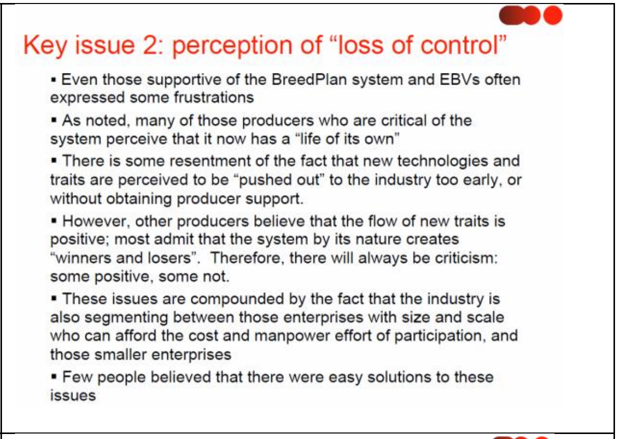
Funding Sources
- Government (indirect - eg projects)
- Profit reinvestment
- Beef sales
- Banks & private capital
- nvestor equity
- Fee for service (eg advice)
- IP/Patents

NB: there are publicly funded, and levy funded projects, activities and subsidies across the board. Some funding sources – eg MLA – appear in most classes of organisation



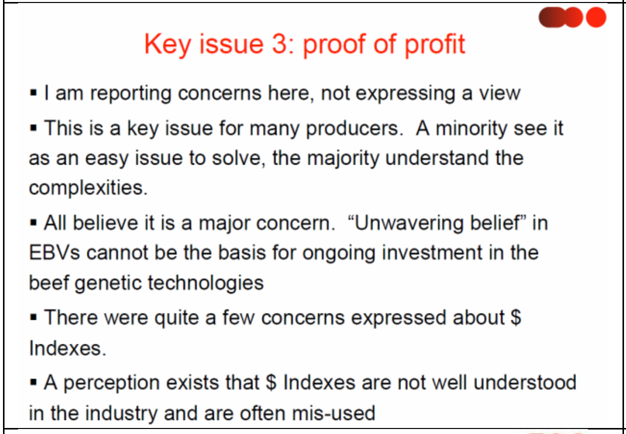
Key issue 1: Education & Extension

- The main concern is enhancing the capacity of both commercial and seedstock producers to continue to keep up with current developments, let alone the next round of changes driven by the emergence of many new markers
- Producers are seen by many to be less committed, or less able, to attend programs and new methods need to be found to pass on knowledge and information
- Many good programs are in place including TBTS, SBTS, BreedLeader, DPI programs, Beef CRC and breed society activities
- However, it was noted by many that an overall plan/and was not in place and that national coordination was not strong
- Australia's producers must be the best informed in the world or we will lose our competitive advantage
- The key question being: *what do we need to put in place to ensure that in 10 years time our producers are continually updated with appropriate knowledge in a way they can understand and use?*



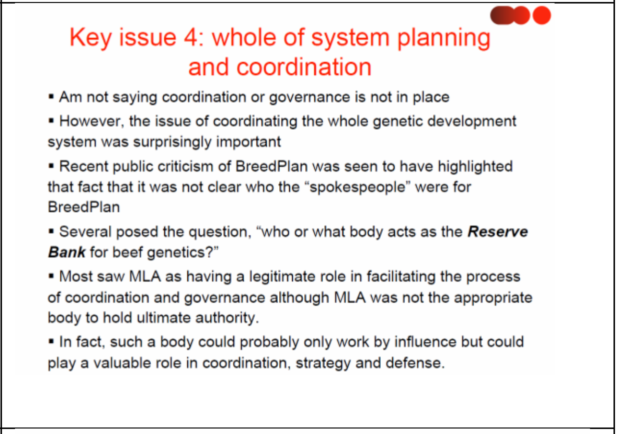
Key issue 2: perception of "loss of control"

- Even those supportive of the BreedPlan system and EBVs often expressed some frustrations
- As noted, many of those producers who are critical of the system perceive that it now has a "life of its own"
- There is some resentment of the fact that new technologies and traits are perceived to be "pushed out" to the industry too early, or without obtaining producer support.
- However, other producers believe that the flow of new traits is positive; most admit that the system by its nature creates "winners and losers". Therefore, there will always be criticism: some positive, some not.
- These issues are compounded by the fact that the industry is also segmenting between those enterprises with size and scale who can afford the cost and manpower effort of participation, and those smaller enterprises
- Few people believed that there were easy solutions to these issues



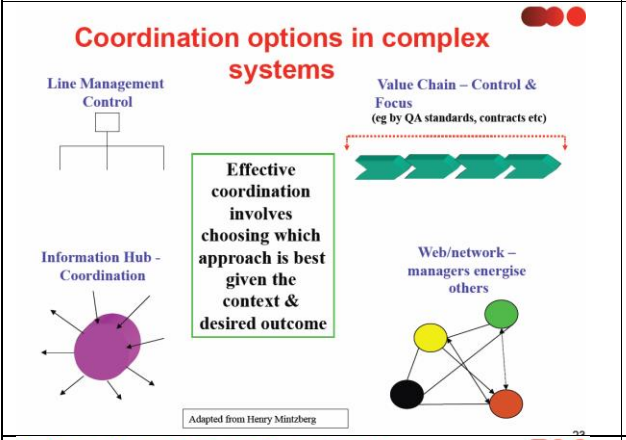
Key issue 3: proof of profit

- I am reporting concerns here, not expressing a view
- This is a key issue for many producers. A minority see it as an easy issue to solve, the majority understand the complexities.
- All believe it is a major concern. "Unwavering belief" in EBVs cannot be the basis for ongoing investment in the beef genetic technologies
- There were quite a few concerns expressed about $ Indexes.
- A perception exists that $ Indexes are not well understood in the industry and are often mis-used



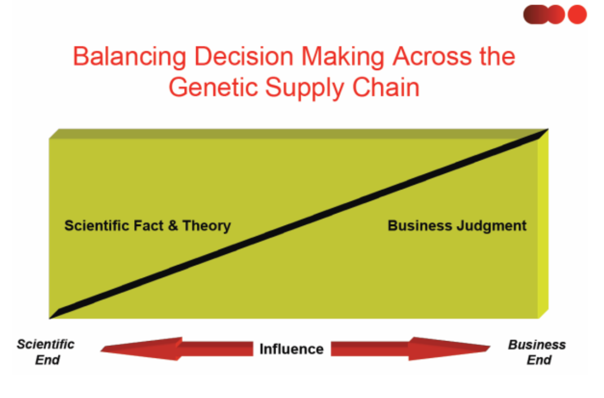
Key issue 4: whole of system planning and coordination

- Am not saying coordination or governance is not in place
- However, the issue of coordinating the whole genetic development system was surprisingly important
- Recent public criticism of BreedPlan was seen to have highlighted that fact that it was not clear who the "spokespeople" were for BreedPlan
- Several posed the question, "who or what body acts as the ***Reserve Bank*** for beef genetics?"
- Most saw MLA as having a legitimate role in facilitating the process of coordination and governance although MLA was not the appropriate body to hold ultimate authority.
- In fact, such a body could probably only work by influence but could play a valuable role in coordination, strategy and defense.



Coordination options in complex systems

Adapted from Henry Mintzberg



Balancing Decision Making Across the Genetic Supply Chain

5. Specific criticisms & concerns

1. How to manage, and who will manage, the integration of gene markers, EBVs and other emerging technologies?
2. How to ensure markers and EBVs are not seen as alternative systems?
3. Encouraging more use of EBVs in Northern Australia
4. Ensuring enough animals – and more animals – are performance recorded
5. Can breeds improve genetically indefinitely?
6. Animals being allocated EBVs derived from their parentage when the producers who own them do not performance record
7. Dealing with the needs of large, corporate producers alongside that of many small herds
8. The need for more people to better understand the whole BreedPlan system (what we have called the value chain) and how it works.
9. Understanding that many of the issues the industry faces are about better technology transfer and more explicit change management
10. Ensuring commercialisation continues to be efficiently and effectively managed – some wanted more competitors to ABRI, others not. The arguments in the negative generally saw the Australian industry as too small to benefit from competitors to ABRI. The arguments in the affirmative wanted more competition and direct access to BreedPlan without going through a Breed Society. "We are essentially dealing with commercialisation issues, the science is good" (a producer)
11. Getting the balance right in EBV calculation between heritage and actual performance. (Several producers expressed concern that at an intuitive level it seemed to them that on balance, too much weight was given to heritage over actual performance).
12. Ensuring more transparency in the system around costs of actual services versus cost of membership of, for example, a breed society.

Key issue #4 identified in the Pogson report directly addresses the question of "whole of chain" planning and coordination, with other slides providing some context.

The working party that was subsequently established to address this specific issue[19] came up with the following recommendations, which remain relevant today:

> In recent years new technologies have emerged that can be used to help improve the accuracy of selection and improve mating decisions. There is a sense that these have not been as well coordinated as they might be in order to secure maximum benefit for industry. Furthermore, DNA technologies are poised to offer breeders a far wider range of choices, most of which will actually complement existing technologies if handled properly. Commercialisation models, lines of communication and accountability for resolving issues and the need for a regular national forum were some matters raised [at a previous meeting of stakeholders]. The working group proposed to address all of these issues by establishing a high level group to have oversight of all beef genetic-related activities (*Beef Breeding Aust Inc).*
>
> The following responsibilities of the "group" were proposed:
> *Help shape long-term strategy for beef genetics;*
> *Creating and overseeing implementation of national beef genetics strategic plan;*
> *Debate issues and recommends policy;*
> *Informs industry about decisions on a regular basis, perhaps through an annual forum;*
> *Sets quality standards, and assessed products against these standards."*

Additional features of the proposed "BBA Inc" are discussed in the working group's full report, extracts of which appear in the box below and the following figure:

> Recommendation: Establish a high level "group" that will have oversight of all beef genetic-related activities (nominally called "Beef Breeding Aust Inc").
>
> Consensus points about the "group":
> - active in shaping long-term strategy for beef genetics;
> - active in creating and overseeing implementation of national beef genetics strategic plan;
> - debates issues and recommends policy;
> - requires resources and clear terms of reference; (MLA a likely source);
> - informs industry about decisions on a regular basis, perhaps through an annual forum;
> - requires an independent chairperson with appropriate skills;
> - requires members with appropriate expertise and industry recognition;
> - sets quality standards, and assessed products against these standards.
>
> Points about the "group" around which clear consensus was not reached:
> - the "group" be constituted as a Board of an incorporated entity;
> - the "group" be constituted of Directors chosen for their skills;
> - the "group" be constituted of senior representatives of the major entities involved in beef genetics;
> - responsible for creating and overseeing implementation of national beef genetics strategic plan;
> - debates issues and is entrusted to make policy decisions that are binding through yet to be defined mechanisms;
> - requires a professional chairman with appropriate skills who is appropriately remunerated;
> - sets quality standards, and formally accredits products in relation to these standards.

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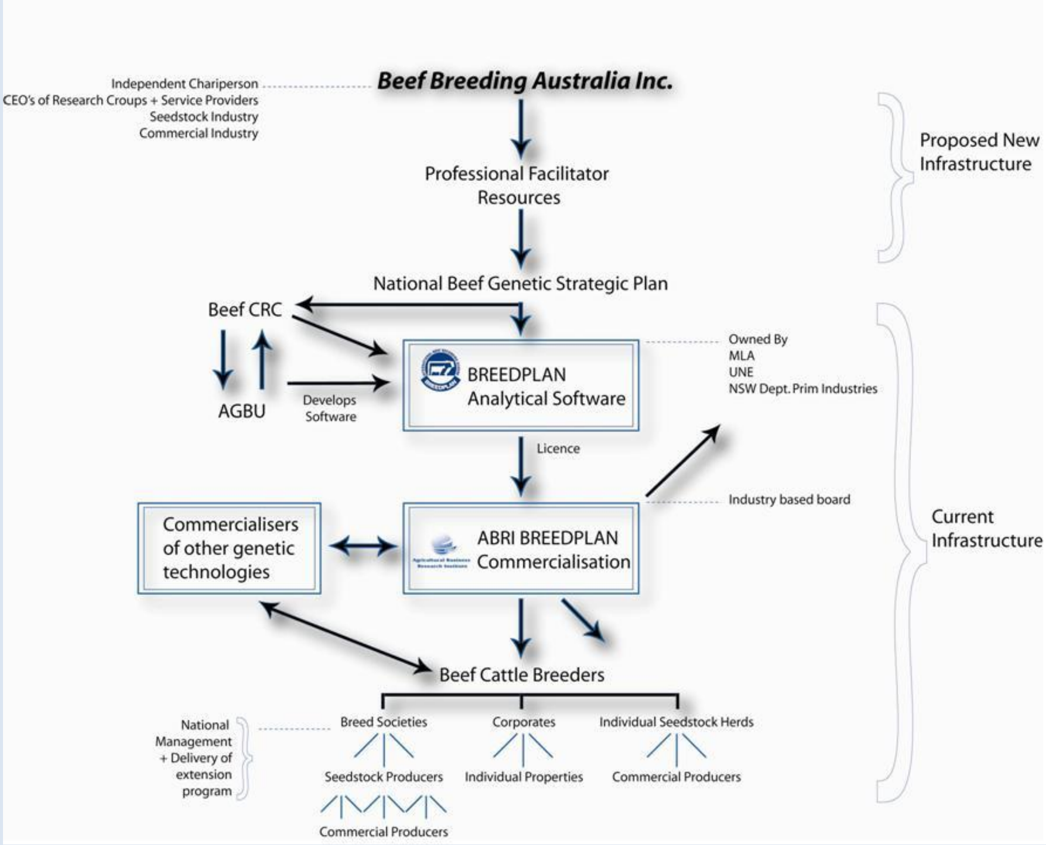
[19] Core members comprised Arthur Rickards, Graeme Mitchell, Graham Truscott, Steve Millard, Mike Stephens, Jason Strong, Greg Harper, Duncan Ferguson.

Supporting members were Jack Allen, Carel Teseling, Jay Hetzel, Alex McDonald, David Falepau, Steve Barwick

Figure 1: Proposed Future Model for Commercialisation of Beef Breeding Technologies



Key elements of the working group's recommendations formed the basis of the fifth strategy of the 2007-2011 Beef Genetics Strategic plan[20]:

5. Improve benefit delivery to producers through better coordination of beef genetic technologies and improved lines of communication and accountability

Key Actions

- MLA to develop the role and focus on a national coordinating entity drawing upon the recommendations of the industry Working Party formed to investigate this issues and further consultations with stakeholders
- Recommendations from the working party suggest this coordinating entity should:
    - be active in shaping long-term strategy for beef genetics;
    - be active in creating and overseeing implementation of national beef genetics strategic plan;
    - debate issues and recommend policy;
    - be resourced by MLA under clear terms of reference
    - inform industry about decisions on a regular basis, perhaps through an annual forum;
    - have an independent chairperson with appropriate skills
    - draw upon members with appropriate expertise and industry recognition;
    - be active in setting quality standards, and assessed products against these standards.
- It is proposed that this group, if established, would be reviewed in 3 years.

The current AGBU Consultative Committee, formed since the 2007-2011 plan was drafted, fulfils some, but not all, of these functions. Feedback received during the "Listening Group" process and the following workshop in July 2011, indicated that there is still support for a wider range of responsibilities as described above.

The model that was described in the 2007-2011 plan has already achieved relatively widespread support, but has not yet been fully implemented. Reconstituting the AGBU Consultative Committee as recommended by the 2006 working group would seem to be the most logical mechanism for achieving the required whole-of-chain planning, monitoring and co-ordination of effort.

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[20] Beef Genetics Strategic Plan 2007-2011, drafted by Philip Pogson (March 2007)

7. What are the rational levels of investment into:

- **Strategic research (> 7 years to implementation)?**
- **Applied research (3-7 years to implementation)?**
- **Extension and delivery (<3 years to implementation)?**

Lead investigator: B Lindner, support from P Amer

Synopsis

The essence of technological progress is a linear pipeline from basic/strategic research to applied research to the discovery of innovations that, if and when adopted, lead to private and/or social benefits.

Basic/strategic research adds to the stock of fundamental knowledge, and in so doing expands the frontier of potential innovations to be discovered by future applied research.
The stock of fundamental knowledge is an indispensable input to applied research, which discovers new innovations, and so adds to the stock of currently available innovations.

Because the link between basic/strategic research and innovation discovery is indirect, the time lag from research to innovation discovery will be longer for basic/strategic research than for applied research, BUT in general the range of innovations enabled by basic/strategic research will be greater than for any particular program of applied research.

Although basic/strategic research might be seen as being more risky in the sense that the dispersion of possible returns from basic/strategic research is greater than for applied research with the same expected value, it is generally accepted by economists that a quasi-government body such as MLA should ignore such uncertainty, and should not discount industry and publicly funded investments for risk so defined.

Even though the research time lags are longer for basic/strategic research, and therefore the consequential benefits from any individual innovation should be discounted more heavily than for applied research, this might be more than offset by the larger number of potential innovations enabled by basic/strategic research. On the other hand, MLA stakeholders may not be able to capture all of the benefits from such broader impacts.

A priori, there are no theoretical grounds for any particular allocation of funding between basic/strategic research and applied research, but some generalisations can be inferred.
With basic/strategic research, but no applied research, no new innovations will be discovered[21], and the “research innovation gap” between the frontier of potential innovations and currently available innovations will expand over time.

With applied research, but no basic/strategic research, the “research innovation gap” will shrink over time, as will returns to applied research.
With both basic/strategic research and applied research, in the long run the former will determine the rate of technological progress, while the latter will determine the size of the “research innovation gap”.

Possible benefits from extension include wider uptake of available innovations, and/or faster diffusion, as well as lower transactions costs from making fewer wrong adoption decisions.

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[21] Except by serendipity.

In the long term, extension will at best shrink the extension innovation gap between currently available innovations and currently used innovations, but will not impact on the long run rate of technological progress.

While decisions about rational levels of investment in basic/strategic research and applied research might be aided by the following guidelines, ultimately they have to be based on subjective judgements informed by available evidence.

- Greater investment in basic/strategic research could be warranted if the long run rate of technological progress is judged to be too slow.
- Greater investment in applied research could be warranted if the long run research innovation gap is judged to be too long.
- Greater investment in extension could be warranted if the long run extension innovation gap is judged to be too long.

In practice, if total beef genetics RDE funding is fixed, the problem is more complicated because any increase in funding for one component of the of the RDE budget needs to be at the expense of one or both of the other components.

With respect to the specific case of rational levels of investment in genomics, there are additional pertinent issues to consider.

There has been a dramatic expansion in the frontier of potential livestock genetic innovations in recent years due to the enormous investment in human genomics.

The main impact to date seems to have been to lengthen the research innovation gap.

The case for government or industry to fund further basic genomics research seems weak.
One response could be to reallocate funds from basic genomics research to applied genomics research in an attempt to increase the pool of available livestock specific genetic innovations.

On the other hand, it might be prudent to defer any increased investment in applied genomics research until the effective cost of applied research declines to a fraction of current levels. Alternatively, industry could rely on the private sector to discover and market additional “adoption ready” genetic innovations, even if this resulted in sub-optimal levels of investment in applied research, and sub-optimal utilisation of available innovations, as well as inhibiting future innovation discovery due to enabling knowledge not being shared.

The alternative to attempting to predetermine rational aggregate levels of investment in basic/strategic research, applied research, and extension, is to continue to identify MLA’s priorities, and judge each RDE proposal on its perceived merits.

Literature Review

There are many different definitions of strategic research, applied research, and extension. For instance, ABS (1993) defines the following research categories:

- Pure basic research: Experimental and theoretical work undertaken to acquire new knowledge without looking for long term benefits other than the advancement of knowledge.
- Strategic basic research: Experimental and theoretical work undertaken to acquire new knowledge directed into specified broad areas in the expectation of practical discoveries. It provides the broad base of knowledge necessary for the solution of recognised practical problems.
- Applied research: Original work undertaken primarily to acquire new knowledge with a specific application in view. It is undertaken either to determine possible uses for the findings of basic research or to determine new ways of achieving some specific and predetermined objectives

MLA does not fund pure basic research in the above sense, but it does fund strategic basic research (hereafter commonly referred to as basic/strategic research) as well as applied research. In addition, MLA also funds extension and delivery activities (hereafter extension), which can be defined as:

- Extension is undertaken to facilitate and accelerate the dissemination and uptake of existing knowledge and innovations developed from applied research, with the aim of producing new or enhanced products or policies, or installing new or enhanced processes.

For reasons to be discussed below, most such classifications of research and development are not especially helpful in addressing the question of how much of the investment in beef genetics and genomics RDE should be allocated to strategic research vis-a-vis applied research vis-a-vis extension. In the early literature, strategic research, applied research, and extension were conceived as a linear pipeline[22] that produces knowledge or information of decreasing generality and increasing direct applicability in the immediate future. In his discussion of the research pipeline, Nelson (1959 pp.300-301) observes that in moving along a continuous spectrum of scientific activity from the applied-science end to the basic-science end, the degree of uncertainty about the results increases, and the goals become less clearly defined and less closely tied to specific practical outcomes. The essence of the nature of the link between basic and applied research is spelt out as follows:

> "Applied research is relatively unlikely to result in significant breakthroughs in scientific knowledge save by accident, for, if scientific breakthroughs are needed before a practical problem can be solved, ... applied research will not be undertaken".

More recently, some polemical publications[23], using definitions of basic and applied research without regard to the purpose to be served by the distinction, have attacked the pipeline model on the grounds that the nature of the linkages between the stages of the pipeline are not always uni-directional, and at times may be bi-dimensional, or even multi- dimensional.

All research is intrinsically uncertain, so ex ante, some anticipated outcomes will not be realised. Similarly, some realised outcomes might be serendipitous, in the sense that ex ante, they were not anticipated. This suggests that for any consideration of rational levels of investment across the RDE spectrum, the most meaningful distinction between strategic research and applied research is the scope, ex ante, of anticipated outputs. Anticipated outputs from strategic research are

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[22] According to Pannell (1999), the linear or `pipeline' model in which the impact of basic research flows in a sequence to applied research, then technology, and finally to economic productivity, was first articulated by Francis Bacon in 1605. Sir Isaac Newton expressed much the same notion in his letter to Robert Hooke (15 February 1676) "If I have been able to see further, it was only because I stood on the shoulders of giants."

[23] For example, see Brooks (1994), Garrett-Jones et al. (1995), Pavitt (1991), Rosenberg (1982), Rosenberg (1990), Rosenberg (1991).

predominantly new knowledge that contributes to the intellectual foundations for further research, and with the potential to lower the cost of applied research. Such research is not anticipated to produce new or improved processes or products that are “adoption ready”. Conversely, anticipated outputs from applied research are predominantly inventions comprising new and novel products, processes or policies that are more or less “adoption ready”, and will have some utility if and when adopted.

Because the crucial link between basic/strategic research and innovation discovery is indirect, one corollary is that the anticipated time lag from initiation of research to eventual realisation of any outcomes will be longer for strategic research than for applied research because the lag for the latter excludes the duration of the strategic research project plus the time until knowledge outputs become inputs to applied research. Non-economists often do not appreciate that research time lags can be extremely long. Studies in the United States and United Kingdom for aggregate agricultural research have found that total lags of 30 years or more are not uncommon (Pannell 1999, p.96).

Another corollary is that the scope of eventual beneficial outcomes anticipated from strategic research is likely to be wider than for applied research because strategic research enables the discovery of a more diverse set of innovations than applied research. Thus, the negative impact of a longer time lag might be offset by the broader scope of inventions made possible by strategic research.

Because the degree of dispersion of the probability distribution of possible returns from strategic research is greater than for applied research with the same expected value, in this sense strategic research involves greater uncertainty, or is more risky, than applied research. In other words, the variance of the probability distribution of possible returns from strategic research is greater than for applied research with the same expected value. Whether this should influence funding decisions by the MLA is moot. As Arrow and Lind (1970) note, risk matters to individuals, and it is widely accepted that most individuals will value an asset with uncertain returns at less than its expected return. It follows that the greater the dispersion of potential returns, the greater will be the discount for risk. In economics, such behaviour is referred to as risk aversion.

However, they also argue that governments should not discount public investments for risk. More specifically, they should ignore uncertainty, and behave as if they are indifferent to risk in the above sense. Essentially, Arrow and Lind argue that governments can better cope with uncertainty than can private investors, in part because it invests in a greater number of diverse projects with uncorrelated returns, and so is able to pool risks to a much greater extent than private investors, and in part because it has such diverse sources of funding. In many respects, the MLA is a quasi-government body with a diverse investment portfolio and diverse sources of funding, so many economists would argue that the MLA also should not discount for risk in allocating funding between the components of RDE.

If this is accepted, then the “risk free” interest rate is the appropriate discount rate to apply when calculating the present value of investments with different research time lags. While there is still some debate amongst economists on both theoretical and empirical grounds about the appropriate risk free rate to apply in practice, there is widespread agreement that the correct rate is somewhere in the range from 5% to 7%.
As noted above, the time lag from research to innovation discovery will be longer for basic/strategic research than for applied research, and the following table illustrates the drastic decline in the present value of research returns as the time lag from research to realisation of first benefits lengthens.

		Time lag to first benefits (yrs)						
	discount rate	0	5	10	15	20	25	30
PV as % of FV of research returns	5%	100%	78%	61%	48%	38%	30%	23%
	7%	100%	71%	51%	36%	26%	18%	13%

Also as noted above, in general the range of innovations enabled by basic/strategic research will be greater than for any particular program of applied research. This is a two edged sword. On the one hand, it is conceivable that this greater number of potential innovations will compensate for discounting more distant potential returns from individual innovations more heavily than more proximate returns from applied research. On the other hand, MLA stakeholders may not be able to capture most, let alone all of the benefits from such broader impacts. Clearly, this should be a key consideration in the evaluation by MLA of proposals for basic/strategic research.

While there are no theoretical grounds a priori, for any particular allocation of funding between basic/strategic research and applied research, the key rationale why a body such as the MLA should fund at least some strategic research derives from its role as one of the principal determinants of the cost of achieving the goals of applied research. This fundamental insight has been pivotal to a number of seminal studies, such as Evenson and Kislev (1976), Huffman and Evenson (1993), and Alston, Norton and Pardey (1995).

In the pipeline model, any backward linkages are inconsequential. This is not to deny that at times, basic research can discover inventions directly, nor that applied research can add to basic knowledge and enhance the productivity of basic research; but by and large, these are exceptions that tend to prove the rule. In any case, they are a distraction in any analysis of the appropriate mix of strategic research, applied research, and extension, and Occam's razor has been applied to excise such considerations from the conceptual framework developed below.

It has been widely observed that in a technologically dynamic economy, there will be a “technology gap” between the best-practice level of technology in use at any given time, and the best-practice level of technology that would prevail if technological diffusion of new innovations was instantaneous.[24] Such a gap between utilised innovations and available innovations will be referred to below as the “extension innovation gap” to distinguish it from the “research innovation gap”. The latter is defined as the gap between currently available innovations, and potential frontier innovations that could be discovered by applied research given the stock of knowledge or body of techniques currently available to innovators.

In a paper on the role of education on technological diffusion, Nelson and Phelps (1966) posited that, in steady state equilibrium, utilised innovations and available innovations will grow at the same rate, while the size of the extension innovation gap will be determined by the level of education. Since both education and extension have the potential to accelerate the rate of diffusion of innovations, both can be expected to shorten the extension innovation gap, but not alter the long run rate of technological progress.

Subsequently, Evenson and Kislev (1976) formalised the concept of a linear pipeline between basic research and applied research in a mathematical model. Applied research was viewed as a search to discover new superior technologies from a given distribution of potential technologies, while basic research shifts the distribution searched. Hence, productivity of applied research effort is a function of the “research innovation gap” between the best innovations currently in practice, and the

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[24] For instance, see Nelson and Phelps (1966).

"research innovation frontier"[25], which is determined by the stock of knowledge from basic research. Without basic research, over time there will be diminishing returns to further applied research, because the innovation gap will asymptotically approach a stationary innovation frontier. Eventually, it will prove too costly to achieve further progress by applied research, which will cease. However, with constant rates of basic and applied research, a steady state will emerge in which the rate of progress of the research innovation frontier is determined by the rate of basic research, and the research innovation gap is determined by the rate of applied research.

In this theoretical framework, the optimal steady state levels of funding strategic research, applied research, and extension could be solved analytically if all of the required information about research productivity, costs, etc., were available, and if the total RDE budget was unconstrained so that each component of the RDE budget could be varied independently of the other components. Clearly, this is not practicable. At best, the above conceptual framework can be used to provide guidance to specialist professionals best placed to provide advice about the allocation of funding between the various RDE components. Such professionals need to knowledgeable about current use and availability of innovations from the beef cattle genetic improvement RDE system, about the science of beef genetics and genomics and potential future innovations, and about the cattle industry generally.

For instance, in a steady state, the greater the investment in extension, the shorter will be the extension innovation gap, ceteris paribus. Hence, subjective judgements about whether the level of investment in extension was optimal or not could be based on an assessment of the benefits of speedier diffusion of innovations relative to the costs of achieving this outcome by extra investment in extension. While this might sound relatively straightforward, inter alia it requires judgements to be made not only about the extent of current use of genetic innovations, but also about available genetic innovations that are currently unused, but which beef producers would adopt if they were better informed. There is a significant body of literature documenting a widespread tendency to over-estimate the latter measure[26], at least in part due to a failure to comprehend that the potential adopter's best self-interest is much broader than just net financial returns. Consequently, many supposedly beneficial innovations are never adopted.

Likewise, the greater the level of investment in applied research, the smaller will be the steady state research innovation gap. In this case, the principal benefit from a shorter research innovation gap is that new innovations will become available sooner once their "discovery" is enabled by new knowledge that is the output from strategic research. Again, the optimal level of applied research will the level that balances such benefits against the costs of applied research necessary to discover inventions quicker. If assessing the extent of available genetic innovations is difficult, then making judgements about the scope of the genetic innovations frontier enabled by the current state of scientific knowledge is many-fold more difficult.

Last, ceteris paribus, the greater the investment in strategic research, the faster will be the overall rate of technological progress once a steady state is achieved. Arguably, the hardest question of all to answer is whether the current rate of technological progress is too fast, or too slow,. The fact that almost all returns to research studies find very high rates of return to investment might suggest that the rate of technological progress is too slow due to under-investment in strategic research. On the other hand, stakeholders who are beneficiaries of beef genetics RDE seem reluctant to fund further increases in the RDE budget.

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[25] That is, the best potential technology in the distribution being searched.

[26] See Lindner (1987) for some references to this literature.

Furthermore, if total beef genetics RDE funding tends to be fixed exogenously in practice, the rational allocation problem is more complicated because a funding increase for a component of the of the RDE budget needs to be at the expense of one or both of the other components.

Investment in genomics RDE

With respect to the specific case of rational levels of investment in genomics, there are additional pertinent issues to consider.

It is widely believed that the enormous investment in human genomics and proteomics research in recent years has enabled a dramatic expansion in the frontier of potential livestock genetic innovations. However, by and large, the main impact to date seems to have been to lengthen the research innovation gap, rather than to increase the rate of discovery of available “adoption ready” genetic innovations. At least in the short run, the case for government or industry to fund further strategic genomics research seems weak, even if it is livestock oriented[27].

One response could be to reallocate industry and/or taxpayer funds from fundamental genomics research to applied and focussed genomics research in an attempt to increase the pool of available livestock specific innovations. On the other hand, given that further human oriented basic genomics research will almost certainly continue to drive down the effective cost of applied research to a fraction of current levels, and so stimulate faster innovation discovery, it might be prudent to defer any increased investment in applied research. At some stage, a critical judgement then will need to be made as to when the technology is close enough to application to warrant an increase in livestock-specific applied research. This assumes there is enough information in the public domain to make such a decision.

Given that many inventions derived from genomic research are patentable, an alternative response could be to allow the private sector to fund more such research, and to discover and market additional “adoption ready” genetic innovations. If the private sector does fund such applied research, the level of investment and consequential innovation discovery will be sub-optimal because a private investor will be unable to appropriate all of the potential gains. This is due to the fact that the price charged by private firms to use these innovations will exceed the social opportunity cost of additional uptake, and so deter some potential adopters from adopting the innovation. A related problem is that producers who do adopt such innovations as are discovered will under-utilise them for essentially the same reason. A further problem is that private firms often are unwilling to share key enabling knowledge with other scientists, which can inhibit future innovation discovery and the rate of technological progress.

Conclusion

To sum up, this is a very vexed problem that is not amenable to definitive solutions based on statistical analysis of empirical evidence, nor on mathematical solutions to elegant theoretical models. At best, a conceptual framework such as that outlined above might assist knowledgeable individuals to provide advice about the direction of any funding reallocation based on subjective judgements about the likely divergence between the current situation and a fuzzy view of more desirable arrangements.

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[27] Apart perhaps from some limited basic/strategic research tightly targeted to overcoming knowledge gaps that are blocking the discovery of new beef genetic innovations by applied research. Furthermore, the extent to which MLA stakeholders can capture the benefits from the likely broader impacts of basic/strategic research should be a key consideration in the evaluation by MLA of such proposals.

The alternative to attempting to predetermine rational aggregate levels of investment in basic/strategic research, applied research, and extension, is to continue to identify MLA's priorities, and judge each RDE proposal on its perceived merits.

Possible future work

- An assessment of the current rate of beef genetic technological progress, and whether it is too slow.
- An assessment of the current beef genetic research innovation gap, and whether it is too long.
- An assessment of the current beef genetic extension innovation gap, and whether it is too long.
- Ex post impact assessment of recent MLA investments in beef genetics applied research.
- Ex post impact assessment of recent MLA investments in beef genetics extension.
- What beef phenotypes, if any, should be given priority for investment in beef genetics RDE?
- Should specific breeds, and breeders within breeds, be targeted in some way?

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Synopsis

Historically, most plant breeding for Australia’s grains industry was performed by public sector RD&E providers.

To the extent that they existed, seed royalties did not include any charge to cover the costs of the breeding program and the intellectual capital embodied in the new varieties.

Most growers chose to minimise the purchase of such seed, and to multiply it themselves by growing “farmer saved seed” to plant subsequent crops.

Private “for profit” companies were not interested in entering the plant breeding business.

In response to scientific developments and changes in the legal framework for intellectual property rights, there is a growing trend to privatisation of plant breeding.

For many major crops, such as wheat and canola, breeding has changed from a mainly public system to a system dominated by private plant breeding companies. For many minor crops, such as lupins, there is still virtually no private sector involvement in plant breeding, and little evidence of any commercial interest in future investment.

Private plant breeding companies contribute little if anything to the cost of pre-breeding research that underpins continued genetic improvement in crop varieties.

Incentives to create plant biotechnologies mushroomed following the extension to the scope of patent law to include living organisms, and many new enabling plant breeding technologies are now routinely protected by patents.

For special cases such as hybrid corn, strong genetic copy protection enabled plant breeders to capture much of the value from other superior traits, as well as from heterosis.
For many broadacre crops, the key driver of privatisation of plant breeding has been the evolution of plant breeders’ rights (PBR).

PBR grants monopoly power to plant breeders over certain uses of crop varieties, but the so called farmer saved seed exemption is a crucial limitation on these rights. This exemption permits farmers to continue the common practice of saving seed at harvest without payment to the plant breeder, and greatly restricts the ability of plant breeders to appropriate varietal value created by plant breeding.

EPRs are now the most prevalent method used by breeding programs in Australia, and particularly by wheat breeders, to recoup value from growers of PBR crop varieties. EPR is based on grain production rather than on seed sales; and is a payment made to the owner/s of a plant variety by a grower for the right to grow that variety. The EPR system provides a commercial incentive for breeders to develop varieties that meet growers’ real needs, because a variety that does not do so will not be adopted.

It is doubtful whether recent funding sources for plant breeding have any relevance for animal breeding due to several differences between plant and animal breeding.

Most of the granted animal patents have been for gene sequences to use as genetic markers. There are no corresponding intellectual property rights to plant breeders rights for animal breeding.

Literature review – Notes on funding plant breeding RDE in the Australia's grains industry

Historically, most plant breeding for Australia's grains industry was performed by public sector RD&E providers (e.g. state agencies, universities, CSIRO) with coinvestment in national and regional programs by industry funded RDCs (e.g. Grains Research and Development Corporation (GRDC) and its precursors). The supporting pre-breeding research in agronomy, plant pathology, entomology, biometry, plant nutrition, plant physiology, and other cognate disciplines also was publicly financed.

Typically, the seed of new varieties from breeding programs was released to particular growers for seed bulk up. Either no seed royalty was charged for this seed, or at most a nominal price was charged that barely covered the cost of producing certified seed. To the extent that they existed, seed royalties did not include any charge to cover the costs of the breeding program and the intellectual capital embodied in the new varieties. Growers purchased seed from seed merchants, again at very low prices that covered little more than the costs of seed multiplication. Effectively, improved varieties were freely released to producers at nominal costs and token seed royalties.

Nevertheless, most growers chose to minimise the purchase of such seed, and to multiply it themselves by growing "farmer saved seed" to plant subsequent crops. Not surprisingly, private "for profit" companies were not interested in entering the plant breeding business.

Since then, plant breeding for crops has been evolving in response to scientific developments, as well as to changes in the legal framework for intellectual property rights, and to consequential economic forces. In particular, there is a growing trend to privatisation of plant breeding for several broadacre crops. For many of the minor crops though, such as lupins, there is still virtually no private sector involvement in plant breeding, and little evidence of any commercial interest in future investment. On the other hand, for many major crops, with wheat and canola being two of the more notable some examples, breeding has changed from a mainly public system to a system dominated by private plant breeding companies.

In Australia, the outcome for wheat breeding has been a transition from as many as eight prior and mainly state-based and focussed breeding programs operated and funded primarily by governments with support from collective industry funding; to three large national wheat breeding companies, and one small company. All four are incorporated "for profit" private companies, and all are part owned by large international plant breeding and seed companies, as follows.

- Australian Grain Technologies Pty Ltd (AGT). Shareholders are:
  Grains Research and Development Corporation (GRDC), the South Australian Research and Development Institute (SARDI), the University Adelaide (UA), and Vilmorin & Cie [subsidiary of Limagrain Holdings].
- Longreach Plant Breeders Pty Ltd. Shareholders are:
  AWB Limited and Syngenta Seeds.
- Intergrain Pty Ltd. Shareholders are:
  the Grains Research and Development Corporation (GRDC), Western Australian Agriculture Authority (WAAA), and Monsanto.
- HRZ Wheats. Shareholders are:
  CSIRO, NZ Plant and Food Research, GRDC, and Dow Agrosciences.

These companies aim to rapidly develop and deliver varieties with improved characteristics to Australian grain growers. They compete for market share and rely on income from the sale of new varieties to fund their breeding activities, but they contribute little if anything to the cost of pre-breeding research that underpins continued genetic improvement in crop varieties. So today, almost all wheat breeding is a commercial business, and GRDC no longer invests grower levies directly in wheat breeding projects, and therefore has no ownership in new varieties.

The pre-breeding part of the plant genetics RDE pipeline is still funded almost entirely by GRDC and public sector partners. Out of a total of about $80m of investment, GRDC invests about $22m of levy money on wheat and barley pre-breeding research, with most of the rest coming from public sector sources. GRDC also funds the National Variety Trials (NVT)– a national program of comparative crop variety testing that provides robust, independent results on the performance of recently released crop varieties.

One of the drivers of this privatisation process has been the development of cereal biotechnologies by multi-national bioscience companies, who are now actively looking to partner with entities with germplasm assets to provide a platform to deliver breeding technologies, including GM varieties. The incentives to create plant biotechnologies mushroomed following the extension to the scope of patent law to include living organisms. As a result, many new enabling technologies are routinely protected by patents.

However, new varieties created by plant breeding typically fail to meet the more stringent tests for patent protection. Hence, private plant breeding companies have had to find other ways to appropriate some of the benefits generated from growing improved varieties in order to be profitable. For a few crops such as corn, the development of hybrid technology provided very strong genetic copy protection that enabled plant breeders to charge high prices for seed and thereby capture much of the value from other superior traits, as well as from heterosis per se. Because hybrid vigour declines in subsequent generations of seed harvested from hybrids, “farmer saved seed” does not jeopardise the profitability of breeding for hybrid varieties.

For many broadacre crops though, no such biologically based copy protection has been available, so the other key driver of privatisation of plant breeding has been the evolution of plant breeders’ rights (PBR). The objective of PBR is to encourage the development of new varieties by providing plant breeders with an opportunity to obtain a reward for producing a new plant variety. Compared with other IP rights, PBR have a unique set of criteria due to the difficulty of reliably reproducing a plant variety. Dating from the Plant Variety Rights Act (1987) and the subsequent Plant Breeder’s Rights Act (1994), plant breeders were provided with limited monopoly power over certain uses of crop varieties for a term of 20 years. While these monopoly rights are significant, important limitations still remain in the PBR Act as amended in 2002. First among these limitations is the so called farmer saved seed exemption, which permits farmers to continue the common practice of saving seed at harvest without payment to the plant breeder, thereby greatly restricting the ability of the latter to appropriate varietal value created by plant breeding. A second and lesser limitation is the breeder’s exemption, which permits other plant breeders to use protected varieties in their breeding programs in order to breed new varieties. So long as these new varieties are not “essentially derived” from a PBR variety, the rights of the PBR holder are not infringed, and no fee is payable.

In their quest for profitability, private plant breeders have trialled a range of possible methods of charging for new crop varieties, including seed royalties, technology use fees, “end point royalties” (EPR), and “Closed Loop Marketing Agreements” (CLMA), to find viable cost effective ways to appropriate varietal benefits. The traditional method of seed royalties has slowly declined in importance, because farmers who pay for the seed need to only buy small amounts of it, which can then be multiplied and saved to plant future crops. Moreover, the larger the royalty, the less they are willing to buy, so realizable returns to breeders of new varieties have been found to be inadequate for plant breeding to be profitable. The practice of technology use fees seems to be limited to crops where there is a patentable invention embedded on the crop variety, while the use of CLMA has not become widespread, and seems best suited to certain niche situations where quality control by the buyer is important.

An EPR is a payment made to the owner/s of a plant variety for the right to grow that variety. As the name suggests, the EPR is paid on production rather than on seed sales; so it is paid when a grower sells grain produced from that variety. Payment can be based on the volume, quantity or weight of the product sold. Hence, breeders and growers share the risk – but also share in the rewards under an EPR system.

EPRs are now the most prevalent method used by breeding programs in Australia, and particularly by wheat breeders, to recoup value from growers of PBR crop varieties. EPRs now provide a substantial source of revenue that supports breeding activities, although as noted above, pre-breeding RDE continues to rely mainly on public and industry levies.

The EPR system provides a commercial incentive for breeders to develop varieties that meet growers' real needs, because a variety that does not do so will not be adopted, thus sending a strong financial message back to the breeding company. As a result, growers have access to superior varieties faster through streamlined research, and the breeding programs are market-driven, meeting end-user requirements to recoup their investment.

To ensure that the system functions effectively and efficiently, it has been found necessary to take several steps to simplify the system and reduce the costs of EPR administration. First, a consistent, industry-standard, grower license agreement has been developed to streamline and simplify the process for growers, and royalty managers have agreed to use a common Grower EPR Harvest Declaration Form, to be distributed by the National Grower Registry (NGR), from the 2010/11 harvest. Second, a standard commodity agreement with traders for EPR collection has been developed to achieve a nationally consistent process for the role that traders have in EPR collection.

There are two methods used to collect EPRs at present. One is automatic deduction of EPRs by the grain traders purchasing the grain directly from a grower. Automatic deduction of EPR collection is supported by most grain traders in Australia, but depends on the EPR variety being declared at the point of delivery. Grain traders can only deduct EPRs when a variety is correctly identified on grain receival documents. When a grower delivers to a bulk handler for sale to a grain trader, the trader relies on the bulk handler's variety declaration system and the grain trader will deduct the EPR automatically according to variety.

When growers decide either to use their grain on their own farm, or to sell it to businesses not automatically deducting EPRs from their grain payments, royalty managers will invoice growers for outstanding EPRs based on the annual EPR Harvest Declaration Form completed by growers, and on grain purchase data supplied, under agreement, from various grain traders.

It is doubtful whether recent funding sources for plant breeding have any relevance for animal breeding. For a start, there are several differences between plant and animal breeding, including basic differences such as the fact that farm animals produce few progeny per female. This leads to a higher market value of the individual animal; and the prevalence of bilateral exchange based on private property rights. Consequently, the farmer owns the animal and its genetic composition after purchasing semen, embryo or animal, and the price of animals traded for breeding purposes is supposedly determined by their genetic value. Moreover, the main resource for genetic change from animal selection is genetic variation within the animal populations, so there is active international exchange of breeding animals by private-private transactions on the basis that accessing different gene pools in other breeding programmes speeds up the rate of genetic improvement.

Due to the exorbitant cost to date of cloning, and because it has proved commercially impossible to achieve homozygosity by inbreeding, animals used for production, as well as those used for selection in breeding programs, exhibit more or less the same amount of genetic variation.

By contrast, homogeneity is achieved in plant breeding by various methods, such as continuous inbreeding, or by cloning. Such pure lines can then be used to breed (rather than just select) production varieties that are very homogenous. In plant breeding, continuous genetic improvement of crop varieties depends on continuous introgression of new genetic material. To achieve this aim, breeders resort to a wide range of tools, including interspecific crosses, changes in the chromosome sets, accessing the genetic variation in related wild species etc.. Therefore, plant breeding depends on access to and exchange of genetic material and information. Hence, protection of plant varieties resembles patent like principles.

In this sense, less homogenous animal breeds are very different from plant varieties, and in animal breeding, the clearest patentable objects are the molecular genetic findings which can be exploited in selection. Hence, most of the patents that have been granted have been for gene sequences in connection with genetic markers. In New Zealand, a company has claimed a patent on the "Booroola" gene, which regulates the ovulation rate in sheep. While the scope of the patent covers animals that are produced in a breeding programme in which the DNA test has been used, apparently it does not cover those animals that carry the gene naturally. Whether the patent also covers the offspring of the animals that have been tested for the presence of the gene is moot.
It is doubtful whether such patents provide the desired incentives for innovation, research and development in the animal breeding sector, and there are concerns that they inhibit the use of animal genetic resources by researchers, breeders, and farmers.

There are no corresponding intellectual property rights to plant breeders rights for animal breeding. For domestic pets, there are some precedents in animal breeding where the vendor claims to lay down conditions for on-selling of germplasm, but whether such conditions would withstand a legal challenge in the absence of clearly applicable intellectual property rights is not clear.

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(Following slides by P Amer)
Potential funders

- **Innovative/adopting breeders**
- All breeders
    - *Generic*
    - *Those breeders who benefit*
- Industry levy
- Feedlot/Processor level
- Tax payer
- Service provider

Innovative adopting breeders

- Motivations
    - *Faster ΔG = increased bull sales*
    - *Faster ΔG = semen sales/royalties*
    - *intellectual stimulation*
    - *ego*
- Disincentives
    - *Bull sales and royalties not driven just by ΔG*
    - *Risk of technology failure*
    - *Costs and inconvenience*

Innovative adopting breeders

- Ways to pay
    - *Genotyping costs (consumables and labour)*
    - *Profit margins associated with genotyping*
    - *Phenotyping (In kind)*
    - *Payment to participate in a BIN*

Australian Plant Breeding Example

- Legal instrument (PBR) grants monopoly power to plant breeders over certain uses of crop varieties
- Farmer saved seed exemption
- Value of PBR realised based on production of grain, rather than paid per unit of seed
- Big driver of plant based genetic improvement
- Breeder motivated to continue improvement due to farmer saved seed exemption
- Intractable for livestock breeding??

Breeder rights structure??

- Clause in bull sales (NZ Dairy AI)
    - Royalty required if selling sons of bulls
- Likely need “whole of breed” regulation or breeders requiring this would be undercut in the “breeder to breeder” bull and semen markets by others without this requirement
- More revenue to leading breeders = leading breeders prepared to invest more to stay leading breeders

Breed society

- **Motivations**
    - *Breed progression*
    - *Exploit natural competitive advantage from technology (e.g. Small Ne), big*

        market share
    - *Revenue from semen royalties*
- Disincentives
    - *Benefits not shared equally among members*
    - *Politically disruptive*
- Ways to pay (Semen royalties)
    - *Condition of BIN participation is that semen from identified top sires made available for "breed development"*
    - *Society manages the distribution of set number of semen units to breeders*
    - *Royalty collected is split between bull owner and BIN*

Processor/Feedlot

- Motivations
    - More supply
    - More secure supply (viable supply chain)
    - More market options (bad genetics = limited market options)
    - Improved industry profile (aids procurement) for "participating" feedlot/processors
    - Technology integrated into supply chain "locks in" stock – aids procurement

Processor/Feedlot

- Disincentives
    - *Less benefits to individual company unless exclusive involvement*
    - *Highly competitive procurement and sales means profit lost*
- Ways to pay
    - *In-kind collection of phenotypes*
    - *Levy investment*

Service providers

- Motivations
    - *Profit on services and add-on product sales*
    - *Profit on solutions provision?*
- Disincentives
    - *Crowded out by public investment*
    - *Prefer generic services (not population specific predictions)*
    - *Leakage of IP to competitors*
- Ways to pay
    - *In-house development*
    - *Contribution to validation process*
    - *Sharing of historic genotypes and phenotypes*
    - *Intellectual development and critical mass of expertise*

Industry good levy

- Motivation
    - *Most benefits of genetic improvement returned to weaned calf sector*
    - *Comes for free, because of competitive bull market*
- Disincentives
    - *Don't see the benefits (lag, season and price variability)*
- Ways to pay
    - *Levy (% of slaughter value would be the fairest mechanism – but probably not the most practical)*

    - *Does not matter where applied, because costs passed back to weaned calf producers through competition*

Tax-payer

- Motivation
    - *Improved meat quality*
    - *Cheaper meat (unlikely because domestic price set by the export market)*
    - *Reduced GHG emissions*
    - *Rural services (e.g. EU landscape management role of livestock)*
    - *Improved animal welfare*
- Disincentives
    - *60% of beef exported means foreign consumers benefit*
    - *Conflict with farmer objectives (e.g. Low gross GHG emissions = unproductive animals)*
- Ways to pay
    - *Matched funds to levy*
    - *Carbon farming incentives (more efficient animals = lower GHG emissions intensity)*
    - *As consumers through higher prices for better quality meat*

Implications

- Commercial farmers are not contributing enough, relative to their large share of benefits
- Core BIN funding should come from industry levy (Producer or feedlot or processor levy)
- Top ups
    - *Progressive breeders (In Kind)*
    - *Individual feedlots and processors (In Kind)*
    - *Service providers (Deal making required)*
- Facilitation
    - *Extension to reduce market failure (need commercial farmers to be convinced of benefits)*
    - *Breed societies – greater "breed development" role*
    - *Carbon farming – linked to genetic merit*
    - *Payment systems to farmers for meat quality*
        - Supply chain integration (e.g. Supermarket specifies bulls)
        - Measurement technologies on slaughter chain

10. Do current charges for using BREEDPLAN (data addition, evaluation) incentivise performance recording, data quality and/or genetic improvement?

Lead investigator: R Woolaston

The short answer is that it depends on breed – some encourage it through their fee structure, others don't.

The standard BREEDPLAN fee structure is set by the ABRI Board, following recommendations from the IBRS (International Beef Recording Scheme) Sub-Committee.

There are three main components to the BREEDPLAN fees –
a) Membership (of BREEDPLAN as distinct from membership of the breed society)
b) Processing of performance information; and
c) GROUP BREEDPLAN (ie. analytical).

This fee structure is used as the basis for ABRI charges to the breed societies for their BREEDPLAN service. The breed societies then offer the BREEDPLAN service to their members, but all implement different systems for recouping the fees that they are charged by ABRI from their members.

The standard fee structure can be altered at the discretion of ABRI management when negotiating the contract for the provision of the BREEDPLAN service to each breed society. In many cases, ABRI offers reduced rates as a way of subsidising the cost of BREEDPLAN to members of that breed society. In addition, some breeds offer minor discounts for electronic submission of information.

Fees for breed association membership and BREEDPLAN use are summarised in Table 10.1, obtained from publicly-available sources as indicated. The charging models vary according to breed:

- BREEDPLAN costs for **Murray Grey, Shorthorn** and **Charolais** are completely absorbed by the membership and registration charges, so those members who use the service are essentially subsidised by those who don't. These breeds have a small discount for volume (i.e. number of cows registered).
- **Angus**, **Hereford** and **Simmental** breeders are charged a relatively modest additional annual BREEDPLAN membership fee but beyond that, charges are the same irrespective of the number of traits measured. Angus has a discount for number of cows on inventory whereas Hereford and Simmental do not. With these breeds, non-users also subsidise users but not quite to the same extent as Murray Grey and Shorthorn, who do not have separate BREEDPLAN membership charges.
- **Limousin** also charge an annual BREEDPLAN fee, but in addition, charge a per-animal fee for BREEDPLAN use. Limousin has a flat cow inventory fee and BREEDPLAN is slightly more "user-pays" than with Angus and Hereford, but there is no disincentive to submit comprehensively-recorded data.
- Tropical breeds (**Brahman** and **Santa Gertrudis**) direct all BREEDPLAN charges to users, with no obvious cross-subsidisation from non-users and with incremental charges for each additional piece of information submitted.

Essentially the incentives for participation decrease in the above order, with Murray Grey , Shorthorn and Charolais offering the most incentive and tropical breeds providing the most disincentive. Charges obviously take no account of how well the resulting data are used for genetic improvement.

There are four relevant components to data quality:

- Absence of errors
- Proportion of a cohort that is represented in the dataset
- Number of traits recorded per animal
- Relevance of traits recorded to the breeding objective

Although data integrity is essentially the breeder's responsibility, ABRI implements checks for outlying observations and also extreme EBVs (where an animal's EBVs is more than 2 genetic standard deviations from their mid-parent, there is no EBVs report) and a range of data checks are applied within the BREEDPLAN code. ABRI also conducts routine data checks prior to each GROUP analysis and employs animal science graduates to process performance data so that it can be monitored for quality.

Observations that appear to be outliers with respect to the contemporary group average are flagged in the breeder reports, and if the relevant data are not corrected or verified it may be excluded from subsequent analyses[28]. Thus the incentive to provide error-free data is limited by the breeders' desire to obtain the best possible accuracies for their animals and by the possibility of not having EBVs returned for outlying animals. There is no discount for data found to be error-free.

For most temperate breeds, once cows are registered, submitting complete data from a complete cohort costs no more than submitting part of a cohort, so there is no financial disincentive for measuring all animals, at least from a data-processing perspective. The tropical breeds are charged for every piece of data – the more animals represented in the data they submit for BREEDPLAN analysis, the more it costs and so there is a strong incentive not to report poor-performing animals which will be steers or cull heifers.

With respect to traits recorded, the fee schedules for most temperate breeds do not discriminate between basic and comprehensive trait lists, so the only cost considerations when determining which traits to record, are those incurred on-farm. Again this is not the case for tropical breeds – the more traits submitted, the more it costs.

The incentive to record traits that are relevant to a breeder's objective is driven by the ease of measurement and by the effect of the trait on breeding value accuracies, not BREEDPLAN charges; although tropical breeders may be tempted to substitute less-informative traits for more informative traits that cost more to submit.

Finally, it should be recognised that in order for breed societies to survive, they must have members. There will naturally be a tendency for fee schedules to be structured in such a way that membership levels are not unduly compromised. Adoption of BREEDPLAN among breeders in northern Australia is considerably less than in southern Australia. Hence tropical breed associations may feel that if they were to adopt the charging schedules of temperate breed associations, there would be opposition from many of their non-BREEDPLAN members, leading to a loss of members. Whether this is necessarily a bad thing from the perspective of genetic gain in the national herd is a separate issue. There may be a case for gaining a greater knowledge of the price sensitivity, particularly in northern Australia. If there are relatively few BREEDPLAN users, the total cost would not be great, so if was distributed across all members, the additional cost to non-users may be quite small.

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[28] E.g. http://www.shorthorn.com.au/assets/files/articles/Breedplan_recording_Update_2.pdf

Table 10.1. Charges ($GST incl) for using BREEDPLAN, including society and BREEDPLAN membership fees for the various breed societies.

Breed	Memb-ership	Number of cows					Additional BREEDPLAN charges	Ref
		1-25	26-100	101-200	201-300	>300		
Angus[29]	220	24.20	24.20	17.60	17.60	15.40	$132 Group BREEDPLAN enrolment pa	[30]
Charolais	220	26.40	22.00	17.60	17.60	17.60	No	[31]
Hereford	110	20.90	20.90	20.90	20.90	20.90	$275	[32]
Limousin	187	20.90	20.90	20.90	20.90	20.90	$93.50-$148.50[33]+$4.40 per cow on inventory	[34]
Murray Grey	330	26.40	26.40	24.20	23.10	23.10	No	[35]
Shorthorn	198	27.50	27.50	26.40	25.30	24.20	No	[36]
Simmental	264	22.00	22.00	22.00	22.00	22.00	$132 membership	[37]
Brahman	220	2.00	2.00	2.00	2.00	2.00	$132 membership $5.69 for Wng wt + 2 later wts $1.41 for each additional wt $2.25 scanning/calf $2.25 carcase/calf $0.57 mature wt/cow $1.13 other traits/calf $5.69 feed intake/animal	[38, 39]
Santa Gertrudis	300						Same as Brahman	[40,41]

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[29] Includes Angus Herd Book register and Red Angus register

[30] http://www.angusaustralia.com.au/asa/AARegulations.pdf

[31] http://www.charolais.com.au/wp-content/uploads/2010/08/Service-Fees-Charges1.pdf

[32] http://www.herefordsaustralia.com.au/images/HAL_Schedule_of_Fees.pdf

[33] BREEDPLAN membership fee depends on the number of cows on inventory, up to 51 cows

[34] http://breedplan.une.edu.au/fees/Limousin%20Fee%20Schedule.pdf

[35] http://www.murraygrey.com.au/pdf/MGBCS_REGS_2011.pdf

[36] http://www.shorthorn.com.au/assets/files/forms/2011_SB_FEE_SCHEDULES.pdf

[37] Membership fees also include a state levy varying between $44 and $100, in addition to the $264 base fee.

[38] http://www.brahman.com.au/animalRegistration.html

[39] http://breedplan.une.edu.au/fees/Brahman%20Fee%20Schedule.pdf

[40] http://www.santagertrudis.com.au/members_fee_schedules.htm

[41] http://breedplan.une.edu.au/fees/Santa%20Fee%20Schedule.pdf

11. Are there simple metrics available for each of these parameters, or could such be developed?

Lead investigator: R Woolaston

Metrics have been developed at AGBU for data quality auditing and to quantify variables lined to rates of genetic progress. Related software has been delivered to ABRI: Data Audit contains a range of checks on data quality; and Takestock is designed to assess at a range of key performance indicators on individual breeding programs. In addition, SBTS/TBTS have developed a herd rating system, which categorises herds on the basis of data completeness, using a five star scale. Herefords Australia has already agreed to adopt the herd rating scheme and will make the information public. The service will also be offered to other breed societies.

Metrics for genetic improvement

TakeStock, originally called "StockTake" [42], was developed to help breeders assess and improve their rates of genetic progress. It derives descriptive statistics for breeds from the National Beef Recording Scheme databases to describe and monitor changes in the basic genetic structure of the breed. It also uses stepwise regression to identify key variables that explain differences in the rate of genetic progress, for a given period, across herds within a breed. Herds are rated for their performance in these variables to provide a benchmark of their breeding program against the average of other herds recorded in the breed.

Johnston & Moore (2005) outlined the variables used in TakeStock:

Variables computed for breed and herds
Genetic progress in period 1 (prior period)
Correlation between sire EBV and number of progeny
Ratio of number of dams per sire
Average EBV of all males, females, steers
Average EBV of sires (weighed number of progeny)
Average EBV of dams (weighed number of progeny)
% of inbred animals
Average % inbreeding of inbred animals
Replacement rates sires and dams
Mean age of sires to breed sires
Mean age of sires to breed dams
Mean age of dams to breed sires
Mean age of dams to breed dams
Number of herds with progeny of common sires
Maximum selection differential of sires
Maximum selection differential of dams

Variables considered for KPI analysis
Correlation between sire and dam EBVs
Herd size

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[42] Johnston, D.J. and Moore, K.L. (2005) *"StockTake" - Genetic audit software for Australian seedstock beef producers.* Proc. Assoc. Advmt. Anim. Breed. Genet. 16: 161-164

Average herd EBV in prior period
Sex ratio of recorded calves
% calves by artificial insemination (AI)
% calves born by embryo transfer (ET)
% males castrated
Selection differential of sires
Selection differential of dams
Selection differential of ET donor cows
Selection differential of sires mated to 2 year old cows
Inbreeding of all animals
Age of dams at first calf
Mean age of sires
Mean age of dams
% sire connectedness of herd (i.e. number of progeny of common sires as a ratio total animals)
Standard deviation of EBV of all animals
Mean square error of birth date for day of the month (i.e. 1-31)
Mean square error of birth day for day of the week (i.e. Mon-Sun)

Metrics for data quality

There are five main aspects to data quality as it relates to genetic improvement:

- Accuracy and depth of pedigree
- Quantity of performance data
- Quality of phenotypic records
- Effectiveness of records
- Quality of genomic information

Pedigree information is clearly important, particularly so for Group Breedplan (across-herd) runs comparisons. Pedigree and birth type errors can frequently be detected by breed societies, particularly for any herds with DNA information available.

A special software package called “Data Audit”, developed by AGBU and delivered to ABRI, is designed to produce a “Quality of Performance Information” score card for individual herds, by trait and by year. The software can scan data files and search for anomalies in distributions, such as deviations from normality, last digit frequency and “jump” records, which refer to the recording precision. It produces a report of these statistics. Although it has been (and is being) used at ABRI, the feasibility of implementing it routinely in BREEDPLAN runs is still under consideration. Nevertheless, BREEDPLAN does contain several other in-built error traps incorporated into its standard data preparation routines, such as the incidence of outlying records.

SBTS/TBTS have developed several other tools to augment DataAudit. One is the capability to produce contemporary group reports for individual breeders, which contain useful statistics on contemporary group size and distributions. They have also developed a Herd Rating System, which categorises herds on the basis of data completeness, using a five star scale. Herefords Australia has already agreed to adopt the herd rating scheme and will make the results public. The service will also be offered to other breed societies. The Herd Rating System currently assesses the proportion of useable data submitted from each year drop (completeness of data), calving spread etc.

Overview of metric options

There are three potential roles of breeder and breed-level metrics and analyses of data as follows:

1. Real time screening software to pick up obvious data errors and stop them from distorting genetic evaluations and other reported information. This can operate in two places:
    a. as data gets loaded on to the database or
    b. between the database and the genetic evaluation process.

In general, the first of these (a) is better because errors get picked up earlier, however, if for some reason they don't get done at (a), they may be deployed at (b).

2. Breeder and bull buyer targeted diagnostics, such as the SBTS/TBTS herd rating system. TakeStock arguably also fits this category as well but probably requires special training for breeders to take full advantage of it.

3. Researcher-targeted diagnostics, such as TakeStock, where researchers and support personnel can get a feel for the good and not-so-good aspects of what breeders are doing. This knowledge could help drive future research direction, (for example there may be both genetic evaluation and breeding scheme design implications), drive the focus for extension activities, and help identify target herds/breeds for new genetic improvement initiatives.

The Researcher-targeted diagnostics could potentially be further updated to include diagnostics that are relevant of genomic selection and targeted breeding initiatives. These could include:

- Calculation of effective population size by year
- Dissection of the breed trend, is genetic superiority imported through foreign or domestic sires, or generated from selection of superior homebred males. This can be done at breed or breeder level.
- A quantification of the dissemination status of the herd (i.e. sum of its genetic contributions through the breed population)
- Relationship profiling, what is the extent of medium distance relationships with other animals and likely accuracy from better prediction of relationships through genomic selection.

12. Are there mechanisms for participation that would incentivise recording, data quality and genetic improvement?

Lead investigator: R Woolaston

In a perfect market, breeders providing top $Index bulls would receive the highest prices, so there would be a natural incentive for them to keep making good progress by recording the most appropriate traits and to provide high quality data. However, the market is not perfect, which greatly dilutes the incentives to invest in good quality and complete records. Furthermore, there are likely to be a certain number of breeders who have built up their clientele through good marketing alone, and who in the short term at least, may be financially better off not informing their clients how well their animals rate on a profit index. It is the job of beef cattle extension services to help remove market imperfections by encouraging bull buyers to make more rational purchases using objective information.

The seedstock market is never likely to be perfect; and even if bull buyers were fully informed, it is quite likely that the optimal level of performance recording from an industry perspective is higher than it is from the perspective of the bull breeding enterprise. Furthermore, from an industry-wide perspective, the marginal value of hard-to-measure traits is likely to be greater in leading herds than it is in lower-ranked herds.

To incentivise high quality recording, the options must obviously revolve around the costs, the rewards, or some combination of the two.

With respect to costs, some breed societies (e.g. Angus Australia[43]) have a flat fee structure so that members who do little or no performance recording effectively subsidise members who do. Others (e.g. Santa Gertrudis[44]) set their charges for using BREEDPLAN according to the number and completeness of records submitted, which could be expected to have the opposite effect. An extreme variation of this, which would probably not be acceptable to the bulk of breed society members, is to actually structure the charges per animal so that they are inversely proportional to the industry value i.e. the more complete the records provided in terms of animals measured and traits covered, the lower the total cost. For this to become a reality, it would probably require external subsidies to be provided e.g. from producer levies, in conjunction with an objective method of determining the value of performance records to the industry as a whole.

Another way of inducing producers to submit complete records is to offer a more comprehensive data management system, such as that offered by the American Hereford Association's Total Performance Records scheme[45]. It is designed to provide the producer with a more complete picture of their herd's performance over time, as well as annual cow production summaries. This information could potentially be used to aid management decisions, in addition to providing a form of data certification.

Incentives might also take the form of subsidised genotyping in exchange for the provision of high-value records. This could lead to what would be essentially a dispersed beef information nucleus.

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[43] http://www.angusaustralia.com.au/asa/AARegulations.pdf
[44] http://www.santagertrudis.com.au/members_fee_schedules.htm
[45] http://www.hereford.org/seedstock/whole-herd-tpr-0

It would also be helpful if there was better information available to breeders on the relationship between their recording program and the expected rate of genetic gain. Work along these lines is included in the current MLA contract with ABGU for sheep (MLA project B.SGN.0127), where it is planned to use a deterministic model to evaluate breeding costs, population structure and parameters and breeding objectives to quantify the benefit of any additional trait measured. Benefit/cost analyses of this nature can be used to compare alternative recording schemes within a fixed budget so that returns on investment in recording can be maximised.

Finally, the questions of data quality and incentives were actually the focus of a working group formed during 2006 to provide input into formulation of MLA's 2006-2011 beef genetics strategic plan. Although the working group's recommendations were not adopted in full, there has been some subsequent progress in establishing data quality standards that should inform breeders of their data quality and encourage them, through peer and client pressure, to improve the quality of data submitted. ABRI/SBTS is in the process of establishing a herd rating system based on results of Data Audit analyses. Because of the complexity of including and explaining all of the issues related to data quality the rating will be based on data completeness. The Limousin Society will probably be the first to publish the ranking for each BREEDPLAN member, expected to be before the end of 2011[46].

An extract of the 2006 working group's report follows:

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[46] Alex McDonald, personal communication

Appendix 1. Report of a working group in 2006 established to examine ways in which improvements could be made to the quality of information on which selection decisions are made[47]

Background

GROUP BREEDPLAN has been available to industry since 1985. Breed Societies have been integrally involved in the development of the databases as stud breeders were the vast majority of users and wanted to link Society pedigree databases to performance records.

The development of BREEDPLAN and identification of traits available for analysis have been based on the assumption that breeders would record the information they found useful in their breeding and marketing strategies. That is, the data available across all traits would expand over time. As such, correlated EBVs have been made available to breeders:

- as encouragement to record
- to indicate early trends (particularly where there are unfavourable correlations between traits)
- and as an aid to make early selection decisions

with the expectation that the performance data would follow. To some extent, this has happened. However, there is growing concern that herds that do minimal recording continue to get EBVs for most traits and this may affect the integrity of the analysis for herds doing more extensive recording.

It is also recognised that the “beef industry” has many and varied forms and that outcomes need to allow for this. In particular, Northern and Southern based systems, feedlot and pasture, intensive and extensive, etc. For many issues, one size may not fit all.

1. Herd Data Quality Recording Classification

This issue has been discussed at some length both during the workshop and since. The following discussions have been put to the extended group as the first “action” describes below. Extra comments from the extended group have been included as well.

Group suggestion was to categorise traits into blocks (see Table 1 for example). Using this example:

- Within these, consider a ‘points’ system based on % recorded (eg >90% = 9 points).
- Traits used and points allocated may need to be breed-specific.
- Need to consider 5 public levels say:
    - Performance (absolute basic)
    - Bronze
    - Silver
    - Gold
    - Platinum (virtually complete)
- Use 3 year rolling base eg in 2006 look at 2004, 2003, 2002.

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[47] The purpose of the group’s investigations was to examine ways in which improvements could be made to the quality of information on which selection decisions are made. The initial discussion group comprised: Carel Teseling, Glen Trengove, James Litchfield (Snr), Jack Allen. The extended group included Wayne Upton, Jason Strong, Don Nicol, Ian Locke, James Laurie, Alex McDonald, Greg Popplewell, Mike Stephens, Bryan Corrigan, David Raff

- Use the AGBU 'data audit' software to advise breeders of their 'quality' issues/ranking. It is considered that this may be given to breeders but not necessarily made public (depending on Society and what is developed).
- Some traits/items are 'all or nothing' i.e. they are either done fully or not included. Pedigree would be part of this. Also days-to-calving where less than complete information makes the analysis useless.
- Where herds do not record a trait block (eg bwt), then they can still attain a high status by recording the other traits very well. Using Table 1 as an example, Bronze may be >= 54 points, Silver >= 69 points, etc. Therefore, Gold status could be achieved even if bwt was not recorded; however, unlikely to achieve Platinum without all traits.
- Could be implemented in 2 stages *viz* P/G/S/B/Perf categories and then AGBU data audit at a later stage.
- How confident are we to include new traits (eg DNA markers)?

Table 1. Example points score to achieve various classifications

	Max point	**Perf.**	**Bronze**	**Silver**	**Gold**	**Plat.**
Pedigree (Sire,dam,dob,sex, twin,ET,recip)	10		9	9	9	9
Birth Wt/Calve Ease/Gest length	10		5	7	8	9
Weaning weight	10		5	7	8	9
Post weaning (400 and/or 600)	10		5	7	8	9
Scan (Fat,EMA,IMF if relevant)	10		5	7	8	9
Carcase abattoir (wt,fat,EMA, MS)	10		3	5	6	7
Scrotal (as% of bulls @ 400)	10		5	7	8	9
Matings (for DC) – matings, preg test	10		9	9	9	9
Docility						
Flight time						
IGF/NFI	10		5	7	8	9
DNA Markers	10		3	4	5	6
Total	**100**		**54**	**69**	**73**	**85**

Further discussion highlighted the need to make the system simple for the commercial clients to understand and, if possible, standardised across breeds. There are other systems in place or have been previously discussed (eg LambPlan, American Hereford Association, Alex McDonald's draft, etc) which will undoubtedly be considered in any further discussions in this area.

Restricting the BREEDPLAN analysis to only include herds that had data that meet a minimum requirement was also discussed. This issue is both political as well as technical and requires careful consideration by Breed Societies. Initial across Society discussion of this would be best done at BTLG and then followed up with the various Breed Society Technical committees. However, it was felt that minimum standards would give the commercial sector more faith in the EBVs and be more easily extended to the industry, although managing a changeover would require careful consideration.

Priority: 1
Actions:

- Draft P/G/S/B/Perf guidelines to this group .
- Then circulate guidelines to BTLG for across Society discussions (Feb 2007)
- Societies get feedback from members for final approval
- Encourage AGBU to report draft Data Audit results to BTLG in February.

Resources: Once/if adopted, use Societies, SBTS and TBTS to promote and explain concept.

2. Price Structure

- Difficult issue due to overlay of Breed Society issues with performance recording. Hence discussion is as much political as economic.
- Societies offer a range of services and may also offer discount/subsidies and/or sliding scale of fees.
- Should MLA consider rebates to say Platinum herds with good data quality as they supply the basis of good evaluations. The on-farm costs of collecting quality data is a herd cost, and is a disincentive to quality recording.
- Another MLA funded/supported initiative may be to develop better and robust electronic recording facilities (i.e reduce manual recording costs).
- Societies may consider herd rebates for quality progeny test programs supplying critical data (e.g NFI abattoir carcase etc).
- Favoured price structures for recording is a single overall fee rather than a fee/trait. However, fee structures are generally a Society by Society issue.
- There is a perceived issue of recording fees. Suggest an MLA sponsored facilitator to look at broader options with ARCBA, Societies and larger breeders in an open forum. Aim is to get fresh ideas on pricing that achieves both Society aims (admin, extension, marketing, development, etc) as well as options for performance recording herds.

Priority: 2

Actions:

- discuss in a Forum with a Facilitator with ARCBA and Societies.
- NBRS to consider implementing single fee for “non-corporate” users.

3. Multibreed/Across Breed BREEDPLAN

- Need to define what the actual industry wants and who would use it.
- Industry has different definitions of what this means e.g.
    - EBVs to single/standard base (*viz* +15 in Angus = +15 in Hereford).
    - All breeds and breed crosses in a single analysis with heterosis allowed for.
- Once we have an idea of what industry wants, look at what is required to achieve it and get it costed.
- Then proceed with knowledge and develop and fund an action plan.

Priority : 2

Actions:

- Draft terms of reference for (MLA?) appointed consultant/committee to investigate/review what industry requires and potential benefits.
- Once review findings available, investigate options to achieve this and cost the work and compare to perceived benefits.

4. DNA [Details of the report are omitted because the group's recommendations have largely been overtaken by events. In brief, the recommendations were:
a) Priority 1 – that commercial markers be accredited by an independent committee, now deemed not to be feasible or necessary;
b) Priority 2 – that markers be included in BREEDPLAN, which has essentially been achieved;
c) Priority 2 – that a national DNA database be formed, which has also been achieved; and
d)Priority 4 – that markers used for parent verification should be standardised within Australia]

5. Reportability of EBVs

Which EBVs are displayed and why is seen more as an education/extension issue, as it is just as easily argued that more EBVs be made available as less. While it is recognised that those herds taking more measurements should be rewarded, reportability of EBVs may not be the best approach as an EBV without direct measures may still give useful information to the prospective buyer of the animal. Also, a measured animal may contribute no information to the analysis if it is in a single animal contemporary group.

It is recommended that SBTS/TBTS/etc continue to educate the industry on understanding accuracies and trait indicators.

This item is somewhat linked to item 1 in that herds want to be rewarded for the effort to record and traits recorded. It is likely that industry discussion on either item 1 or this item will include both.

Priority: 5 (re: altering reportability criteria).
1 (re: extension and education).

Actions:

- encourage continued education of industry on EBVs and accuracy through SBTS, TBTS, etc.
- Societies further consider this issue at BTLG

13. Is it possible to compare the economic and technical efficiency of a nucleus-multiplier model for the seedstock sector with the current distribution of herd size, recording accuracy and selection response?

Lead investigators: J van der Werf, P Amer

Notes on pedigree and herd data provided for Breed A.

Peter Amer, AbacusBio Ltd, Updated, 20th October 2011

Multiple (4) indexes provided, but across all animals these were correlated to each other by at least 0.91 and so results here only consider index 1 and index 4. These were the two most different indexes. Indexes 2 and 3 were almost identical to each other in terms of ranking across all animals, and they were intermediate between indexes 1 and 4.

Terminology in these results uses “exporters” to reflect breeders that provide bulls for use by other domestic Australian breeders (the process of dissemination) and “importers” to reflect the breeders that use bulls or semen from bulls bred by other domestic Australian breeders. “Foreign” sources comes from overseas, as opposed to “domestic “ sources of bulls and/or semen.

Figure 1. Average genetic merit (**Index 1**) of animals born in different breeder herds (these breeders have produced the most widely used sires by other Australian breeders) or different countries relative to all other animals (rest). Note that animals born in different countries are a selected subset of all animals born in those countries.

Figure 2. Average genetic merit (Index 4) of animals born in different breeder herds (these breeders have produced the most widely used sires by other Australian breeders) or different countries relative to all other animals (rest). Note that animals born in different countries are a selected subset of all animals born in those countries. Results are effectively weighted average by number of animals.

Notes to Figures 1 and 2.

- Breeders 1 to 7 generate the sires with the most progeny in other herds (i.e. sire breeder different to progeny breeder). These breeders have substantially better merit than the remaining herds. For example, the herd with the most exports is 9 years of genetic trend ahead of the “rest” of the industry for index 1, and 6 years for index 4.
- Breeder 4 is a substantial exporter and ranks below the rest for index 1, but ranks well for index 4. This is strong evidence that there are meaningful variations in breeding strategy and target markets.
- Average breeding values for foreign born animals in the pedigree file is typically higher than the main body of breeders. These will be a highly selected group of foreign born animals, but never the less, they appear to be a significant contributor to genetic progress for Index 1.
- For index 1, the main “exporting” breeders appear to have overtaken the foreign born animals, and the main body of breeders have caught up.
- Foreign born animals still appear to be superior for index 4. Numbers of foreign bulls from recent birth years are very low, as most foreign animals in the pedigree probably reflect older semen producing bulls still resident in the source country.

Figure 3. Origins of sires by year of birth. Outside sires have birth breeder herd code different to calf breeder herd code, while foreign sires are identified as being from overseas in the pedigree file.

Figure 4. Average genetic merit for Index 1 for calves with different origins of sires by year of birth.

Figure 5. Average genetic merit for Index 4 for calves with different origins of sires by year of birth.

Notes to Figures 3, 4 and 5

- Foreign born sires have contributed to between 1/3 and ¼ of calves born over the past 20 years, but with some evidence of a recent decline in this statistic.
- There is again evidence of a convergence between calves of domestic sires versus foreign sires. This convergence in stronger for Index 1 than for Index 4.
- Calves from outside sires have been noticeably better than calves of homebred sires for index 1, although the effect is not as strong as foreign sires, appears to be declining, and is possibly slightly weaker for Index 4.

Figure 6. Cumulative contributions of different countries and some specific Australian herds to the genetic trend in Index 1 based on partitioning of the Mendelian Sampling component of breeding values according to birth country or herd. (The method used is described in Gorjanc, G. Potocnik, K. Garcia-Cortes, L. A., Jakobsen, J., Durr, J. (2011) Partitioning of international genetic trends by origin in Brown Swiss bulls. InterBull open meeting, Stavanger, Norway and based on Garcıa-Cortes et al Animal (2008), 2:6, pp 821–824)

Notes to Figure 6

- Results in Figure 6 suggest that most genetic progress in the Mendelian sampling component of breeding value (superiority of parents over their own parent average) can be traced back to importation of high merit sires from Country A.
- Importation from Countries B and C is also significant, but selection applied within Export Herd 1 has made a greater contribution than imports from countries B and C combined.
- Selection applied within the other Exporting herds (Exporting Herds 2 to 4) has made only a very small contribution, although they have likely played an important role through dissemination via the progeny of imported sires, but without making a lot of selection within these sires for Index 1.
- Exporting Herd 1 appears to have contributed at least one quarter of the total combined and cumulative added value of genetic progress through selection among animals born within Australian herds.

Figure 7. Proportions of calves born in 2010 by import and dissemination status of their birth breeder herd. Dissemination category is defined according to number of calves born in other herds from sires born in the breeder herd over the past year. The higher ranges indicate higher levels of dissemination. Import status identifies herds where more than 50% of calves sires are imported

from other Australian breeders, or where more than 50% of calves sires are from foreign sources, of where more than 50% of calves are from either source, conditional on them not having already been assigned to one of the other two categories.

Figure 8. Average value for index 1 in calves born in 2010 by import and dissemination status of their birth breeder herd.

Figure 9. Average value for index 4 in calves born in 2010 by import and dissemination status of their birth breeder herd.

Notes to Figures 7, 8 and 9.

- More than 50% of calves are born in herds with minimal dissemination, and these herds are the lowest genetic merit for Index 1 and Index 4. The herds that use a high (>50%) proportion of domestic imported bulls are slightly superior to those that use a majority of homebred bulls.
- Herds with a high rate of use of foreign semen tend to be either substantial exporters, or minimal exporters, with few intermediates. Out of these two groups, the exporters are very high in merit for Index 1.
- For the herds with high rates of dissemination, being in the>50% Domestic Importer category does not mean higher genetic merit for either index 1 or 4, relative to being in the >50% homebred breeder category.
- The relationship between dissemination status and index merit appears to be stronger for index 1 than for index 4.

Figure 10. Number of progeny of bulls from a breeder herd born in other herds, relative to breeder herd size. Both axis transformed to a log 10 scale. (i.e. 2=100 and 3 = 1000)

Figure 11. Number of progeny of bulls from a breeder herd born in other herds ("Exports" expressed on Log 10 scale), relative to breeder herd average genetic merit for Index 1 in 2010.

Table 1. Correlations between breeder herd characteristics and numbers of exports

	Non exporters included		Exporters only	
	Normal	Log10 Exports	Normal	Log10 Exports
Herd size	.49	.49	.55	.65
Herd Ave index 1	.18	.14	.31	.38
Herd Ave Index 4	.16	.22	.26	.35

Notes to Figures 10 and 11 and Table 1.

- Index 1 seems to be slightly more important than Index 4 in determining exporters
- Herd size is more related to the extent a herd is an exporter, than the average genetic merit of the herd.
- Higher correlations with Log 10 transformation of number of exports (for the exporter only analysis) indicates that influence of variables on other herds is more exponential than linear. i.e. the effect of index and herd size on number of exports is greater at higher levels of either than at lower levels.
- Relationships are stronger when the analysis is restricted to exporting herds. This suggests that some large and/or high merit herds are either unable to export (no demand) or choose not to export.

Figure 12. Number out of 100 randomly selected 2009 born animals with a medium distance relationship with varying proportions of all animals in year cohorts from 2004 to 2009.

Notes to Figure 12.

- Medium distance relationships involve 3 or 4 meiosis distance separation, corresponding to A matrix coefficients of 0.0625 to 0.125.
- There is only a modest effect of year cohorts. Bars for the 2004 and 2005 cohorts are only modestly higher on the left side of the chart (lower numbers of medium distance relationships).
- Fifty percent of selection candidates drawn from the 2009 cohort have medium distant relationships with 20% or more of all of the animals born within each of the year cohorts considered.
- One third of selection candidates have a medium distance relationship with at least 25% or more of all of the animals born within each of the year cohorts considered.
- If 1000 training animals were genotyped at random from each year cohort for three years, then one half of selection candidates should have a medium distance relationship with at least 1000 x 3 x 50% x 20% = 300 animals.
- The opportunity to have much higher numbers of medium distance relatives genotyped would occur with selective choice of selection candidates and training animals.

Figure 13. Distribution of relatives in the same year cohort by numbers of Meiosis of distance for alternative samples of distantly and more closely related selection candidates. For example, the “Closest 20%” sample constitutes the 20 animals (out of 100) which are most closely related on average with the whole 100.

Notes to Figure 13.

- Most random pairs of animals are between 4 and 6 meiosis differences apart.
- There is a lot of variation in the population in the extent to which an animal is related to all of the other animals.

Figure 14. Average inbreeding trend

Notes to Figure 14.

- Animals with an unknown sire, unknown dam, or unknown year of birth were excluded.
- The importation of animals from the 1970’s until the early 2000’s may have kept a cap on inbreeding.

Table 2. Effective population size estimated from the pedigree using relatedness among samples of animals drawn from various year cohorts.

Year of birth of animals sampled	Estimate of effective population size
1985	379
1990	402
1995	281
2000	192
2005	119
2010	103

The method used to compute effective population size is described by Cervantes et al. 2011. J. Anim. Breed. Genet. 128 (2011) 56–63

Notes on pedigree and herd data provided for Breed B.

Peter Amer, AbacusBio Ltd, 27th October 2011

Only a single index was available for this breed. A relatively modest proportion of animals in the pedigree had an index.

Terminology in these results uses “exporters” to reflect breeders that provide bulls for use by other domestic Australian breeders (the process of dissemination) and “importers” to reflect the breeders that use bulls or semen from bulls bred by other domestic Australian breeders. “Foreign” sources comes from overseas, as opposed to “domestic “ sources of bulls and/or semen.

Figure 1. Average genetic merit (**Index 1**) of animals born in different breeder herds (these breeders have produced the most widely used sires by other Australian breeders) or different countries relative to all other animals (rest). Note that animals born in different countries are a selected subset of all animals born in those countries.

Notes to Figures 1.

- Breeders 1 to 10 generate the sires with the most progeny in other herds (i.e. sire breeder different to progeny breeder). Only some of these breeders have better merit than the remaining herds and there is a substantial amount of spread in average genetic merit across breeders.
- Breeder 1 (the most disseminating breeder) appears to have substantially higher merit than the other exporting breeders, due to a steadily higher rate of genetic progress.
- Breeder 2 (the 2nd most disseminating breeder) has closer to average genetic merit.
- There is only one country supplying bulls, and the genetic merit of the imported animals has remained relatively static and has been overtaken by the genetic trends within Australian herds.

Figure 2. Origins of sires by year of birth. Outside sires have birth breeder herd code different to calf breeder herd code, while foreign sires are identified as being from overseas in the pedigree file.

Figure 3. Average genetic merit for Index 1 for calves with different origins of sires by year of birth.

Notes to Figures 2 and 3

- Foreign born sires have contributed to between 20% and 10% of calves born over the past 20 years, with a steady decline in this statistic.
- Calves with indexes sired by homebred domestic bulls have overtaken the merit of calves with sires from foreign and outside sources.

Figure 4. Cumulative contributions of different countries and some specific Australian herds to the genetic trend in Index 1 based on partitioning of the Mendelian Sampling component of breeding values according to birth country or herd. (The method used is described in Gorjanc, G.

Potocnik, K. Garcia-Cortes, L. A., Jakobsen, J., Durr, J. (2011) Partitioning of international genetic trends by origin in Brown Swiss bulls. InterBull open meeting, Stavanger, Norway and based on Garcıa-Cortes et al Animal (2008), 2:6, pp 821–824)

Notes to Figure 4

- Results in Figure 4 suggest that most genetic progress in the Mendelian sampling component of breeding value (superiority of parents over their own parent average) can be traced back to importation of high merit sires from Country A. The component of genetic trend due to “Other Aust Herds” is substantial as is the component due to Export Herd 1, the herd with the highest level of dissemination.
- The low contribution by many of the other exporting herds might in part be explained by the limited numbers of animals with indexes to be partitioned.

Figure 5. Proportions of calves born in 2010 by import and dissemination status of their birth breeder herd. Dissemination category is defined according to number of calves born in other herds from sires born in the breeder herd over the past year. The higher ranges indicate higher levels of dissemination. Import status identifies herds where more than 50% of calves sires are imported from other Australian breeders, or where more than 50% of calves sires are from foreign sources, of where more than 50% of calves are from either source, conditional on them not having already been assigned to one of the other two categories.

Figure 6. Average value for index 1 in calves born in 2010 by import and dissemination status of their birth breeder herd.

Notes to Figures 5 and 6.

- More than 50% of calves are born in herds with minimal dissemination.
- There are very few herds that use a high (>50%) proportion of imported bulls, these have lower average index, and do not disseminate genes via wider use of sires born in their herds.
- The relationship between dissemination status and index merit appears to be quite weak.

Table 1. Correlations between breeder herd characteristics and numbers of exports

	Non exporters included		Exporters only	
	Normal	Log10 Exports	Normal	Log10 Exports
Herd size	.58	.24	.57	.33
Herd Ave index 1	.21	-.03	.52	.48
Trend Index 1	.11	.02	.24	.25

Notes to Table 1.

- Herd size is as equally important as average genetic merit of the herd when determining the extent to which a herd is an exporter.

Figure 7. Number out of 100 randomly selected 2009 born animals with a medium distance relationship with varying proportions of all animals in year cohorts from 2004 to 2009.

Figure 8. Distribution of relatives in the same year cohort by numbers of Meiosis of distance for alternative samples of distantly and more closely related selection candidates. For example, the “Closest 20%” sample constitutes the 20 animals (out of 100) which are most closely related on average with the whole 100.

Notes to Figures 7 and 8.

- Most random pairs of animals are between 4 and 8 meiosis differences apart.

- There would be minimal opportunity for genomic selection to operate through better prediction of medium distance relationships unless genotyping is highly targeted.

Figure 9. Average inbreeding trend

Notes to Figure 9.

- Animals with an unknown sire, unknown dam, or unknown year of birth were excluded.
- The importation of animals from the 1970's until the mid 1990's may have kept a cap on inbreeding.

Table 2. Effective population size estimated from the pedigree using relatedness among samples of animals drawn from various year cohorts.

Year of birth of animals sampled	Estimate of effective population size
1985	180
1990	356
1995	390
2000	354
2005	381
2010	213

The method used to compute effective population size is described by Cervantes et al. 2011. J. Anim. Breed. Genet. 128 (2011) 56–63

Notes on pedigree and herd data provided for Breed C.

Peter Amer, AbacusBio Ltd, Updated, 27th October 2011

Multiple (4) indexes provided, but across all animals these were correlated to each other by at least 0.96 and so results here only consider index 1.

Terminology in these results uses “exporters” to reflect breeders that provide bulls for use by other domestic Australian breeders (the process of dissemination) and “importers” to reflect the breeders that use bulls or semen from bulls bred by other domestic Australian breeders. “Foreign” sources comes from overseas, as opposed to “domestic “ sources of bulls and/or semen.

Figure 1. Average genetic merit (**Index 1**) of animals born in different breeder herds (these breeders have produced the most widely used sires by other Australian breeders) or different countries relative to all other animals (rest). Note that animals born in different countries are a selected subset of all animals born in those countries.

Notes to Figures 1.

- Breeders 1 to 10 generate the sires with the most progeny in other herds (i.e. sire breeder different to progeny breeder). These breeders tend to have better merit than the remaining herds although there is a substantial amount of spread in average genetic merit across breeders.
- Breeder 6 (the 6th most disseminating breeder) appears to have substantially higher merit than the other exporting breeders, due to a steadily higher rate of genetic progress.
- Average breeding values for foreign born animals in the pedigree file are typically higher than for the main body of breeders. These will be a highly selected group of foreign born animals.
- Foreign born animals still appear to be superior. Numbers of foreign bulls from recent birth years are very low, as most foreign animals in the pedigree probably reflect older semen producing bulls still resident in the source country.

Figure 2. Origins of sires by year of birth. Outside sires have birth breeder herd code different to calf breeder herd code, while foreign sires are identified as being from overseas in the pedigree file.

Figure 3. Average genetic merit for Index 1 for calves with different origins of sires by year of birth.

Notes to Figures 2 and 3

- Foreign born sires have contributed between 17% and 6% of calves born over the past 20 years, with a steady decline in this statistic.
- There is little evidence of a convergence between index 1 merit of calves of domestic sires versus foreign sires. The lag of genetic merit of calves of domestic sires versus calves of imported sires is approximately 2 to 3 years, and is highly variable.
- Calves from outside sires are not noticeably better than calves of homebred sires.

Figure 4. Cumulative contributions of different countries and some specific Australian herds to the genetic trend in Index 1 based on partitioning of the Mendelian Sampling component of breeding values according to birth country or herd. (The method used is described in Gorjanc, G. Potocnik, K. Garcia-Cortes, L. A., Jakobsen, J., Durr, J. (2011) Partitioning of international genetic trends by origin in Brown Swiss bulls. InterBull open meeting, Stavanger, Norway and based on Garcıa-Cortes et al Animal (2008), 2:6, pp 821–824)

Notes to Figure 4

- Results in Figure 4 suggest that most genetic progress in the Mendelian sampling component of breeding value (superiority of parents over their own parent average) can be traced back to importation of high merit sires from Country A and Country C. While the component of genetic trend due to “Other Aust Herds” is substantial, this same contribution was apparent back in 1970, and the value-add since then has been quite modest.
- Export Herds 1 and 4 have made a noticeable contribution to the genetic trend.

Figure 5. Proportions of calves born in 2010 by import and dissemination status of their birth breeder herd. Dissemination category is defined according to number of calves born in other herds from sires born in the breeder herd over the past year. The higher ranges indicate higher levels of dissemination. Import status identifies herds where more than 50% of calves sires are imported from other Australian breeders, or where more than 50% of calves sires are from foreign sources, of where more than 50% of calves are from either source, conditional on them not having already been assigned to one of the other two categories.

Figure 6. Average value for index 1 in calves born in 2010 by import and dissemination status of their birth breeder herd.

Notes to Figures 5 and 6.

- More than 50% of calves are born in herds with minimal dissemination, and these herds are the lowest genetic merit for Index 1, particularly when there is a major reliance on homebred sires. There are very few herds that use a high (>50%) proportion of domestic imported bulls, these have lower average index, and do not disseminate genes via wider use of sires born in their herds.
- The relationship between dissemination status and index merit appears to be quite weak.

Figure 7. Number of progeny of bulls from a breeder herd born in other herds, relative to breeder herd size. Both axis transformed to a log 10 scale. (i.e. 2=100 and 3 = 1000)

Figure 8. Number of progeny of bulls from a breeder herd born in other herds ("Exports" expressed on Log 10 scale), relative to breeder herd average genetic merit for Index 1 in 2010.

Table 1. Correlations between breeder herd characteristics and numbers of exports

	Non exporters included		Exporters only	
	Normal	Log10 Exports	Normal	Log10 Exports
Herd size	.47	.48	.37	.53
Herd Ave index 1	.29	.31	.30	.39

Notes to Figures 10 and 11 and Table 1.

- Herd size is more related to the extent a herd is an exporter, than the average genetic merit of the herd.
- Higher correlations with Log 10 transformation of number of exports (for the exporter only analysis) indicates that influence of variables on other herds is more exponential than linear. i.e. the effect of index and herd size on number of exports is greater at higher levels of either than at lower levels.

Figure 9. Distribution of relatives in the same year cohort by numbers of Meiosis of distance for alternative samples of distantly and more closely related selection candidates. For example, the "Closest 20%" sample constitutes the 20 animals (out of 100) which are most closely related on average with the whole 100.

Notes to Figure 9.

- Most random pairs of animals are between 6 and 8 meiosis differences apart.
- There would be minimal opportunity for genomic selection to operate through better prediction of medium distance relationships without careful structural design.

Figure 10. Average inbreeding trend

Notes to Figure 10.

- Animals with an unknown sire, unknown dam, or unknown year of birth were excluded.
- The importation of animals from the 1970's until the early 2000's and the large effective population size (below) may have kept a cap on inbreeding.

Table 2. Effective population size estimated from the pedigree using relatedness among samples of animals drawn from various year cohorts.

Year of birth of animals sampled	Estimate of effective population size
1985	936
1990	990
1995	884
2000	647
2005	585
2010	462

The method used to compute effective population size is described by Cervantes et al. 2011. J. Anim. Breed. Genet. 128 (2011) 56–63