Final report

Impact assessment of MLA investment in the Genetics program

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Abstract

The net benefits of investment into genetics research, development, and adoption programs must be estimated to produce cost-benefit analyses and evaluate efficacy. Quantifying the economic benefits of genetic improvement is challenging because the economic value of genotypes is not directly measurable. This project sought to develop a methodology and Excel based tools for assessing the net benefits of investments in MLA's genetics programs.

These modelled business as usual and counterfactual scenarios, with assumptions for adoption of registered animals and rate of genetic improvement entered in the model. The net present value benefits of MLA's investments in genetics programs were estimated to be \$348M for the 2016 – 2040 period and \$342M for the 2021 – 2045 period.

Approximately 75% of the benefits were earned in the sheep industry, with the southern and northern cattle industries sharing in 20% and 5% of the benefits, respectively. The Assessment tools can be used for ongoing and routine use by MLA, with reference to the user guide, to quantify net benefits of the genetics program.

Executive summary

Background

The net benefits of investments into genetics programs must be routinely evaluated to benchmark research and development performance against alternatives. In the case of genetics, benefits assessment is difficult because the effect of genotype on farm and supply chain profitability is not directly measurable.

This project sought to develop a methodology for estimating the net benefits of MLA genetics programs and provide initial estimates of net benefits. In doing so, Assessment tools were developed for routine and ongoing use by MLA.

Objectives

The project objectives were:

- To develop and compare methods of benefit estimation for MLA's investments in genetic programs across the grassfed sheep and beef industries.
- To provide a method, process, and recommendations for ongoing, annual benefits estimations and evaluations of the genetics program.
- To estimate net benefits of investments in genetics programs for the periods 2016 – 2040 and 2021 – 2045.

This report addresses each of the objectives by detailing the methodological approaches tested, presenting results from the Genetics Impact Assessment tools developed, and providing a user guide for its use.

Methodology

Three methods for valuing genetic improvement were tested: $Indexes (estimates of animals' genetic potential for profitability), herd modelling (Breedcow & Dynama), and trait-productivity regression analysis. The annual values of genetic improvement were used as inputs in the Assessment tools which modelled business as usual and counterfactual scenarios. Counterfactual assumptions for adoption of registered animals and rate of genetic improvement were entered in the tools.

Results/key findings

The net present value[1] of benefits of MLA's sheep and beef investments in genetics programs were estimated to be $348M for the 2016 – 2040 period and $342M for the 2021-2045 period. For both periods, approximately 75% of the benefits were earned in the sheep industry, with the southern and northern cattle industries sharing in 20% and 5% of the benefits, respectively.

Approximately 33% of the benefits from the $254M benefits from sheep genetics are attributable to clean fleece weight. The remaining two-thirds of benefits are attributable to red meat production traits such as weaning rate, yearling weight, eye muscle depth, and lean meat yield.

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[1] Net present value is calculated over a 25-year period using a discount rate of 5% and a base year of FY23.

The Genetics Impact Assessment tools can be used for routine and ongoing assessments with reference to the user guide provided.

Benefits to industry

The initial estimates of net benefits and development of assessment tools advance the sector by providing a current estimate of net benefits from the genetics program for the red meat sector which can be compared against program costs and used for cost benefit analysis. Further, the Excel tools and the associated user guide can be used for ongoing and routine use by MLA to quantify net benefits of the genetics program.

Future research and recommendations

EBV and $Index databases were critical to this project, as were producer intentions and adoption surveys. Uncertainties for genetic merit, adoption, and lag in genetic merit between the seedstock and commercial sectors could be reduced by genomic recording and development of multi-breed EBVs, depending on how widely the technologies are adopted and applied.

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1. Background

The impacts of all investments made by research and development (R&D) organisations must be regularly evaluated so that performance can be assessed, and resource allocation decisions can be informed. Investment in livestock genetic improvement is critical to industry productivity growth, sustainability, and the ability of meat producers to meet market specifications.

Meat and Livestock Australia (MLA) invests directly in genetics programs through initiatives such as BREEDPLAN, LAMBPLAN, and MERINOSELECT. Separate programs apply to tropical and temperate beef (northern and southern Australia, respectively), merinos, and prime lambs. Furthermore, these investments can be distinguished as technical innovation for genetic improvement itself, and support for the adoption of technical innovation among both seedstock and commercial producers. Both technical innovation and adoption must occur for MLA investments to produce industry benefits.

There is interest and value in quantifying the performance of MLA’s investments in genetics programs. However, the impacts of genetic improvement are not directly measurable or observable and are incremental in nature. It is therefore necessary to develop rigorous estimation methods for the impacts of investments in genetics so that interpretable metrics, such as return on investment and total benefits at the farm gate, can be used to evaluate performance and for comparison with other investment opportunities.

This project sought to develop an impact assessment methodology for the genetics programs that produced a net benefits value estimate for industry segments: northern cattle, southern cattle, and sheep. The assessment tools were developed with the aim of being routinely used by MLA to assess the genetics programs on an ongoing basis.

The immediate net benefits results presented in this report can be used by MLA to benchmark the performance of the genetics program. The results can also inform the relative performance of industry segments in terms of genetic improvement. Additionally, the assessment tool can be used to inform prioritisation of investment. For example, a greater share of investment in commercial adoption may be more desirable in the northern cattle industry compared with merino sheep. Therefore, the assessment tool can be used to produce net benefits results as well as model the impacts of potential investments.

2. Objectives

The project objectives were:

- To develop and compare methods of benefit estimation for MLA’s investments in genetic programs across the grassfed sheep and beef industries.
- To provide a method, process, and recommendations for ongoing, annual benefits estimations and evaluations of the genetics program.
- To estimate net benefits of investments in genetics programs for the periods 2016 – 2045 and 2021 – 2045

This report addresses each of the objectives by detailing the methodological approaches tested, presenting results from the Genetics Impact Assessment tools developed, and providing a user guide for its use.

3. Methodology

3.1 Overview of methodology

The methodology requires evaluating the economic benefits of genetic improvement across several scales: the animal unit level, farm gate level, and regional or national flock scale. At the animal unit level, methods must connect genetic trends in specific traits with economic gains. This project tests three approaches:

1. Calculating the annual change (delta) in $Index values, expressed as dollars per cow or ewe mated, for specific breeds and production systems (e.g., Brahman Live Export).
2. Estimating annual changes in gross margin per animal unit based on gains in key traits (such as sale weight, reproductive rate, and survival rate) using herd modelling software.
3. Estimating productivity gains per animal unit (e.g., kilograms of beef produced per adult equivalent, AE) based on improvements in key traits, derived from empirical relationships.

Methods 2 and 3 were applied exclusively to Brahman cattle in Central Queensland (ABARES Region 322), and Northern Territory (NT) Victoria River Downs (VRD) & Katherine (ABARES Region 713) for comparative analysis.

Method 1 was ultimately applied to each industry in aggregate: northern Australian cattle, southern Australian cattle, and sheep (national).

To translate these estimates into nationally relevant values, it is essential to account for the time lag between genetic improvement in $Index values—primarily recorded in the seedstock sector—and their subsequent impact in the commercial sector. Additionally, only the segment of the national herd or flock actively using MLA-supported genetics and purchasing recorded animals should be included, factoring in the adoption rate of these recorded genetics.

This assumption means that genetic improvement is assumed to apply to all animals in herds or flocks that purchase registered animals. For example, if there is a nucleus herd or flock in a commercial setting, but a few registered sires are purchased each year, genetic improvement will be accounted for. Conversely, if a commercial herd or flock transfers unregistered animals to another herd or flock which does not identify as purchasing registered animals, genetic improvement in that herd or flock will not be included in this assessment.

Multiplying the derived values by the corresponding herd or flock segment (e.g., Merino ewes) provides a gross estimate of the benefits from investments in genetic recording and improvement. This estimate must, however, be evaluated against a counterfactual scenario, or the level of improvement and adoption expected without MLA investment. The counterfactual considers two factors:

- A slower adoption rate in the commercial sector
- A reduced rate of genetic improvement (slower change in $Index or Estimated Breeding Value (EBV) values)

The counterfactual results are then subtracted from the base case scenario to yield the final benefit estimates. Figure 1 provides a summary of this process.

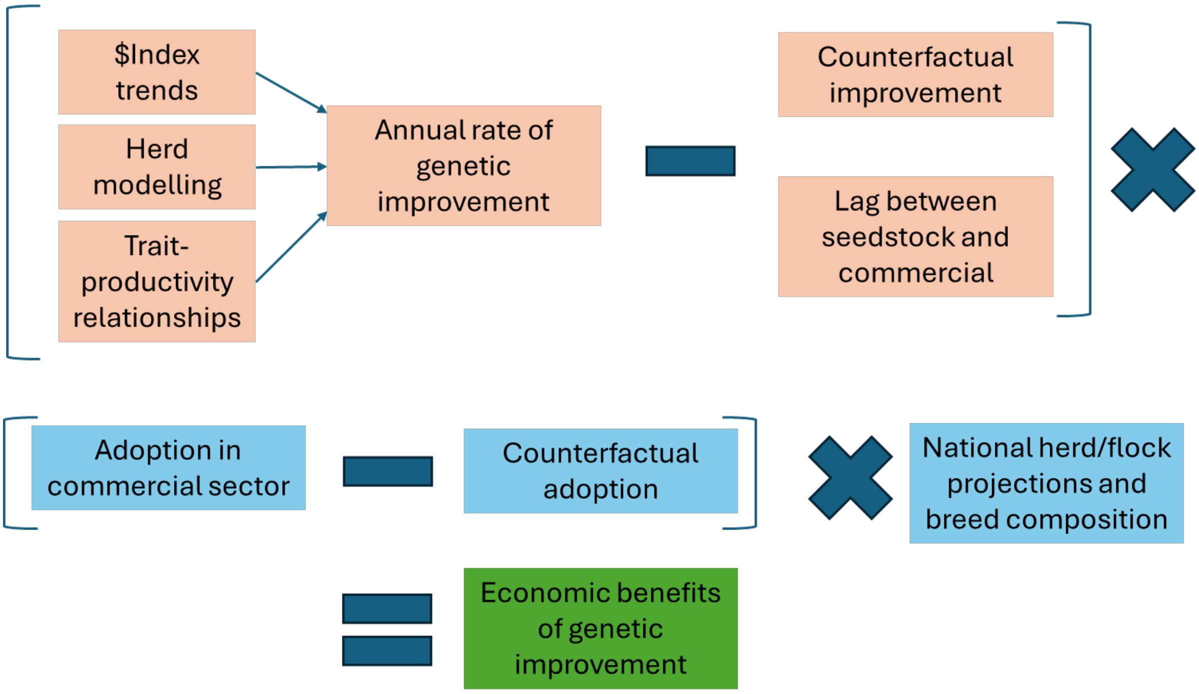


Figure 1: Flowchart of methodology overview showing the chain of logic and data inputs required to estimate the economic impacts of genetic improvement.

The process can also be expressed through a series of equations. First, the impact for a given year is calculated as:

$$I_{by} = \Delta\$Index_{y-lag} \quad \text{(Eq. 1)}$$

Where:

- I_{by} is the base case (b) impact (I) of genetic improvement in the commercial sector in a given year (y), expressed as $ per cow or ewe mated.
- $\Delta\$Index$ is an annual change in $Index value.
- $y - lag$ is the year of interest minus the lag in improvement between the seedstock and commercial sector, discussed further in Section 3.3.1.

Subsequently, the benefit estimation for a population is estimated as:

$$B_y = \left(I_{by} - I_{cy}\right) \times \left(A_{by} - A_{cy}\right) \times p \quad \text{(Eq. 2)}$$

Where:

- B_y is the annual benefit, at national scale, of genetic improvement.
- $\left(I_{by} - I_{cy}\right)$ is the difference between the base case impact and the counterfactual impact, as defined in Eq. 1
- $\left(A_{by} - A_{cy}\right)$ is the difference between base case and counterfactual adoption of registered animals, expressed as a percentage.

The following sections detail each of the elements described here with documentation of their implementation in an Excel tool.

All future benefits are discounted to present values under a standard discounting methodology. The rate applied was 5% for all scenarios as per guidance from MLA. The methodology follows the same principles as the cumulative discounted expressions (CDE) method which has been widely used to estimate the long-term value of a trait (Berry et al., 2006). For this project, the value of the entire national herd or flock is considered, rather than individual trait(s), so the method has not been directly employed. However, the principles of accounting for generation intervals and discounting future values were applied.

3.2 Estimating benefits from genetic improvements

3.2.1 $Indexes

This assessment leverages genetic trends in breeding values and $Indexes to estimate recorded genetic improvement rates. $Indexes consolidate various traits into a single dollar figure per cow or ewe mated, weighting traits according to their relevance in a specific production system while accounting for genetic correlations among traits. For example, $Indexes for tropical breeds are often heavily weighted to fertility, given the relative importance of fertility traits to performance in tropical herds (Bell & Sangster, 2023; Fordyce et al., 2022; Holmes, 2015; McLean et al., 2018; McLean et al., 2014; McLean et al., 2020; Rolfe et al., 2016; Walsh & Holmes, 2022).

Trait weightings are presented on the BREEDPLAN and Sheep Genetics websites, the links to which are provided in Table 1. Given the focus on red meat in this evaluation, only dual purpose and carcase production $Indexes were used for sheep to limit the influence of wool traits on calculated outcomes.

The primary purpose of $Indexes is to facilitate the identification and selection of superior animals. However, in this project, trends in $Indexes over time are used as indicators of a cohort's rate of genetic improvement. This approach aligns with Fennessy et al. (2014), which used $Index trends as a validation check in a genetics impact assessment.

The $Indexes used in this assessment were developed through BREEDPLAN Breed Object software and provided by the Animal Genetics and Breeding Unit (AGBU). MLA also supplied the Sheep Genetics LAMBPLAN and MERINOSELECT Indexes.

Table 1 lists all $Indexes used in the assessment, which according to the Insights Survey, accounts for most of the herd and flock (Sloane & Walker, 2023). However, the list does not include $Indexes collected by pastoral companies on composite breeds which may account for many cattle. These could be incorporated into the tool if available.

Table 1: BREEDPLAN, LAMBPLAN and MERINOSELECT $Indexes used as inputs to the evaluation of MLA's investment in genetics programs.

Species	**Breed/Line**	**Index Hyperlinks**
Sheep	Merino	*Merino Dual Purpose Plus (DP+)*
	Terminal	*Terminal Carcase Production (TCP)*
	Maternal	*Maternal Carcase Production Plus (MCP+)*
Cattle	Brahman	*Brahman Central Production*
		Brahman Live Export
	Droughtmaster	*Droughtmaster JapOx*
	Angus	*Angus Breeding Index*
		Domestic Index
	Charolais	*Charolais Northern Maternal*
		Charolais Domestic Terminal
	Hereford	*Hereford South SR Grass*
		Hereford SR BBaldy

	Limousin	*Limousin Domestic Maternal*
		Limousin Export Maternal
		Limousin Northern Terminal
		Limousin Vealer Terminal

Breed average $Indexes in more recent years have greater uncertainty and lower accuracy. Accuracy increases as more progeny are recorded over progressive years. This means that trends are smoother further back in time, with more recent years showing greater volatility in $Index values.

$Index trends were extrapolated from known years into the future on a linear basis. The impact of extrapolated values is limited by the lag applied between the seedstock and commercial sectors, where $Index values recorded in the present year do not incur benefits for 7 or 12 years into the future for sheep and cattle, respectively.

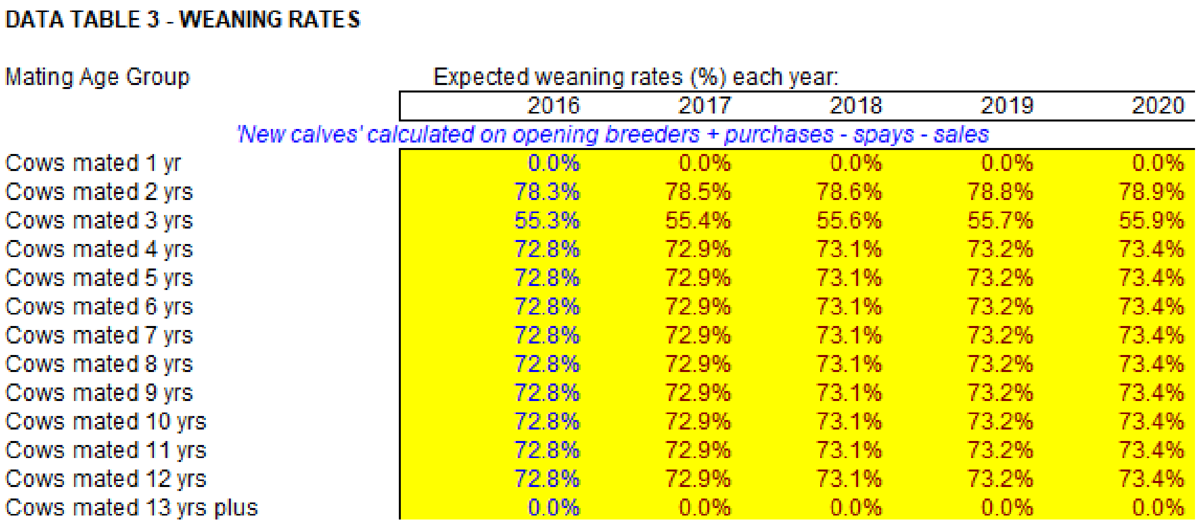
3.2.2 Herd Modelling

The use of holistic herd modelling has been proposed and used as a method to investigate the impact of genetic improvement on herd productivity and profit (Chudleigh et al., 2019; Griffith et al., 2003). This project follows Griffith et al. (2003) in using the trends of Breed Object traits as inputs into a herd modelling exercise, using both Central Queensland Brahmans and NT VRD & Katherine as production systems for the purposes of comparative analysis.

In this case, genetic trends for sale weights, cow survival (inverse of mortality), mature cow weights, and weaning rate were applied as inputs in Breedcow & Dynama software. Baseline herd conditions were set by consulting the default templates provided and from Australian Beef Report data for the relevant region (Chudleigh, 2013; McLean et al., 2023).

Trends were derived from linear regression analysis of the Breed Object trait trends, like the approach taken by Griffith et al. (2003) and Wellington & Walmsley (2020). Figure 2 shows that these are generally linear in nature with some annual variation. The slope coefficients were added to baseline figures for sale weights, mature weights, weaning rates, and mortality for each year of the model. Figure 3 shows how the trends in weaning rate were entered in Data Table 3 of the Dynama element of the Breedcow & Dynama software package. Similarly, trends in mortality were entered in the Dynama Data Tables 1 and 2: female and male death rates, and sale weight trends were entered in Prices tab Table 1: paddock weight/head which fed into Table 3: sale weight/head.

Figure 2: Linear trends in Estimated Breeding Values (EBVs) over time for the four traits derived from the Brahman Central Production Index and entered as inputs in both the herd modelling and trait-productivity regression analyses. EBVs compare genetic merit to the current population, so values should be interpreted as deviations from a reference population rather than absolute.



DATA TABLE 3 - WEANING RATES

Mating Age Group	Expected weaning rates (%) each year:				
	2016	2017	2018	2019	2020
	'New calves' calculated on opening breeders + purchases - spays - sales				
Cows mated 1 yr	0.0%	0.0%	0.0%	0.0%	0.0%
Cows mated 2 yrs	78.3%	78.5%	78.6%	78.8%	78.9%
Cows mated 3 yrs	55.3%	55.4%	55.6%	55.7%	55.9%
Cows mated 4 yrs	72.8%	72.9%	73.1%	73.2%	73.4%
Cows mated 5 yrs	72.8%	72.9%	73.1%	73.2%	73.4%
Cows mated 6 yrs	72.8%	72.9%	73.1%	73.2%	73.4%
Cows mated 7 yrs	72.8%	72.9%	73.1%	73.2%	73.4%
Cows mated 8 yrs	72.8%	72.9%	73.1%	73.2%	73.4%
Cows mated 9 yrs	72.8%	72.9%	73.1%	73.2%	73.4%
Cows mated 10 yrs	72.8%	72.9%	73.1%	73.2%	73.4%
Cows mated 11 yrs	72.8%	72.9%	73.1%	73.2%	73.4%
Cows mated 12 yrs	72.8%	72.9%	73.1%	73.2%	73.4%
Cows mated 13 yrs plus	0.0%	0.0%	0.0%	0.0%	0.0%

Figure 3: Linear trends over time for weaning rate entered as inputs in the Breedcow and Dynama model.

The need for numerous manual inputs to create different scenarios in the Breedcow & Dynama modelling platform highlighted a risk of transposition errors, which would be undetectable in the online platform due to the lack of formula visibility. Therefore, it was decided to use an earlier, offline version of the software (V6.02), which allows data entry through Microsoft Excel spreadsheets, providing greater accuracy in inputs and visibility of formulas used in the calculations that produced the final results. While there are some minor differences between the current online version and V6.02—particularly in the valuation of spay cattle—this did not impact the modelling, as the quantity of spay cows was assumed to be zero in all years.

Despite using the offline templates, challenges remained in modelling consecutive 10-year periods. Specifically, the “Closing Value” of cattle in the 10th year was set to equal the “Opening Value” of cattle in the 11th year (which was zero), leading to an artificial reduction in GM/AE in the 10th year. To address this, three overlapping 10-year periods were created, effectively eliminating the drop in profitability in the 10th year of the calculations.

Since the modelling aimed to assess productivity and profitability improvements from genetic gains, both the QLD and NT scenarios assumed no debt or surplus cash deposits. Additionally, asset provisions, depreciation, and family drawings were standardized at $80,000 per year across scenarios.

There is assumed to be no additional cost of improving genetics, beyond costs of larger animals if applicable, which are reflected in AE and DSE ratings. This assumption is based on producers replacing genetics at a constant rate and no additional cost for maintaining industry standard genetic merit.

Data on husbandry costs, operational expenditures, mortality rates, herd size, property size, and other factors were based on long-term regional averages from the Australian Beef Report (McLean et al., 2023). To establish a consistent baseline scenario for each region, some herd AEs varied slightly from the long-term averages reported. This variation is due to differences in herd composition, assumed cattle weights by category, and sale dates.

Although it could be argued that operational costs increase as the number of AEs increase, for the purpose of this analysis, these costs were held static throughout all periods and were calculated based on the long-term operational expenditure per AE for each region (as reported in the Australian Beef Report), multiplied by the number of AEs in the first year of this analysis.

In scenarios where genetic gains were applied, herd numbers showed a modest increase over 20 years due to reduced mortality and improved weaning rates. This increase varied by region, ranging from 0.9% to 2.7%, which, when compared with trends reported in the Australian Beef Report, is relatively conservative given the typical growth in herd size, often influenced by land expansion that may or may not increase stocking rates.

Each scenario required several assumptions, including sale distance, freight costs ($/deck/km), turnoff/sale weights, and weight-for-age metrics. Where available, published data specific to regions (such as CSIRO’s Transporting Livestock in Northern Australia) was used. In cases where published data was unavailable or inconsistent, the best estimates were made based on practical experience.

The assumptions around growth-paths and baseline weaning rates for each scenario were based upon the work published by Bray et al. (2015). The definition of 1 AE was taken to be a 450kg steer with zero weight gain, this was used for both the models analysing *Bos indicus* herds and *Bos taurus* herds.

Pricing assumptions for all models were based upon the Australian Beef Report’s 60th decile long-term average to Dec 23 (in 2023 dollars) for Yearling Steer/Heifer; Steers & Bullocks and Grown

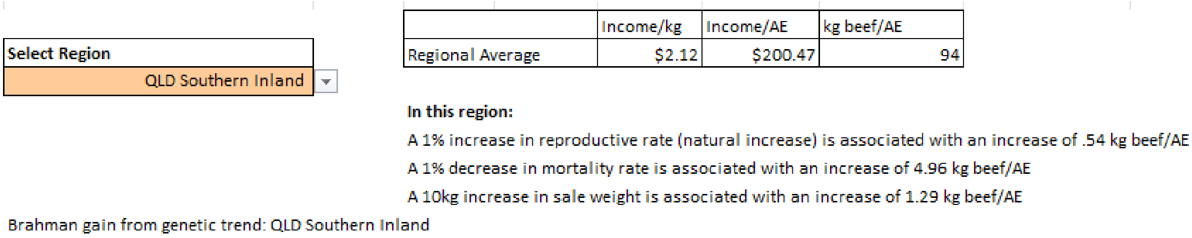
Females for Queensland. These values per kg were reduced as age increased for categories where reported data was not available.

3.2.3 Trait-Productivity Regression

The relationships between performance traits and beef productivity are well-established and have been applied widely. For example, the response in kilograms of beef/AE to reproductive rate, sale weight, and mortality rate have been extensively referred to in the northern Australia beef industry (Bell & Sangster, 2023; Fordyce et al., 2022; Holmes, 2015; McLean et al., 2018; McLean et al., 2014; McLean et al., 2020; Rolfe et al., 2016; Walsh & Holmes, 2022). This approach also formed the basis of the 'proof of profit' project (L.GEN.1810) which developed a tool to assess the likely profit outcomes from investing in genetic improvement (Wellington & Walmsley, 2020). The method of analysis used in L.GEN.1810 is repeated in this project with updated input data.

As for herd modelling the methodology was applied to the Central Queensland and NT VRD & Katherine regions, using trends from the Brahman Central Production and Live Export $Indexes to enable comparison.

The Excel tool developed for L.GEN.1810 was used with updated genetic trend input. This tool uses regionally specific relationships between traits and productivity derived from empirical analysis and applies a regionally specific value for income/kg, as per Figure 4, which is then applied to kilograms of beef produced per AE, to give a change in income per AE.



Select Region
QLD Southern Inland

	Income/kg	Income/AE	kg beef/AE
Regional Average	$2.12	$200.47	94

In this region:
A 1% increase in reproductive rate (natural increase) is associated with an increase of .54 kg beef/AE
A 1% decrease in mortality rate is associated with an increase of 4.96 kg beef/AE
A 10kg increase in sale weight is associated with an increase of 1.29 kg beef/AE

Brahman gain from genetic trend: QLD Southern Inland

Figure 4: Screenshot from the trait-productivity relationship tool showing data entry and values applied in the Central/Southern Inland Queensland analysis.

The analysis methodology applied in the trait-productivity relationship method penalises increasing mature cow weight by increasing the AE rating. The result can be visualised with the contribution of each trait apportioned, as per Figure 5. The increase in income/AE is generally analogous to the measure produced from Breedcow & Dynama and the $Indexes (noting differing denominators – cows/ewes mated versus AEs), so can be used for comparison.

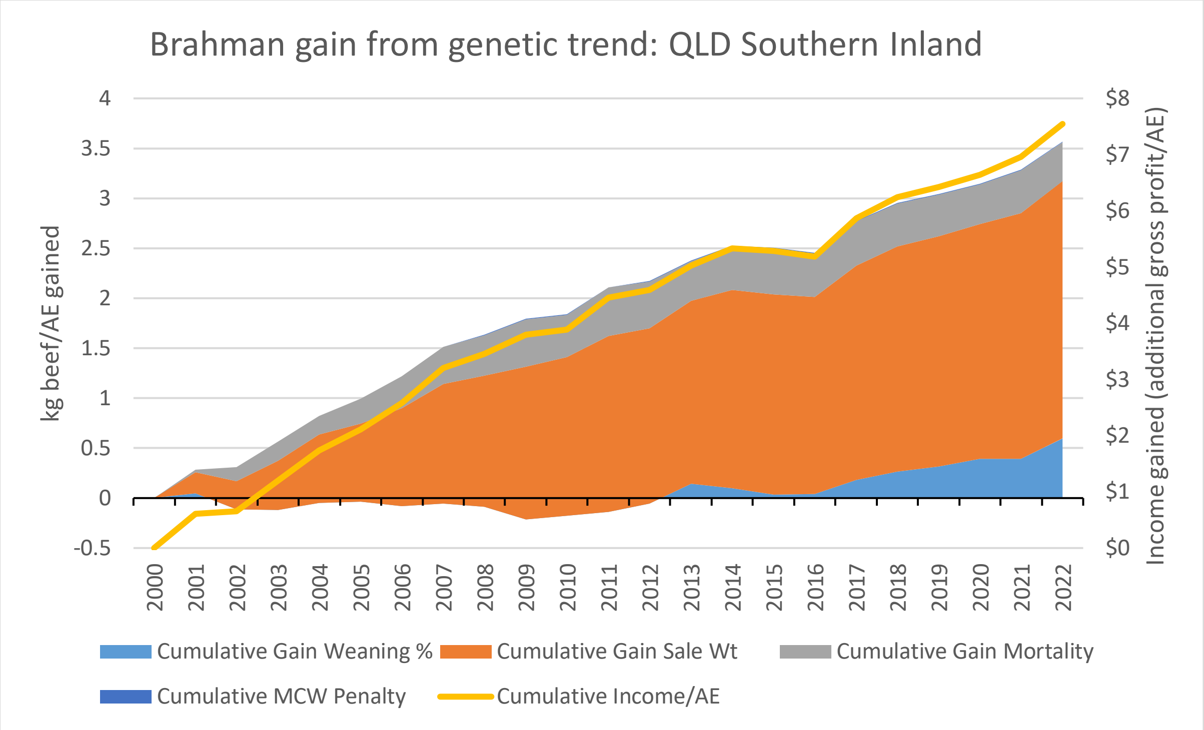


Figure 5: Income and productivity gained per AE as calculated in the trait-productivity relationship tool for Brahmans in Central/Southern Inland Queensland.

3.3 Counterfactual assumptions

3.3.1 Adoption

It is assumed that, without MLA investment, the rate of adoption would be slower. This is referred to as counterfactual adoption. It's also assumed that this rate would differ across industry segments. For instance, Fennessy et al. (2014) applied counterfactual adoption rates of 10-25% for the northern beef industry, whereas adoption rates for southern beef and sheep were higher, closer to base case levels. At the start of the evaluation period, the counterfactual adoption rate matches the base case, with user-defined inputs guiding the rate of increase, which would generally be set lower than the base case, as illustrated in Figure 6.

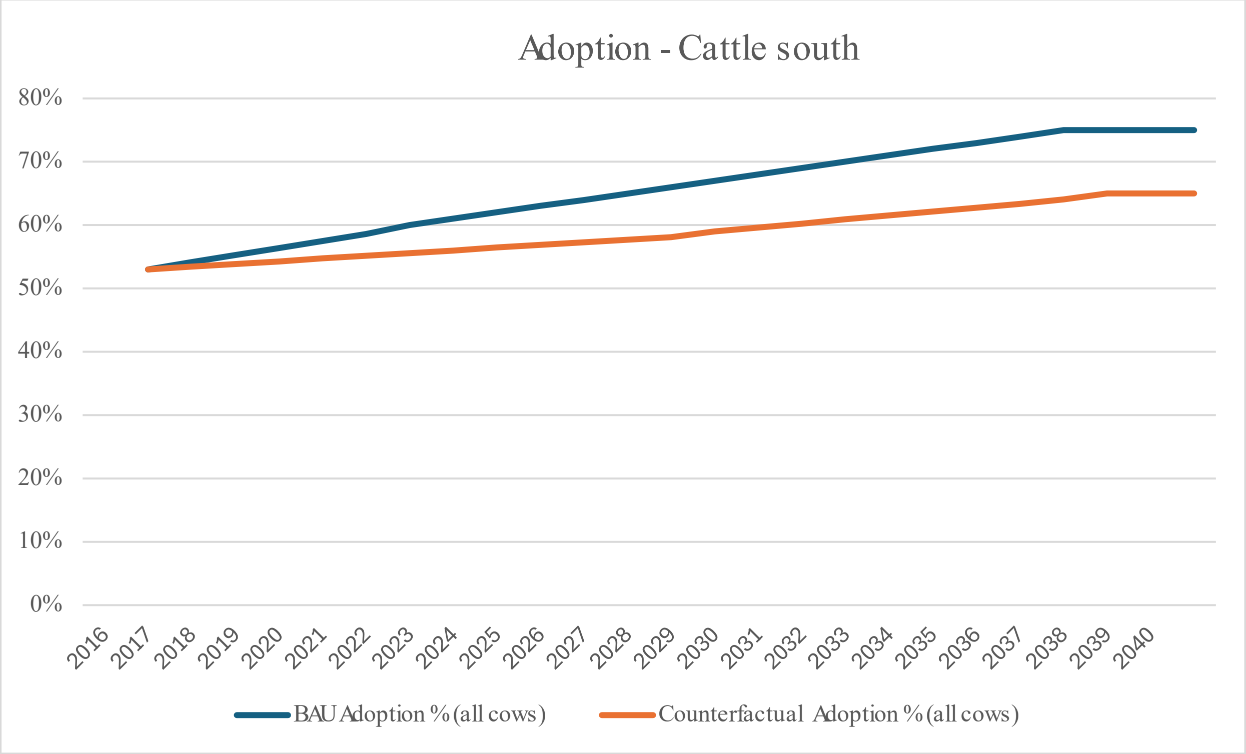


Figure 6: Business as usual (BAU) and counterfactual adoption in the southern beef from the 2016-2040 analysis period.

There is considerable uncertainty associated with estimating the counterfactual adoption. The presence and effect of alternative service providers must be considered, as shown in Table 2. Due to the uncertainty, it is recommended that the assumptions underpinning the counterfactual adoption estimate are considered and recorded each time the assessment is run.

Table 2: 2022 'base case' (actual) adoption figures for each of the cohorts evaluated in the evaluation of MLA's investment in genetic programs alongside adoption figures used in the counterfactual scenario.

Species/Region	2022 Adoption (MLA Insights)	2022 Counterfactual Adoption (2016-2040 analysis period)	2022 Counterfactual Adoption (2016-2040 analysis period)
Sheep	57% (commercial producers using ASBVs)	54%	56%
Cattle – North	51% (tropical producers using BREEDPLAN EBVs)	47% (assume absence of TBTS)	50% (assume absence of TBTS)
Cattle – South	60% (temperate producers using BREEDPLAN EBVs)	56% (assume absence of SBTS)	59% (assume absence of SBTS)

3.3.2 Rate of genetic improvement

The second component of the counterfactual is the rate of genetic improvement without MLA investment. Like adoption rates, this rate is specific to each industry segment and is challenging to estimate precisely. Griffith et al. (2003) and Fennessy et al. (2014) used historical improvement rates as proxies for counterfactuals. For instance, Fennessy et al. (2014) applied the trend from 1993-1997 to project improvements from 2000-2040. Griffith et al. (2003) did not model a complete counterfactual for the entire population but instead applied a longer lag to the segment of producers not adopting registered animals.

Although the “delayed rate of genetic trend” method made sense in previous evaluations, it is not used for this project due to two main reasons:

- Genetic improvement rates have generally followed a linear and cumulative trend since around 1990, making the concept of delayed improvement rates less applicable.
- A more flexible method for defining the counterfactual rate of genetic improvement allows for testing assumptions and evaluating sensitivity.

In this evaluation, the reduction in the rate of genetic improvement is defined as a percentage decrease, set through an input cell in the evaluation workflow explained further in the User Guide. The figure used for development was a 20% reduction in the rate of genetic improvement. This value was selected in consultation with MLA genetics managers based on a reduction in selection accuracy in the absence of objective measurement.

3.4 Assessment tools

Genetics Impact Assessment tools have been developed and applied to each industry segment: northern cattle, southern cattle, and sheep. The tools were developed to accept annual $Index values as inputs, though they could be adapted to accept annual gains expressed in dollar figures derived from any of the benefit estimation methods explained in Section 3.2.

The main components of the Impact Assessment tools are the inclusion of benefit estimates for two periods, 2016 – 2040 and 2021 – 2045. The former assumes that genetics funding continued from 2016 and delivered benefits for 25 years from that date. The latter counterfactual date range assumes that there was no funding until 2021 and hence the 25-year benefits are reduced accordingly. The difference between the two time periods indicates the 5-year benefit between 2016 and 2021. This difference is relatively small, reflecting that benefits from the program are small in the first 7 years owing to lags in the counterfactual index impact and adoption rates.

A detailed User Guide is available in a separate document, and builds on the methodological principles outlined in this section.

4. Results

4.1 Net benefits of genetic improvement

The net present value benefits of all of MLA’s investments in genetics programs were estimated to be $342M from 2021 to 2045 and $348M for the 2016 – 2040 period. For both periods, approximately 75% of the benefits were earned in the sheep industry, with the southern and northern cattle industries sharing in 20% and 5% of the benefits, respectively (Table 3). Benefits can be traced to the trait weightings in $Indexes listed in Table 1.

Table 3: Net present value benefits of MLA’s investments in genetics programs based on a discounted cash flow assessment of 5% and a baseline year of FY25.

	Southern Cattle ($M)	Northern Cattle ($M)	Sheep ($M)	Total ($M)
2016 - 2040	72.55	17.76	257.49	347.80

2021 - 2045	70.73	17.16	254.04	341.93

There are several likely reasons for the proportionally larger benefits earned by the sheep industry compared with cattle:

- Sheep have a shorter generation interval than cattle, so the lag between improvement in the seedstock and commercial sectors is shorter.
- The Dual-Purpose Plus Merino $Index incorporates clean fleece weight with a trait weighting of 40%. A further 5% of the $Index is determined by staple strength and fibre diameter. This $Index was applied to an average of 74% of the sheep population (Merinos) considered in the evaluation, so approximately 33% of the benefits from improvement in sheep genetics are attributable to clean fleece weight.
  The remaining two-thirds of benefits are attributable to red meat production traits such as weaning rate, yearling weight, eye muscle depth, and lean meat yield.
- The national flock is large, so benefits per ewe mated are multiplied across a large population.
- For northern cattle in particular, rates of $Index improvement are low.

These estimated benefits are lower than those provided by Fennessy et al. (2014) which totalled $1,445M across the sector. The discrepancy between these estimates and the Fennessy et al. (2014) estimates are likely to be most attributable to different herd and flock size outlooks between periods, and, to a lesser extent, differences in counterfactual assumptions.

The Impact Assessment tools allow net benefits to be plotted on an annual basis (Figure 7, Figure 8 & Figure 9). Annual benefits are small in early years of the analysis period when the gap between the business as usual and counterfactual scenarios is lowest. The annual values, especially the relativity between breeds, are mostly dependent on forecast herd or flock sizes. Volatility from 2029 to 2032 for sheep, and 2029 and 2036 for cattle, are due to higher uncertainty and more variation in $Index values in more recent years, noting the lag between the seedstock and commercial sectors. Values are smoother after the transition between actual and forecast index change values.

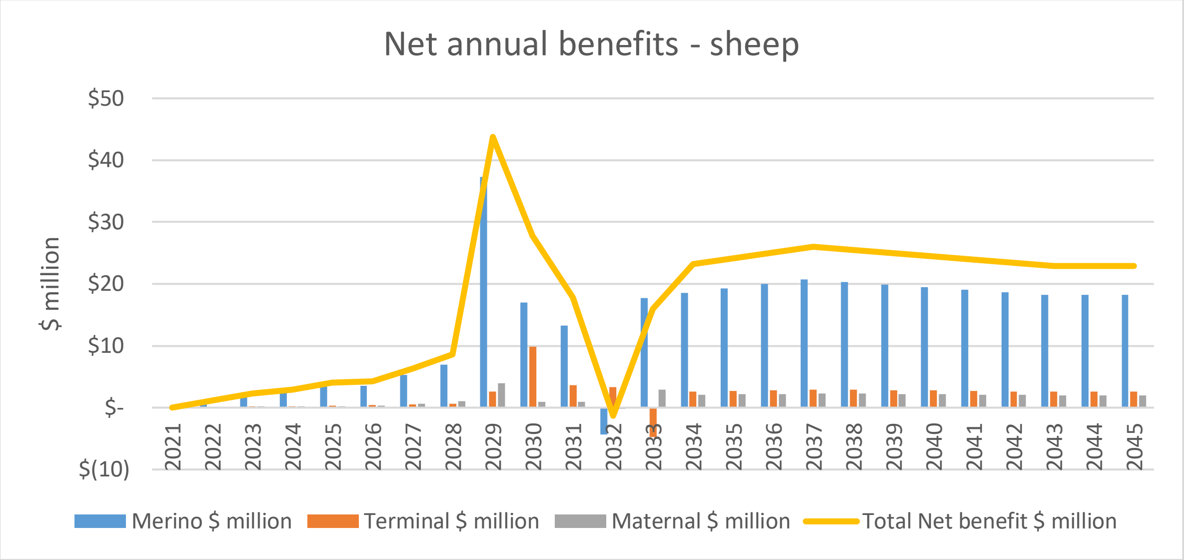


Figure 7: Annual net benefits of genetic improvement for the sheep industry from 2021 – 2045, from the genetics Impact Assessment tool.

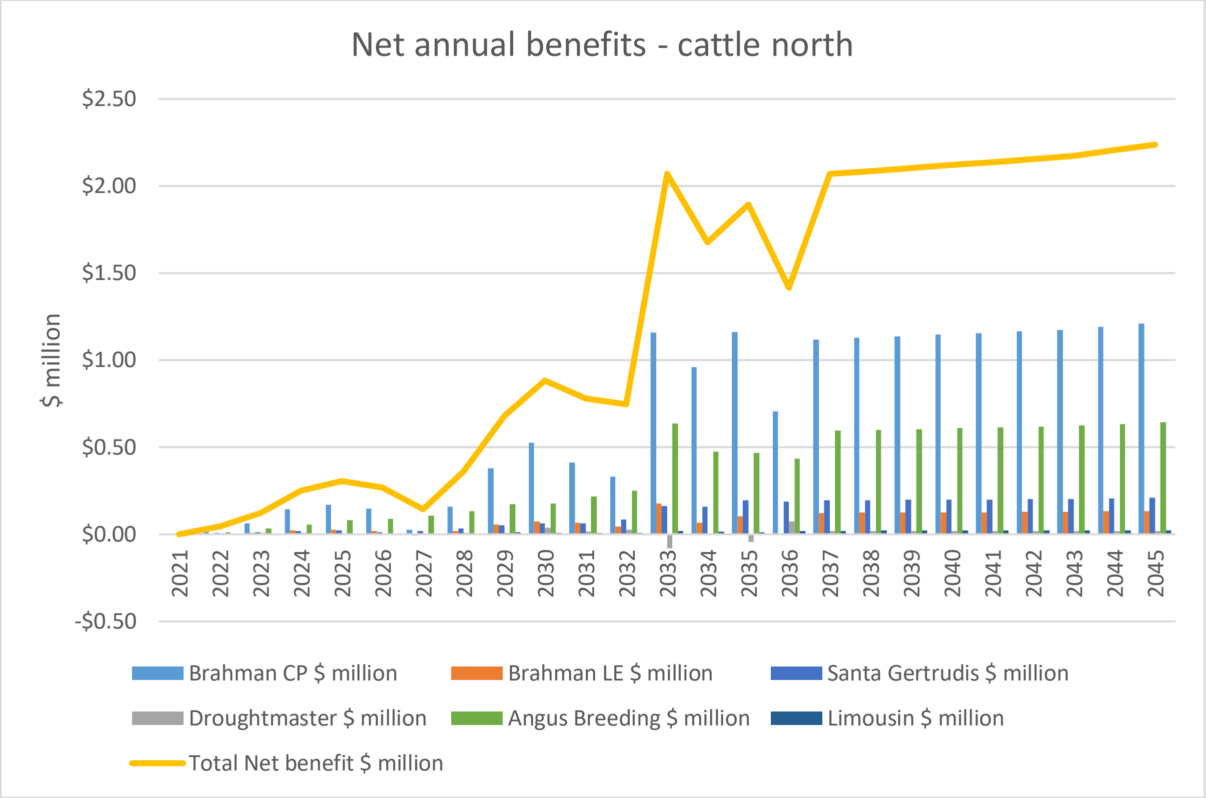


Figure 8: Annual net benefits of genetic improvement for the northern cattle industry (selected breeds) from 2021 – 2045, from the genetics Impact Assessment tool.

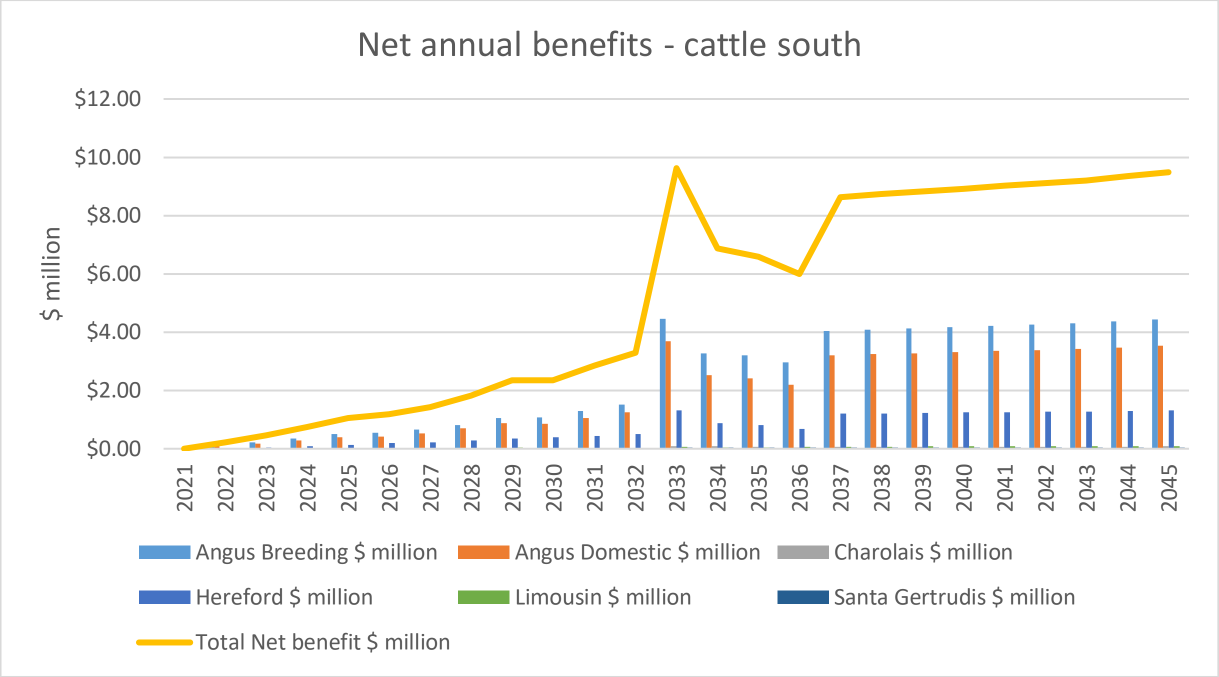


Figure 9: Annual net benefits of genetic improvement for the southern cattle industry (selected breeds) from 2021 – 2040, from the genetics Impact Assessment tool.

4.2 Comparison of benefits estimation methods for genetic improvement

The relativity of benefit estimation methods varied between the Central Queensland and NT VRD & Katherine testing regions (Figure 10 and Figure 11). $Indexes go beyond the farm gate and encompass the entire supply chain, thereby producing larger estimates of annual gain than methods which are restricted to the farm domain (Chudleigh et al., 2019; Wellington & Walmsley, 2020). This is evident in Figure 10 where the cumulative gains in $Index values exceed gains estimated from the herd modelling (Breedcow and Dynama) and regression methods. In Figure 11, the Breedcow and Dynama, and regression methods produce very similar results, with the $Index lagging for most of the period. However, the difference between all methods at the end of the period is within $2, providing assurance of cross-validity between methods.

The lesser difference in NT VRD & Katherine compared with Central Queensland is explainable as the Live Export $Index reflects a 300kg export weight and lesser slaughter weight than the Brahman Central Production $Index, so there are less expected benefits earned beyond the farm gate for the Brahman Live Export $Index.

Given the differences in scope of each approach, findings from the Assessment tools rely on $Indexes as inputs and should be presented as relating to the entire supply chain. In aggregate, $Indexes represent the red meat sector.

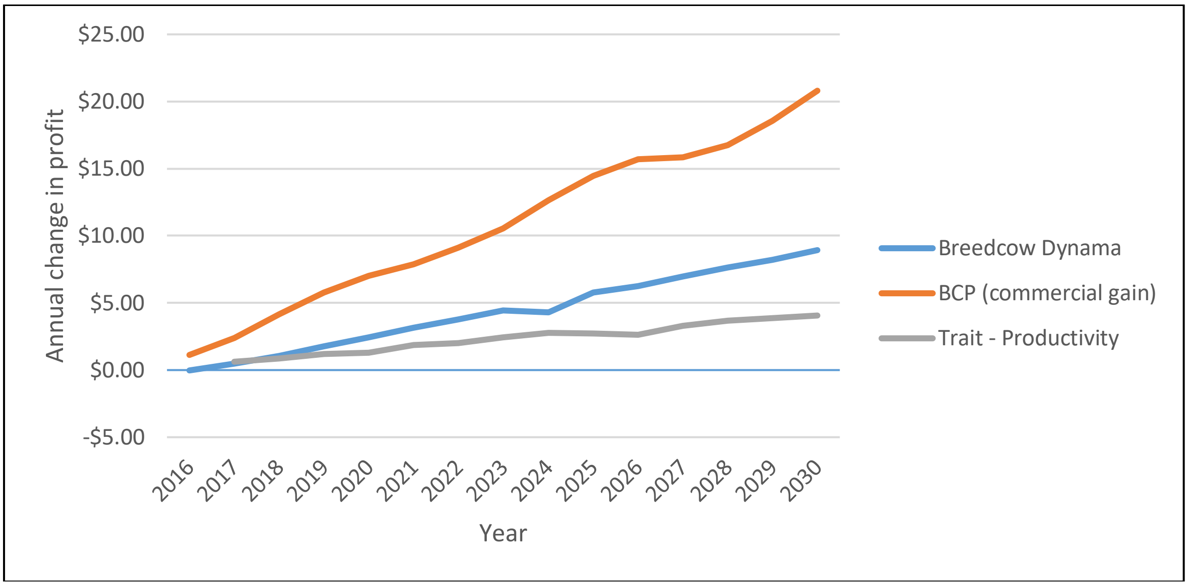


Figure 10: Cumulative improvement in profits derived from three estimation methodologies: the Brahman Central Production (BCP) $Index, Breedcow & Dynama herd modelling, and trait-productivity regression analysis.

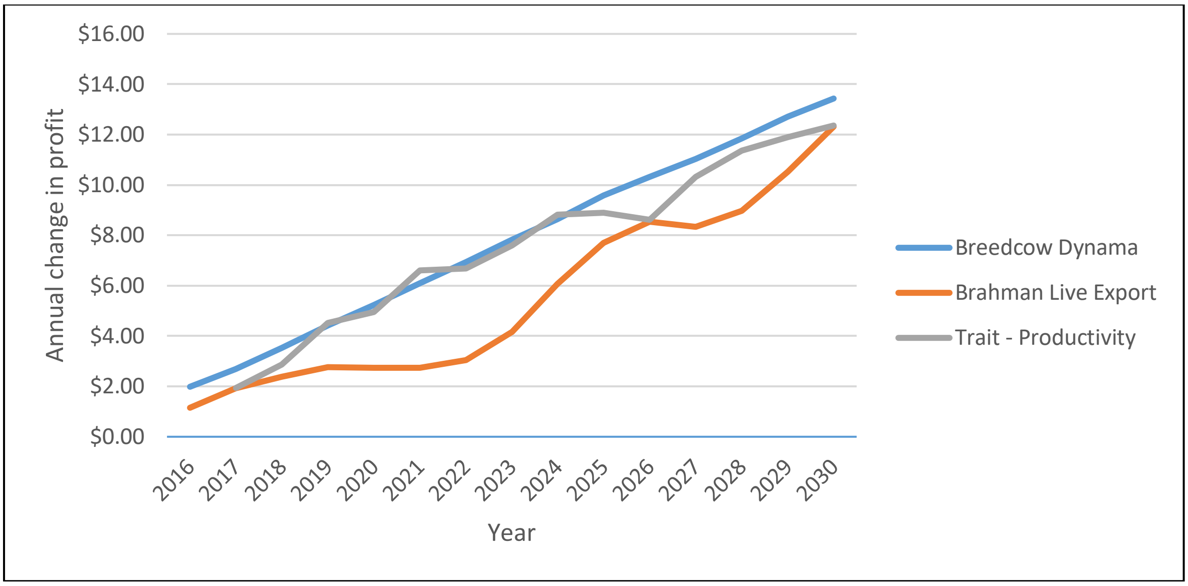


Figure 11: Cumulative improvement in profits derived from three estimation methodologies: the Brahman Live Export $Index, Breedcow & Dynama herd modelling, and trait-productivity regression analysis.

In selecting a preferred methodology for input data into the Assessment tools, consideration was given to the 'Occam's Razor' philosophy of seeking acceptable and logical solutions with the fewest possible assumptions. This was especially because the Assessment tools were developed for routine and ongoing use by MLA. In view of this, the $Index trends are an 'off-the-shelf' product requiring the fewest assumptions among the methods tested. The Assessment tools were therefore developed to accommodate $Indexes as inputs, though the workflow can accept any commercial gain values expressed as dollars per head.

There are evaluation cases where a herd modelling or empirical regression analysis may be desirable, generally at a more disaggregated level than an industry-wide assessment. For example, herd modelling is a valuable means of testing how changes in price relativity of stock classes (e.g. bullocks worth more than weaners) interacts with optimum genotypes. Similarly, a trait-productivity regression analysis can be applied as a cross-reference to trait weightings in $Index formulae. Outputs from herd modelling could be used as inputs to the Assessment tools to produce a national scale assessment of the impact of genetic improvements on farm-gate profit under hypothetical conditions, though this would be a labour-intensive process.

5. Conclusion

5.1 Key findings

- The assessment methodology and tools developed indicates that investment in MLA genetics programs yields considerable net present value benefits of $342M from 2021 – 2045 with modest counterfactual assumptions.
- Trends in $Indexes are an acceptable 'off-the-shelf' measure of genetic improvement across the entire supply chain which can be used as inputs to sector impact assessments. Other means of estimating genetic improvement, such as herd or flock modelling, and empirical regression analysis, can be used as alternative measures relating specifically to farm-gate impacts.
- The sheep industry earned around 75% of the total sector benefits, southern cattle earned 20%, and northern cattle earned 5%. This could be attributed to rates of adoption of

registered animals, rates of genetic improvement, inclusion of wool related benefits and outlooks for the national herd and flock population.
- Approximately 33% of the benefits from sheep genetics are attributable to clean fleece weight. The remaining two-thirds of benefits are attributable to red meat production traits such as weaning rate, yearling weight, eye muscle depth, and lean meat yield.
- The Genetics Impact Assessment tools can be used for routine and ongoing assessments with reference to the User Guide.

5.2 Benefits to industry

The initial estimates of net benefits and development of the Assessment tools advance the sector by:

- Providing a current estimate of net benefits from the genetics program for the red meat sector and the sheep meat, northern and southern beef industries which can be compared against program costs and used for cost benefit analysis.
- Presenting insights, such as the relative contribution of industry segments to net benefits from the genetics program.
- Providing tools and a user guide for ongoing and routine use by MLA to quantify net benefits of the genetics program.

6. Future research and recommendations

A challenge for any assessment of genetic improvement is that the effects of genotype on productivity and profitability are not directly measurable. This means that estimates in improvement must be valued from EBVs and derivatives, such as $Indexes.

For aggregate assessments, such as the one this project has undertaken for the entire red meat sector, the uncertainty of valuing genetic improvement is compounded by uncertainty of adoption rates for improved genotypes in the commercial sector, and the lag between improvement in the seedstock and commercial sectors. There are several avenues of future research which could address some of these uncertainties:

- Producer surveys for both adoption and intentions (especially breed composition) provided critical information for this project. It is recommended that these continue.
- To complement the information from surveys, genomic recording and genomic EBVs in the commercial sector would enable more accurate estimation of adoption rates of registered animals, and the lag in genetic merit between seedstock and commercial herds/flocks.
- Simultaneously, this project has demonstrated the usefulness of the current EBV and $Index databases maintained by the breed societies and AGBU. These should continue to be well resourced.
- Multi-breed EBVs and $Indexes would simplify the Assessment tools, depending on the number of breeds and proportion of the herd/flock they cover. It is possible that multi-breed EBVs would support further adoption of registered animals, which would enhance the accuracy of the assessment and overall outcomes of MLA investment.

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