Opportunities for utilizing DNA-based technologies to enhance traceability and profitability in the Australian red meat industry

– A scoping study

(Project Code FA073)

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Abbreviations and Acronyms

ABARES	Australian Bureau of Agricultural and Resource Economics and Sciences
ABRI	Agricultural Business Research Institute
ABS	Australian Bureau of Statistics
AGBU	Animal Genetics and Breeding Unit
ALEC	Australian Livestock Exporters' Council
ALFA	Australian Lot Feeders' Association
ALPA	Australian Livestock and Property Agents
AMIC	Australian Meat Industry Council
AMPC	Australian Meat Processor Corporation
ARCBA	Australian Registered Cattle Breeders Association
AUS-MEAT	A joint venture between AMPC and MLA, responsible for management of trade descriptors and national accreditation standards for red meat
BCA	Benefit-cost analysis
BSE	Bovine Spongiform Encephalopathy
CCA	Cattle Council of Australia
CSIRO	Commonwealth Scientific and Industrial Research Organisation
DAFF	Department of Agriculture, Fisheries and Forestry (now Department of Agriculture)
DNA	Deoxyribonucleic Acid
EBV	Estimated Breeding Value
EID	Electronic Identification
EQ	Eating Quality
FI	(Net) Feed Intake
FMD	Foot and Mouth Disease
GBS	Genotyping by Sequencing
ICAR	International Committee for Animal Recording
ISC	Integrity Systems Company
LDL	Livestock Data Link
LPA	Livestock Production Assurance
LPS	Low Pass Sequencing
MLA	Meat and Livestock Australia
MS	Marbling Score (AUS-MEAT)
MSA	Meat Standards Australia
N_e	Effective population size
NLIS	National Livestock Identification System
NPV	Net Present Value
NSW DPI	New South Wales Department of Primary Industries
NVD	National Vendor Declaration
P.A.	Per annum
PIC	Property Identification Code
R&D	Research and Development
SNP	Single Nucleotide Polymorphism
SPA	Sheep Producers Australia
TAT	Turn-around Time
TSU	Tissue Sampling Unit
UNE	University of New England

Abstract

The potential role of genomics to further improve traceability levels in the red meat industry was investigated, as DNA-based technologies offer unambiguous identification with a range of auxiliary benefits. Modelling indicated that genotyping the entire national beef herd for traceability is unlikely to compensate for the additional costs involved. However, potential additional benefits (faster genetic gain and better management decisions) make several implementation models appear to be highly attractive. Genotyping the national sheep flock is impractical, but the cost of using DNA judiciously to augment NLIS could be quite cost effective.

Perceptions, concerns and experiences around traceability, DNA technologies, costs and willingness to pay were explored through industry consultations. Application of genomic technology for traceability alone was not generally seen as attractive, but the ancillary benefits that accompany lifetime traceability would make the value proposition more attractive.

There are instances of DNA already being used to augment traceability and there is a strong argument for taking a proactive approach to coordinating its wider use. The longer the delay, the greater the costs and difficulties arising from fragmentation. A program of work with a series of stop/go decision points is proposed, to be coordinated and overseen by an appropriately-qualified steering group.

Executive summary

Background

Participants in Australia's red meat industry have a strong incentive to have the ability to track their products through the supply chain. The National Livestock Identification Syss (NLIS) is believed to achieve 97% traceability for beef and 90% traceability for sheep, where traceability is measured by the proportion of animals that can be successfully traced between defined points in the supply chain or over time. Genomic information can potentially deliver exceptionally high levels of traceability, even after other means of identification (tags) have been removed or paper-work misplaced. Consequently, this project was initiated to investigate the potential role of genomics to underpin even better traceability in the red meat industries.

Objectives

This is a scoping study that

- Assesses the genotyping (DNA) technologies that are best suited for traceability
- Evaluates the benefit/cost of using DNA for traceability as well as ancillary benefits that are achievable
- Describes how such a traceability system could work and the distribution of benefits
- Identifies the risks, costs, barriers to adoption and how these should be addressed
- Describes a process to resolve technical and strategic issues prior to implementation

Methodology

The benefits of improved traceability in both beef and sheep were evaluated using an existing economic model, with the levels of traceability assumed to vary according to the proportion of animals genotyped. Auxiliary benefits were evaluated by a) using genetic modelling with typical economic breeding objectives; and b) modelling the value of improved ability to predict optimal production pathways.

An industry survey was conducted and interviews were held with major stakeholders and technology providers. The purpose was to identify industry perceptions, barriers to adoption and practical issues related to DNA technologies.

Results/key findings

Modelling indicated that the additional value of traceability expected from genotyping the entire national beef herd is unlikely to compensate for the additional costs involved. However, tactical genotyping can lead to a net increase in benefits due to traceability of 11-37% compared with NLIS alone. When additional benefits were taken into account, the net benefits of genotyping were 32-45% higher than the benefits currently attributed to NLIS.

Genotyping the national sheep flock is prohibitively expensive and clearly impractical. However, augmenting NLIS with tactical genotyping could be cost-effective in improving traceability and lead to better-inform ram purchasing decisions.

There are already instances of DNA being used to augment traceability and any implementation of a national program should be preceded by careful planning to avoid added costs and difficulties arising from fragmentation.

Benefits to industry

Improved traceability enhances the industry's ability to track, manage and control major exotic disease outbreaks. Using DNA to augment NLIS can lead to a range of additional benefits related to livestock evaluation, disease detection, pathway decisions, product specification and proof of provenance.

Future research and recommendations

A program of work with a series of stop/go decision points is proposed, potentially leading to implementation of a national genotyping program designed to augment NLIS and to realise the additional benefits. This should be coordinated and overseen by an appropriately-qualified steering group.

Project outputs against objectives

Objective	**Relevant outputs**
This is a scoping study	A scoping study is defined as "A preliminary study to define the scope of a project"[1]. In this instance, the "project" is assumed to be the potential implementation of a DNA-based traceability system for the red meat industry. Investigating this requires a thorough understanding of: - Industry structures and how each sector relates to the others (Section 2) - What is meant by "traceability" and some systems currently in use (Section 3) - Industry views on traceability options (Section 4) - The logistical requirements of a DNA-based system (Section 5) - Estimates of the direct and indirect economic benefits (Section 6) - A consideration of strategy and governance (Section 7) - Risks and opportunities (Section 8) - A potential pathway to implementation, taking account of the above (Section 9)
Detail what technologies for genotyping are now available that could be deployed for the purpose of animal tracking and tracing as well as to support raising and product provenance claims.	Genotyping panels of fewer than a hundred SNPs have been found to provide for unique identification within a breed, but larger arrays with 50k SNPs are widely used in both beef and sheep. The difference in cost is relatively small but the latter can be used to provide a range of additional benefits. A key factor in the cost is the collection and extraction of DNA which will be similar for low and higher density chips This is discussed in Sections 3 and 8 of the report.
Identify which ones are most suitable and the refinements/improvements that may be required.	These issues are discussed in Sections 4, 5 and 8 of the report. Small panels (several hundred SNPs) can be used for identification, pedigree ascertainment detection of genetic defects *etc.*, but 50k SNP panels offer a range of additional benefits. The value of extra genetic gain that can be achieved with the larger panel, if used judiciously (such as some of the options evaluated in Tables 1-3), can greatly outweigh any additional cost. Larger panels (*e.g.* 750k) have been extensively trialed and found to offer very few benefits over 50k panels. Technology improvements have resulted in the standard 50K panels being upgraded to 70-100K recently at the same costs. For the purposes of this report the term '50K panel' will refer to this family of panels that now ranges from 40K-100K and offer similar outcomes. Full or partial genome sequencing is neither necessary nor cost effective for the applications considered in this report. According to genotyping companies, race-side genotyping technologies are not feasible, at least cost-effectively, now or in the foreseeable future. A likely solution is that all samples are genotyped with a genomic profile in the order of 50K SNP, as commonly used in genetic applications in cattle and sheep. These genotypes would be stored in the database. Then if there is an animal, or a product from an animal, where the identity is not known, this sample could be genotyped for a reduced targeted list of SNPs, which are a subset of the full genomic panel. This reduced genotype could be obtained much faster and be queried against the entire database to determine its identity.
Assess technologies regarding cost vs benefits, scalability and timeliness of response	

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[1] https://www.collinsdictionary.com/dictionary/english/scoping-study

Objective	**Relevant outputs**
Detail additional value adds -can the same sample be used for multiple purposes and what sector of the value chain would be interested in these?	A number of other applications of genomic information are described Section 3.
Detail how a verification process would work from any point in the supply chain including live animal and carcass sampling as well as time frames and critical success factors.	Discussed in Section 5 (Requirements of an operational DNA-based tracing system).
Explore storage options, risks and costs - should items be stored as samples, DNA or data? Identify key barriers to adoption and develop a plan to overcome these.	Discussions with genotyping companies and people experienced with using DNA for these applications indicate that long-term storage of samples or DNA for traceability purposes is not feasible (Section 4). Rather, DNA should be extracted from samples and genotyped as soon as possible. Genomic data, stored in an appropriate database, is the safest and most flexible option. Barriers to adoption are also identified and discussed in Section 4, opportunities for resolution are discussed in Section 8 and an appropriate plan is described in Section 9. A primary concern is data ownership, access and utilization. These issues will have to be managed through extensive industry consultation.
Explore options of what a feasible business model could look like for using DNA for verification of provenance or other claims.	These options are explored in Sections 7, 8 and 9. Appropriate actions to underpin implementation are detailed in Section 9.
This study will be backed by practical, validated learnings.	The industry-wide survey (Section 4) provided significant insights into the practicalities of genomic technology implementation and potential prices that industry would be willing to pay. Relevant information was also sought from personnel in vertically integrated companies that have developed their own traceability systems, from genotype providers experienced in providing DNA-based traceability solutions and from colleagues who have been involved in implementing national genotyping programs in other countries (notably Switzerland and Ireland).

1. Introduction

Today's consumers require and expect integral knowledge about their food – its origins, how it is produced, how it is prepared and whether it is safe. Consequently, to protect brands and allow accountability, livestock producers have a strong incentive to develop and participate in systems that can track red meat products through the supply chain and inform consumers. Governments also have an inherit interest in biosecurity, public health and safety and ensuring that agricultural industries have ready access to export markets.

The Australian red meat industries are dominated by beef, veal, mutton and lamb, so this study will be focused on cattle and sheep with an emphasis on the former, which represents the greatest dollar value. According to Meat and Livestock Australia (MLA), the off-farm meat value of the Australian beef industry was approximately $20.2b in 2019. This figure includes domestic expenditure plus export value, including live exports; and compares with the off-farm meat value of $7.2b for the Australian sheepmeat industry over the same period. Around 189,000 people are employed in the red meat industry, including on-farm production, processing and retail[2].

The amenability of a product to be tracked through the supply chain is commonly referred to as its traceability. Australia's red meat industries have been proactive in developing traceability for its products. SAFEMEAT (a national partnership between industry and government[3]) provides the policy direction and oversight for the national integrity system, whilst the Integrity Systems Company (ISC) was established in 2017 as a wholly owned subsidiary of MLA to manage and deliver the three industry integrity programs being the National Livestock Identification System (NLIS), Livestock Production Assurance (LPA) program, and National Vendor Declarations (NVDs). The system currently in place appears to work very well, but it does have some inherent weaknesses as it primarily relies on physical labelling – initially ear tags in animals (which can become lost) and subsequently on information being passed along the processing and marketing chain (box labels) without error. Note that this information transfer is not automatic or embedded (*i.e.* in the sense that the information is contained in a tag that stays with the animal and its component products).

This project was initiated to investigate the feasibility of using genomic technologies to enhance traceability along the red meat supply chain; and to determine whether its inclusion in the current system (NLIS, LPA *etc*.) presents a clear value proposition for both sheep and cattle. Establishing the value proposition requires the consideration of numerous factors, including:

- the effectiveness of the technology in aiding traceability
- potential ancillary benefits
- the likely costs
- logistical issues including sample and data management
- genotyping methodology
- which animals (and their products) should be genotyped
- turnaround times
- the receptiveness of key participants
- potential implementation models
- the availability of service providers

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[2] MLA State of the Industry Report (2020) https://www.mla.com.au/globalassets/mla-corporate/prices--markets/documents/trends--analysis/soti-report/mla-state-of-industry-report-2020.pdf

[3] https://www.safemeat.com.au/

To provide the context for potential implementation, this report briefly describes how the red meat industries are structured, identifies the main markets, examines the need for traceability, and outlines the processes currently being used to underpin traceability. We also explore the views of industry participants and potential service providers, before modelling the benefits and costs of some potential options for using genomic information for traceability. Important considerations include the suitability of alternative technologies, the capabilities of potential service providers, the logistics of sample storage and data management, implementation models and user incentives.

2. Industry structures

A detailed study of the structure of the Australian beef herd can be found in DAFF (2006)[4], which describes the various production sectors, their main geographic locations and factors influencing movements of livestock between them. The structure of the Australian sheep flock and factors influencing sheep movements were reported in detail by East and Foreman (2011)[5] and Perrett (2015)[6]. For the purpose of this study, participants involved in the passage of red meat from producer to consumer can be categorised into one or more of the following:

- Seedstock breeders
- Commercial producers
- Backgrounders and Finishers
- Lot feeders
- Processors
- Wholesalers, retailers and smallgoods manufacturers
- Exporters
- Consumers

In addition, there are numerous service providers who operate within and across each of the sectors including livestock agents, veterinarians, consultants, *etc*. who have direct engagement with the NLIS and traceability.

The flow of animals and animal products between the various participants in the red meat industries is depicted in Figure 1.

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[4] https://www.agriculture.gov.au/sites/default/files/sitecollectiondocuments/animal-plant/animal-health/livestock-movement/beef-movement-ead.pdf

[5] East, I. and Foreman, I. (2011), The structure, dynamics and movement patterns of the Australian sheep industry. Australian Veterinary Journal, 89: 477-489. https://doi.org/10.1111/j.1751-0813.2011.00852.x

[6] Perrett, E. (2015). Are we killing the golden sheep? The changing size and composition of the Australian sheep flock: Implications for production and profitability. Australasian Business Perspective Paper 101(No. 398-2016-24420). https://ageconsearch.umn.edu/record/234412/

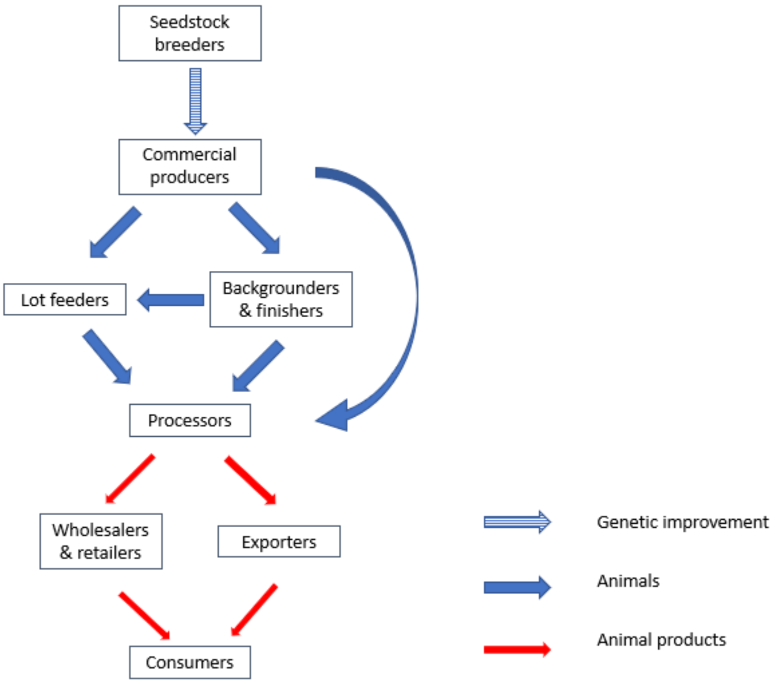

Figure 1. Sectors of the beef and sheep industries

Seedstock breeders

The value chain arguably starts with breeders of seedstock, who are primarily responsible for genetic improvement; and who are also likely to have an interest in DNA technology as a tool to aid in selection.

Successful genetic improvement is a complex and costly process, and in Australia most of the genetic improvement effort is undertaken by specialised seedstock breeders. These breeders are often known as "stud breeders", because they have registered their herd/flock with a breed society. Strictly speaking however, seedstock breeders do not have to be registered studs and many are not.

Typically, these breeders supply entire males (and surplus females) to commercial producers for use as breeding stock. They may also sell semen and/or embryos to commercial producers but in general, this practice is much more prevalent in the dairy industry.

According to the Australian Registered Cattle Breeders Association (ARCBA), there were approximately 145,000 cattle registered as seedstock in 2020, about half of which were British breeds, with almost 25% tropical breeds and the remainder European and other breeds[7]. These were distributed among approximately 7,000 registered breeders.

There are approximately 900 sheep seedstock breeders registered with the Australian Association of Stud Merino Breeders and 570 with the Australian Stud Breeders Association (which covers non-Merino breeds). Although there are almost 30 recognised breeds of sheep in Australia, according to Sheep Genetics (the national genetic information and evaluation service for the meat and wool sectors), six breeds of sheep account for 90% of the commercially active seedstock sector in Australia: Merino, Poll Merino, Poll Dorset, White Suffolk, Suffolk and Border Leicester[8].

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[7] http://arcba.une.edu.au/reports-downloads/registration-statistics/

[8] www.sheepgenetics.org.au

Among the large number of seedstock breeders registered for beef cattle and/or sheep, a relatively small number contribute to the majority of genetic improvement; although the exact balance is difficult to quantify. Figures from BREEDPLAN[9] (the major genetic evaluation service for Australian beef breeders) indicate that among its clients, about 67% of the registered animals come from the largest 23% of the herds. In sheep, 57% of the animals in the Sheep Genetics database come from about 27% of the participating flocks.

Commercial producers

This is the sector in which the great bulk of calves and lambs are born and weaned. Although commercial producers typically maintain their own self-replacing herds or flocks, they generally source their improved breeding stock from the seedstock sector. This is mostly in the form of breeding males and to a lesser extent breeding females but can also be via semen and/or embryos.

Tables released by the Australian Bureau of Statistics (ABS) in May 2021 show the total number of calves less than one year old to be about 5m, and the total number of marked lambs younger than one year to be a little over 20m[10]. These are likely to under-estimate the true numbers weaned, which can be estimated from survey data published by the Department of Agriculture, Water and Environment[11]:

a) In the case of cattle, the branding rates and numbers of cows mated indicate that the average number of calves branded over the past 20 years is approximately 6.6m p.a.

b) For sheep, the average number of lambs marked per farm and the total number of farms indicate that the average number of lambs marked over the past 20 years is approximately 33m p.a.

Recently, Fordyce *et al*. (2021)[12] argued that survey data published by ABS and ABARES consistently under-estimate the true number of cattle in Australia and calculated that since 1985, the average number of calves weaned annually has been approximately 9.8m. For the modelling described later in this report (Section 6), we have assumed the number of calves weaned to be 7.5m p.a.; and the number of lambs weaned to be 35m p.a.

The number of sires used across Australia is of interest in this study, because genotyping sires may be a cost-effective alternative to genotyping all livestock for the purpose of assisting traceability. Sire numbers are not readily available, but Fennessy *et al*. (2014)[13] estimated, using 2012 figures, that an annual intake of 86,000 beef sires would be needed to mate the Australian beef cow herd; and an intake of 254,100 rams would be needed for the national sheep flock. Our computations using the most recent farm survey data from ABARES suggest that these are probably the right order of magnitude but are more likely to be under-estimates than over-estimates.

Commercial producers may elect to finish their young livestock themselves ready for sale to processors or focus on breeding and then sell progeny as store stock to specialist growers or feedlotters. Breeding animals in commercial herds or flocks that are surplus to requirements (usually because of their age or their unsuitability for breeding) are generally sold to processors,

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[9] https://breedplan.une.edu.au

[10] https://www.abs.gov.au/statistics/industry/agriculture/agricultural-commodities-australia/2019-20/71210DO001_201920.xlsx

[11] https://apps.agriculture.gov.au/mla/

[12] Fordyce, G., Richard, R.,Moravek, T and McGowan, M.R. (2021) “Australian cattle herd: a new perspective on structure, performance and production”. Animal Production Science , https://doi.org/10.1071/AN20342

[13] https://www.mla.com.au/contentassets/24b7d0ea1bb44f7097ae83bab1f7932f/b.eva.0001_b.eva.0002_final_report.pdf

either directly or through sale yards; but they may also be on-sold for finishing at pasture or through feed lots.

According to ABS statistics for 2019-20, over half of Australia's beef cattle are in Queensland and the Northern Territory (Figure 2), implying that at least half of Australia's beef cattle are born under relatively extensive conditions. This was illustrated in the report by DAFF (2006)[14], where breeding cow numbers in the northern herds averaged 3,000 head, with some holdings up to 25,000 head, compared with average breeder numbers of 150-400 cows in more temperate regions.

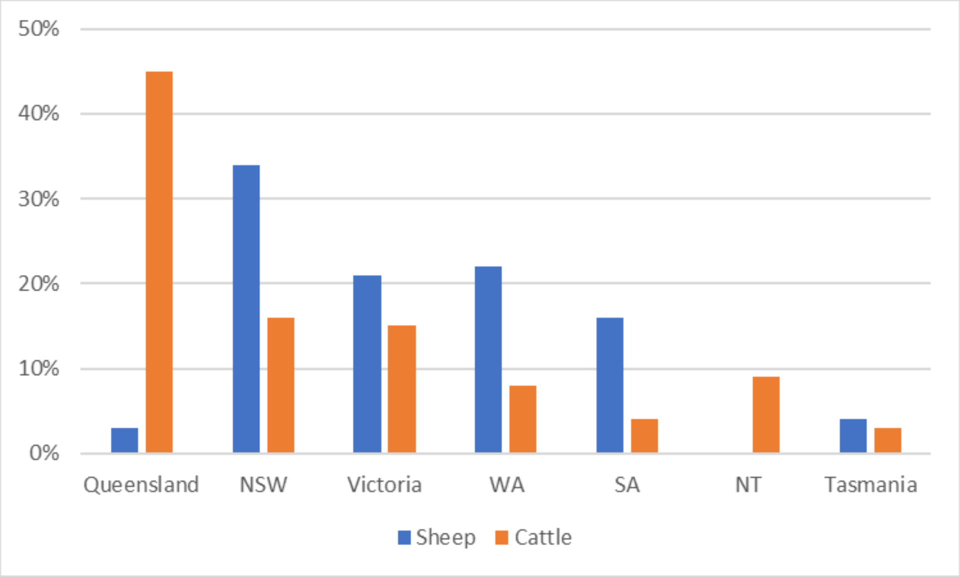

Figure 2. Distribution of beef cattle and sheep by State[15]

In contrast with cattle, the majority of Australia's sheep population is located in New South Wales (34% in 2019-20) and Western Australia (22%), with 21% in Victoria and 16% South Australia (Figure 2). Survey information from ABARES indicates that in 2019-2020, the largest 10% of beef farms produced almost 61% of Australia's beef. This contrasts with the distribution in sheep, where the the largest 10% of farms produced 34% of Australia's output from sheep (Figure 3).

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[14] https://www.agriculture.gov.au/sites/default/files/sitecollectiondocuments/animal-plant/animal-health/livestock-movement/beef-movement-ead.pdf

[15] https://www.abs.gov.au/statistics/industry/agriculture/agricultural-commodities-australia/2019-20/71210DO003_201920.csv

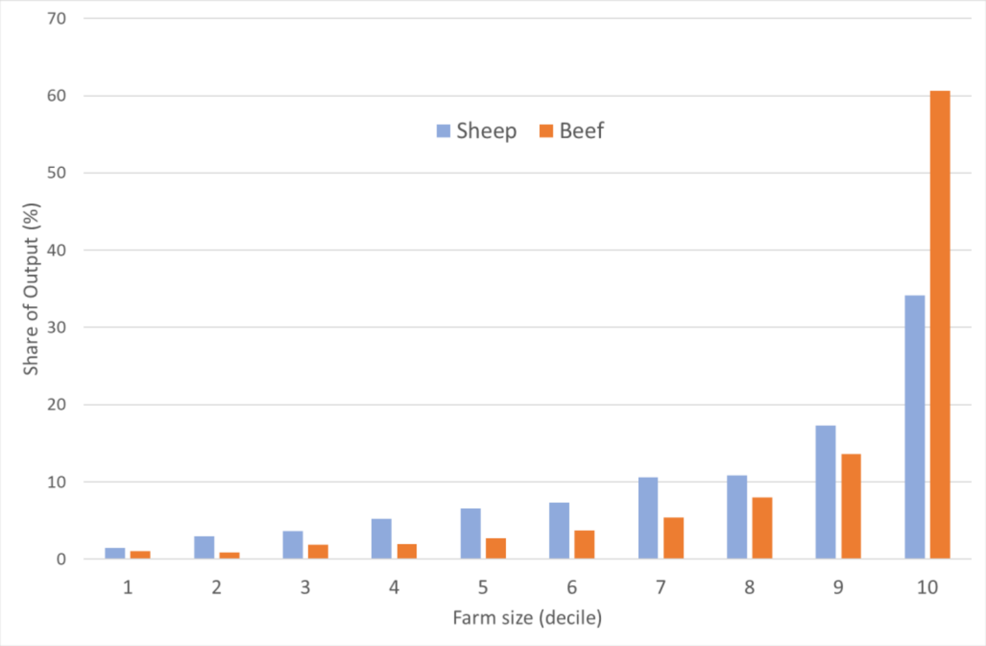

Figure 3. Contribution to national industry output in 2019-2020 according to farm size[16] for sheep and cattle[17]

As of June 2019, breeding ewes (aged one year and over) accounted for 57% of the national flock, while lambs under one year made up 30%[2]. In the same year, 52% of the beef herd were cows and heifers (aged one year and over) and 22% were calves under one year.

Backgrounders and Finishers

These are producers who are generally located in more favourable environments and have the resources to grow (and fatten) livestock to an optimal weight prior to finishing in a feedlot or alternatively, for slaughter. MLA describes the backgrounding process for beef as follows[18]:

> **Backgrounding** refers to the grouping and acclimatisation of animals prior to entry into the feedlot or intensive finishing system. This practice delivers significant production benefits once the cattle are on feed including:
> - Improved socialisation
> - Improved feed intake
> - Reduced health issues
>
> Each of these benefits result in increased weight gain on-feed and increased productivity. Backgrounding also allows cattle to be grown out to a uniform weight before entering the feedlot, providing for easier management on feed and improved production.

Finishers generally use high performance pastures and/or grazing crops to target grass-fed markets. Carcase weight ranges from 260-400kg are typical and there are a multitude of dedicated brands for grass-fed animals. The primary markets are domestic consumption and the US.

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[16] ABARES uses farm total cash receipts to define farm size

[17] https://www.agriculture.gov.au/abares/research-topics/surveys/disaggregating-farm-size

[18] https://www.mla.com.au/research-and-development/feeding-finishing-nutrition/Lotfeeding-intensive-finishing/backgrounding/

Lot Feeders

Feedlots are usually located close to grain-growing areas and focus on fattening livestock on grain-dominant rations for a relatively short period (averaging 50-120 days in cattle), prior to slaughter. There are also specialist lamb lot feeders but these are less common and range in scale from small (<1000 head) to large (>50,000 head).

According to the Australian Lot Feeders' Association (ALFA), *t*here are up to 400 accredited cattle feedlots in Australia with capacities ranging from 500 to over 50,000+ head[19]. At any one time, 2-3% of Australia's total cattle population are in feedlots and grain fed beef contributes 30-40% of Australia's total beef production. In 2020/21 ALFA reported that approximately $2.9 million animals were fed from 70 days (short-day) through to 450 days (long-day) on feed.

It is difficult to provide accurate information on the size of the lamb feedlot industry as there is no central register/survey available from which to obtain this data. However, according to MLA, ABARES estimated that from 2012-2014, approximately 6% of slaughter lambs were produced in feedlots[20]. On a state basis, Western Australia had the highest proportion of lambs finished on grain at 8%, compared with 4% in the eastern states. However, estimates of the numbers of feedlot-produced lambs vary considerably. This is not unexpected as many lamb feedlots are opportunistic and will feed lambs when either market prices or grain prices are favourable. In addition, a proportion of lambs are supplemented with grain during the finishing phase, which is largely a consequence of significant sheep numbers in both the sheep-wheat zone and in the highly seasonal (Mediterranean) regions of southern Australia.

Processors and smallgoods manufacturers

Processors purchase livestock for slaughter and break down the carcases in a form that is ready for domestic or export consumption. The Australian Meat Industry Council (AMIC) is the peak body representing retailers, processors and smallgoods manufacturers across the country. It currently values the domestic smallgoods market at $4b p.a., compared with red meat exports of around $17.2b p.a. and domestic red meat sales of $11.3b[21]. AMIC has estimated that barriers to trade could potentially lead to losses of the order of $3b:

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[19] https://www.feedlots.com.au/overview

[20] https://www.mla.com.au/prices-markets/market-news/2015/grain-finished-lambs-yield-higher-returns--abares/

[21] https://amic.org.au/about-us/

> *More than 70% of the beef and sheep meat produced in Australia is exported, to over 100 international markets. Free trade agreements are essential to gaining market access and there have been some good wins on this front in recent years – but FTAs are not enough to help our members maximise their market potential. Technical barriers to trade must be addressed too.*
>
> *Our calculations show these barriers create the potential for loss of business in the order of more than $3 billion.*
>
> *Barriers include things like detailed export plant accreditation, product shelf-life restrictions and labelling issues.*
>
> Source: https://amic.org.au/market-access/

Research and development for the processing sector is coordinated by the Australian Meat Processor Corporation (AMPC)[22], with membership free to levy-paying red meat processors but funded indirectly through mandatory slaughter levies paid to the government. It has 102 members operating in 130 meat processing establishments, representing more than 90% of Australia's red meat processing capacity. However, the distribution of employee numbers among the largest red meat processors[2] suggests that about 10 companies employ 80% of the processing workforce, with the largest employer accounting for over three times that of the second-largest employer.

Wholesalers and retailers

MLA estimated that in 2018-19, there were about 550 wholesale and 2180 retail businesses in Australia selling red meat[2]. This compares with about 670 businesses involved with processing and over 73,000 businesses involved directly in on-farm production. Wholesale and retail sales accounted for 19% of overall (red meat) industry turnover, compared with 29% for processing and 52% for the production sector. In the domestic market, 83% of fresh meat is sold in supermarkets (mainly Woolworths and Coles) with butchers making up the other 17%[23].

Exporters

Approximately 76% of Australia’s beef and veal production is exported; and of this, the majority is in packed form (88% by value, ~2/3 of which is chilled and 1/3 frozen) with the balance in the form of live animals. In 2020/21, the greatest proportion of Australia’s beef and veal exports (78%) went to China, Japan, the US and South Korea. Live cattle are exported to numerous countries, predominantly in South East Asia and the Middle East[24].

The proportion of Australia’s sheepmeat production that is exported is somewhat lower at about 64%. In 2020/21, China and the US accounted for 51% of Australia’s sheepmeat exports. Approximately 1m head were exported as live sheep to Middle Eastern countries.

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[22] https://www.ampc.com.au/about/ampc-membership

[23] https://www.mla.com.au/globalassets/mla-corporate/prices--markets/documents/os-markets/red-meat-market-snapshots/2019/mla-ms-australia-beef-sheep-2019.pdf

[24] https://www.agriculture.gov.au/animal/welfare/export-trade/cattle_and_sheept_export_destinations

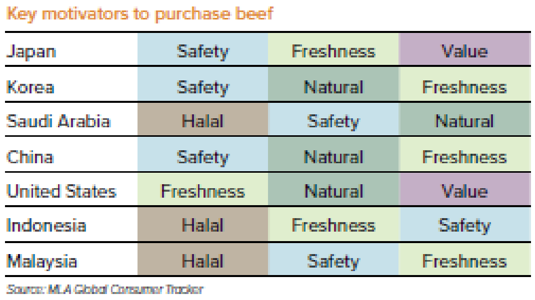
The peak industry body representing Australia's livestock export sector is the Australian Livestock Exporters' Council (ALEC), which is responsible for determining industry policy, providing strategic direction and representing Australia's livestock export trade both nationally and across the world.

Consumers

MLA's State of the Industry Report (2020) noted that over the most recent year, 94% of Australian households had purchased fresh beef and 75% had purchased fresh lamb. It also found that a range of factors influence purchasing decisions for red meat, with freshness, price and ease of preparation the main factors.

According to a survey conducted by MLA in 2020, two in three Australians feel good about the beef and lamb industry, becoming more positive about its impact on society and the environment[25]. More than half Australians agree that producers are ethical and trustworthy, that farming is humane, and that the industry is sustainable and doing all it can do reduce its environmental impact. However, despite becoming increasingly important to Australian consumers, sustainability and animal welfare considerations are typically not paramount in the purchasing decision.

The increasing importance to consumers of sustainability and welfare are also reflected in Australia's export markets for both beef[26] and sheep meat[27], where there is growing consumer interest and awareness of provenance, sustainability, animal welfare, food safety and traceability. MLA has identified the key factors influencing consumer choice for beef and sheep meat in some of Australia's main export markets (box).

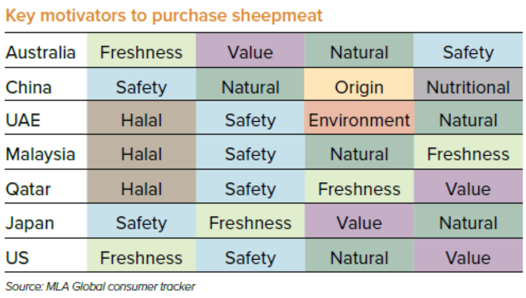


Key motivators to purchase beef

Japan	Safety	Freshness	Value
Korea	Safety	Natural	Freshness
Saudi Arabia	Halal	Safety	Natural
China	Safety	Natural	Freshness
United States	Freshness	Natural	Value
Indonesia	Halal	Freshness	Safety
Malaysia	Halal	Safety	Freshness

Source: MLA Global Consumer Tracker

https://www.mla.com.au/globalassets/mla-corporate/prices--markets/documents/os-markets/red-meat-market-snapshots/2021/global-beef-industry-and-trade-report.pdf



Key motivators to purchase sheepmeat

Australia	Freshness	Value	Natural	Safety
China	Safety	Natural	Origin	Nutritional
UAE	Halal	Safety	Environment	Natural
Malaysia	Halal	Safety	Natural	Freshness
Qatar	Halal	Safety	Freshness	Value
Japan	Safety	Freshness	Value	Natural
US	Freshness	Safety	Natural	Value

Source: MLA Global consumer tracker

https://www.mla.com.au/globalassets/mla-corporate/prices--markets/documents/os-markets/red-meat-market-snapshots/2021/global-sheep-industry-and-trade-report.pdf

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[25] https://www.mla.com.au/marketing-beef-and-lamb/consumer-sentiment-research/

[26] https://www.mla.com.au/globalassets/mla-corporate/prices--markets/documents/os-markets/red-meat-market-snapshots/2021/global-beef-industry-and-trade-report.pdf

[27] https://www.mla.com.au/globalassets/mla-corporate/prices--markets/documents/os-markets/red-meat-market-snapshots/2021/global-sheep-industry-and-trade-report.pdf

3. Traceability and associated applications

Traceability

Food Standards Australia has provided a comprehensive definition of food traceability and its essential features (box):

Food traceability

(January 2017)

Traceability is the ability to track any food through all stages of production, processing and distribution (including importation and at retail). Traceability should mean that movements can be traced one step backwards and one step forward at any point in the supply chain.

For food processing businesses, traceability should extend to being able to identify the source of all food inputs such as:

- raw materials
- additives
- other ingredients
- packaging.
-

Why is traceability important?

Traceability enables corrective actions (such as a product recall) to be implemented quickly and effectively when something goes wrong. When a potential food safety problem is identified, whether by a food business or a government agency, an effective traceability system can help isolate and prevent contaminated products from reaching consumers.

Traceability allows food businesses to target the product(s) affected by a food safety problem, minimising disruption to trade and any potential public health risks. It is important for all food businesses (including retailers and importers) to be able to trace products.

What are the characteristics of a traceability system?

An effective traceability system relies on being able to track product one step forward and one step back at any point in the supply chain. The system a food business has in place includes any procedures for identifying producers, suppliers, customers and products and the records kept including:

- name and address (and other contact details) of suppliers and a description of products or inputs supplied
- name and addresses (and other contact details) of customers and a description of the product supplied to them
- date of transaction or delivery
- batch or lot identification (or other markings)
- volume or quantity of product supplied or received
- any other relevant production records

Source: *https://www.foodstandards.gov.au/industry/safetystandards/traceability/Pages/default.aspx*

For the purpose of this report, we will adopt the definition used by Dwyer & Clarke (2015), which is ***'the proportion of animals that can be successfully traced between defined points in the supply chain or over time'.***

MLA has overseen the development of a comprehensive system for traceability in the Australian red meat industry to help protect Australia's reputation as a supplier of clean, safe and natural food products, including red meat. MLA established the Integrity Systems Company (ISC) in 2017 as a wholly owned subsidiary to initiate, oversee and coordinate related activities. Its stated purpose is to provide food safety measures, product assurance and traceability along the entire red meat supply chain in order to protect and promote Australia's reputation as a supplier of safe food products, produced ethically and responsibly. It has oversight of three elements of the industry's strategy to ensure on-farm assurance and traceability from farmer to processor: the Livestock Production Assurance (LPA) program, the National Vendor Declaration (NVD) and the National Livestock Identification System (NLIS).

This system provides traceability from paddock to plate with an essential role in collecting and collating data from all participants in LPA. In addition, Livestock Data Link (LDL) provides an important facility for producers and other industry stakeholders to gain valuable data insights into animal health and carcase performance. These are summarised by MLA:

Livestock Production Assurance (LPA) program - The LPA program is the Australian industry's on-farm assurance program. It provides evidence of livestock history and on-farm practices when transferring livestock through the value chain. The LPA National Vendor Declaration (LPA NVD) is the declaration communicating the food safety status of every animal as it moves through the supply chain.

National Vendor Declarations (NVD) - The NVD communicates the food safety status of every animal every time it moves along the value chain – between properties, to saleyards, or to processors. Producers can use paper NVDs or the new mobile-friendly eNVD system.

National Livestock Identification System (NLIS) - NLIS is Australia's system for the identification and traceability of cattle, sheep and goats. The NLIS combines three elements to enable the lifetime traceability of animals:

- a visual or electronic ear tag
- a Property Identification Code (PIC)
- an online database to store and correlate the data.

Source: *https://www.mla.com.au/meat-safety-and-traceability/red-meat-integrity-system/*

ISC has also overseen the development of a software system known as **Livestock Data Link (LDL)** which is designed to enable producers and processors to share information about each consignment with respect to disease status, carcase defects and alignment with defined quality specifications.

The flow of genes, animals and animal products between the various industry sectors has been depicted in Figure 1, with "paddock to plate" referring to the pathways between producers and consumers. Traceability of animals to the processor stage is enabled by NVDs and NLIS tags. Thereafter, traceability relies on documentation through the AUS-MEAT program.

In 2015, MLA supported a benefit-cost assessment of NLIS, LPA and associated food safety research (Dwyer and Clarke 2015)[28]. That study estimated the benefit cost ratio for the combined programs to be between 7.4 and 8.9, equating to a projected net benefit over 30 years of $8.7b to $10.6b (in 2014 dollars). NLIS contributed the majority of the benefits, but all three components yielded positive returns. The figures for NLIS were deemed to be lower-bound estimates, predominantly reflecting the benefits of reducing the impacts of foot and mouth disease but excluding the benefits of reducing the impact of a wide array of other potential exotic and endemic diseases. Their analyses assumed that NLIS increased the traceability in beef from 65% to 97% and in sheep from 65% to 90%.

A subsequent study (White *et al.*, 2019)[29] using slightly modified assumptions, revised the net benefits upwards and made a number of recommendations, including work to increase the levels of traceability through ongoing system and technology enhancements, as well as to explore opportunities for deriving additional value from collected data, *inter alia.*

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[28] https://www.mla.com.au/contentassets/1583d850bfa546d098a18dfb07c50d5e/v.lim.1505_final_report.pdf

[29] https://www.mla.com.au/globalassets/mla-corporate/research-and-development/final-reports/2020/v.isc.1918-final-report.pdf

Vulnerabilities

There are two places along the red meat supply chain where identities / identification (and therefore full traceability) can potentially be lost.

The first stems from the fact that animals can (and sometimes do) lose their ear-tags. Often the animal has a second management tag which can be used to enable its identity to be tracked when the lost tag is replaced. However, this is not always the case. There appear to be no official reports published on tag loss rates, but anecdotal evidence (from stakeholder consultations, the rural press[30] and the survey summarised later in Section 4) indicates that estimates of total identity loss due to lost ear tags typically range from 3% to 10% in cattle; and from 3% to 8% in sheep. One Australian processor estimated that lost identity due to lost tags averages about 2% in cattle. The lost value associated with traceability loss (tag loss) varies with the type of market, carcase weight and potential carcase quality. Quantifying the loss is a subject of this current study; however early discussions with processors indicated that discounts were primarily associated with the transfer from one market to another. The resulting loss could be as much as 15% of the total value of a carcase, which can be in the hundreds of dollars for high value markets (long-fed Wagyu).

The second potential loss of identity occurs at slaughter, after which time the product is tracked by physical or electronic records. From this point, proving the veracity of identification becomes more difficult if there is a dispute or a need to determine the source of a contaminant or pathogen, particularly when meat cuts are combined or blended during the packing process or through mincing.

A recent report for MLA by Asymmetric Innovation Pty Ltd claimed a loss in traceability of beef cattle of around 4% in 2018-19 due to tag problems (losses, damage and non-reconciled breeder tags) as well as failure to scan between PICs[31]. The project's authors recommended that further work be done on implantable tags to overcome these losses, which were estimated to be worth $10m p.a. in direct costs and over $2b in increased biosecurity risks.

Systems allowing complete trace-back

The two main methods currently in use rely on intrinsic properties of the animal tissue, namely chemical composition and genotype.

Chemical composition

A useful review of chemical provenancing of foodstuffs and the methodology in use can be found in the PhD thesis of Kreitals (2013)[32], which also provides estimates of the historical costs associated with food-borne pathogens, fraudulent labelling and product substitution. Chemical provenancing relies on the fact that the trace element concentrations in plant and animal tissue are affected by relatively small variations in the environment in which they are grown, giving them a unique chemical "signature". This signature can be used to help trace products along the supply chain.

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[30] https://www.beefcentral.com/news/tag-retention-nlis-tag-losses-still-frustrating-producers/

[31] https://www.mla.com.au/research-and-development/reports/2021/project-summary-v.rda.0002---assessing-the-feasibility-of-an-implantable-id-for-cattle/

[32] Kreitals, N.M. (2013). "Use of multi-element profiling for the traceability of Australian pork offal and its relationship to the pork meat Physi-Trace database", PhD thesis, University of Western Australia https://research-repository.uwa.edu.au/files/3223911/Kreitals_Natasha_2013.pdf

The Australian pork industry has developed a traceability process called Physi-trace™, to verify and defend provenance claims and to support the supply of consistently high eating quality Australian pork to its customers (described by Channon *et al*. 2018)[33]. It is used in conjunction with a paper-based livestock and identification movement system called a PigPass National Vendor Declaration (NVD) that is linked to the PigPass database[34]. Physi-trace™ relies on systematic variations in the chemical composition of pork from different sources. Trace elements in a given sample can be compared with known reference samples to validate country, state and farm of origin. Physi-Trace™ uses TSW Analytical Pty Ltd laboratories for processing its samples. TSW Analytical is part of the Source Certain group[35], which also provides supply chain traceability services for a wide range of products including minerals, pharmaceuticals, foodstuffs (incl. meat), artworks *etc*. using TSW Trace™ methodology[36]. Source Certain depicts the general process as shown in Figure 2.

APL's 1920/21 Annual Report indicates the cost of a single traceback event to be around $6,600. According to APL (V. Gore, *pers. comm.*), this is because the library must be updated with samples from the putative piggery to ensure currency of the database, as trace element profiles can change with water supply, feed additives *etc*. Turn-around time is thought to be approximately 5 days, but this can vary considerably depending on laboratory availability. APL is currently supporting projects to enhance the technology using machine learning[37].

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[33] H.A. Channon, H.A., D'Souzac, D.N., Jarrett, R.G., Lee, G.S.H., Watling, R.J., Jolley, J.Y.C and Dunshea, F.R. (2018). "Guaranteeing the quality and integrity of pork – An Australian case study". Meat Science 144:186-192

[34] https://pigpass.australianpork.com.au/faq

[35] https://sourcecertain.international/about.php

[36] https://www.tswanalytical.com.au/projects

[37] https://australianpork.com.au/search-projects?keyword_text=physitrace&project_date%5Bmin%5D=&project_date%5Bmax%5D=&project_category=All&project_status=current&sort_bef_combine=title_ASC&sort_by_date=1

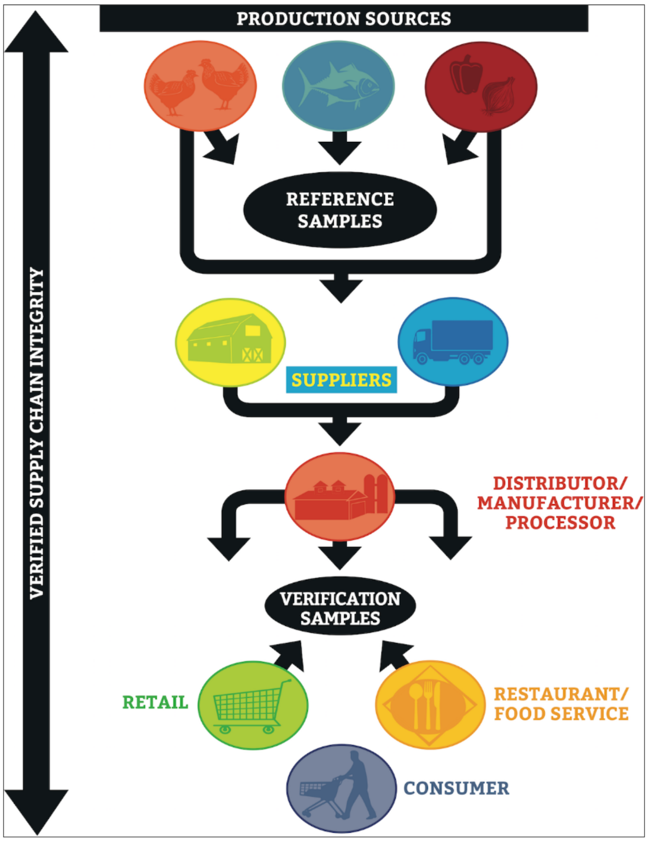

Figure 4. The TSW Trace™ system.
(Source: https://sourcecertain.international/technology.php)

Oritain™ is another company offering a service that uses trace elements and isotopes in a product to help ascertain its source. According to Oritain's web site, the technology is built on criminal forensic techniques and claims to be acceptable as evidence in a criminal court of law, delivering results in 1-5 days[38]. It works in the fields of aquaculture, eggs, fibre, honey, horticulture, meat, wine and pharmaceuticals, *inter alia.* A recent MLA Donor Company project demonstrated Oritain's ability to distinguish Australian beef and lamb from meat produced in other countries by developing a "Fit for purpose Origin Fingerprint"[39]. Reference sets were established for both beef and lamb by collecting samples from a wide range of abattoirs across Australia. The profiles of 75 samples were determined and were found to be statistically distinguishable from samples taken in other countries – 14 countries in the case of beef and eight for lamb.

The effectiveness of systems that rely on chemical composition obviously depend on the comprehensiveness of the reference library and on the background profiles of farms being sufficiently different from one another and reproducible over time. Given the variability of soil types, water, pasture, rainfall, feeding supplements and even breed within a typical beef or sheep property, we consider it unlikely that chemical profiling could reliably distinguish between products grown on neighbouring farms with similar production systems, for example; at least not without a very large and frequently updated reference library of tissue samples.

Genomics

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[38] https://oritain.com/how-it-works/the-science/

[39] https://www.mla.com.au/research-and-development/reports/2020/compositional-traceability---origin-fingerprints-for-australian-beef-and-lamb/

Genotypic information is used widely in the animal industries, particularly in the seedstock sector, and relies on the fact that each animal has a unique genetic profile (monozygotic twins and clones being notable exceptions). Although there are now numerous applications of genomic technologies, those principally used by breeders in the cattle and sheep industries can be classified as being primarily for ancestry ascertainment/verification and/or genetic evaluation (although the two applications are not unrelated). The latter includes diagnostics for a wide range of genetic defects and poll/horn status and is being used increasingly for performance prediction and sorting for specific production and finishing pathways. DNA is typically extracted from tail hair samples, blood cards, semen or an ear punch using a tissue sampling unit (TSU). According to Allflex, the latter is the method preferred by most laboratories as it is reliable, provides a clean sample, is easy to transport, is bar coded and can be readily matched to NLIS and management tags[40].

With the rapid evolution of genomic technologies, the possibility now exists that DNA information could be used to help overcome some of the perceived vulnerabilities in the current traceability system. This idea was explored as early as 2006 in an MLA-supported project by id-DNA Pty Ltd[41], who held a relevant patent position involving genotyping animals and loading genomic information back onto RFID ear tags. These patents appear to have lapsed[42].

More recently, both Ireland and Switzerland have implemented a national DNA-based identification system for their cattle herds. In the UK, a pilot project was launched in early 2021 to assess the potential for a DNA traceability system through the UK's beef supply chain and some beef supply chains in Australia are already using the technology on a limited basis.

Other applications of genomic information

As indicated previously, a growing number of seedstock breeders (both cattle and sheep) are using genomic technologies in some form. The most common applications are for genomic prediction and for pedigree ascertainment/verification.

In recent years, about one-third of the flocks contributing data to Sheep Genetics supply at least some genomic information for one of these purposes. This is substantially greater than the proportion of animals in the Sheep Genetics dataset with genomic information, but it does indicate that many sheep breeders have at least had some experience with the process of collecting and submitting tissue samples for genomic analysis. In beef, there is wide variation between breeds, but overall, around 30-50% of animals entering BREEDPLAN analyses within a year now have genomic information included, reflecting use by approximately 20-30% of breeders. The adoption rate in both sheep and beef, as measured by numbers of genotypes being submitted, is growing rapidly.

Genomic prediction Genomic tests allow selections in the seedstock sector to be made at an earlier age (thus reducing the generation interval) and can provide predictions for important traits that are difficult and/or expensive to measure directly. This can lead to greater rates of genetic gain in traits of economic importance. Recent software developments in BREEDPLAN and Sheep Genetics allow all phenotypic and genomic information to be used simultaneously in national evaluations, at least in the major breeds. The number of genotyping providers servicing breeders in Australia continues to increase, with AGBU recently developing a set of industry standards for genotype panels (Connors and Ferdosi 2019)[43].

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[40] https://www.allflex.global/au/product/tsu-sampling-units/

[41] https://www.mla.com.au/contentassets/4163752b65d843eab5317a54e5aba0db/a.scc.0018_final_report.pdf

[42] Patent applications 2006209790 and 2005900456

[43] Connors, N.K. and Ferdosi, M.H. (2019) "Genotype panel requirements for inclusion into BREEDPLAN single step evaluations". Proceedings Assoc. Adv. Anim. Br Genet. 23: 382-385.

The marginal benefits of genomic information as an aid to selection are relatively small in traits that are easy to measure (such as body weight or fleece weight), but there are significant advantages for traits that are difficult or expensive to measure (such as feed efficiency or methane emissions), are sex-limited (female fertility), are only expressed in some environments (such as disease resistance) or are only expressed later in life (lifetime reproduction) or *post mortem* (carcase and eating quality traits).

Genomic tests also exist to detect carriers for a number of genetic conditions. For example, Angus Australia routinely monitors for nine such conditions including dwarfism and horns[44]; and Sheep Genetics lists 11 simply-inherited traits included in commonly-used genomic panels (yellow fat, hairy lamb, callipyge, myostatin *etc*.)[45]. Panels used for genomic prediction typically contain 50-60,000 SNPs and cost the breeder in the vicinity of $50, but lower density tests with lower predictive power are also available (*e.g.* in Angus) for around $40.

Parentage tests: Smaller panels containing several hundred SNPs are also available for parentage tests in either sheep and cattle, costing in the vicinity of $20-$30. Apart from the obvious applications related to genetic selection, results from these tests can be (and have been) used to help resolve disputes over ownership, sire/semen usage and proof of genetic ownership.

Poll/horn test: A diagnostic poll haplotype test is available for cattle in Australia, largely driven by animal welfare concerns. Connors *et al*. (2018) [46] reported that by January 2017, the test had been applied to more than 25,000 animals. That number was steadily increasing and included animals from over 50 breeds, but most were from either Brahman, Santa Gertrudis, Hereford, Charolais, Droughtmaster or Limousin cattle.

Genomic tests have also been developed for use in the commercial breeding and finishing sectors, intended to predict an animal's performance, including post farm-gate. The utility of predictions for such traits as growth, carcase quality, disease, fertility *etc*. is only limited only by the quantity and quality of reference data for a particular breed or breed mix. Examples include tests for:

Replacement females: Angus Australia (in partnership with both Zoetis and Neogen) have recently released an updated version of Angus HeiferSelect™, which predicts performance for nine maternal, growth and carcase traits, as well as providing a rating for aggregate breeding value and which can be used for optimal sire assignment. It is intended for use in commercial cattle with at least 87.5% Angus ancestry and is intended as a management tool to assist in identifying heifer replacements (and culls) and mating allocations at a cost of around $40 per sample. The product is showing accelerating levels of uptake and is supported by a recent Zoetis case study showing a positive return on investment from using the product[47].

Feedlot performance: Growth rate, marbling and feed efficiency are all key profit drivers in feedlot performance. Hines *et al.* (2021) [48] recently published a study of a new product called Angus SteerSelect™, which predicts carcase weight, marbling score and ossification score in purebred

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[44] https://www.angusaustralia.com.au/education/breeding-and-genetics/genetic-conditions-in-angus/

[45] https://www.sheepgenetics.org.au/resources/genomics/

[46] Connors N.K., Tier, B. and Johnston D.J. (2018) "Current status of Australia's diagnostic poll haplotype test". Proc. World Congr. Genet. App. Livest. Breed. 11: 344-352.

[47] https://www.youtube.com/watch?v=rKGFWIHBRdA

[48] Hine, B.C., Duff, C.J., Byrne, A., Parnell, P., Porto-Neto, L., Li, Y., Ingham, A.B., Reverter, A. 2021) "Development of Angus SteerSELECT: a genomic-based tool to identify performance differences of Australian Angus steers during feedlot finishing: Phase 1 validation." Animal Production Science 61, 1884-1892.

Angus lot-fed steers. Animals ranked in the top quartile for predicted carcase value were worth approximately 20% more than those in the bottom quartile, in both short-fed and long-fed steers. This equates to differentials of $351 and $712, respectively. Further work is under way to expand the number of traits to nine, including immune competence.

The American Angus Association provides similar tests for commercial producers in the US, which provide index values for a range of maternal, growth and carcase traits, as well as docility and cow costs[49]. Pricing is currently around USD28 (compared with standalone parentage or sire verification costs of USD18).

General performance profiling: Neogen Australasia offers a genomic profile test (Igenity® Beef) [50] designed for crossbred commercial cattle, using DNA to predict genetic merit in both heifers and steers to provide an additional heifer selection tool for cattle producers. Producers also use the test in the production of high-value steers and to score commercial bulls being used as sires. The test includes 16 maternal, performance, and carcass traits plus parentage, with customised versions available for different breeds including Brangus and Santa Gertrudis. Neogen claims that the test is backed by the world's largest multi-breed genetic evaluation (International Genetic Solutions, or IGS), which includes at least 16 North American breed societies and has access to a database with over 20m animal records and 350,000 genotypes.

Flock profile: The Cooperative Research Centre for Sheep Industry Innovation (Sheep CRC) developed a test specifically for commercial sheep producers which allows them to benchmark the performance of their flock against industry averages. It requires DNA to be collected from a random sample of 20 animals from the same drop and processed by a commercial genomics laboratory. Sheep Genetics then provides benchmarking information for a range of traits and genetic conditions.

In addition to providing specific applications for individual users, widespread adoption of genomic technologies can also offer broader industry benefits apart from traceability and the above applications, for example:

a) To help determine the degree of connection of a cohort of animals to a genomic reference population, so that commercial data collected by industry can contribute to specific reference populations, thereby adding value – larger reference populations will deliver more accurate genomic predictions, therefore speeding up rate of genetic gain in the industry.

b) This could be extended to linking with other means of tracing (such as chemical profile) to help differentiate between genetic and environmental fingerprints in the context of establishing provenance.

c) Uses in animal health, including by estimating proportion of population at risk from pathogens *etc*. For example, in Ireland, the ICBF uses its genomic database to enable the identification of sires with enhanced genetic resistance to tuberculosis and liver fluke[51]. This can potentially be extended to infer risk using genetic similarity to one or more reference populations by linking incidence database(s).

In summary, with appropriate data collection and management systems in place, having a large proportion of the population genotyped can potentially lead to larger reference populations and

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[49] https://www.angus.org/AGI/pages/CommercialTests/AGICommericalTestingOptions.pdf

[50] https://www.neogen.com/categories/igenity-profiles/igenity-beef/

[51] https://www.icbf.com/?page_id=12693

much more accurate selection decisions (faster genetic gain) in the seedstock sector, as depicted in Figure 5, benefitting the entire value chain. Not represented in this diagram are the direct benefits that genomic information can offer other participants in the value chain by providing access to predicted performance attributes; or other potential ancillary benefits describe above.

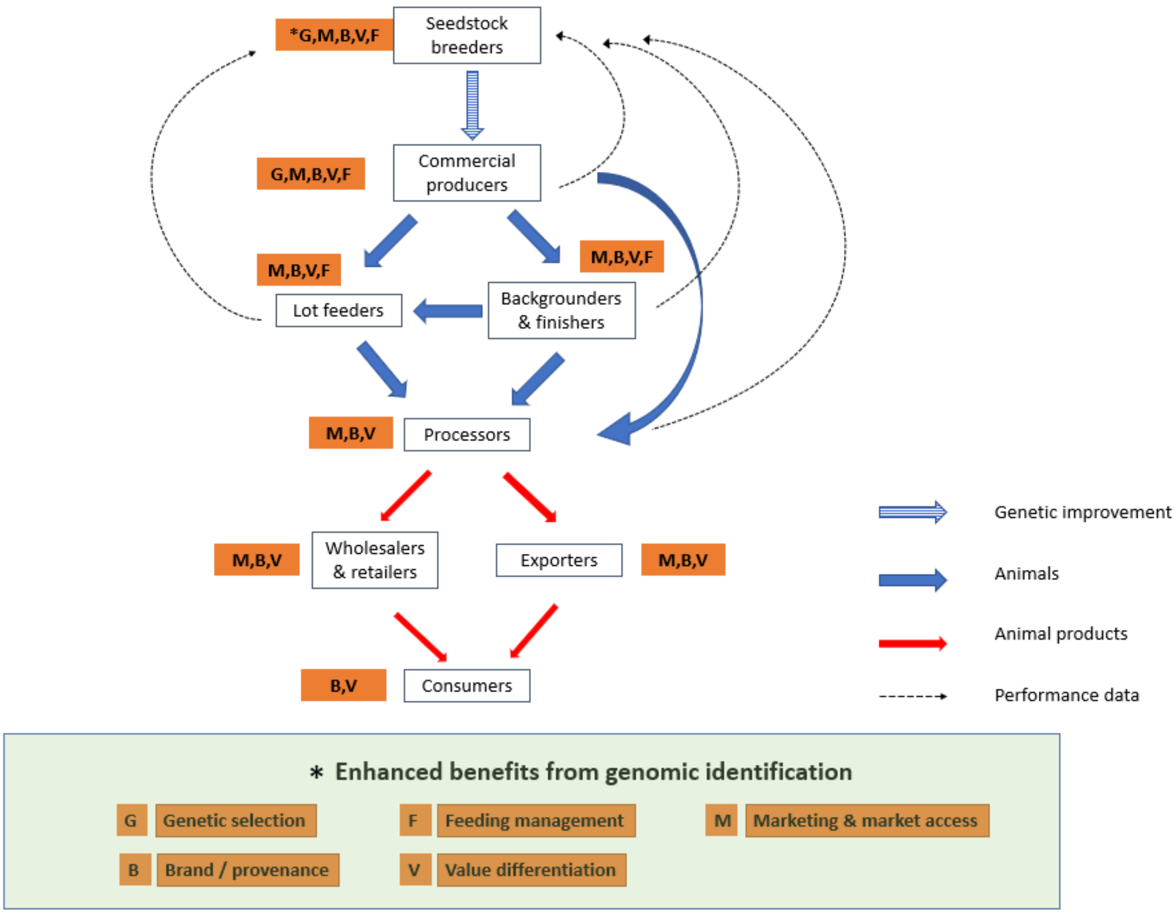


Figure 5. Flow of animals, products and information between sectors, showing benefits from genomic identification

4. Industry views on traceability options

One of the key objectives of this project was to seek significant industry feedback and perceptions concerning their understanding of the current traceability system and the potential role that genomics may play in red meat traceability. This was comprised of two phases, being an online survey (through Survey Monkey®) and targeted one-on-one interviews. The survey methodology is detailed in Appendix 1 and was used to gather a broad range of opinions from various industry stakeholders, eliciting 100 responses.

A smaller number (20+) of targeted one-on-one interviews were then used to explore some issues in greater depth. These included known genomic technology providers, key service providers (breed societies) and significant stakeholders such as stud breeders, feedlots, agents and processors. The main aims were to:

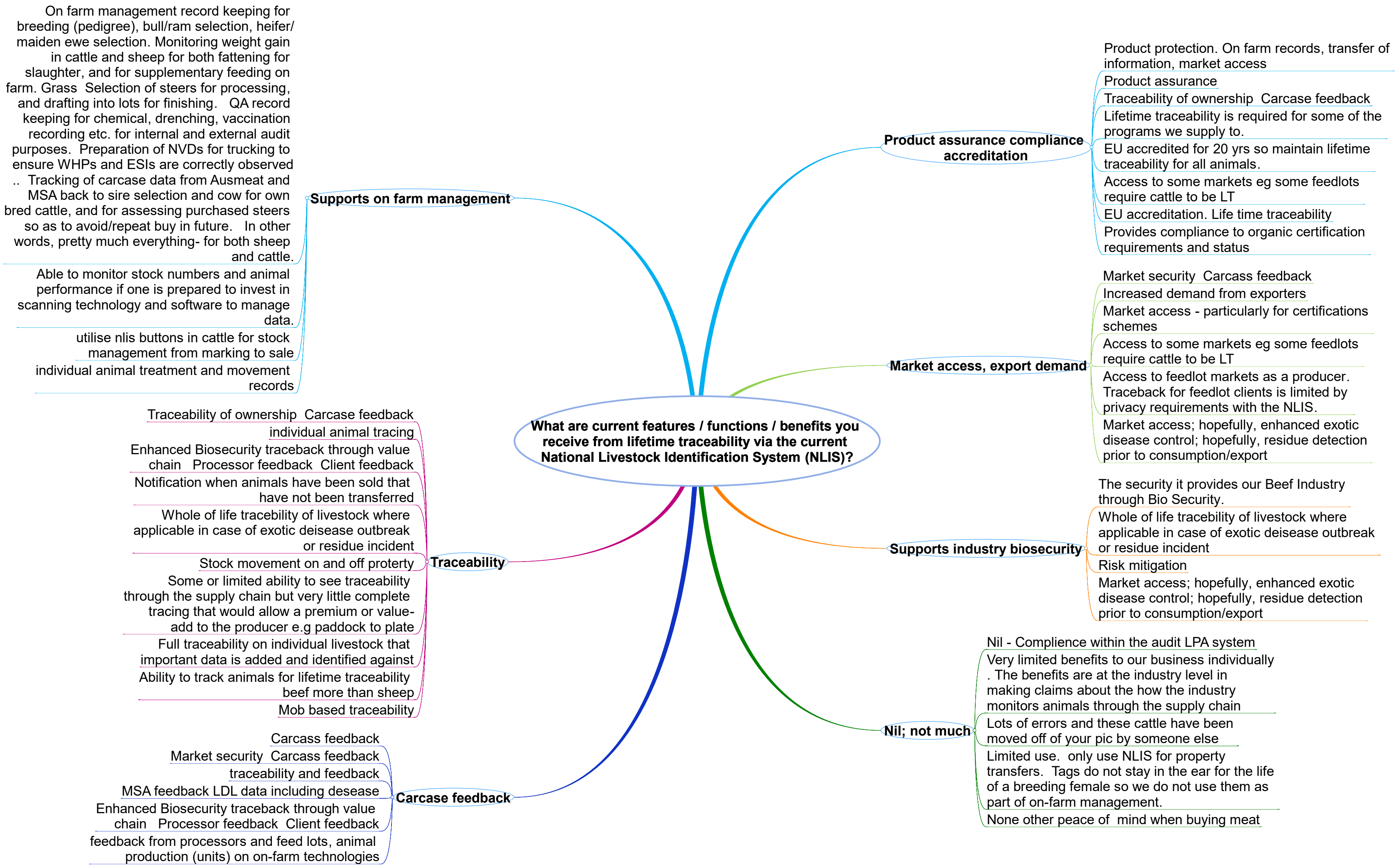
a) further explore how genomic technologies may influence traceability;
b) better understand potential barriers to adoption and utilisation; and
c) identify future possibilities that genomic technologies may offer.

Online survey questionnaire

The primary objective and outcome of the online survey was to obtain feedback and opinions on a range of questions relating to utilisation of the current system, awareness and utilisation of genomic and DNA technologies, opportunities for genomics in traceability and barriers that may occur. The survey responses provided both qualitative and quantitative information. The qualitative information has been aggregated into thematic areas within a mind map construct to allow visualisation of the information. The quantitative information was analysed within various sub-cohorts and is presented in a series of graphs.

Expectations, features and benefits of the current traceability system

Red meat stakeholders identified a range of features and benefits that they expect to obtain from the current NLIS lifetime traceability system. Figure 6 depicts a thematic analysis of the responses.



What are current features / functions / benefits you receive from lifetime traceability via the current National Livestock Identification System (NLIS)?

- **Supports on farm management**
  - On farm management record keeping for breeding (pedigree), bull/ram selection, heifer/maiden ewe selection. Monitoring weight gain in cattle and sheep for both fattening for slaughter, and for supplementary feeding on farm. Grass Selection of steers for processing, and drafting into lots for finishing. QA record keeping for chemical, drenching, vaccination recording etc. for internal and external audit purposes. Preparation of NVDs for trucking to ensure WHPs and ESIs are correctly observed .. Tracking of carcase data from Ausmeat and MSA back to sire selection and cow for own bred cattle, and for assessing purchased steers so as to avoid/repeat buy in future. In other words, pretty much everything- for both sheep and cattle.
  - Able to monitor stock numbers and animal performance if one is prepared to invest in scanning technology and software to manage data.
  - utilise nlis buttons in cattle for stock management from marking to sale
  - individual animal treatment and movement records
- **Traceability**
  - Traceability of ownership Carcase feedback
  - individual animal tracing
  - Enhanced Biosecurity traceback through value chain Processor feedback Client feedback
  - Notification when animals have been sold that have not been transferred
  - Whole of life tracebility of livestock where applicable in case of exotic deisease outbreak or residue incident
  - Stock movement on and off proterty
  - Some or limited ability to see traceability through the supply chain but very little complete tracing that would allow a premium or value-add to the producer e.g paddock to plate
  - Full traceability on individual livestock that important data is added and identified against
  - Ability to track animals for lifetime traceability beef more than sheep
  - Mob based traceability
- **Carcase feedback**
  - Carcass feedback
  - Market security Carcass feedback
  - traceability and feedback
  - MSA feedback LDL data including desease
  - Enhanced Biosecurity traceback through value chain Processor feedback Client feedback
  - feedback from processors and feed lots, animal production (units) on on-farm technologies
- **Product assurance compliance accreditation**
  - Product protection. On farm records, transfer of information, market access
  - Product assurance
  - Traceability of ownership Carcase feedback
  - Lifetime traceability is required for some of the programs we supply to.
  - EU accredited for 20 yrs so maintain lifetime traceability for all animals.
  - Access to some markets eg some feedlots require cattle to be LT
  - EU accreditation. Life time traceability
  - Provides compliance to organic certification requirements and status
- **Market access, export demand**
  - Market security Carcass feedback
  - Increased demand from exporters
  - Market access - particularly for certifications schemes
  - Access to some markets eg some feedlots require cattle to be LT
  - Access to feedlot markets as a producer. Traceback for feedlot clients is limited by privacy requirements with the NLIS.
  - Market access; hopefully, enhanced exotic disease control; hopefully, residue detection prior to consumption/export
- **Supports industry biosecurity**
  - The security it provides our Beef Industry through Bio Security.
  - Whole of life tracebility of livestock where applicable in case of exotic deisease outbreak or residue incident
  - Risk mitigation
  - Market access; hopefully, enhanced exotic disease control; hopefully, residue detection prior to consumption/export
- **Nil; not much**
  - Nil - Complience within the audit LPA system
  - Very limited benefits to our business individually . The benefits are at the industry level in making claims about the how the industry monitors animals through the supply chain
  - Lots of errors and these cattle have been moved off of your pic by someone else
  - Limited use. only use NLIS for property transfers. Tags do not stay in the ear for the life of a breeding female so we do not use them as part of on-farm management.
  - None other peace of mind when buying meat

Figure 6. Thematic analysis of the key features, functions and benefits that red meat stakeholders receive from the current traceability system via NLIS

As expected, there was a strong connection between lifetime traceability, carcase feedback (performance) and on farm management and decision making. That connection highlighted the importance of data collection and the ability to link a unique NLIS identifier (record; animal) with data collected either on farm or further down the supply chain. Specifically, data from MSA and AUS-MEAT carcase feedback was frequently mentioned. From the responses, it is evident that such carcase feedback is an important ancillary benefit which is, in the main, also seen as a 'key ancillary benefit' from the national traceability system.

Furthermore, there was a strong connection of product assurance, compliance and accreditation with access to markets (particularly export markets). There was an additional connection identified with whole of industry biosecurity, residue tracking and risks of disease. Most producers and lot feeders identified the current traceability system as key to market access.

A small proportion of respondents failed to identify benefits and had quite negative opinions on the current NLIS. That sentiment is often observed in industry commentary, but in reality (from our experience and backed by the number of LPA registered users) is likely to reflect the view of only a very small percentage of the overall industry.

When prompted to categorise or identify the additional benefits from a defined sets of themes that are linked to lifetime traceability via NLIS, beef and sheep stakeholders both identified food safety, product integrity and animal health and welfare as the most prominent benefits (Figure 7). Carcase benchmarking and provenance rated higher for beef than sheep, which potentially reflects the impact of the MSA program, and the number of beef brands linked to quality and breed.

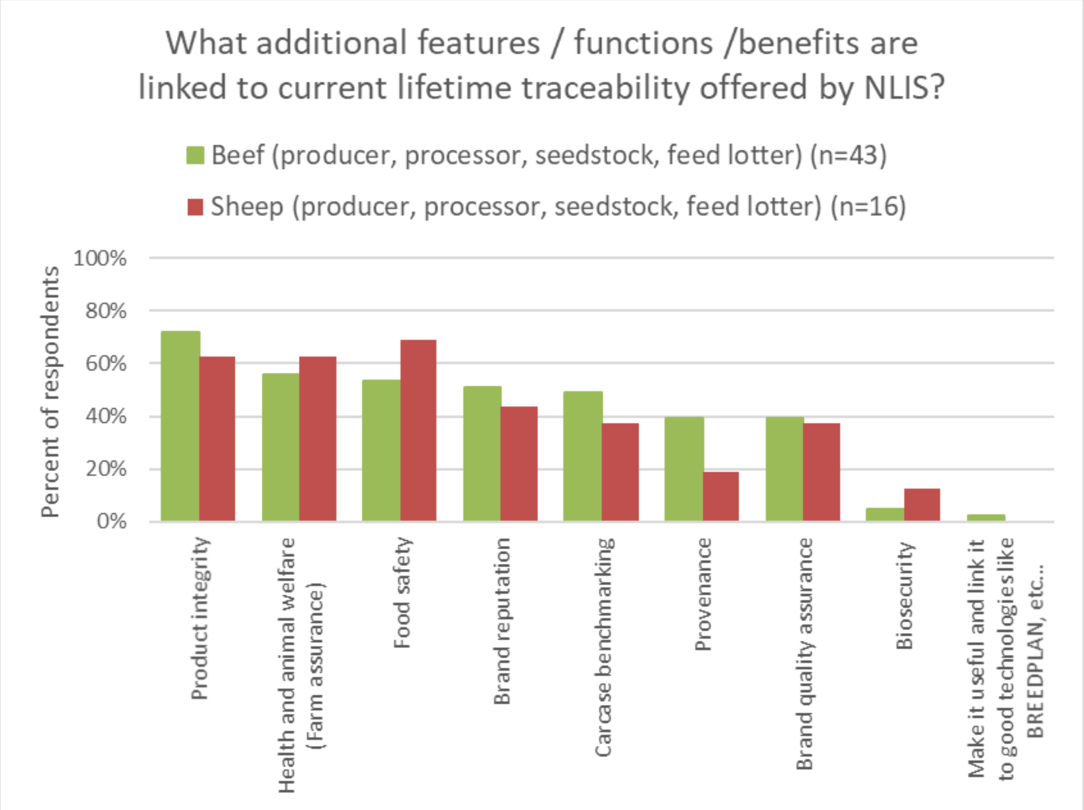


Figure 7. Additional benefits linked to NLIS tags

In general, respondents from the production sector identified additional benefits with the same frequency as those from the processing sector (Figure 8); however, processors identified a higher proportion of the suggested themes more often, except for provenance. Interestingly, the benefits of biosecurity ranked last amongst those identified by survey respondents.

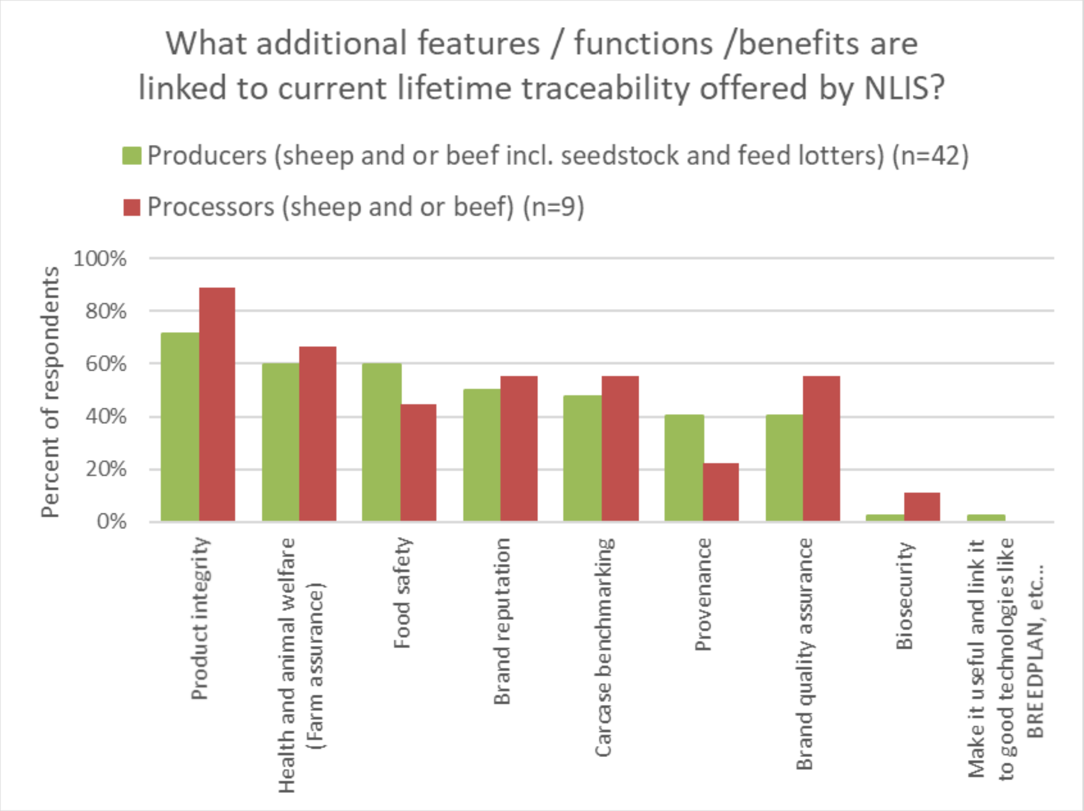


Figure 8. Additional benefits linked to NLIS tags (producers and processors)

There was an interesting but not unexpected response to the timeframes required to verify lifetime traceability. Processors indicated either real time (44%) or within a 24-hour timeframe (45%; 89% cumulative), with 100% verification (cumulative) required within a week. Production sector respondents also had a relatively short timeframe requirement with 38% real time, 38% within 24 hours (68% cumulative) and 80% cumulative within a week. This response has some very important implications for the application of genomics in lifetime traceability, which with current technology will not be able to satisfy the real time aspiration and will require sophisticated systems to meet the 24 hour and 1 week expectation.

Loss of Lifetime traceability in current system

Accurately assessing the business case for incorporation of genomic technologies into the current and future traceability system requires some understanding of the loss (perceived and real) of NLIS tags across industry. Over a five-year period, purchases of post-breeder tags have represented 3% of total NLIS tag purchases in beef[52], suggesting that this has been the annual incidence of tag losses; however, there is ample anecdotal evidence to suggest that tag loss may be higher in many instances. Respondents to our survey generally reported low rates of tag loss, with 84% indicating less than 5% in the beef sector and 93% less than 5% in the sheep sector. Of note, 8% of the beef sector respondents (1 producer and two processors) indicated loss rates of between 5-10%; and 5% (one producer, one beef seedstock) indicated above 10% tag loss (both of whom were in Northern Australia). In contrast only one sheep producer observed tag losses as high as 5-10% (see Figure 9).

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[52] https://www.beefcentral.com/news/tag-retention-nlis-tag-losses-still-frustrating-producers/

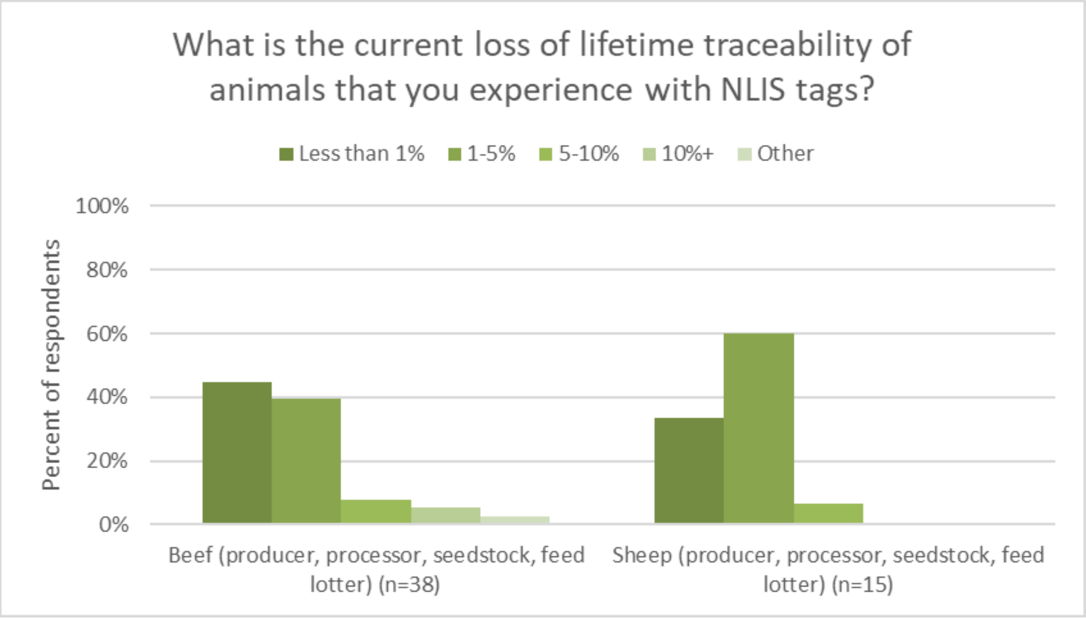


Figure 9. Current loss of lifetime traceability with NLIS tags

When asked to estimate the costs (loss of value) associated with the loss of the NLIS tags and therefore lifetime traceability in cattle, there was an unexpectedly wide range from less than $5 per head (39%) to greater than $50 per head (27%) for those respondents from the beef production sectors (seedstock, producers and lot feeders; see Figure 10). Processors also indicated significant variation in the costs, with 25% indicating a $5-10 loss and 63% a cost greater than $50.

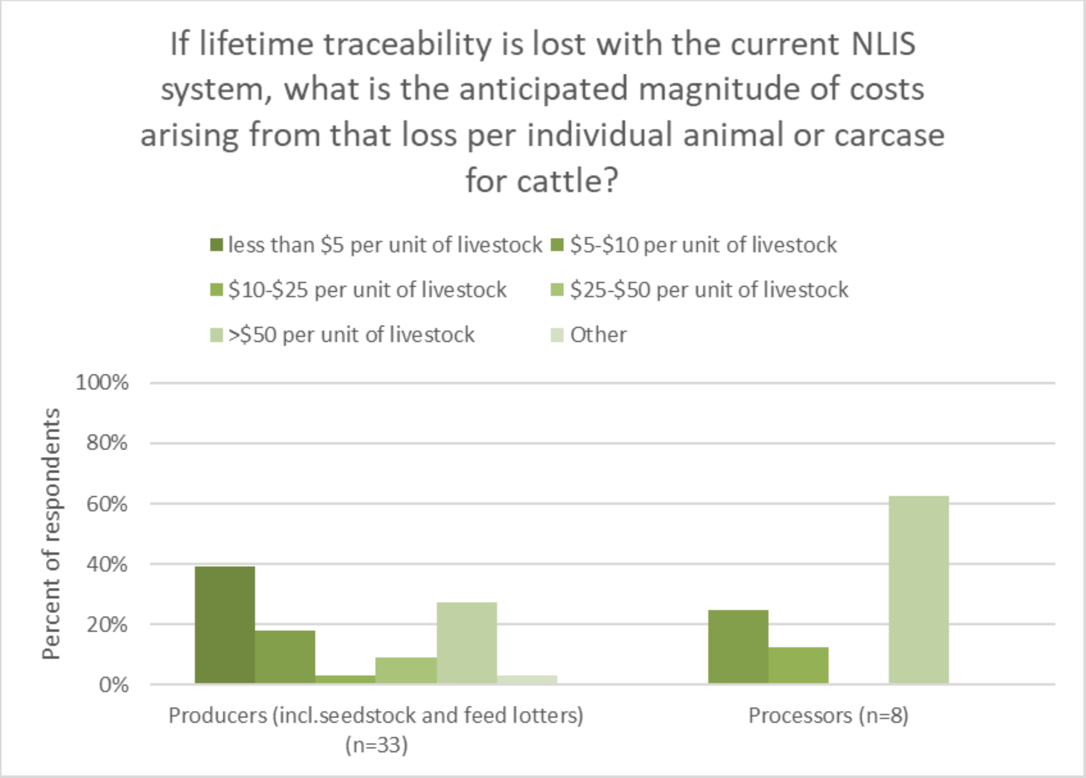


Figure 10. Estimates of current costs associated with loss of NLIS tag for cattle

As expected, the costs associated with loss of NLIS tags for sheep or lambs was generally lower (Figure 11), with 47% of the production sector indicating a loss of less than $5, however 9% did indicate a loss of $50 or greater (seedstock). There was a high other comment response rate which were generally associated with either zero or negligible losses. Sheep processors again showed significant variation with 29% indicating a loss less than $5 and 29% indicating a loss greater than $50 per carcase.

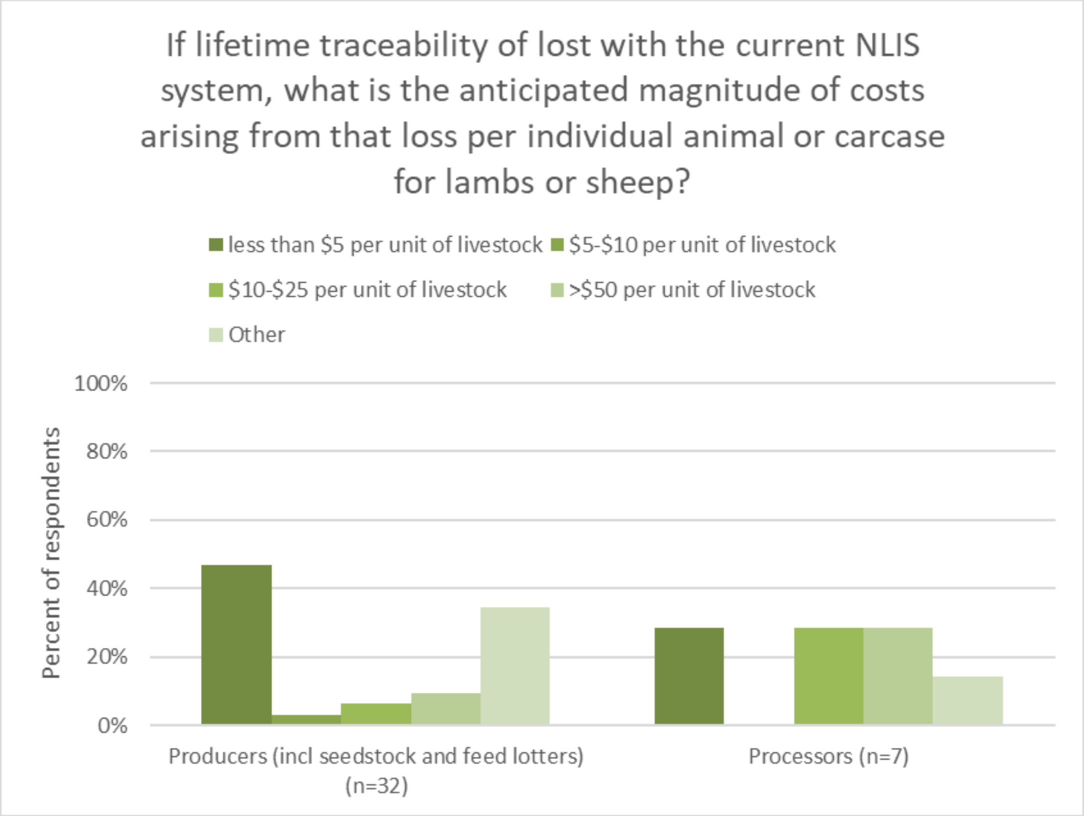
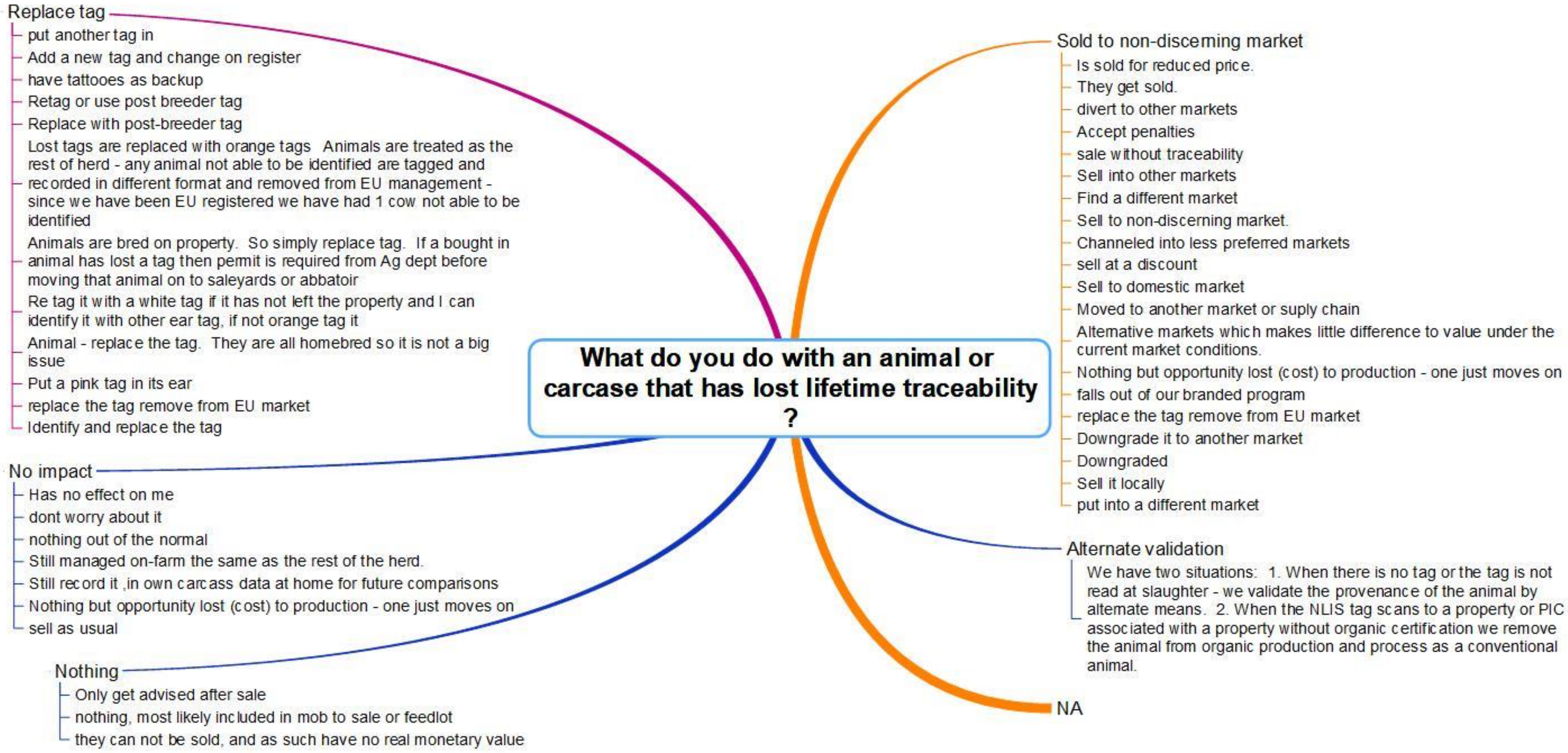


Figure 11. Estimates of current costs associated with loss of NLIS tag for sheep or lambs

A thematic analysis of the responses to an open-ended question on what people do with animals or carcases that have lost tags is shown in

Figure 12. There was a strong theme of simply replacing the tag; however, there were some variations in how those tags were replaced as indicated in the commentary. The other strong theme that emerged (both for producers and processors) was that animals without lifetime traceability are usually directed to a less discerning market, with again some variations in approaches used (as shown). A small proportion of respondents indicated that either nothing is done or there is little impact from the loss a tag.



What do you do with an animal or carcase that has lost lifetime traceability ?

- Replace tag
  - put another tag in
  - Add a new tag and change on register
  - have tattooes as backup
  - Retag or use post breeder tag
  - Replace with post-breeder tag
  - Lost tags are replaced with orange tags Animals are treated as the rest of herd - any animal not able to be identified are tagged and recorded in different format and removed from EU management - since we have been EU registered we have had 1 cow not able to be identified
  - Animals are bred on property. So simply replace tag. If a bought in animal has lost a tag then permit is required from Ag dept before moving that animal on to saleyards or abbatoir
  - Re tag it with a white tag if it has not left the property and I can identify it with other ear tag, if not orange tag it
  - Animal - replace the tag. They are all homebred so it is not a big issue
  - Put a pink tag in its ear
  - replace the tag remove from EU market
  - Identify and replace the tag
- No impact
  - Has no effect on me
  - dont worry about it
  - nothing out of the normal
  - Still managed on-farm the same as the rest of the herd.
  - Still record it ,in own carcass data at home for future comparisons
  - Nothing but opportunity lost (cost) to production - one just moves on
  - sell as usual
- Nothing
  - Only get advised after sale
  - nothing, most likely included in mob to sale or feedlot
  - they can not be sold, and as such have no real monetary value
- Sold to non-discerning market
  - Is sold for reduced price.
  - They get sold.
  - divert to other markets
  - Accept penalties
  - sale without traceability
  - Sell into other markets
  - Find a different market
  - Sell to non-discerning market.
  - Channeled into less preferred markets
  - sell at a discount
  - Sell to domestic market
  - Moved to another market or suply chain
  - Alternative markets which makes little difference to value under the current market conditions.
  - Nothing but opportunity lost (cost) to production - one just moves on
  - falls out of our branded program
  - replace the tag remove from EU market
  - Downgrade it to another market
  - Downgraded
  - Sell it locally
  - put into a different market
- Alternate validation
  - We have two situations: 1. When there is no tag or the tag is not read at slaughter - we validate the provenance of the animal by alternate means. 2. When the NLIS tag scans to a property or PIC associated with a property without organic certification we remove the animal from organic production and process as a conventional animal.
- NA

Figure 12. Thematic analysis of approaches and responses to loss of lifetime traceability

Responses to the question on the costs of establishing and maintaining lifetime traceability for cattle provide two important pieces of information (Figure 13). The first is the estimate of costs over and above the purchase price of NLIS electronic identification (EID) tags ($3-5), which are usually associated with labour and software; and the second being the magnitude of expense that people are committing to achieving lifetime traceability. As with previous questions, there was significant variation in the estimated costs from 27% of beef production sector participants indicating less than $5, to 11% indicating greater than $20 per head (which were not all seedstock). Processors also indicated a wide variation from 17% at less than $5, to 17% being greater than $20, with 50% at $5-10.

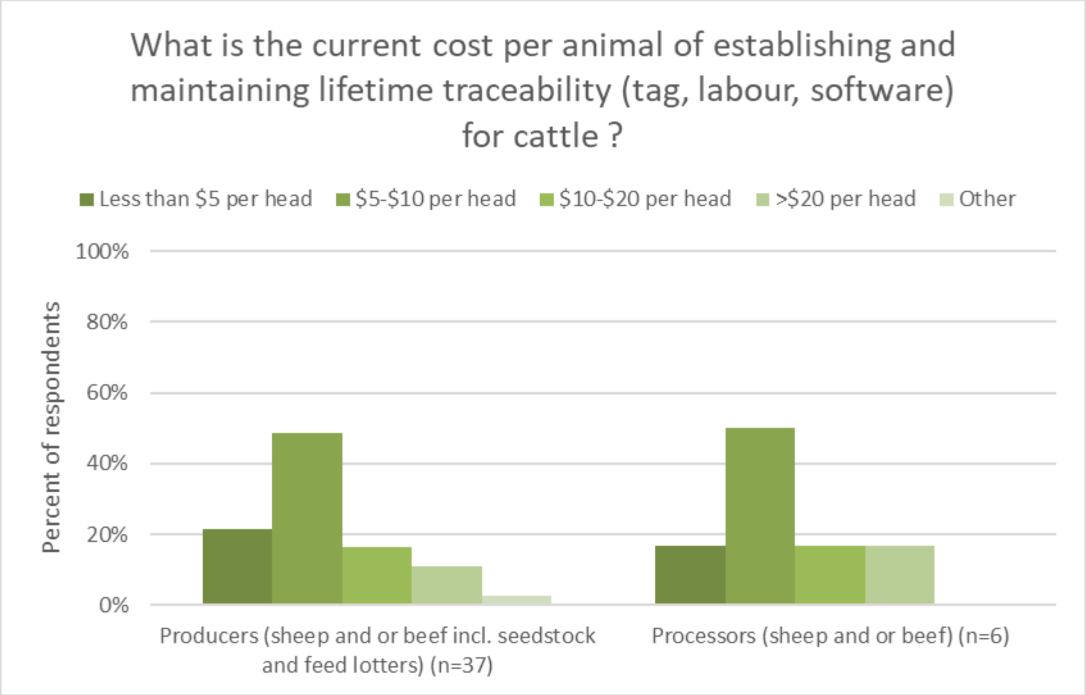


Figure 13. Estimated costs of establishing and maintaining lifetime traceability in cattle

In contrast, 83% of respondents in the sheep production sector indicated a cost of less than $5 for establishing and maintaining lifetime traceability in sheep and lambs with the current NLIS system. Processors also generally reported a lower cost for sheep, but one processor did indicate a >$20 cost which was associated with a detailed hook-tracking and feedback system (see Figure 14).

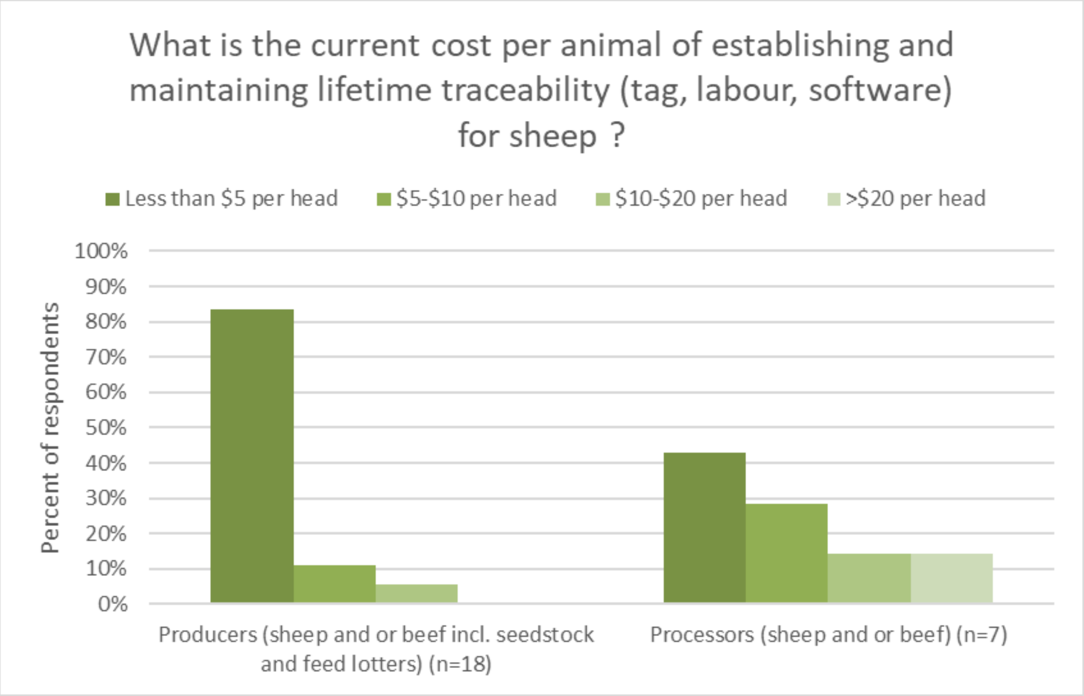


Figure 14. Estimated costs of establishing and maintaining lifetime traceability in sheep

There were very similar approaches or additional steps (methods) used in protecting or ensuring lifetime traceability. Management and or/ dual tags are widely used by both beef seedstock and beef producers, with some use of tattooing, freeze branding (of animal identity) and DNA sampling in the seedstock sector. Some producers also use additional tags that include both PIC and NLIS number. Of interest, no respondent from these sectors indicated that they use genotyping specifically to protect lifetime traceability. The beef lot feeders indicated very similar practices to beef producers in the use of management and or dual tags (see Figure 15). In contrast, sheep producers (Figure 16) generally indicated lower rates of protecting lifetime traceability which would be primarily linked to the current mob-based tracking system.

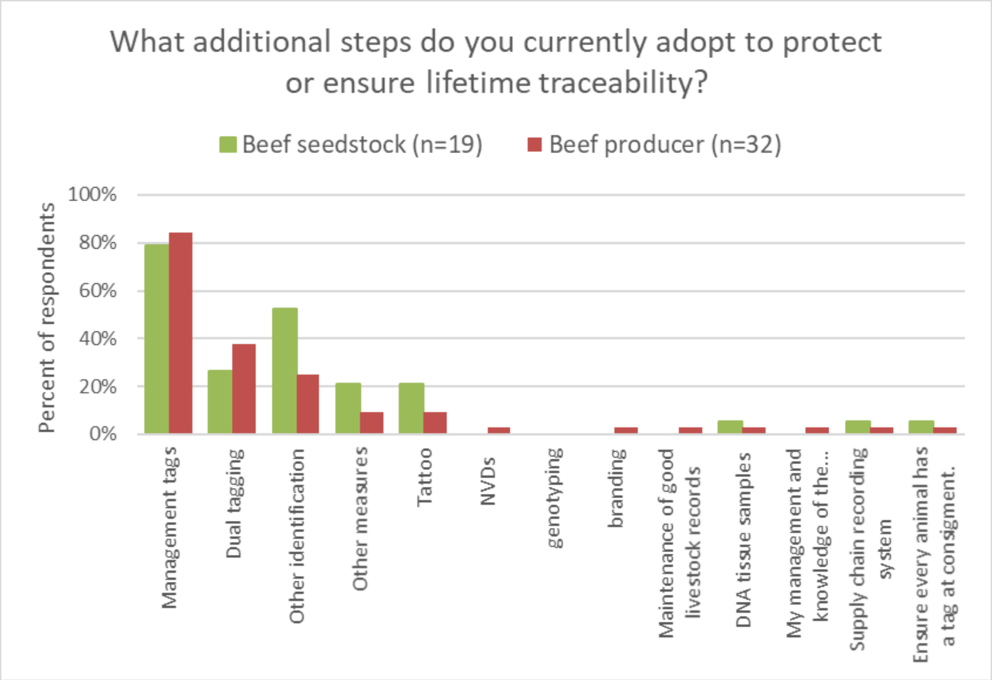


Figure 15. Practices used in the beef production sectors to ensure lifetime traceability

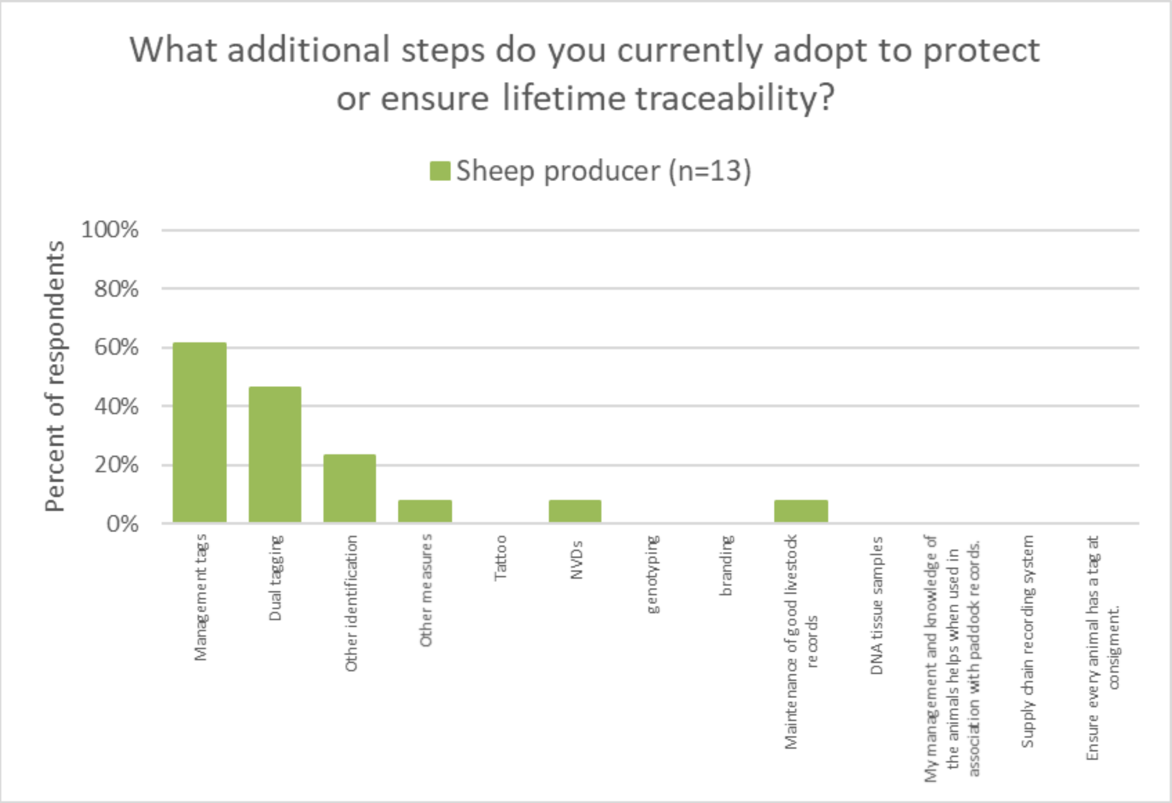


Figure 16. Practices used by sheep producers to ensure lifetime traceability

When asked to contrast the key differences between the two species in terms of lifetime traceability there were some very clear themes that emerged. These included:

- More market demand for lifetime traceability
- EID and individual management for cattle vs mob-based for sheep
- Linkage to carcase and animal health feedback for cattle vs mob-based feedback for sheep, summarised as more value add in cattle than sheep
- Perception that the cattle system is far more robust and accurate when compared to sheep
- Belief that traceability is more important in cattle compared to sheep

These observations are important as they tend to indicate that cattle industry participants are generally more aware of the value of lifetime traceability and see more tangible value-add than sheep industry participants, which is primarily a function of individual animal identification as opposed to mob-based traceability that exists within the current sheep system.

Genomic technologies and traceability

Importantly, this survey revealed the awareness, application, barriers and preparedness to pay for genomic technologies in both the beef and sheepmeat industries. These data provide an indication of how receptive both industries may be towards implementation of genomic technologies for lifetime traceability; and notably what price points may have to be reached for such technologies to be an attractive value proposition. The responses also provide some insights into key differences between the beef and sheep industries.

As expected, current applications of genomic technologies are most frequent in seedstock selection and related parentage identification for breeding. Application was higher in the beef industry compared to the sheep industry (see Figure 10). There was moderate application of genomics for commercial animal performance, which reflects the emergence of new genomic-based selection tools such as Heifer Select™[53] and Flock Profiling[54]. Some respondents have had experience in testing for genetic diseases or adverse genetic conditions, but generally these are now included in seedstock genotyping services offered by breed societies. Notably, there was one supply chain that indicated that they are using genomics to back a beef brand.

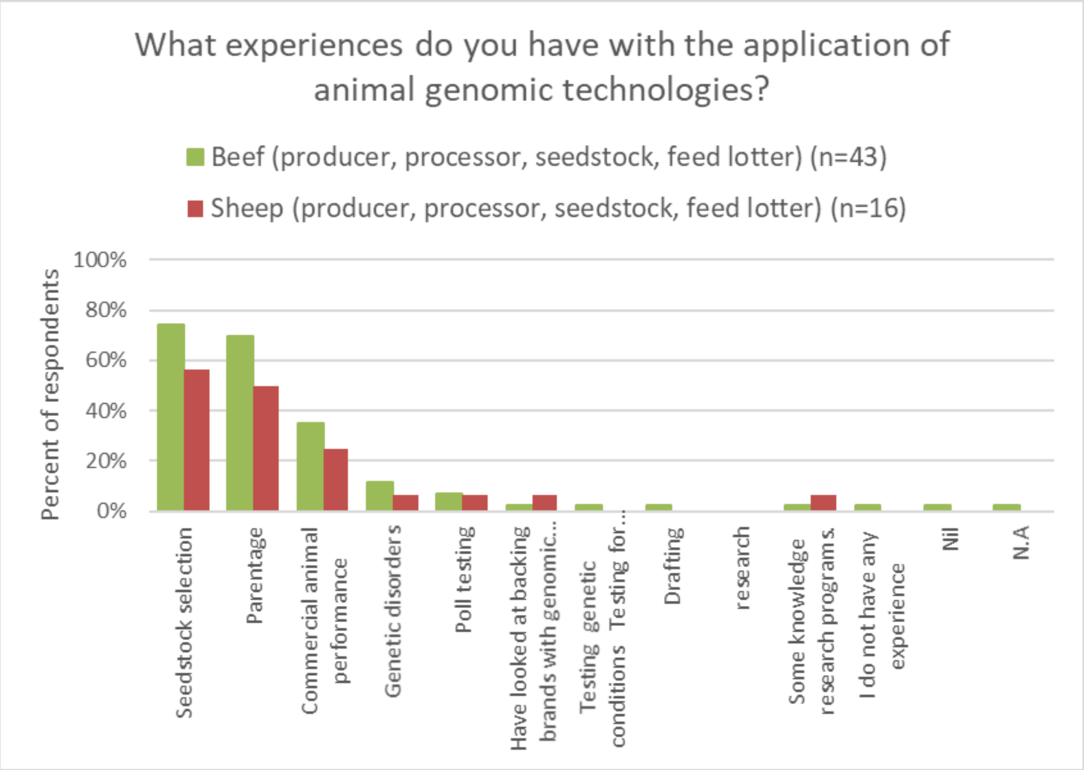


Figure 17. Types of applications of genomic technologies identified by beef and sheep industry participants

Not surprisingly, service providers and researchers had strong awareness and experience of genomics in both seedstock and commercial selection. It is highly likely that the service providers in this survey are strongly linked either to genomic companies or to beef breed societies. Another important observation was that four processors indicated that they have had experiences in seedstock and commercial selection using genomics, which potentially reflects the vertical supply chain structures that those processors are engaged with.

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[53] https://www.angusaustralia.com.au/breeding/animal-selection/angus-heiferselect/

[54] https://www.sheepgenetics.org.au/resources/genomics/

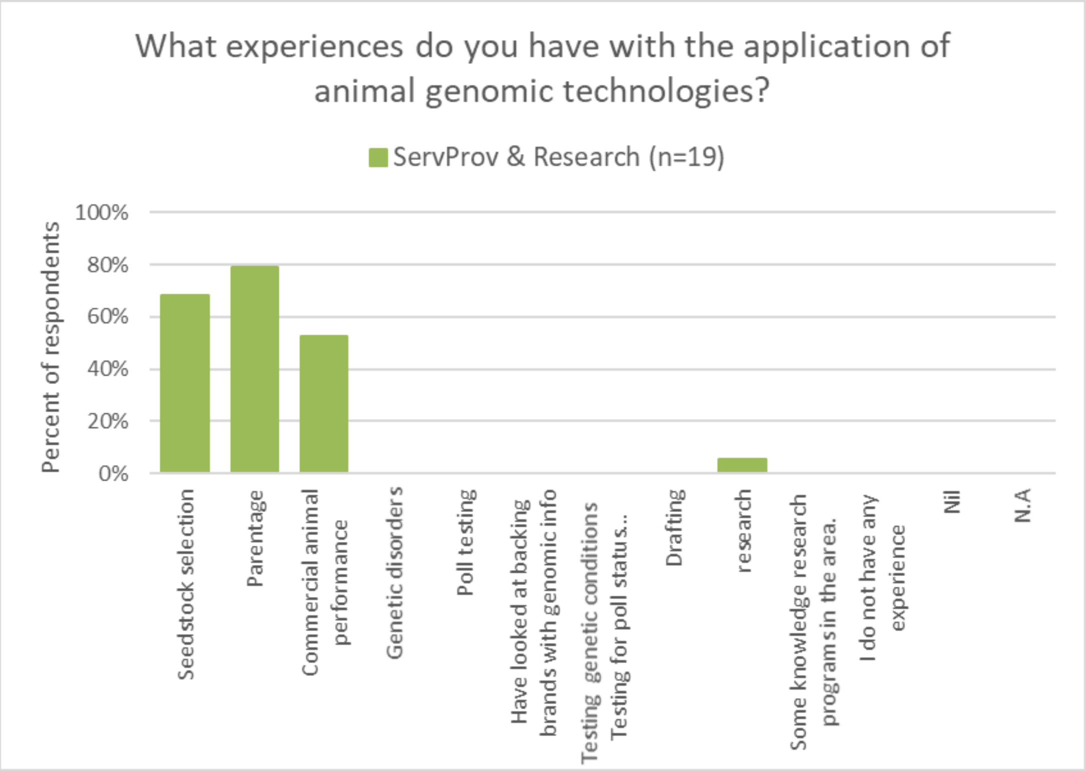

Figure 18. Types of applications of genomic technologies identified by beef and sheep industry service providers and researchers

Given the current experiences with genomic technologies, it was notable that only around 60% of the respondents in both industries expressed an interest in using genomic tools for lifetime traceability. Thirty percent in both industries were unsure and 10% stated no interest (see Figure 19). Notably, lot feeders were more interested than producers, with 85% indicating that they would be interested and 15% unsure. There was some difference between producers and processors in their levels of interest, with no processor indicating that they would not be interested and a third indicating they are still unsure at this stage.

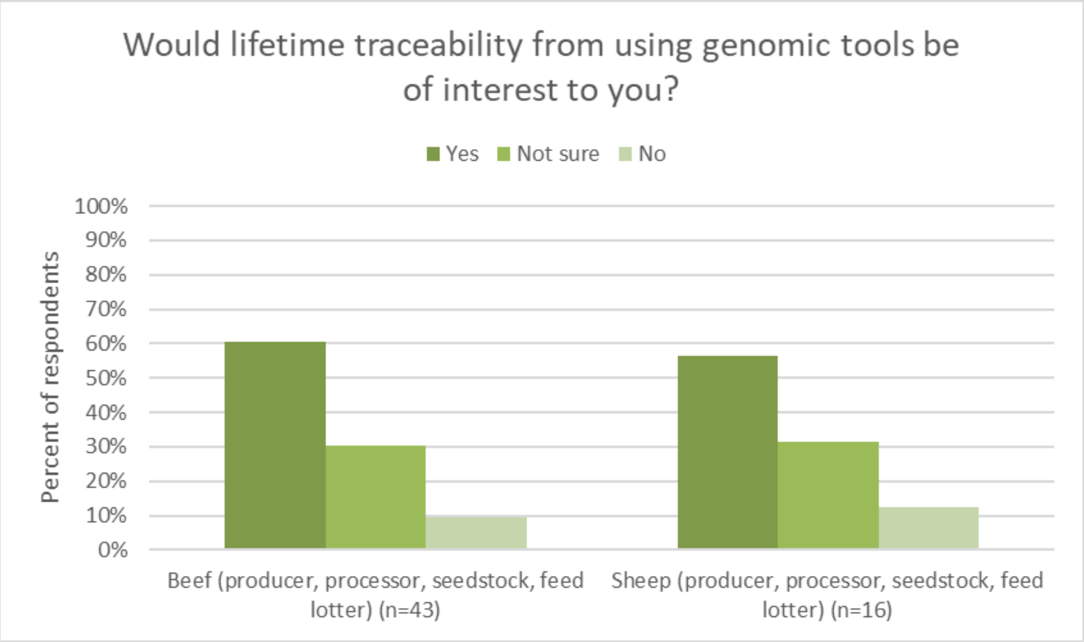

Figure 19. Interest in use of genomics for lifetime traceability

There was a consistent moderate response to the directed question (prompted answers from list) on additional benefits that beef, and sheep industry participants would require (expect) from genomic lifetime traceability. There were no obvious differences between sheep and beef industry participants (see Figure 20), except for animal health and welfare prediction, which were higher in sheep and parentage / inbreeding which were higher in beef.

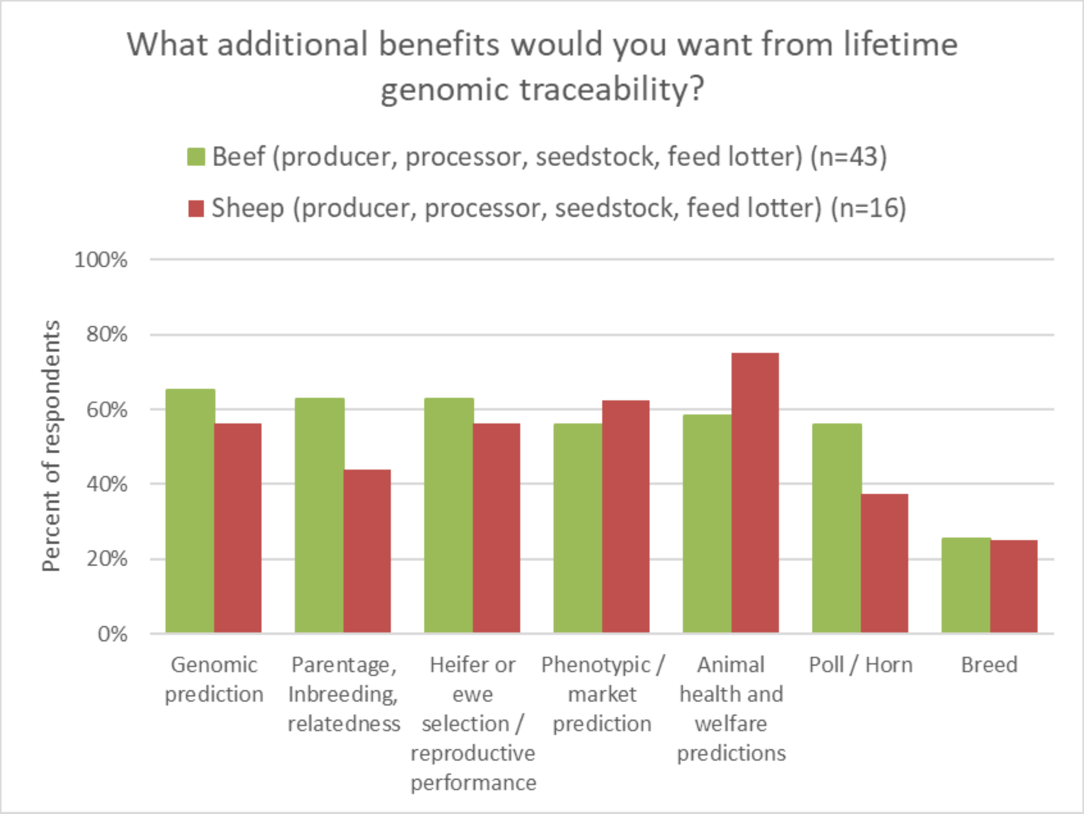

Figure 20. Additional benefits required from lifetime genomic traceability, classified by beef vs. sheep industry participants

As expected, producers tended to be more focussed on breeding outcomes, whereas processors were more focussed on commercial prediction of performance, health and welfare. Interestingly, as shown in Figure 21, a higher proportion of processors saw benefits from poll /horn testing and breed characterisation (which are linked to welfare and brand provenance claims).

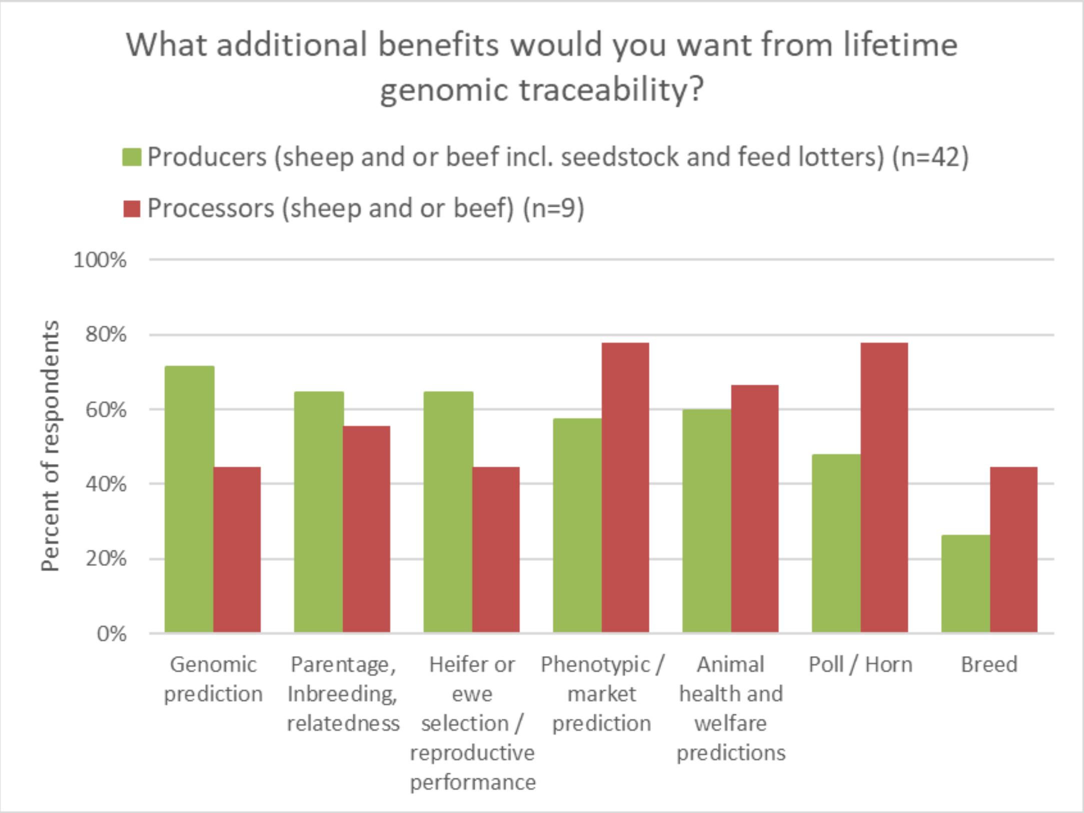

Figure 21. Additional benefits required from lifetime genomic traceability, classified by producers vs. processors

When participants were asked to nominate other potential benefits from genomic lifetime traceability, there was a very strong theme of linking carcase data with genomic data to improve prediction of performance. That theme was also linked to other areas of new attributes (breed and animal health) and better selection. Supporting supply chain activities was another identified theme, with provenance and brand security key expectations. A small but important theme was ability to detect and defer theft (see
Figure 22).

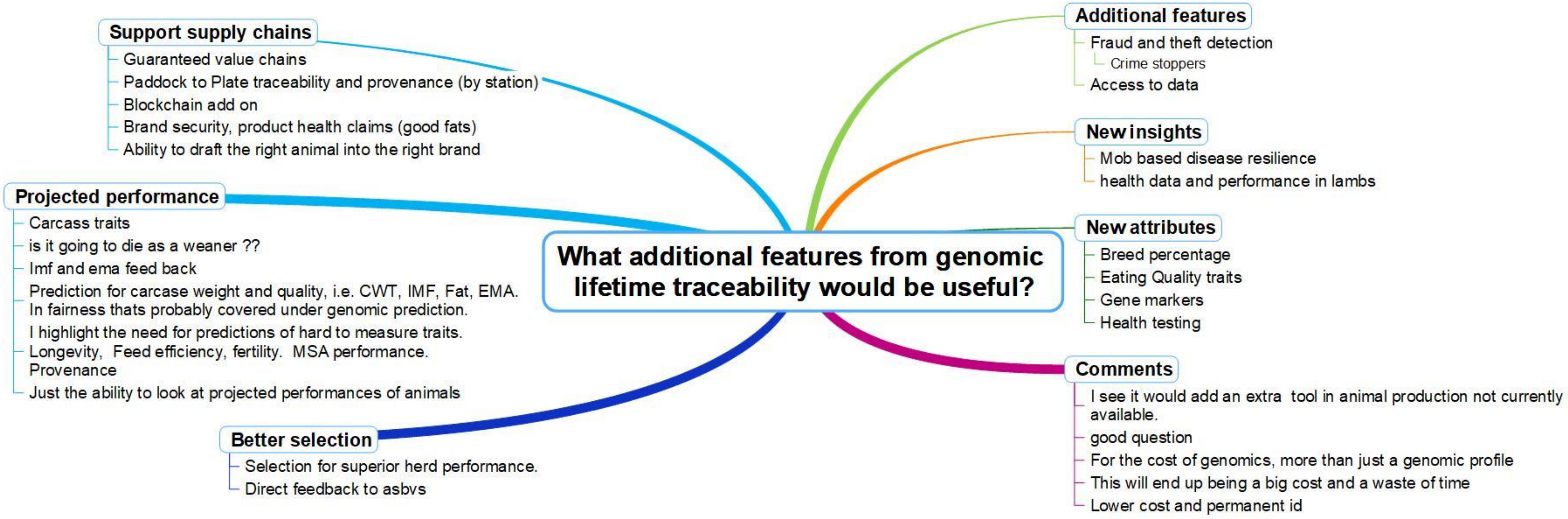

Figure 22. Mind map of themes related to additional benefits sought from genomic lifetime traceability

When asked to consider barriers to adopting lifetime genomic traceability, there was a very strong response, consistent across the beef and sheep sectors (see Figure 23). In general, the production sector identified more barriers and at a greater frequency than processors, consistent between the seedstock sector, producers and lot feeders. Cost dominated responses from the production sector and was the most frequently identified barrier for processors (although lower in magnitude). The effort required for collection and the continuing need of other forms of identification, visually and for tracking, were other notable barriers.

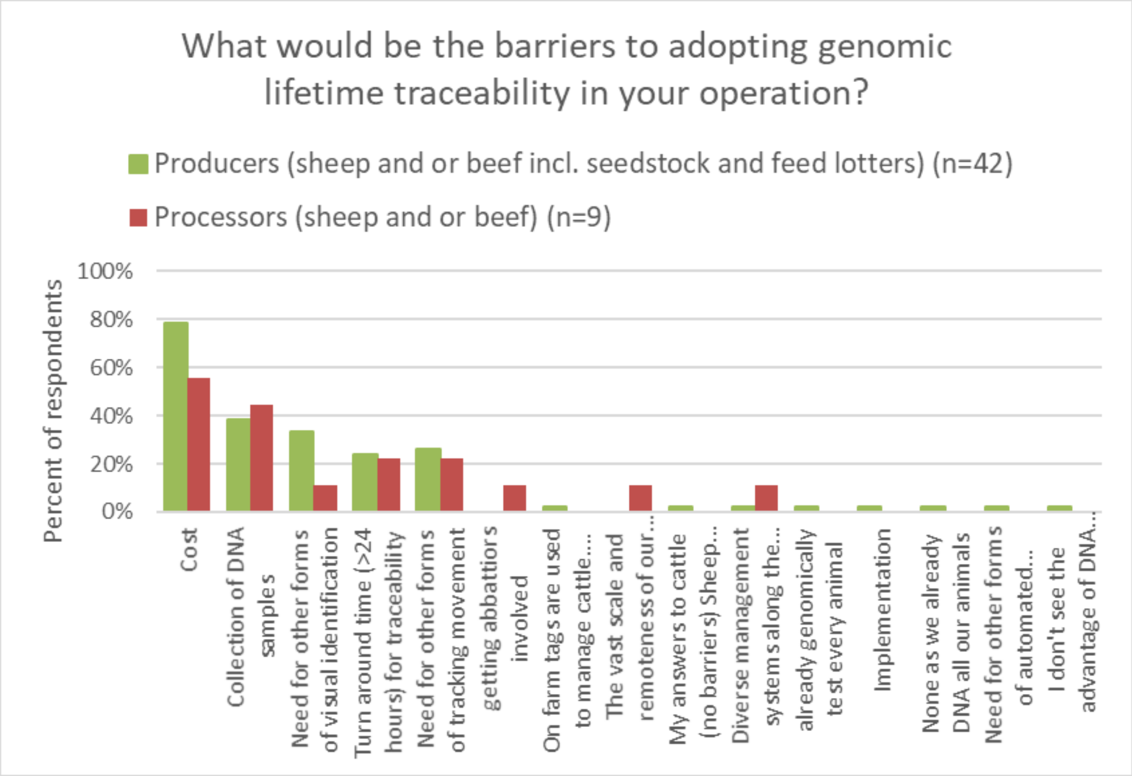

Figure 23. Identified barriers to adoption of genomic lifetime traceability

Survey participants were then asked what concerns that they would have with genomic data and ownership. This question prompted an expansive and extensive set of responses, often with more than several concerns identified by an individual. Those concerns have been grouped into major themes and are shown in

Figure 24. Direct ownership of data was seen as important, with several comments indicating that the person paying for the data should have ownership rights. This belief is consistent with the attitudes to data ownership across many agricultural industries[55] and is the subject of several current cross-sectoral initiatives.

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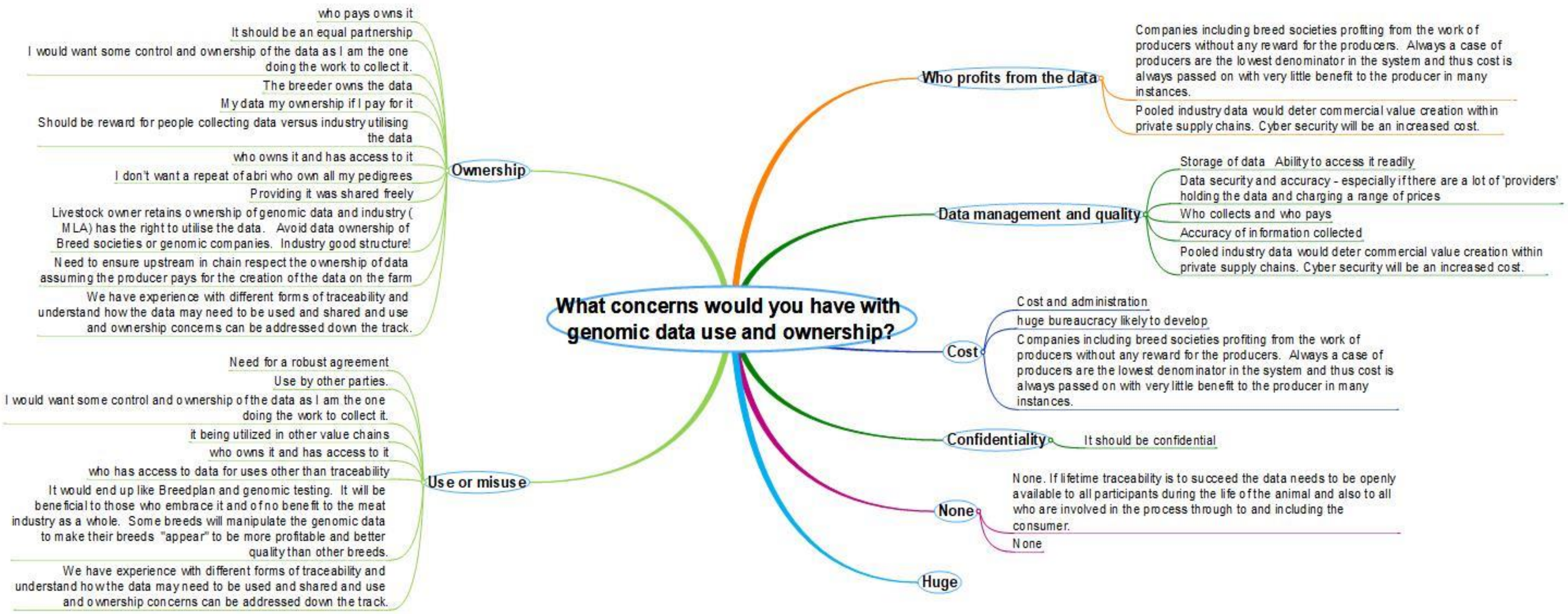
[55] https://www.farminstitute.org.au/product/the-implications-of-digital-agriculture-and-big-data-for-australian-agriculture/



What concerns would you have with genomic data use and ownership?

- **Ownership**
  - who pays owns it
  - It should be an equal partnership
  - I would want some control and ownership of the data as I am the one doing the work to collect it.
  - The breeder owns the data
  - My data my ownership if I pay for it
  - Should be reward for people collecting data versus industry utilising the data
  - who owns it and has access to it
  - I don't want a repeat of abri who own all my pedigrees
  - Providing it was shared freely
  - Livestock owner retains ownership of genomic data and industry (MLA) has the right to utilise the data. Avoid data ownership of Breed societies or genomic companies. Industry good structure!
  - Need to ensure upstream in chain respect the ownership of data assuming the producer pays for the creation of the data on the farm
  - We have experience with different forms of traceability and understand how the data may need to be used and shared and use and ownership concerns can be addressed down the track.
- **Use or misuse**
  - Need for a robust agreement
  - Use by other parties.
  - I would want some control and ownership of the data as I am the one doing the work to collect it.
  - it being utilized in other value chains
  - who owns it and has access to it
  - who has access to data for uses other than traceability
  - It would end up like Breedplan and genomic testing. It will be beneficial to those who embrace it and of no benefit to the meat industry as a whole. Some breeds will manipulate the genomic data to make their breeds "appear" to be more profitable and better quality than other breeds.
  - We have experience with different forms of traceability and understand how the data may need to be used and shared and use and ownership concerns can be addressed down the track.
- **Who profits from the data**
  - Companies including breed societies profiting from the work of producers without any reward for the producers. Always a case of producers are the lowest denominator in the system and thus cost is always passed on with very little benefit to the producer in many instances.
  - Pooled industry data would deter commercial value creation within private supply chains. Cyber security will be an increased cost.
- **Data management and quality**
  - Storage of data Ability to access it readily
  - Data security and accuracy - especially if there are a lot of 'providers' holding the data and charging a range of prices
  - Who collects and who pays
  - Accuracy of information collected
  - Pooled industry data would deter commercial value creation within private supply chains. Cyber security will be an increased cost.
- **Cost**
  - Cost and administration
  - huge bureaucracy likely to develop
  - Companies including breed societies profiting from the work of producers without any reward for the producers. Always a case of producers are the lowest denominator in the system and thus cost is always passed on with very little benefit to the producer in many instances.
- **Confidentiality**
  - It should be confidential
- **None**
  - None. If lifetime traceability is to succeed the data needs to be openly available to all participants during the life of the animal and also to all who are involved in the process through to and including the consumer.
  - None
- **Huge**

Figure 24. Thematic analysis of concerns to genomic data use and ownership

However, there was consistent commentary that breed societies should not own this type of data as they do with data underpinning genetic improvement systems. Use and misuse of data was a common theme that was linked to ownership but extended to include elements such as who are the beneficiaries and what controls should be in place. Concerns around who profits from genomic data was a third theme, with data management and quality and costs also prominent. Of note, there was a small but consistent proportion of respondents that indicated that they have no concerns.

Survey respondents were asked to nominate the maximum that they would be prepared to pay, within a range from 0-$100. Given the variation in responses, the most appropriate way of presenting the data was a count of responses relative to price brackets (maximum), as shown in Figure 25. For Sheep, the most common price was $5 (38%), followed by $10 (16%), with a median of $5. For beef cattle, the most frequent response was $10 (21.5%) followed by $30 (14%), with a median of $20.

This difference was surprising given the amount that respondents pay for current lifetime traceability (almost double the current cost of the NLIS tag). There was a difference between processors (median $29) and producers (median $17.50). These estimates of the preparedness to pay provide critical information in determining market readiness for genomic traceability and the magnitude that costs must be to be attractive for adoption across the livestock industry.

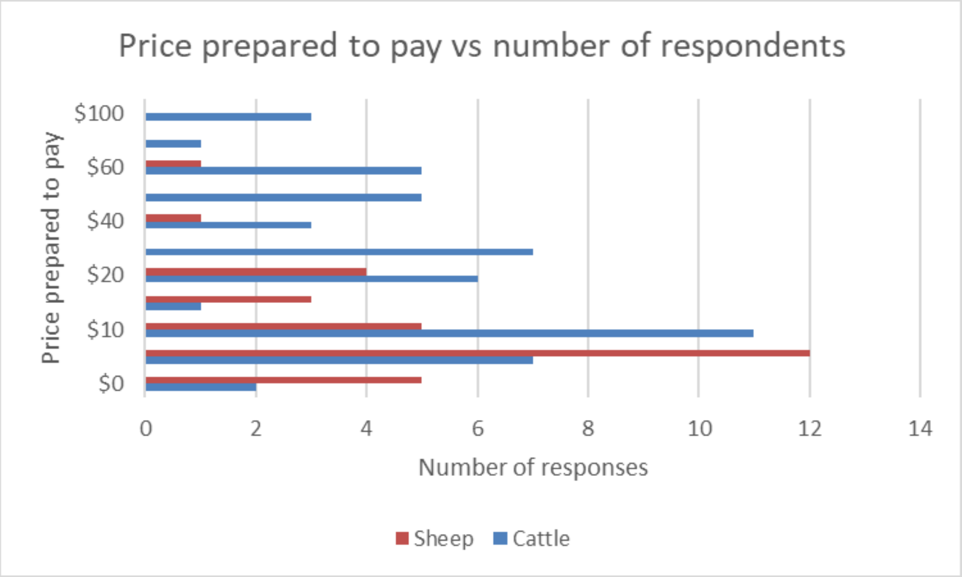


Figure 25. Maximum price prepared to pay vs number of responses for genomic lifetime traceability

As expected, (due to NLIS regulations), a very high proportion participants in the beef industry use EID technologies and a high proportion of beef seedstock and beef producers indicated that they would continue to use EID even if genomic lifetime traceability was available (63% and 72% respectively (Figure 26). A moderate but significant number indicated that they were unsure of whether they would continue to use EID; and only a very small proportion indicated that they would not continue to use EID technologies of lifetime traceability was available.

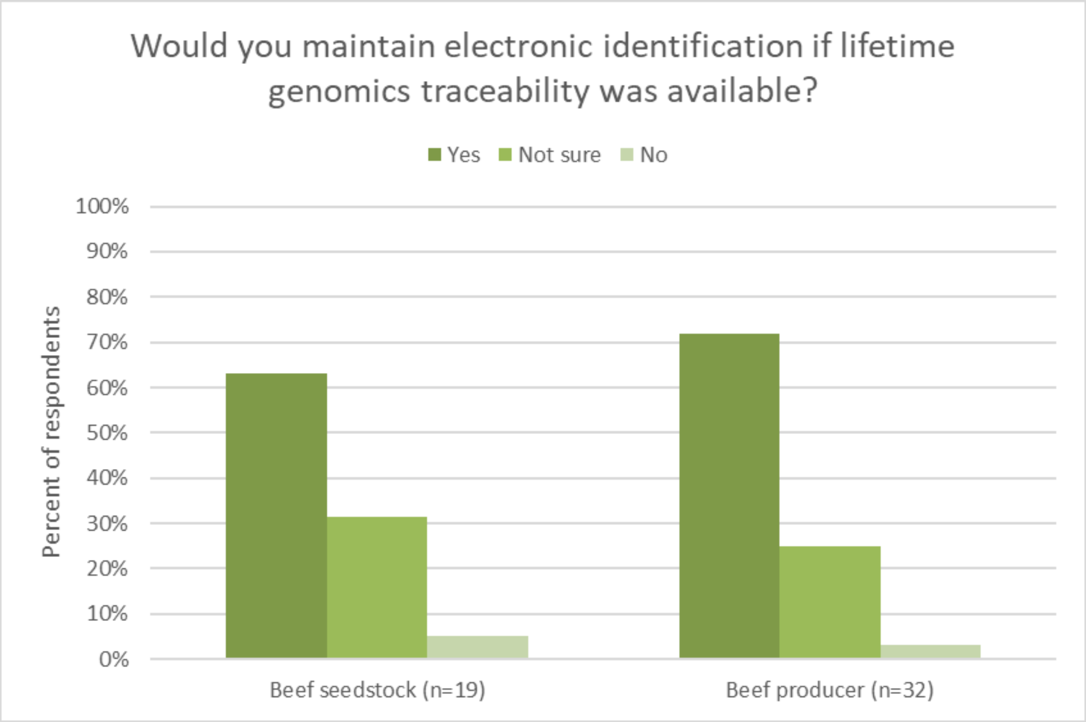


Figure 26. Percentage of respondents (beef seedstock and producers) that would continue to use of EID technologies if lifetime genomic traceability was available

Although only a small number of respondents from the beef lot feeders and beef processors answered this question, there was a very strong belief that EID use would continue even if lifetime traceability was available (100% and 88% respectively; see Figure 27.

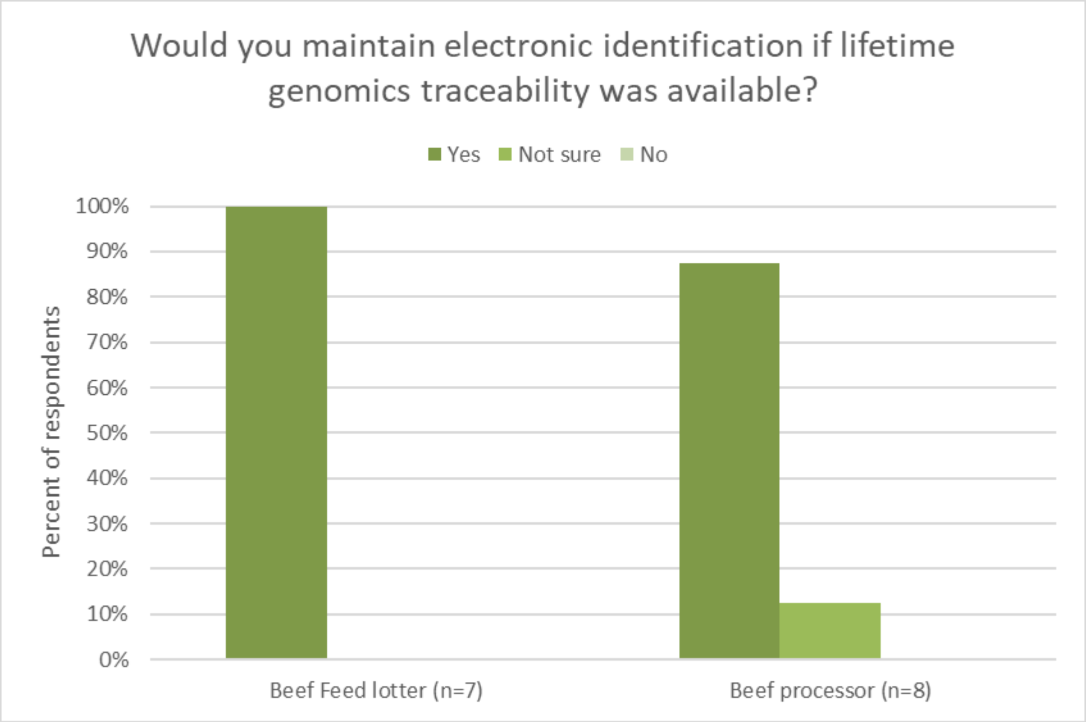


Figure 27. Percentage of respondents (beef lot feeders and processors) that would continue to use of EID technologies if lifetime genomic traceability was available

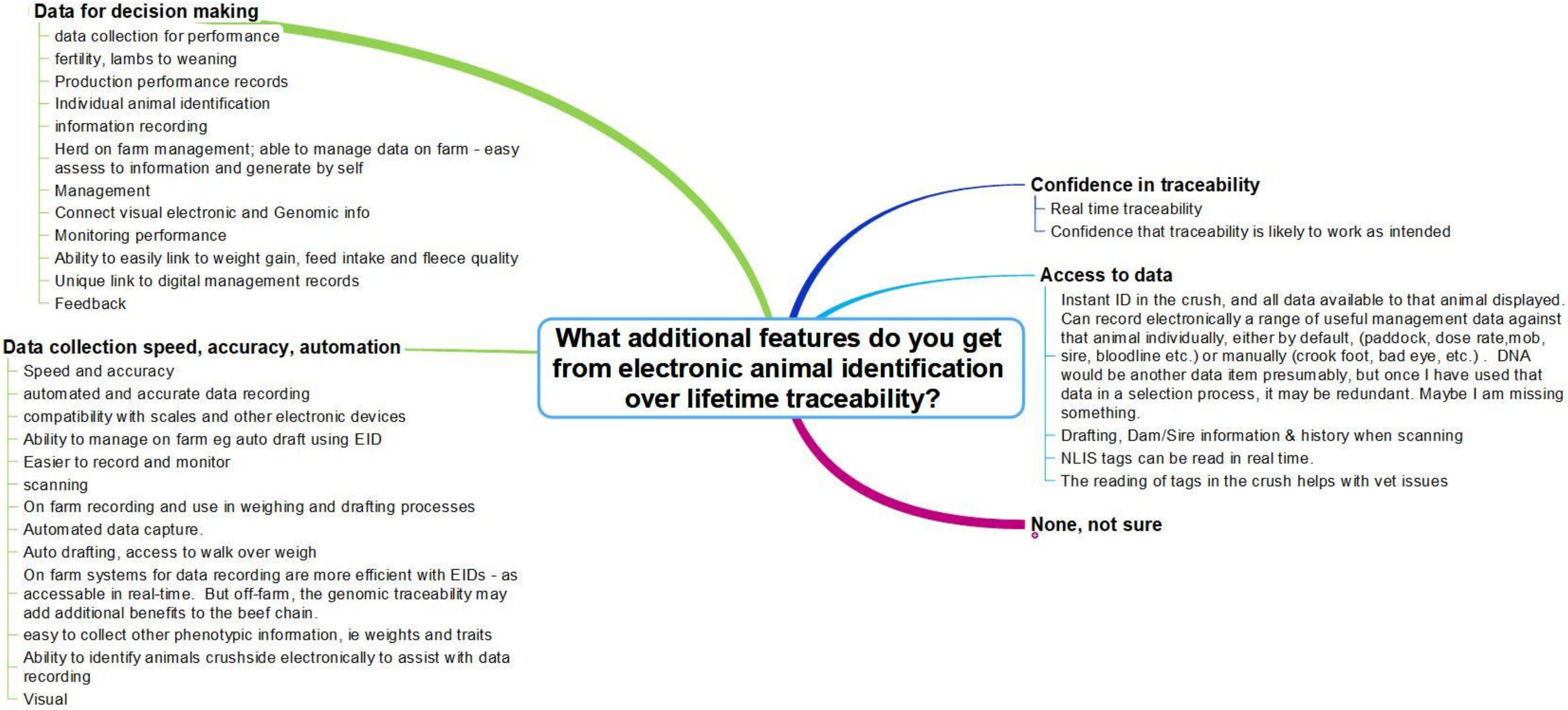
Overall, these responses would indicate that lifetime genomic traceability is currently seen as an add-on rather than a replacement to the current lifetime traceability system that is underpinned by

EID tags. Potential reasons for why EID technologies would be maintained are shown in Figure 28. Clearly EID tags are seen as an important tool in collecting accurate data in these industries, particularly data that informs decisions related to management or genetic selection. As noted, potential automation, accuracy and speed of collection of data were identified as key ancillary benefits of EID lifetime traceability. However, a proportion of all respondents saw little or no extra benefits from EID technologies.

The final question in the survey sought additional commentary by respondents on their views of lifetime genomic traceability. This commentary was summarised into three themes (see Figure 29), being:
1. Questions by the respondents, seeking answers;
2. Commentary that supported the implementation of genomic traceability; and
3. Commentary that opposed the implementation of genomic traceability.

Some respondents were still interested in where the value proposition or benefits would accrue from the introduction of lifetime genomic traceability. Most saw potential opportunities, primarily linked to genetic selection and the ability to increase both the volume of information and the ability to transfer it along the value chain. Those same respondents did identify costs, timelines for genomic test information and integration with visual systems as barriers to overcome.

A smaller but still significant proportion of respondents saw little or no benefit, were concerned about bureaucracy and would be strongly opposed to the introduction of genomic lifetime traceability.



What additional features do you get from electronic animal identification over lifetime traceability?

Data for decision making
- data collection for performance
- fertility, lambs to weaning
- Production performance records
- Individual animal identification
- information recording
- Herd on farm management; able to manage data on farm - easy assess to information and generate by self
- Management
- Connect visual electronic and Genomic info
- Monitoring performance
- Ability to easily link to weight gain, feed intake and fleece quality
- Unique link to digital management records
- Feedback

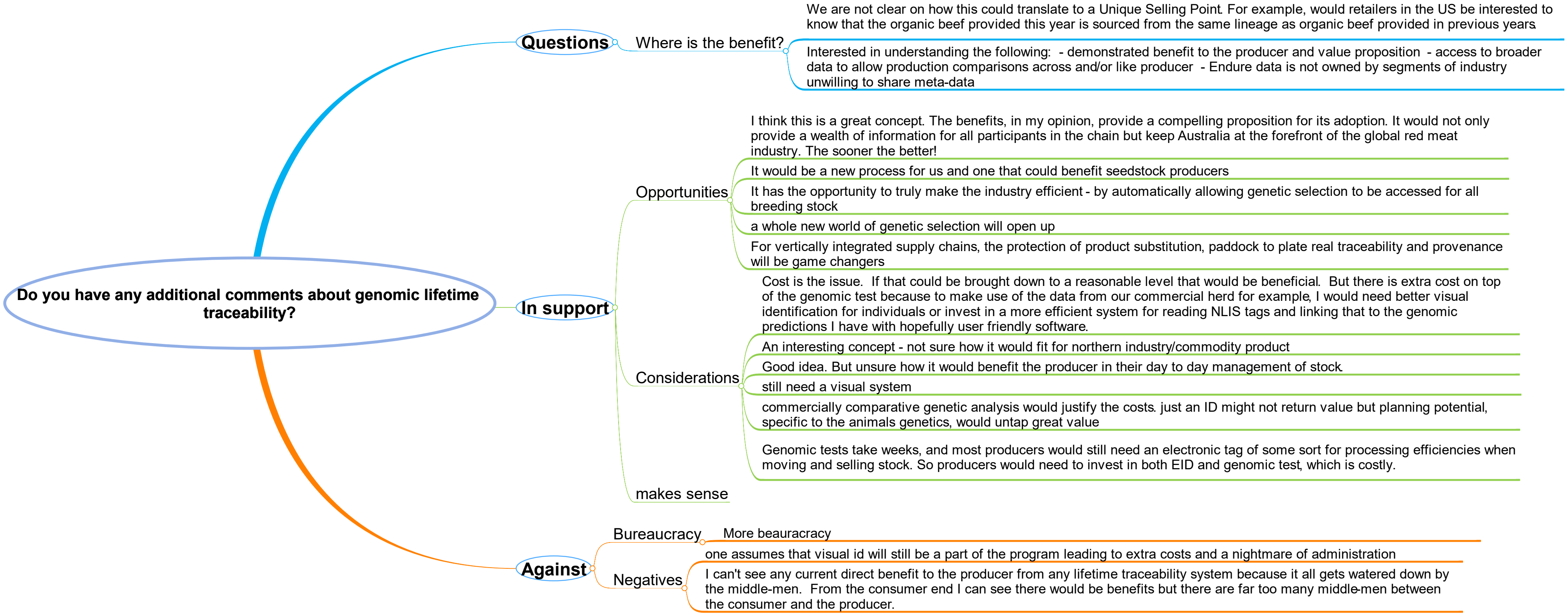
Data collection speed, accuracy, automation
- Speed and accuracy
- automated and accurate data recording
- compatibility with scales and other electronic devices
- Ability to manage on farm eg auto draft using EID
- Easier to record and monitor
- scanning
- On farm recording and use in weighing and drafting processes
- Automated data capture.
- Auto drafting, access to walk over weigh
- On farm systems for data recording are more efficient with EIDs - as accessable in real-time. But off-farm, the genomic traceability may add additional benefits to the beef chain.
- easy to collect other phenotypic information, ie weights and traits
- Ability to identify animals crushside electronically to assist with data recording
- Visual

Confidence in traceability
- Real time traceability
- Confidence that traceability is likely to work as intended

Access to data
- Instant ID in the crush, and all data available to that animal displayed. Can record electronically a range of useful management data against that animal individually, either by default, (paddock, dose rate,mob, sire, bloodline etc.) or manually (crook foot, bad eye, etc.) . DNA would be another data item presumably, but once I have used that data in a selection process, it may be redundant. Maybe I am missing something.
- Drafting, Dam/Sire information & history when scanning
- NLIS tags can be read in real time.
- The reading of tags in the crush helps with vet issues

None, not sure

Figure 28. Key additional benefits obtained from EID lifetime traceability



We are not clear on how this could translate to a Unique Selling Point. For example, would retailers in the US be interested to know that the organic beef provided this year is sourced from the same lineage as organic beef provided in previous years.

Interested in understanding the following: - demonstrated benefit to the producer and value proposition - access to broader data to allow production comparisons across and/or like producer - Endure data is not owned by segments of industry unwilling to share meta-data

I think this is a great concept. The benefits, in my opinion, provide a compelling proposition for its adoption. It would not only provide a wealth of information for all participants in the chain but keep Australia at the forefront of the global red meat industry. The sooner the better!

It would be a new process for us and one that could benefit seedstock producers

It has the opportunity to truly make the industry efficient - by automatically allowing genetic selection to be accessed for all breeding stock

a whole new world of genetic selection will open up

For vertically integrated supply chains, the protection of product substitution, paddock to plate real traceability and provenance will be game changers

Cost is the issue. If that could be brought down to a reasonable level that would be beneficial. But there is extra cost on top of the genomic test because to make use of the data from our commercial herd for example, I would need better visual identification for individuals or invest in a more efficient system for reading NLIS tags and linking that to the genomic predictions I have with hopefully user friendly software.

An interesting concept - not sure how it would fit for northern industry/commodity product

Good idea. But unsure how it would benefit the producer in their day to day management of stock.

still need a visual system

commercially comparative genetic analysis would justify the costs. just an ID might not return value but planning potential, specific to the animals genetics, would untap great value

Genomic tests take weeks, and most producers would still need an electronic tag of some sort for processing efficiencies when moving and selling stock. So producers would need to invest in both EID and genomic test, which is costly.

More beauracracy

one assumes that visual id will still be a part of the program leading to extra costs and a nightmare of administration

I can't see any current direct benefit to the producer from any lifetime traceability system because it all gets watered down by the middle-men. From the consumer end I can see there would be benefits but there are far too many middle-men between the consumer and the producer.

Figure 29. Additional commentary provided for genomic lifetime traceability

Targeted Interviews

At the commencement of this project, the project team identified several key stakeholders who could provide deeper insights into the application of genomics for lifetime traceability than was possible through the on-line survey. Those stakeholders were contacted, and interviews were held either face to face or via video conferencing. These targeted interviews involved eight genotyping providers, two peripheral technology providers, three processors, two major vertically integrated beef operations, several leading seedstock providers, two breed societies and two technology companies. The interviews followed a semi-structured questionnaire and examined a number of themes relating to genomics. The following sections are from aggregated and de-identified summaries of those interviews.

Genotyping companies and service providers

Representatives of several international genotyping companies were interviewed. In general, there was strong interest in the concept of considering genomics for traceability, with most companies keen to see the outcomes of this project and potential involvement in any proof-of-concept trials. All companies represented in these interviews provide genomic tests for beef and sheep seedstock selection and for management decisions, with retail prices ranging from $15 (parentage) through to $40-$70 (100K SNP chips). All indicated that they see those costs decreasing somewhat, although with current technologies it would be difficult to get tests below $10.

Several companies are offering commercial genomic testing services for traceability. This is usually within dedicated supply chains and those companies are integrating genomics with blockchain technologies (either internally developed or with third parties) to deliver more information beyond the current traceability, including breed, provenance, animal welfare and brand. However, those supply chains were usually focussed on high quality, high value brands where there are greater incentives for lifetime traceability and product assurance. In fact, most companies indicated that branded beef value chains are the most likely entry point for genomic applications for traceability. It was noted that the owners of such brands may be reluctant to participate in a national scheme that allows competitors to view data and in particular, genomic predictions; although they were generally amenable to participation in some form if it brought economies of scale.

When asked whether genomics would offer value for whole of industry traceability, all companies indicated that this would require a significant shift to rapid throughput genomic platforms which would need to be linked to a large integrated databases with sophisticated analytics and integration procedures. Interviewees indicated that long-term storage of DNA is not feasible, at least not a large scale, meaning a significant investment in data infrastructure would be required. Some companies opined that only a fully integrated genomic selection system would have a positive whole-of-industry benefit cost ratio.

Several companies considered that the magnitude of the task would require inter-company cooperation using a common platform, whilst others thought that genomic technology would be adopted supply chain by supply chain, which in turn would allow time to build new capacity and capability if a whole of industry solution is required. Some companies commented that emerging technologies such as genotyping-by-sequencing (GBS), nanopore and low pass sequencing (LPS) may have application for this task and would improve throughput and reduce time lags in obtaining results, but most thought that it will be at least 2-5 years before commercial implementation of such innovations will be possible.

Another notable viewpoint was that the dairy industry will drive innovation in cattle genomics and potentially will adopt lifetime traceability more readily, due to greater use of genomics for performance prediction. Interviewees also indicated a belief that genomics will not provide a solution that allows movement tracking, so that integration with EID or similar technologies will be required. Notably, several of these companies are investing in alternative technologies to tags, including facial recognition and retinal scanning as a value-add to genomics.

Vertically integrated companies

Some major vertically integrated companies (those with production, feedlot and processing) were interviewed. In general, there was solid interest in the application of genomic technologies, but more for screening and prediction of animals' merit, rather than traceability. In fact, those companies indicated that they see genomic traceability as an additional benefit rather than a direct goal. Most companies were interested in being contacted about further pilot work and are probably the most likely candidates for trialling implementation of genomic technologies for traceability.

5. Requirements of an operational DNA-based tracing system

There are three main components to a DNA-based traceability system:

Genotyping

This requires a tissue sample from the animal, which needs to be transported to a laboratory for DNA extraction and genotyping. The genotype, probably containing about 50k DNA loci, is then stored in a dedicated database. If necessary and with an adequate reference established, a 50k genotype can be imputed to a full genomic sequence with a high degree of accuracy.

Database

The genomic database must be linked to the current NLIS database to establish identity, PIC and initial ownership. There is also the potential to create links with other databases such as MSA, BREEDPLAN, Sheep Genetics, a chemical profile database etc.

Analytics

DNA taken from a case animal or animal product is genotyped and matched to genotypes in the database by determining similarity to an individual or alternatively, to a sire, sire team, herd or flock sample, breed etc. If necessary, the DNA identity can be aligned with other indicators of origin (*e.g.* PIC or mineral profile) and the genetic profile can be used, in conjunction with a phenotypic database, to predict an animal's merit for specific production pathways and/or breeding.

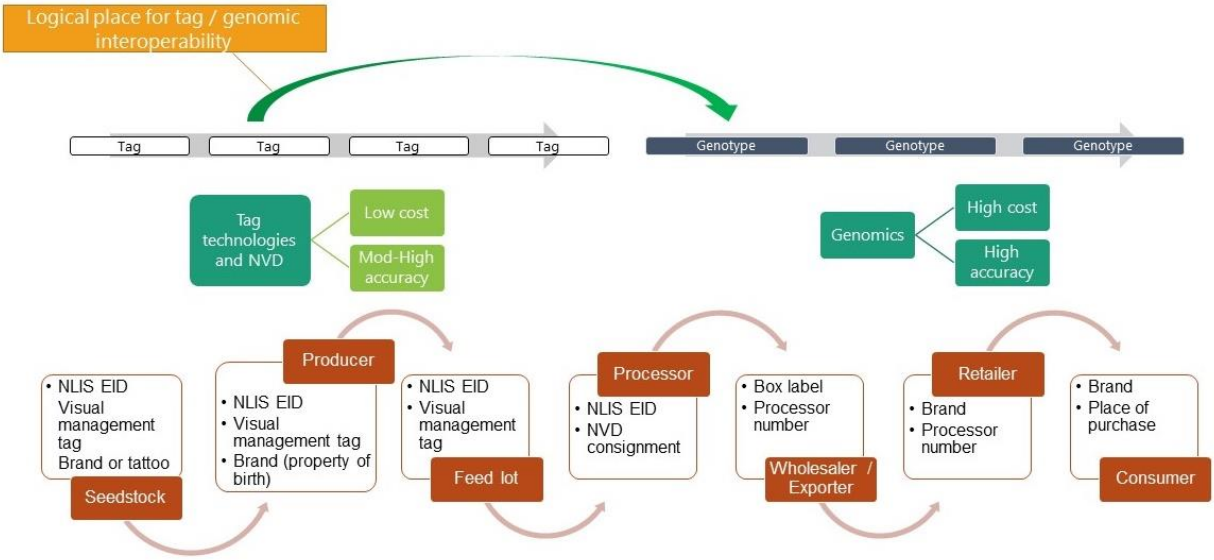


Figure 30. Components of the current tracking system, illustrating how identification through genotyping can augment NLIS tags

Benefits of genotyping

In principle, genotyping can be a relatively simple procedure, requiring the taking of a tissue sample and despatching it to a processing laboratory where it can be automatically logged into a database. This process is already well-established when genotyping for the purpose of genetic evaluation.

With good laboratory practice, sample matching can essentially be error-free and DNA profiles can be stored in perpetuity in electronic form. Information can be made accessible to the entire value chain through to consumers.

Direct benefits include enhanced provenance ascertainment as well as estimates (from the genome) of disease risk and other animal performance attributes. In principle, it should be relatively straightforward to link samples to an individual, a breed, a sire team or a composite mob-based sample. A major ancillary benefit is the ability to employ a suite of predictive tools to enhance decision-making on samples taken as early as birth or weaning, as is done already by progressive breeders. Others to potentially derive direct benefits are the production, finishing, processing and marketing sectors. A significant opportunity exists with many animals genotyped that industry wide collected data on animal attributes, e.g. data from abattoirs, can be linked with the DNA profile of these animals, and this would contribute to larger reference populations that can be used for more accurate genomic prediction of future animals. Linked databases could also provide a powerful resource for related R&D along the value chain.

Additional benefits identified included the identification of fraudulent claims on genetic origin (that is animals being ascribed to a particular parent or breed, which could be extended to the identifying illegal importation of genetics to unlawful use of breeding stock.

Balanced against the potential advantages are additional infrastructure costs and well as implementation costs of $40-$50 per animal, compared with around $5 for the current tag-based NLIS. Consequently, some initial modelling has been undertaken to determine the economic case for a range of implementation models.

6. DNA technology and traceability – economic aspects

An important tenet used to justify the introduction of traceability through the NLIS is the greatly increased power it brings for the tracking, management and control of major exotic disease outbreaks. Several studies have been undertaken to determine the potential costs of such outbreaks (Productivity Commission 2002[56]; Matthews 2011[57]; Buetre *et al*. 2013[58], ABARES 2014[59]). Estimates from these studies have been used in benefit-cost analyses of NLIS in the past, and will help in evaluating the potential impact of using genomic information to enhance traceability.

Previous approaches to assess benefit-cost of NLIS

An ex-post benefit-cost assessment of MLA's Product Integrity Programs was released in 2015 (Dwyer and Clarke 2015[60]), which examined the economic benefits of NLIS, the LPA program and supporting scientific research. The benefit-cost ratio of the three programs combined was estimated to lie between 7.4 and 8:1. Traceability (the NLIS component) made by far the greatest contribution, with net benefits, accumulated over 30 years, estimated at $8.3b. This was considered to be a lower bound estimate because it mainly reflected the assumed benefits of reducing the impacts of foot and mouth disease (FMD) and excluded the benefits of reducing the potential costs of other diseases.

Modelled benefits from NLIS were distributed as shown in Figure 31. Consumers were the major beneficiaries in both beef and sheep, with beef producers receiving about 30% of the total benefits and sheep producers about 24% of the total benefits.

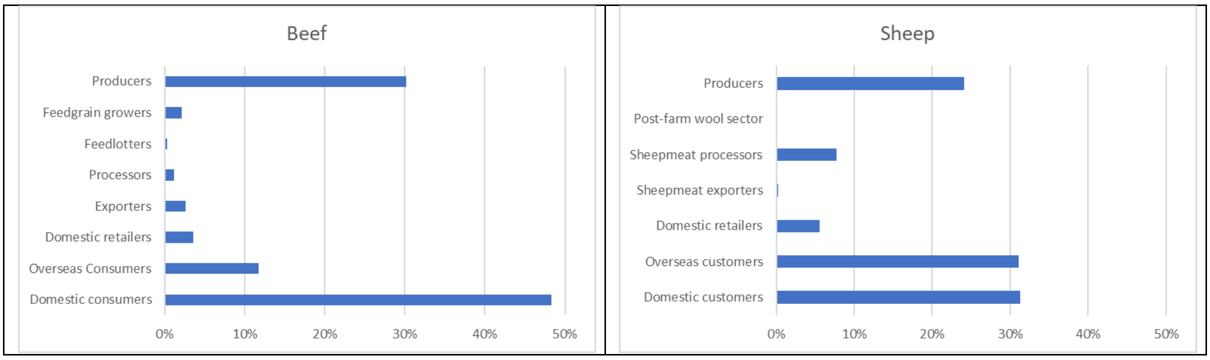


Figure 31. Distribution of estimated benefits from NLIS
(Source: Dwyer and Clarke 2015, Tables 46 & 47)

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[56] Productivity Commission (2002). *Impact of a Foot and Mouth Disease Outbreak on Australia*, Research Report, AusInfo, Canberra. (https://papers.ssrn.com/sol3/papers.cfm?abstract_id=315882)

[57] Matthews, K. (2011) *A review of Australia's preparedness for the threat of foot-and-mouth disease*. Australian Government Department of Agriculture, Fisheries and Forestry, Canberra. (https://www.awe.gov.au/sites/default/files/sitecollectiondocuments/animal-plant/pests-diseases/animal-pests-diseases/footandmouth.pdf

[58] Buetre, B, Wicks, S, Kruger, H, Millist, N, Yainshet, A, Garner, G, Duncan, A, Abdalla, A, Trestrail, C, Hatt, M, Thompson, LJ & Symes, M (2013) *Potential socio-economic impacts of an outbreak of foot-and mouth-disease in Australia*, ABARES Research Report, Canberra, September. (https://www.awe.gov.au/sites/default/files/abares/documents/RR13.11PotSocEcoImpctOfFMD_v1.0.0.pdf)

[59] ABARES (2014) *Implementation of improvements to the National Livestock Identification System for sheep and goats: Decision Regulation Impact Statement* (https://data.gov.au/data/dataset/pc_inlisd9abbl20141022_11a)

[60] Dwyer, G. and Clarke, M. (2015) *Ex-post benefit-cost assessment of MLA's Product Integrity Programs* MLA Report V.LIM.1505

A subsequent study by White *et al*. (2019)[61] assessed the impact of Integrity Systems covering the period 2015-2020. The authors commented on four important aspects of the earlier study, viz:

- Benefits due to avoided disease costs were over-estimated (by not annualising the cumulative costs over the multi-year period of disease spread)
- There were inconsistencies in the counter-factual case (related to ISC operations outside the assessment period)
- The assumed probability of an FMD outbreak in any given year was considered to be too low (at 0.6%)
- The attribution of price premiums in export markets were considered to be too low (as they were discounted twice)

The net effect of changing these assumptions was to increase the modelled benefits over the assessment period; although the authors did note that the evaluation model is extremely complex and involves a large number of assumptions. They also outlined a number of additional benefits apart from those modelled *i.e.* avoided disease costs and export price premiums, viz:

1. Avoided indirect or secondary impacts to the broader Australian economy from exotic disease incursion;
2. Benefits from NLIS and state-based Property Identification Code (PIC) databases, supporting a range of secondary disease surveillance and management activities;
3. Improved economic prosperity of Australian meat and livestock businesses, providing additional resources for improved environmental outcomes;
4. Reduced risk of human health impacts from the fatal variant Creutzfeldt-Jakob Disease (vCJD) and other pathogens;
5. Avoided social impacts from severe livestock disease outbreak, including mental health, financial hardship, unemployment *etc*.; and
6. Improved animal welfare outcomes through avoiding the widespread destruction of livestock typically required to eradicate exotic diseases

Logically, any technology that increases the effectiveness of traceability should increase the modelled economic benefits as well as the additional benefits listed; although any additional costs obviously need to be factored in. White *et al.* recommended, *inter alia*, that MLA/ISC might consider *"…exploring opportunities to derive additional value (or revenue) from collected data, while maintaining the integrity of the systems, and the confidentiality and support of industry and individual users."* Clearly, increasing the effectiveness of traceability using genomic technology presents such an opportunity that is worth exploring.

Key sensitivity/parameters

If a dollar figure can be assigned to the cost of a disease outbreak, it follows that a control strategy can be valued by the extent that it mitigates that risk. In determining the cost, past studies have included costs of lost production, costs of treatment and response costs. The approach we have taken is to build on the work of Dwyer and Clarke (2015) and others*,* whereby the parameters of the Gross Value of Production are defined as well as the risk of an event, the scale of event (*i.e.* how much of industry is impacted) and the duration of an event.

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[61] White, M., Han, S-H., and Hoban, S. (2019) *Integrity Systems Sub-Program Impact Assessment (2015-2020)* MLA Report V.ISC.1918

This logic can then be readily extended by assuming increased traceability using DNA technologies. Modelling any additional benefits also requires factoring in any additional costs, which in turn require assumptions to be made about how the enhanced system might operate. In short, genomic-assisted traceability provides a back-up system that connects an animal to all of its products – a connection that in theory a least, cannot be lost as it is integral to both the animal and its products – but which brings additional costs.

In our modelling, we have relied largely on the work of Dwyer and Clarke (2014)[60], which described the probable relationship between levels of traceability and expected benefits, and attempted to quantify some of the additional opportunities and costs that genomic traceability brings. The results can then be compared with any alternative technology that offers traceability through to end products, such as chemical profiling.

Basic proposition for traceability

In calculating the value of traceability, the basic proposition is that a traceability system can:

i) reduce the time an industry loses during a disease outbreak, in order to-
    a) quarantine the source and enable treatment (and hence duration of lost production); and
    b) Reduce the time out of market(s);
ii) reduce costs, including:
    a) treatment costs; and
    b) the opportunity cost of lost production and/or sales.

In their calculations, Dwyer and Clarke (2015) used the ABARES (2014) estimate of $52b losses over a ten-year period from a large foot and mouth disease (FMD) outbreak. Using various other assumptions, including an annual probability of an FMD outbreak at 1.5% and traceability with NLIS of 97% in cattle and 90% in sheep (compared with 65% without NLIS), they arrived at an annualised "benefit" (*i.e*. avoided costs) due to NLIS of around $615m, or a net present value (NPV) of $8.3b using a 30-year timeframe. Projected benefits increased to $9.43b when a slow-moving disease (bovine spongiform encephalopathy, or BSE) was also included.

Dwyer and Clarke postulated that the relationship between the level of traceability and disease cost is curvilinear, based on NPVs estimated at various levels of traceability; although they pointed out that several points on the curve can be defined, but its exact shape is not actually known. They postulated that the most likely relationship between disease cost due to an outbreak and traceability level is described by Curve A in Figure 32. (Curve B, which lies half-way between Curve A and the dashed line, was simply tested in a sensitivity analysis).

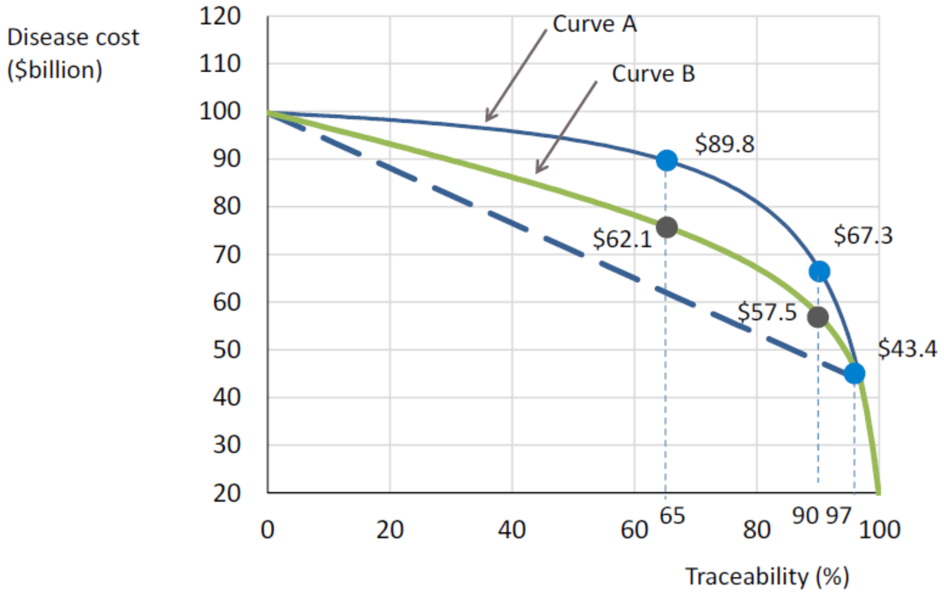

Figure 32. Assumed relationship between disease cost and traceability
(Source: Dwyer and Clarke 2015, Figure 4)

The relationship shown in Figure 32 for a disease outbreak was used by Dwyer and Clarke to derive expected annual benefits from NLIS, assuming the likelihood of an outbreak occurring in a single year to be 1.5%. We note that some of the details of Dwyer and Clarke have been subsequently questioned by White *et al*. (2019) but do not expect this to have a major impact on our main conclusions.

The beef and sheep industries currently have different NLIS protocols resulting in different traceability levels; and furthermore, the additional benefits derived from genomic information take a different form in the two industries, so they will be considered separately.

a) Beef

Traceability in the beef value chain

Dwyer and Clarke (2015) assumed that traceability in the beef industry with NLIS is 97%, which compares with 65% pre-NLIS. Results from our survey and stakeholder interviews suggest that given levels of tag losses being experienced and other imperfections in the system, 97% may be too high, but we have used 97% as the base case in favour of erring on the conservative side. We also assume that the addition of genomic identification on all cattle increases traceability levels to 99.5%. Given the high cost of genotyping (assumed here to be $33 per sample), have also examined a scenario where only half of the national herd is genotyped in order to reduce costs, leading to 99% traceability. This level seems reasonable, given that NLIS is already assumed to provide 97% and the half to be genotyped could be chosen to be highly representative of the national herd (*e.g.* all of the males). This would obviously include all of the sires, except for those used in the form of imported semen. To further reduce costs, a fourth scenario is modelled where only sires are genotyped for the reference database. The traceability level for this is also set at 99%, to allow for the fact that in some northern beef operations, sires may include some males that were not marked and are not likely to be sampled (although their close relatives most likely are).

Thus our particular interest is in the part of Curve A in Figure 32 that lies between 97% traceability and 100% traceability. As the curve is not mathematically defined, we have assumed that the relationship between traceability and disease cost is linear over this range (passing through the points in Figure 32), and interpolated a value for intermediate levels of traceability. We have then converted this to an annual traceability benefit using the average relationship derived by Dwyer and Clarke (2015) and allowed for only 76% of the total benefit coming from beef (with the remainder from sheep).

Table 1 shows the estimated annual benefits of traceability at four levels, using the methodology described above and assuming:

1. NLIS with 97% traceability
2. NLIS + 100% genotyping (giving an expected level of traceability of 99.5%)
3. NLIS + 50% genotyping (i.e. half the beef herd, giving 99% traceability)
4. NLIS + sire genotyping, also giving 99% traceability.

Table 1. Estimated costs and benefits using genotyping to aid traceability.

Note	Parameter	NLIS	NLIS & genotyping		
a	Proportion genotyped	0%	50%	100%	Sires
b	Traceability	97%	99%	99.5%	99%
	Cost ($m p.a., industry)				
c	National (database *etc.)*	$5	$6	$6	$6
	Implementation (tags, readers, labour)	$45	$45	$45	$45
d	Implementation (genotyping)		$111	$223	$3
	Benefit ($m p.a., industry)	$468	$626	$665	$626
	Benefit - Cost ($m p.a., industry)	$418	$464	$392	$572
	Marginal benefit ($m p.a.)		+$45	-$27	+$153

<u>Notes</u>
a. Proportion of national beef herd genotyped. Assume 7.5m head p.a. with 10% culled prior to sampling.
b. Approximate traceability levels, as described previously
c. Allows $1m p.a. for annual operation of national genotype database, in addition to existing NLIS costs. It does not include development costs. This figure is uncertain but it is unlikely to affect the main conclusions
d. Genotyping at $33 per sample. Assume 10% of animals culled prior to tissue sampling and 100,000 new bulls p.a., based on annual requirement of new bulls estimated by Fennessy et al. (2014)[13] at 86,000.

This indicates that the additional value of traceability expected to be realised by genotyping the entire national herd is unlikely to compensate for the additional costs involved. However, genotyping half the herd is estimated to lead to a net increase in benefits due to traceability of 11% compared with NLIS alone; with genotyping all sires increasing net benefits by 37% compared with NLIS.

Obviously, these estimates are highly contingent on the veracity of the model used by Dwyer and Clarke (*op cit.*); and it is worth emphasizing that we were unable to obtain a copy of the source document on which they based their model. However, we can be confident that traceability has value, which has been estimated for individual diseases by a range of authors and found to be very high and our sensitivity analyses (not reported here) suggest that the addition of genotyping to augment the existing NLIS system is most likely to be worth somewhere in the range of $5m - $27m p.a. for each extra 10% of the herd that is genotyped. This is encouraging at an industry level. However, achieving them comes at a significantly increased implementation cost, which we assume will fall predominantly or wholly on the individual farm enterprise or value chain – *i.e.* producers will pay the genotyping costs, just as they pay the costs of electronic identification now.

Notably, however, the additional benefits of traceability identified by White *et al*. (see box on page 61) are not included in Table 1. The additional value of these benefits is likely to be appreciable and has the potential to offset the additional farm-level costs. Consequently, in the following section we attempt to evaluate some of the ancillary benefits that might accrue through genotyping.

Ancillary benefits from DNA information

Modelling the magnitude of potential ancillary benefits requires assumptions to be made about levels of genotyping within the seedstock sector as well as in other parts of the production pipeline. Rates of improvement generated in the seedstock sector will, after a delay, lead to equivalent rates of gain in the commercial sector. This was described by Santos *et al*. (2018)[62] with reference to the Australian sheep industry, who also examined the genetic and economic impact of performance recording and genotyping in commercial sheep (*i.e*. sheep not in the seedstock sector). In short, commercial data has the potential to improve selection accuracies in the seedstock sector as well as reduce the delay taken for the benefits to flow through the industry.

We have attempted to model the dynamics resulting from the above factors with both limited and widespread levels of adoption.

Additional data for genomic selection

The relationship between the volume of reference data and the accuracy of genomic selection has been well described (*e.g*. Meuwissen *et al.* 2001[63];Goddard and Hayes, 2009[64]) and is widely accepted. In this context, reference data refers to data collected on animals that provide both genotypic and phenotypic information; and these collectively form what is widely referred to as a “genomic reference population”.

Rates of genetic gain and the impact of additional genomic information at an industry level depend on the:

- number of seedstock cows
- number of bulls entering production per year per cow
- number of lifetime matings of those bulls

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[62] Santos, B.F.S., Amer, P., Granleese,T., Byrne, T.J., Hogan, L., Gibson, J.P and van der Werf, J.H.J. (2018). “Assessment of the genetic and economic impact of performance recording and genotyping in Australian commercial sheep operations” J. Anim. Br. Genet. 135:221-237.

[63] Meuwissen, T.H.E., Hayes, B.J. & Goddard, M.E. (2001) “Prediction of total genetic value using genome-wide dense marker maps”. Genetics 157, 1819–1829.

[64] Goddard, M.E.., Hayes, B.J. Mapping genes for complex traits in domestic animals and their use in breeding programmes. Nat Rev Genet 10, 381–391 (2009). https://doi.org/10.1038/nrg2575

- current rate of genetic progress in dollar terms (typically measured in units of an economic index or $Index expressed as dollars per cow mated per year)
- the increase in accuracy due to the extra information (where accuracy is the correlation between true and estimated breeding value)

Appendix 2 contains a presentation (developed previously for a sheep breeding forum), which outlines the parameters that determine the value of additional records for genomic selection. These are basically:

- The number of such records
- The correlation of the trait(s) with the breeding objective of the population

As an illustration, assume a situation where 50% of young animals are genotyped (*i.e.* approximately 3.75m per year in the case of beef cattle). If all those animals provided phenotypic data, and that data was correlated 100% with the economic breeding objective, then there would be 3.75m "effective records" added to the reference population each year, which would generate accuracy of genomic selection that in theory approaches 100%.

Such a high level of phenotyping is of course impractical, so in our modelling, we have assumed that only a fraction of animals genotyped also provide phenotypic data, and that data is only weakly correlated with the breeding objective. (This is because records obtained from commercial animals are less accurate and cannot be appropriately adjusted for many environmental effects). Under these assumptions, we estimate that an additional 4,500 effective records would lead to an increase in selection accuracy (and therefore rate of genetic gain) of 20% compared with current levels. As there are three main groupings of beef cattle breeds (European, British and Tropical), the total number of effective records required to achieve this aim is 13,500. Thus the ratio of effective phenotypic records to animals genotyped being modelled here is 13,500, or about 13,500/7,500,000 = 0.18% of the annual crop of calves weaned. For comparison, the same logic implies that ~30,000 additional records would be required to increase selection accuracies by about 35% above current levels, or 0.4% of the annual calves weaned. By modelling the resulting increases in genetic progress and the flow of benefits through the industry over a number of years, we can calculate the average annual benefit. This is summarised in Appendix 3.

Note that obtaining these additional phenotypic records will obviously come at a cost. We have not included this cost in our modelling as it is such a small proportion of the national herd, the required data can be accumulated over several years and the cost could probably be absorbed by the industry. Nevertheless, any implementation of such a model would need to consider what incentives might drive the collection of this data by individual producers.

Genomic screening to guide management decisions

As described previously, genomic tests are already being used in the beef production sector to inform management decisions, where young commercial cattle are genomically tested to predict adult performance or feedlot performance. Appendix 4 uses a simple example to demonstrate the principle involved. Using actual data, Hine *et al*. (2021)[48] recently reported the differentials that could be created by genomically testing steers in a commercial feedlot with the AngusSELECT product and using a reference population of 2,973 steers. The accuracies of genomic predictions for carcase weight and marbling score were 75% and 73%, respectively. When steers were ranked according to their predicted carcase values, those in the top quartile had actual carcase values some 20% higher than those in the bottom quartile, in both short-fed and long-fed cohorts, equating to differentials of $354 and $712, respectively.

At an industry level, the extent to which the production sector can benefit from the additional information afforded by genomic predictions will depend on:

- the extent of between-sector contracting
- the accessibility of relevant reference data
- whether this simply shifts benefits between enterprises, and/or reduces opportunity costs (*i.e.* whether animals culled using this information are diverted from a path where they would generate an industry loss).

We have developed a simple model to examine the general case for using genomic screening in commercial populations. The principle can be applied to any testing purpose, such as screening replacement heifers, screening for animals requiring preventive treatment (to reduce risk of some known disease or condition), different feeding regimes (as shown here, but could be extended to grain *vs* grass, short-fed, *etc*.) and others.

It is not intended to imply that this is how genomic screening tests could or will be marketed, or their properties explained - but it does capture the principles of evaluating return on investment in such a test. Here, it is used to show how we can estimate the return to industry from applying genomic screening tools.

Three scenarios have been modelled:

1. Screening for short-fed steers
2. Screening for long-fed steers
3. Screening for heifer replacements

We assume that approximately 500,000 animals genotyped have their data submitted for genomic prediction and subsequently screened using the results, which is a relatively small proportion of the annual number weaned. The accuracy assumed for the genomic tests is as for genomic selection at the respective levels of overall genotyping *i.e.* 45% or 60%. This simple approach likely overestimates the accuracy of genomic screening tests – which will depend on the accuracy of genomic EBVs (estimated breeding values) in the reference and the screened animals' relatedness to the reference.

Given that we have only included three genomic screening examples in Appendix 4 but there are likely to be many more, the industry benefits available may actually be underestimated if other applications are developed.

Total benefits

Some results from our modelling are summarised in Table 2, with benefits aggregated across traceability, genetic gain and screening applications. For the sire-only scenario, there are no additional genetic benefits indicated, because increasing the amount of reference data would require additional genotyping as well as additional phenotyping. It is worth noting, however, that if every beef sire is genotyped, then it is relatively straightforward to compute their breeding values; and this information could potentially influence bull buying decisions, thereby driving better practices across the seedstock sector. No attempt has been made to evaluate such additional benefits.

Table 2. Net benefits of using genotyping as an aid to traceability in beef.

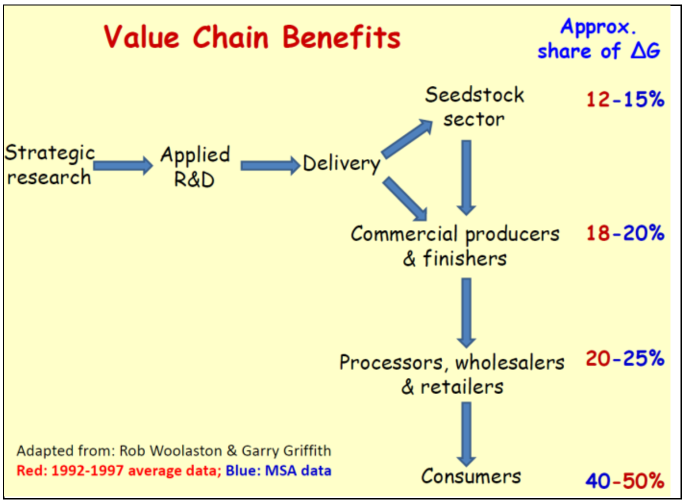
Note	**Parameter**	**NLIS**	**NLIS & genotyping**		
a	Proportion genotyped		50%	100%	Sires
b	Number phenotyped p.a. for genomic reference (both sexes)		13,500	30,000	0
c	Prediction accuracy		45%	60%	na
d	Proportion managed using DNA test		33.3%	33.3%	0
Cost ($m p.a., industry)					
e	National	$5	$6	$6	$6
e	Implementation (tags, readers, labour)	$45	$45	$45	$45
e	Implementation (genotyping – beef)		$111	$223	$3
Benefit ($m p.a., industry – beef)					
e	Traceability (v pre-NLIS)	$468	$626	$665	$626
f	Faster genetic progress due to data		$20	$34	-
g	Genomic screening – SF steers		$11	$28	-
g	Genomic screening – LF steers		$19	$51	-
g	Genomic screening - heifer retention		$38	$101	-
Marginal benefits less marginal costs ($m, p.a.)					
h	Traceability		$46	-$27	$153
i	Genetic gain		$87	$215	$0
j	Total		$133	$188	$153
Total net benefit, beef ($m, p.a.)		**$418**	**$551**	**$606**	**$572**
Total increase due to genotyping			*32%*	*45%*	*37%*

Notes
a. Proportion of national beef herd genotyped
b. Size of genomic reference population (see p. 101)
c. Expected prediction accuracy given size of reference population
d. Proportion of commercial steers and heifers that are managed according to predicted performance based on genotypes
e. Figures from Table 1
f. From Appendix 3
g. From Appendix 4
h. Traceability benefits less extra costs (same as Table 1).
i. Genetic progress + screening
j. h+i

The results summarised in Table 2 should be regarded as somewhat speculative, particularly those for traceability, which rely heavily on the report by Dwyer and Clarke (*op cit).* Furthermore, projected benefits from genetic applications are obviously dependent on the assumptions we have used.

Distribution of benefits by sector

Benefits from increased traceability in beef were estimated by Dwyer and Clarke 2015) as shown in Figure 31. Burrow and Banks (2011)[65] argued that benefits from genetic gain in beef also accrue at all points of the value chain, distributed as shown in Figure 33. The proposition that consumers realise up to half of the benefits from traceability and genetic gain is an argument for at least some public funding of activities directed at improving these.



Adapted from: Rob Woolaston & Garry Griffith
Red: 1992-1997 average data; Blue: MSA data

Figure 33. Distribution of benefits from genetic improvement
(from Burrow and Banks 2011[66])

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[65] Burrow, H.M. and Banks, R.G. (2011) "Increasing uptake of genetic technologies across the beef value chain". Proceedings Assoc. Adv. Anim. Br Genet. 19: 391-398.

[66] Slide 8 of presentation by Burrow and Banks (2011), accessible through http://www.aaabg.org/aaabg19/proceedings19

b) Sheep

Traceability in the sheep value chain

Modelling potential benefits of DNA traceability in the sheep industry, and of potential ancillary benefits, is not as straightforward as for beef cattle, for two reasons:

a. NLIS in sheep is currently mob-based and predominantly based on paper recording (apart from in Victoria where EID is mandatory). Accordingly, a point of comparison for DNA-based traceability in sheep is not an EID system, which would be assumed to have accuracy around 90%, but a paper-based system which, drawing on earlier studies might be assumed to have accuracy in the 65-70% range.

b. The cost of genotyping relative to the value of individual animals is higher in sheep (than cattle) - approximately $35-45 genotyping against nominal 5-year rolling average lamb values of c. $150 per head, compared with similar price for genotyping against steer values of c. $1000-1500 per head.

Taking the second challenge first, it is worth setting out how DNA technologies are already being used in sheep (see Section 3):

- In the stud or seedstock sector, there is steadily growing adoption of genotyping for parentage, horn/poll (Merinos) and increasingly for genomic prediction. This is individual animal genotyping.

- In the commercial sector, there is modest but growing adoption of mob-based genotyping via the Flock Profile service supported by Sheep Genetics. Here, tissue samples from c. 20 animals in a flock are submitted for genotyping, and the genotype is then used to predict flock mean genetic merit for traits evaluated by Sheep Genetics. This service costs approximately $700 per flock.

The methodology for estimating flock mean is based on estimating genetic relationship of that flock sample to the overall genomic reference population (the dataset of animals with genotypes and phenotypes which underpins the genomic analyses delivered by Sheep Genetics). This is analogous to matching an animal to its sire (for example) via DNA, except that in the case of Flock Profile, the matching is actually to all animals with genotypes in the Sheep Genetics database.

An alternative to basing traceability on Flock Profiling would be to genotype all the sheep sires used in Australia. Fennessy *et al*. (2012)[13] estimated that 254,000 new rams are needed each year for the national sheep flock. We have used a figure of 300,000 and each of these is genotyped. At $33 per test, this would probably cost around $33m in the first year if all existing sires are genotyped, but about $10m every year thereafter if just new sires are genotyped. This is likely to lead to slightly more accurate traceability than Flock Profiling but at a greater cost.

Flow-on or ancillary benefits

The approach described has a second-level benefit, in that it automates the provision of information from which breeding and (potentially) management decisions can be made. The Flock Profile service delivers flock mean EBVs, with the primary expectation that producers can use that information to review their ram-buying decisions – both in terms of the ASBVs (the sheep industry version of EBVs) they might focus on, but also, potentially to change their ram source(s).

The value of providing information to assist in such changes in ram source has been modelled by Atkins (1993)[67], and with appropriate updating of prices, can serve as a basis for approximation of benefits of such use of Flock Profile information. Note that Atkins' modelling was solely in Merinos. Switching to genetically superior ram sources is potentially the main "management" benefit of DNA information – primarily because the use of flock sampling overcomes the hurdle of the high cost relative to individual animal value.

It should be noted that a number of studies have investigated use of genotyping in the multiplier level of operations where there is a stud or nucleus, then a multiplier "tier" which in turn supplies flock rams to a large commercial operation. This is not really an ancillary benefit of genotyping for traceability, because such flocks would likely have a genomic profile based on animals in the stud or nucleus – such that the flock will already be obtaining the benefits of genomic selection, or at least is able to.

Additional data for genomic selection

Although we have developed a model to predict the value of increased selection accuracy that would arise if more phenotypic and genotypic records are added to the existing sheep reference populations, we will not report that work here (except to note that elements of the relevant modelling in sheep are also included in Appendix 3). In sheep, where only samples of flocks (or alternatively, sires) are genotyped, increasing the number of records for the reference populations is essentially a separate exercise. This contrasts with the situation in beef where the genotypes of many individual animals become available if DNA is used to strengthen traceability.

More informed ram buying decisions

Profiling every flock using a sample of its DNA essentially means that all flocks can be assigned EBVs for the main traits affecting profitability using existing reference data. A similar situation exists of all sires that are genotyped. This means that ram buyers have the information required to compare ram sources and consequently they have the opportunity (and possibly the motivation) to change their ram supplier.

Notably, Atkins (1993) provided a detailed analysis of the potential values from higher rates of genetic progress and of ram buyers switching sources, for the wool industry. He concluded that the increased adoption of more effective breeding practices together with improved client mobility could result in an additional $1,400m (in 1993 dollars) over 30 years. Using these results as a basis, to approximate a value of this outcome in today's values we have estimated the intervening changes in wool prices, increases in the value of surplus animals, reductions in size of the national flock and assumed that half of the NPV is due to ram-buyer mobility. We have made no allowance for ram-buyer mobility in the terminal sire and maternal sectors. This leads to an estimate of this ancillary benefit of $23m p.a.

Total benefits

For sheep, we present modelling results from three alternatives:

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[67] Atkins, K.D. (1993) "Benefits of genetic improvement to the Merino wool industry", Wool. Tech. Sheep Breed. **41**: 257-268.

1. The existing NLIS system, with traceability assumed to be 90%.
2. NLIS augmented by Flock Profiling, with every flock sampled every three years and traceability assumed to be 99%. No benefits are assumed for extra genetic gain due to genotyping but the value from changing ram sources is included.
3. NLIS + sire only genotyping. All sires are genotyped and traceability is assumed to be 99.5%. No extra benefits accrue for genetic gain but same value from changing ram sources.

The results are summarised in Table 3.

Table 3. Net benefits of using genotyping as an aid to traceability in sheep.

Note	Parameter	NLIS	NLIS & flock profiling	NLIS & sire genotyping
a	Number of flocks submitting genotypes		16,667	-
b	Number of sires genotyped			100,000
c	Traceability	90%	99%	99.5%
Cost ($m p.a., industry)				
d	Implementation (genotyping – sheep)		$12	$3
Benefit ($m p.a., industry – sheep)				
e	Traceability (v pre-NLIS)	$148	$213	$218
f	Faster genetic progress due to data		$0	$0
g	Changing ram sources		$23	$23
Net ($m p.a., sheep), base case		***$148***	***$224***	***$231***
Increase due to genotyping			***51%***	***56%***

<u>Notes</u>
a. Assumes every flock (or sub-flock) sampled every 3 years
b. Annual number of new sires
c. Assumes $700 for flock profile and $33 per sire
d. Proportion of commercial steers and heifers that are managed according to predicted performance based on genotypes
e. Based on Figure 32, assigning 24% of the value to sheep and to allow for curvilinearity, assuming that 1/3 of the benefit of increasing traceability from 90% to 100% occurs between 90% and 95%, with 2/3 of the benefit occurring between 95% and 100%.
f. Assumes no additional reference data – see text
g. Based on Atkins (op cit.)

These results indicate that using DNA to augment the current NLIS system in sheep could potentially be quite cost effective, provided that sampling of the national sheep flock is done judiciously. Most of the additional benefit is likely to arise from improvements in traceability. However, our modelling suggests that the potential value through stimulating ram buyer mobility is still significant. It might be expected that initially, much of the additional value is achieved simply by ram buyers identifying sources of more profitable sires, but in the longer run, most of the additional benefit is likely to be caused by improved ram breeding practices driven by greater competition.

Distribution of benefits by sector

Benefits of NLIS in sheep were estimated by Dwyer and Clarke (2015) to be distributed as shown in Figure 31, with domestic consumers and overseas customers each realising over 30% of the total. There are no published estimates of how the benefits of genetic gain in sheep are distributed, but it is reasonable to assume that they are probably similar to beef (see Figure 33).

Other ancillary benefits

The examples shown above are just a subset of applications that are possible once a system links identity, genotype and some form(s) of performance data. For example, Appendix 6 outlines how the Irish national genomic identification system is being linked to animal health databases enabling therapeutic response, but also enabling R&D into (in this case) the genetics of particular conditions. Once such R&D is complete, it will be possible to detect at-risk animals as soon as a genotype is available. The Irish experience demonstrates the power of linked data as a learning or research vehicle, which will underpin future search tools and services. This distinction underlies the discussion of opportunities in the section “Strategic and Governance Considerations”.

Economic modelling - summary

Not unexpectedly, our initial modelling shows results to be very sensitive to assumptions around:

- ***Risk parameters***. As indicated by White *et al.* (2019)[61], the likelihood and extent of a disease outbreak or contamination event are a major determinant of industry benefit and these are particularly difficult to evaluate.

- ***Genotyping costs***. Current levels are known but there is uncertainty around likely future costs with greatly increased throughput and technological developments.

- ***Adoption levels***. These could be influenced by policy or simply by market forces, with a range of possibilities ranging from totally voluntary with user pays, through to mandatory with industry and/or government subsidies. We do not consider that DNA traceability could totally displace the current tag-based system for the foreseeable future, so have not considered such a scenario.

- ***Animal prices***. Prices of red meat have increased significantly in recent times but there is no certainty that current price premiums will be maintained into the future. Assumptions around prices received relative to the cost of genotyping have a significant effect on the scale of benefits modelled.

If adoption levels are sufficiently high, it is clear that the ancillary benefits (*i.e*. apart from traceability) can greatly outweigh implementation costs and are scalable in that the greater the participation rate, the higher the overall benefits and the greater the potential synergies between systems. Some form of industry-wide genotyping clearly has the potential to be transformational both across and along value chains.

It therefore seems clear that high levels of adoption of DNA-based tools can make large contributions to both increasing industry rate and value of genetic progress, and to profitability of management decisions in individual enterprises and value-chains. Under high levels of adoption, these ancillary benefits can plausibly offset the implementation costs, and create a situation where DNA-based traceability becomes almost a “free by-product”. These potential benefits are the same under the (arguably) optimistic modelling of benefits of traceability, and remain just as important – because the on-farm costs must be offset by value perceived by each individual decision-maker. An overall, key point then, is to think about the nature of the benefits accruing from traceability and other applications of DNA technologies:

- Traceability is a somewhat intangible “insurance” good – with its extent or distribution varying with the extent of an incident. This is not to say that the benefit is intangible to any affected individuals or businesses, but even there, it is of the form of a reduced (or even absent) loss, rather than an actual cash gain.

- Faster genetic progress is also somewhat intangible – individuals have some influence over what they capture through their individual sire purchasing, but individually have little impact on the overall rate of progress … but everyone is better off if that is higher.

- The individual business or value chain applications are much more like private benefits – you make an investment, you see an effect (as long as you have some financial records).

Our conclusion is that using DNA to augment traceability is highly aligned with the IS2025 strategy (see Figure 34). However, it raises a number of strategic questions which require resolution:

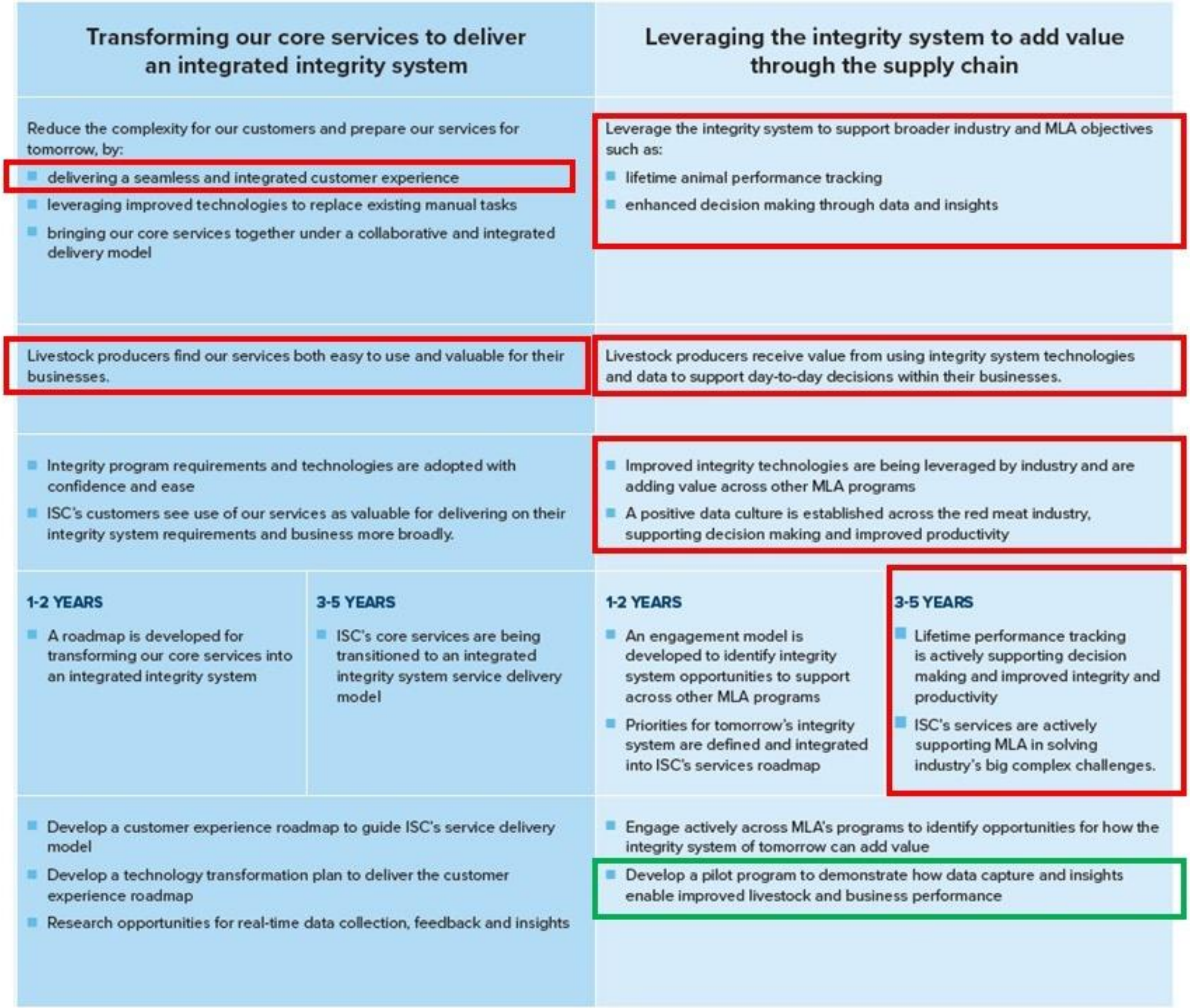
- What is an appropriate implementation model? Should participation be mandatory, voluntary, simply market-driven or opportunistic as is currently the case? Most people basically find the cost of NLIS to be acceptable for industry benefit, but adding DNA significantly increases enterprise costs, and is likely to be resisted because the benefits are not sufficiently obvious or direct.

- How can an acceptable governance system be set up that oversees coordination of the different databases but also recognises the value of participation and determines the ownership of data?

- How can genotyping providers be best co-ordinated and can appropriate standards be established? (Note, however, that these issues have already been effectively addressed when using genomics for genetic evaluation, albeit at a far lower scale).

- Can current turn-around times and the costs of genotyping be reduced through economies of scale?

  Such questions are not trivial and will be addressed in the following sections.



Transforming our core services to deliver an integrated integrity system	Leveraging the integrity system to add value through the supply chain
Reduce the complexity for our customers and prepare our services for tomorrow, by: ▪ delivering a seamless and integrated customer experience ▪ leveraging improved technologies to replace existing manual tasks ▪ bringing our core services together under a collaborative and integrated delivery model	Leverage the integrity system to support broader industry and MLA objectives such as: ▪ lifetime animal performance tracking ▪ enhanced decision making through data and insights
Livestock producers find our services both easy to use and valuable for their businesses.	Livestock producers receive value from using integrity system technologies and data to support day-to-day decisions within their businesses.
▪ Integrity program requirements and technologies are adopted with confidence and ease ▪ ISC's customers see use of our services as valuable for delivering on their integrity system requirements and business more broadly.	▪ Improved integrity technologies are being leveraged by industry and are adding value across other MLA programs ▪ A positive data culture is established across the red meat industry, supporting decision making and improved productivity
1-2 YEARS ▪ A roadmap is developed for transforming our core services into an integrated integrity system **3-5 YEARS** ▪ ISC's core services are being transitioned to an integrated integrity system service delivery model	**1-2 YEARS** ▪ An engagement model is developed to identify integrity system opportunities to support across other MLA programs ▪ Priorities for tomorrow's integrity system are defined and integrated into ISC's services roadmap **3-5 YEARS** ▪ Lifetime performance tracking is actively supporting decision making and improved integrity and productivity ▪ ISC's services are actively supporting MLA in solving industry's big complex challenges.
▪ Develop a customer experience roadmap to guide ISC's service delivery model ▪ Develop a technology transformation plan to deliver the customer experience roadmap ▪ Research opportunities for real-time data collection, feedback and insights	▪ Engage actively across MLA's programs to identify opportunities for how the integrity system of tomorrow can add value ▪ Develop a pilot program to demonstrate how data capture and insights enable improved livestock and business performance

Figure 34. Elements of the IS2025 strategy, showing those that would be augmented with genomic identification (framed)

7. Strategic and governance dimensions

Data Dependence

Whether for traceability purposes alone, or for delivering the ancillary benefits discussed here, there are several developments that must be in place for any benefit of use of DNA technologies:

a) **Appropriate database** There must be a DNA database established under the control of, or at least with the access for, the traceability organisation. Such databases exist, including several over which MLA has some level of control (*e.g.* Sheep Genomics database, beef R&D project databases managed by AGBU and likely by other research providers such as CSIRO, NSW DPI *etc*.). Those databases could be replicated quite simply, and are scalable essentially infinitely, subject to access to suitable servers (or the cloud). By replicate, we mean copy the structure so that new genotypes could start to be added to an empty "box". It is important to note that genotype databases already exist, many of which involve MLA; and so development of a database is not starting from scratch.

b) **Linkage with other databases** The DNA database must be linked to the existing NLIS database via some standard and universal identification protocol. This is in order to enable the linking of a genotype to a known animal (with known origin, ownership *etc*). The most likely such ID system would be the NLIS itself. At least some of the DNA databases in existence include NLIS number for animals, so the principle and method are established. Detailed specifications of the database are beyond the scope of the project but clearly some key considerations would include the capability for uploading and storing large volumes of genotype data, DNA matching algorithms, permissions *etc*.

c) **Performance databases** For the ancillary benefits to be realised, there must be access to databases of performance data (called here reference databases). The linking data field here can be ID, or simply genotype. Examples of such databases include the R&D project databases referred to above, along with databases held and managed by breed societies (either directly, or via contracts with ABRI). Technically, this is relatively straightforward – once data formats are defined between any two players, data can flow in either direction very simply, even very large files. The aspect of this linking that is most challenging to achieve, is the data access and use agreements: agreements that define what party A can do with data owned or managed by party B (and any others), and whether there are commercial components *i.e.* party A has to pay some form of royalty for use of data owned or managed by party B (and any others). The challenging aspect here is not the development of such agreements itself – examples exist of licenses for use of R&D data, for instance. Rather, the challenge is ensuring robust agreements are put in place *i.e.* that can be trusted, and defining any commercial terms *i.e.* what payments are due for access to data. The value proposition for doing this basically applies across all possible uses of genotype data, whether traceability and/or the ancillary benefits: that the accuracy, or decision-making power available to any individual or business or set of businesses increases with the amount of data. Using the example of parties A, B *etc.* above, it is that whatever decision-making power is available to A as a result of collecting data, it will be greater when data collected by A is combined with data collected by B *etc*. This is illustrated for the accuracy of genomic selection in Figure 35, which is the chart of Goddard and Hayes (2009).

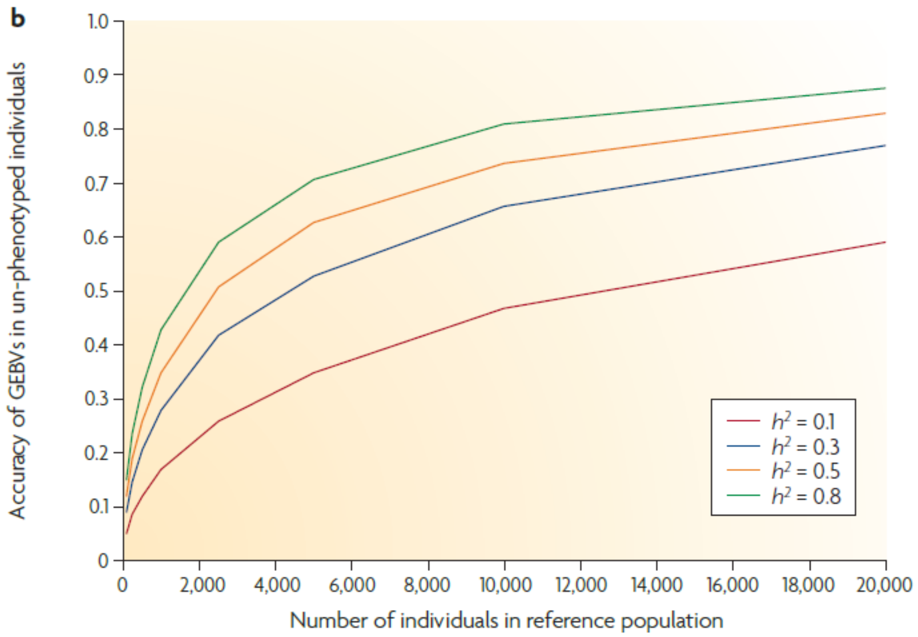


Figure 35. Calculation of number of animals in a reference population and accuracy of breeding values (From Goddard and Hayes 2009)

a. To achieve an accuracy of 0.7 for estimated genomic breeding values (GEBVs) calculated from SNPs requires an increasing number of animals in the reference population as the heritability declines or the N_e of the population increases. b. Accuracy of GEBVs of un-phenotyped individuals with increasing number of phenotypic records in the reference population used to estimate SNP effects, for different heritabilities (h^2). N was 100.

The chart shows that for traits of different heritability, the accuracy of genomic prediction rises with increasing size of the reference population. The shape of this relationship – the rate at which accuracy of some decision or search increases with the number of individuals in the database with some form of data (which can simply be genotype – will vary for different searches or decisions, but the general principle is expected to hold.

This principle will be fundamental to obtaining buy-in from businesses and organisations who are seeking to protect and exclusively exploit, for the benefit of their stakeholders, the value of their data holdings – obvious examples being breed societies.

This benefit of linking or combining datasets is the “why”. The “how” will depend on access agreements. These will almost certainly be based on some form of access charges. Establishing and implementing such charges is a new area or question for animal industries: typically the costs of data are either submerged in some form of overall service charge, or are met by industry or government. These approaches are unlikely to be sufficient in the NLIS case, where the data needed to underpin ancillary benefits is usually at least partly owned by independent businesses, each seeking to maximise the value they can generate and capture from their investments in data.

8. Risks and opportunities

Economies of scale

In our modelling, we have assumed laboratory costs of around $33 for genotyping. Genotyping companies have been understandably non-committal about likely discounts with large volumes of samples, but they did indicate that there is likely to be scope for a meaningful reduction in costs, given a) sufficient volume and b) the ability to plan ahead with a high degree of certainty. We have been told that one genotyping company recently filled an order for about 200,000 bovine tests (>50k SNPs) for AUD20. It seems likely that if/when large scale genotyping becomes a reality, routine tests will become much cheaper, with fast-tracking testing of queried samples, in much smaller numbers, available at a premium.

Some coordination of genotyping procurement is likely to be more beneficial and cost-effective than an *ad hoc* approach; as will the establishment of appropriate standards for genotyping. Critical questions are whether scale can indeed reduce the cost of genotypes and whether there is also scope for reducing turnaround times.

Notably, many of the key stakeholders we interviewed (some of whom are already using DNA tracing in some form) expressed enthusiasm for sharing infrastructure costs with other industry participants. This included at least one of the vertically integrated beef producers/processors.

Potential role of reduced SNP panels

The modelling work in this study has focussed on genotyping panels of sufficient density for genomic prediction of genetic merit and phenotype. When panels of this density (~50K SNP) are used, a host of other tools become available as well, including traceability of course, but also pedigree and breed composition, horn/poll and other diagnostics.

Recent work by Dominik *et al*. (2021)[68] has shown how individual animals can be uniquely identified in larger groups (up to about 80,000 individuals within a breed) using as few as 20-23 SNPs. However, to uniquely identify an animal in a population as large and diverse as proposed here, the number of SNP required is greater and would need to be determined.

Undoubtedly if traceability was the only aim and all the ancillary benefits were to be passed up, smaller panels could be employed. Exactly how much this would reduce the cost would also need to be determined. It is our assumption that with economies of scale, a reduced panel for traceability only and the density proposed here, which allows all the additional information to be provided, would become similar in price when all costs are considered.

One use of the reduced panel may be to reduce the Turn Around Time (TAT) for when a test sample needs to be queried against the database. The laboratory time required for these smaller panels is shorter than the full genomic panel we have proposed (which according to one service provider has a TAT that could be up to a week); whereas the smaller panel could be accomplished same day in the laboratory.

Consequently, one solution we are proposing is that all samples are genotyped with a genomic profile in the order of 50K SNP, as commonly used in genetic applications in cattle and sheep

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[68] .Dominik S., Duff C. J., Byrne A. I., Daetwyler H. and Reverter A. (2021) “Ultra-small SNP panels to uniquely identify individuals in thousands of samples”. Animal Production Science 61, 1796-1800.

today. These genotypes would be stored in the database. Then if there is an animal, or a product from an animal, where the identity is not known, this sample could be genotyped for a reduced targeted list of SNPs, which are a subset of the full genomic panel. This reduced genotype could be obtained much faster and be queried against the entire database to determine its identity. We expect algorithms would be developed to allow this searching and matching to be done in a fast and efficient manner.

Data standards

Issues relating to standards in a range of commercial applications are well explored in the economics literature, including discussion of how standards systems can arise, what happens if they don't, situations which can justify interventions (such as by government), and the economic benefits of having standards.

NLIS (through SAFEMEAT) currently sets standards for the manufacture of electronic ear tags (ISC 2017)[69] as well as the software that processes electronic declarations. If genomics is to become part of the national traceability system, a robust set of standards will need to be developed for two activities: the actual genomic testing; and then the processing of data derived from those tests.

In our assessment, the general standards currently in place around genotyping (and more particularly the ability to read genotypes taken on a diverse range of chips), are probably sufficient for a traceability system. However, it is essential that such a system has the ability to use genotypes from the range of chips currently available now or likely to be available in future. Such ability is well-developed in the software that AGBU has developed for BREEDPLAN and Sheep Genetics, for example.

If the goal is to aim for wide and rapid uptake, it seems likely that the ancillary uses of DNA will become paramount, and that brings up questions of some forms of standardisation, or at least validation of tools. As an example, there are breed composition tests available based on widely differing reference populations, and algorithms (how many SNP are used etc.), and there are global initiatives to provide standards (via ICAR, the International Committee for Animal Recording). Having a process for informing the market of what different tools or algorithms do, would seem to be useful.

The issue of standards in data agreements is a further challenge. This may require the development of a convention describing principles for data access. Such a convention could be the basis of a universal, or at least national platform for data sharing, which would reduce the amount of legal time that individual stakeholders would have to invest, and ideally reduce the risks of both duplication on the one hand, and conflicting, or "heterogeneously and overlappingly incomplete" agreements on the other.

National system *vs* fragmentation

The previous discussion regarding the benefits of combining data in terms of decision-making power highlights one dimension of benefit from combining; the other dimension is simply the additional costs arising from duplication of databases and analytics, as well as transaction costs arising if connecting or combining data is not a built-in feature of the overall system. Note that it is not essential to have one "super-database", as long as the connection protocols and systems are well-designed and essentially seamless.

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[69] Integrity Systems Company (2017) "NLIS – Standard for Radio-Frequency Identification Devices"

An appropriate governance system linking the relevant databases will clearly be needed; one that provides acceptable levels of access while at the same time being equitable to participants and providing appropriate incentives and rewards. High levels of participation will maximise industry benefits, as the power of analytics (including traceability) increases with scale. How this is best set up and overseen is yet to be determined but may, for example, be set up and managed by an industry consortium.

NLIS in sheep

DNA technologies have the potential to transform the adoption of NLIS in sheep (which is currently mob-based apart from in Victoria). If DNA tools offer management benefits for sheep producers at a mob level, then flocks could be sampled at that level, providing a genomic reference point for each flock. Our view is that the current Flock Profile service supported by Sheep Genetics is in fact a model for this, and could be either re-purposed to include a traceability component, or used as the basis of a separate NLIS DNA Flock Tracing option. Some R&D into the accuracy properties of this approach would be valuable, but at face value, having a flock sample of every flock would enable a more objective basis for traceability than simple paper-based identification. The pilot project outlined later in this report would expand the foundation for such an approach, building on the existing genomic reference data managed by Sheep Genetics, and could include trialling traceability applications.

Selection for disease resistance

A potentially valuable application of genomic information is its use as a tool to greatly increase our power to select for disease resistance. Recently, Reverter *et al.* (2021)[70] described a genomic test aimed at improving the immune competence of Australian Angus cattle.

As mentioned previously, genomic databases are used in Ireland in conjunction with other forms of data to provide animal health information services (see Appendix 6). Local experience indicates that obtaining reliable animal health data from farms and feedlots is not a simple task. However, it is likely that data from processors has great potential, particularly as it can cover a wide range of diseases and conditions. For example, observations on large hearts, lung lesions, liver abscesses *etc.* could all be potentially captured, perhaps even using automation, to collect a large volume of health data, which in turn could be used to inform genomic predictions.

Distribution of benefits

The estimates of benefits and costs from introducing DNA technologies to the traceability system can be interrogated to consider how benefits and costs are distributed. This is important when devising a strategy of who should initiate, and possibly fund, a traceability system, and whether there is a role for governments or industry funding bodies. Other workers have estimated how the benefits of traceability are distributed in beef and sheep (see Figure 31) and how the benefits of genetic improvement are distributed in beef (Figure 33). The attribution shown in these studies may or may not be correct, but the following considerations are pertinent.

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[70] Reverter, A., Hine, B. C., Porto-Neto, L., Alexandre, P.A., Li, Y., Duff, C.J., Dominik, S. and Ingham, A.B.(2021) “ImmuneDEX: updated genomic estimates of genetic parameters and breeding values for Australian Angus cattle”. Animal Production Science 61, 1919-1924.

The first point to note is that the implementation costs of NLIS are predominantly borne by producers (tags and tag readers on-farm, plus on-farm labour which is not costed explicitly here but is included in our model as an estimate based on survey feedback). This preponderance of on-farm costs, borne by individual businesses, increases with any implementation of DNA technologies.

When we consider benefits, a distinction is needed between a) industry and community benefits which all enterprises share, and b) benefits which are largely or wholly captured by individual enterprises.

Traceability It can be argued that the benefits of traceability are essentially shared by all enterprises in industry, in a similar way to the existence of a public fire service. If this perspective is accepted, then the total value assigned to the NLIS column in our tables conveys a false impression – enterprises in total contribute an implementation cost estimated at $45m p.a., and obtain a benefit estimated at $616m p.a. from beef and sheep under the methodology applied here. In reality, the share of costs borne by enterprises rises with increasing scale of genotyping, even after allowing for an industry investment in increased database and analytics capability.

Genetic progress The distribution of other benefits is less straightforward. Taking the benefits from faster genetic progress first, these accrue to all enterprises sourcing genetics from breeds and herds using BREEDPLAN (if we assume that BREEDPLAN is the delivery channel for genetic progress that is enhanced by the additional data modelled here) – this is a high proportion of industry now, and under the model of widespread genotyping, likely higher.

This benefit is initially captured through purchase of bulls which are genetically better than those born in previous years, but then flows through the value chain, according to the genetic improvement increment in traits expressed at various points in the chain. In essence this benefit is a sort of combination industry and enterprise good.

Genomic screening The benefits obtained through genomic screening (as modelled here) can be considered to be enterprise or private benefits to a much greater extent. For example, if a feedlot avoids buying less profitable animals through use of genomic information, that feedlot obtains a benefit, and at face value, industry overall is better off through a reduction in “waste”. However, the net effect actually depends on what happens to those animals not entering the feedlot: if they simply go to some other enterprise, there may or may not be an overall industry benefit, depending on their impact on profit in that other enterprise – if for example they simply went to another feedlot with the same feeding regime and market, that feedlot would lose an amount per animal equivalent to the benefit obtained by the feedlot which rejected them; for no overall industry benefit. The cautious modelling here of the potential benefits of genomic screening to an uncertain extent accommodates this uncertainty: we are not inflating the potential overall value to industry.

Extending this point, there is an industry benefit from reducing the waste arising from having animals being managed inappropriately for their genetic potential (in this simple example, animals entering a feedlot that will not be profitable there). Regardless of whether losses associated with such animals are considered as industry or private losses, they are losses incurred by the overall value chain, which accordingly reduce overall competitiveness (NB: economic theory says that benefits and costs incurred at any point in a value chain ultimately end up being shared according to the shares of economic value-added for each link in the chain, adjusted by the market power of different links). Ideally, animals would be genomically screened at birth or soon after using a highly accurate test, and would enter the value chain path for which they are most profitable – this would, by definition, minimise opportunity costs for all enterprises through the entire chain.

The faster genetic progress benefit is similar to an annuity (*i.e.* a benefit obtained every year, and to a large extent, without requiring particular management decisions). The benefits from genomic screening are more like "once-off" decision outcomes – once-off in the sense that the enterprise must make a decision to invest in a test, and act on the results. The tests could be applied every year, but they require that active decision each year.

Overall, this short discussion of the distribution of benefits from DNA technologies implemented around a traceability platform, suggests that:

- Implementation costs are borne predominantly by individual enterprises
- Two forms of benefit – traceability and faster genetic progress – are essentially industry goods *i.e.* all, or virtually all, industry can benefit from them (they are what economists refer to as *club goods*). Other potential benefits of this form are available, including for example more efficient (*i.e.* better outcomes for the same investment) R&D, but have not been modelled or estimated here.
- Other benefits, based on genomic screening, are much more private – the enterprise making the investment in the test obtains much or all of the benefit. There can be collateral industry benefits at the same time.
- Overall, to obtain the potential benefits from improved traceability, these observations suggest that everything possible should be done to enhance potential for the ancillary benefits – thereby making the necessary or primary investment in genotyping more attractive to individual enterprises.

Replace existing system, or extend/enhance it?

On first tackling this project, we considered whether replacing the existing NLIS was an option. It very rapidly became apparent that for traceability purposes, data on ownership and location of animals is essential. This means that if NLIS were replaced with a DNA-based system, elements of the current NLIS would have to be replicated or remain in place.

Accordingly, the modelling and discussion here have only considered models of augmentation *i.e.* where DNA capability and services are added to the existing NLIS platform.

National governance and data rights

It is outside the direct scope of this project to develop or define governance model(s) for an expanded NLIS, but some brief comments can be provided (these draw on earlier points made in this section).

Industry decisions around expansion of NLIS to incorporate DNA capability fall into two broad categories:

1. *Core infrastructure* Building database and analytic capability to support an expanded NLIS is relatively straightforward in investment terms, in that it does not require a suite of new relationships to be established. The complexity here arises from the fact that the justification for making the investment depends on one's view of the likelihood that such a system will in fact be established, because most of the upside required to drive adoption of DNA to enhance traceability, depends on those relationships.

2. *Data relationships.* These are critical to a feasible implementation model (ie one where industry players will invest in genotyping at a scale that adds traceability benefits), but will require a new era of relationships amongst organisations such as MLA, breed societies, feedlots, processors, and wider, state veterinary departments, pharmaceutical and genotyping companies, Animal Health Australia *etc*. The basic principles are relatively simple:

   -Shared protocols for data transfer

   - Agreed protocols for data access, almost certainly involving some form of payment, or at least preferential access to services in return for use of data.

   Because this is not a "green-field" space, developing a strategy for this aspect of implementation is likely to require its own project investment, including considerable consultation. The potential degree of difficulty around data relationships may initially deter industry from tackling it. However, in our view this virtually guarantees considerable problems of fragmentation, opportunity cost (including for example, faster genetic progress not achieved), and duplication.

   In reality, a more practical perspective is to assume that DNA will and should be part of the traceability system, and so a range of options to start towards such a system should be identified and trialled – and recognising that this is a decade-long process.

Catalytic or transformative opportunities

The following points have been touched on already, but are worth repeating:

1. While DNA can enhance traceability, it is the opportunity to extend traceability and simultaneously build new information services on the NLIS platform that is potentially transformative both across and through value chains

2. The non-traceability opportunities are extremely significant:
   - Taking genetic evaluation to effectively 100% coverage of seedstock and commercial animals
   - Reducing waste (cost) arising from misalignment of animals with feeding-marketing pathways
   - Underpinning MSA with genomic prediction and integrating it with genetic evaluation (*e.g.* BREEDPLAN) through the ID-genotype link
   - Establishing a data platform for R&D in animal health, and likely for much broader information service innovation
   - Opening a door for closer collaboration with the dairy industry, which could touch not just NLIS but also the genetic improvement and R&D systems. Integration of databases for genetic and genomic analysis would, for example, be an obvious opportunity to consider

9. Implementation pathway

This study strongly suggests that there is a clear role for using genomic technology in some form to aid lifetime traceability, if for no other reason than that the additional opportunities are substantial. However, the major issues and hurdles appear to be that:

- Calculations to assign a dollar value to an increase in traceability rely heavily on previous work that was used to evaluate MLA's investments in ISC, principally Dwyer and Clarke (2015). Although that study remains highly relevant, the workings underpinning its model are not entirely transparent.

- Mandating DNA collection across the entire production sector is not realistic and unlikely to be palatable to industry at current genotyping prices, even in beef cattle.

- The infrastructure requirements are significant. Creating a large DNA database is feasible but the establishment and maintenance costs are not trivial. Who owns and manages that data is a key barrier that was highlighted by numerous stakeholders.

- Linkages with other databases (*e.g*. MSA, BREEDPLAN, Sheep Genetics or chemical reference data such as Oritain) would involve serious issues to be resolved around access, data security, confidentiality, *etc*.

Genomic technologies are becoming increasingly adopted by industry for use in a range of applications including livestock evaluation, disease detection, pathway decisions, product specification and proof of provenance. **There is some urgency to be proactive in coordinating related activities – the longer the delay, the greater the costs and difficulties arising from fragmentation that will inevitably occur if nothing is done.**

Recommendation

It is recommended that a program of work with a series of stop/go decision points is initiated, coordinated and overseen by a small, appropriately qualified steering group. This should be commenced as soon as possible, with the following objectives:

- Verify that DNA technologies can achieve the degree of traceability assumed in our modelling, using *in silico* analyses, which in turn requires that:
    - An appropriate experimental design identified
    - agreements are in place to access the necessary data
    - appropriate genotypic data already exists to provide sufficient statistical power; and if not identify:
        - suitable criteria for additional sampling with a focus on ensuring that maximum value can be extracted from extra expenditure; and
        - an appropriate funding source is identified including the possibility of collaborating co-investors
- Ensure that relevant agreements are feasible if ongoing data access to industry data is required for incorporation of genomic information into the national traceability system (NLIS)
- Evaluate the feasibility of partial sampling strategies including those outlined in this report, such as sire-only, male (or female) only, flock (or herd) profile *etc*., taking account of whether (and how) additional information might be used to increase the power of existing genomic reference populations

- Better scope requirements for a national DNA database and matching algorithms, which can be integrated with the existing NLIS database. This should include proposed rules for data ownership, access, use and confidentiality.
- Ensure industry engagement at all levels, from breeder through to retail and exporters as well as service providers. It is important to engage with service providers as that group has quite different expectations on whether a national system is required and what rules of engagement should be applied.
- Identify opportunities to reduce costs and turn-around times in a fully operational system.
- Develop a draft strategy for establishing an integrated industry-owned flexible data platform, which includes traceability and for which DNA forms the critical link across multiple forms of knowledge and decision-making.

The coordinating group should ideally include adequate skills and awareness of:

- Project management and budgeting
- Current ISC procedures
- Likely data access and privacy implications
- Existing DNA databases held by industry and research organisations and how best to negotiate access
- Statistical analysis of DNA data and experimental design
- Relevant features of the red meat pipeline and critical players
- Developments internationally that are relevant to DNA-assisted traceability

Simulated tracing

It is important that *in-silico* simulation of the tracing process (as outlined above) is based on existing resources already held in industry databases, and if necessary, supplemented by tactical genotyping of additional animals. The requirements appear to be that:

a) The databases contain genotypic data from commercial animals whose sire genotypes are also included. (Most genotypic data is derived from 50k SNP chips, or equivalent, but subsets of those SNPs can be used to simulate smaller panels, if required)
b) Animals with known genotypic data have an associated NLIS identity and a full lifetime traceability.
c) Some of the animals to be "traced" using simulation are closely related but come from different PICs.

Simulation and testing should be based on animals in the major breeds, which would involve negotiating access to the necessary data. This in turn would highlight the issues that need to be addressed in building a working traceability system. The study could involve data from beef, sheep or both, as determined by the coordinating group. However, the findings should be relevant to both species, with a focus on identifying which approach is most suited to each. It is proposed that a case study be constructed for the Northern beef industry, the southern beef industry and the sheep meat industry. AWI should be consulted to determine whether there is an appetite for a wool specific case study that integrates with traceability in the wool industry.

Timeline

The coordination group to be established within 6 months, with proof of concept to be demonstrated within 18 months and if appropriate, a draft industry implementation strategy prepared within two years.

Appendix 1. Survey methodology

The online survey was developed based on the stated objectives. The survey was submitted to the UNE Human Ethics committee for approval (Approval number HE21-121), with several modifications made to ensure that the survey met requirements from that committee.

The survey consisted of six sections:

1. *Consent*. Agreeing to participate on the understanding that this participation is voluntary, that the participant can withdraw at any time, and that the information provided is confidential and only for use in the current research project. Project participants must 18 years or older.
2. *Demographics*. This section gathered background information on the participant – which sector of the industry they operate in.
3. *Awareness and utilisation of current system*. These questions sort opinions on the current system, features and benefits, utilisation of EID, costs etc.
4. *Awareness and utilisation of genomic and DNA technologies*. Current industry uses, benefits etc.
5. *Potential application of genomics in traceability*. Features, benefits, costs barriers etc.
6. *Other comments*

Survey Delivery

The survey was opened to the potential participants on July 18th, 2021. Promotion of the survey was led by one of the consultants and included targeting as many channels of promotion as possible. This included direct emails to targeted industry participants, direct emails to industry bodies including MLA, AMPC, AMIC, ALFA, CCA, ALPA, SPA, beef breed societies, ARCBA and Sheep Genetics, with requests to include the survey link as an inclusion in the newsletters and social media platforms. The survey was also directly circulated to a contact list of processing stakeholders for inclusion in their communications with producers.

Those promotions resulted in substantial survey activity (see Figure A1). The survey was closed on August 13th April, 2021 (25 days duration) after a 24-hour period of no further responses. There were 100 respondents. However, only 57 provided data that was deemed appropriate (sufficiently complete) for analysis.

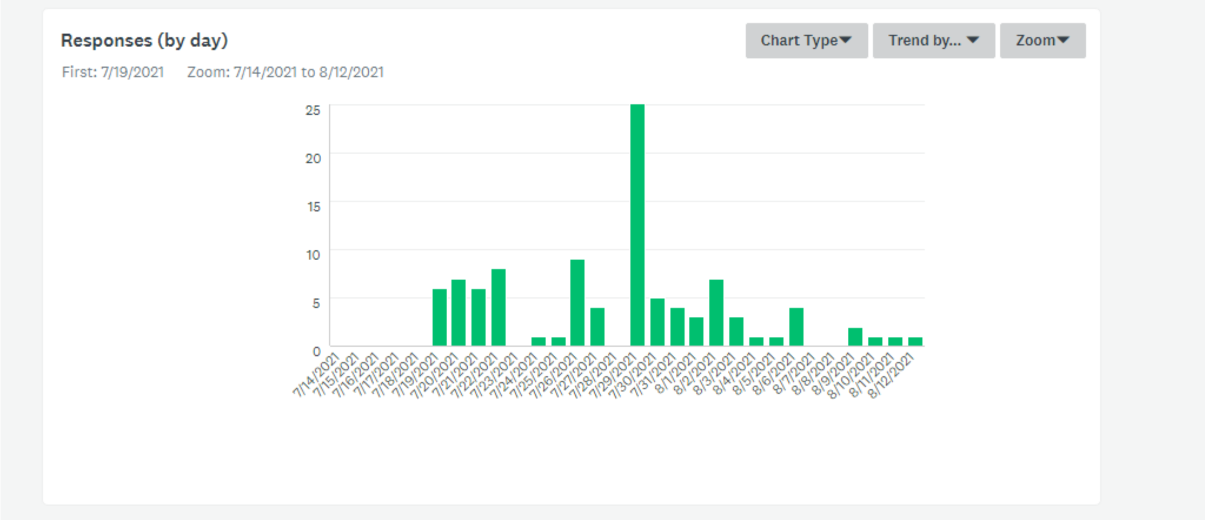


Figure A1. Number of survey responses by day

Survey analysis

The survey responses were downloaded from Survey Monkey® in Microsoft Excel format and analysed using a combination of MATLAB by MathWorks and Microsoft Excel.

Standard statistics (mean, median) and frequency distributions were used to characterise the responses. A MATLAB Unbalanced Analysis of Variance procedure (ANOVAN) was used to test for significant differences between sub-samples of the data.

Respondent demographics

At the close of the survey, there were 100 responses recorded by SurveyMonkey, however only 63 answered the demographics question and of that 57 provided complete responses to the survey.

The majority of the responses were from commercial beef producers and beef seedstock producers, with only a few responses from the sheep seedstock industry despite a concerted attempt to promote the survey to a wide network of sheep industry participants.

Table A1.1. Distribution of completed responses by red meat industry sector.

Role within red meat industry	Responses
Sheep processor	4
Beef processor	8
Sheep and beef processor	3
Sheep producer	13
Beef producer	32
Sheep and beef producer	10
Sheep seedstock	1
Beef seedstock	19
Beef Feed lotter	7
Sheep Feed lotter	2
Service provider / consultant	14
Research	5
Total	**57**

In order to complete more detailed analysis, some key sectors were aggregated (for example beef and sheep, producers, lot feeders and processors etc), those aggregated numbers are shown in Table A1.2.

Table A1.2. Number of responses for aggregated sectors.

Aggregated sectors	Responses
Beef	43
Sheep	16
Processor	9
Producer	42
Seedstock	20
Feed lotter	7
Service Provision & Research	19
Total Respondents	57

Appendix 2. The value of data

(Presentation delivered to a sheep breeding forum by Prof J.H.J van der Werf)

Reference Population Options

- Commercial industry e.g. Abattoir data
    + Ideally cheap (on per animal basis)
    + Large volume
    + Across supply chain

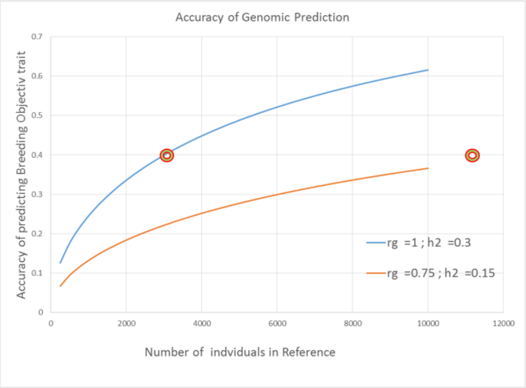
    - Data quality – fixed effects, DOB, dam age, management groups
    - Relationship to whole population
    - Progeny numbers per sire
    - Bias and “harvesting”
    - Coordination and planning

Assessing the value of different reference populations

Is genotyping commercial data a better investment?

Data Source	Phenotype Records Required	Genotype Cost	Phenotype Costs	Total
R&D Project h2 = 0.30, rg = 1	3000	$30	$270	$900,000
Commercial data $h^2 = 0.15$, $r_g = 1$	6000	$30	$120	$900,000

Assessing the value of different reference populations



Is genotyping commercial data a better investment?

Data Source	Phenotype Records Required	Genotype Cost	Phenotype Costs	Total
R&D Project h2 = 0.30, rg = 1	3000	$30	$270	$900,000
Commercial data h^2 = 0.15, r_g = 0.75	11000	$30	$51	$900,000

Is genotyping commercial data a better investment?

Data Source	Phenotype Records	Genotype Cost	Phenotype Costs	Total
R&D Pr h2 = 0.				
Comm h^2 = 0.15, r_g = 0.75				

Can do cost-benefit, depends on parameters

Commercial data can also be biased

Appendix 3. Modelling genetic benefits

This appendix sets out the logic and method used to estimate possible industry benefits arising from additional data collection through generating increased accuracy of genomic selection, in turn enabling faster genetic progress for value chain profit.

The core principle is that if numbers of commercial animals are genotyped, and some have performance data collected on them, and that data is made available to genomic reference populations, accuracy generated by those reference populations will increase. In essence, the modelling simply estimate the benefit of that higher accuracy.

Modelling genetic progress - the base situation

Current rates of genetic progress, and the parameters underpinning that, are used. Statistics on numbers of Australian animals evaluated through BREEDPLAN and Sheep Genetics, and the rates of progress in $Index terms, for the periods 2011-2015 and 2016-2020 were collated for planning purposes in early 2021:

Table A3.1. Genetic evaluation statistics for BREEDPLAN and Sheep Genetics

BREEDPLAN

Time period	#s - British	#s - Tropical	#s - European	Average Index trend - British	Average Index trend - Tropical	Average Index trend - European	Impact - #s x index trend summed
2011-2015	114,297	25,357	21,811	3.95	0.85	1.91	514,686
2016-2020	**113,554**	**25,200**	**18,713**	**5.44**	**1.67**	**1.98**	**696,870**

Sheep Genetics

Time period	#s - Terminal	#s - Maternal	#s - Merino	Average Index trend - Terminal	Average Index trend - Maternal	Average Index trend - Merino	Impact - #s x index trend summed
2011-2015	93,112	29,041	104,414	1.31	1.77	1.84	365,501
2016-2020	**97,896**	**36,521**	**106,642**	**1.99**	**2.99**	**4.32**	**764,704**

NB: the impact measure calculated and presented in the right-hand column is a simple way to assess changes in impact of genetic evaluation and improvement. It is not used here.

The two shaded rows contain the data forming the base case for the modelling here.

Modelling the value of additional data

To calculate rates of progress with additional data (and hence increased accuracy), the parameters of the response equation were derived from the rates of progress shown above, using either population statistics obtained from ABRI (S Skinner, *pers. comm.*), AGBU (A Swan, *pers. comm.*), or estimated based on industry experience.

The modelling was performed for each of the 6 sectors in Table A3.1 – northern cattle, British breed cattle (predominantly southern), European breed cattle, and terminal sire sheep, maternal breed sheep and Merinos. The base parameters used, and brief comments regarding their derivation are shown in Table A3.2. In this table, Southern Beef comprises both British and European cattle.

Table A3.2: Base/current population parameters for genetic improvement, BREEDPLAN and Sheep Genetics

		Beef		**Sheep**		
Note	**Parameter**	**North**	**South**	**Terminal**	**Maternal**	**Merino**
a	Animals evaluated per year	25,200	132,267	97,896	36,521	106,642
b	Males sold per animal evaluated	0.25	0.25	0.40	0.45	0.33
c	Females mated per sire lifetime	70	100	150	150	150
d	Index standard deviation	$12.00	$16.00	$10.00	$8.00	$6.60
e	i/L	0.14	0.31	0.20	0.38	0.36
f	Current response per year ($ per female mated per year)	$1.68	$4.96	$2.00	$3.00	$2.38

Notes:

- *a.* *Numbers of animals evaluated per year are from table A2.1 (S Skinner and A Swan, pers. comm.)*
- *b.* *Males sold per female evaluated are estimates based on industry knowledge*
- *c.* *Females mated per sire lifetime are estimates based on industry knowledge – and branding or marking rate is assumed to be 1 i.e. 100 females mated generates 100 commercial progeny*
- *d.* *Index standard deviation is:*
  - *Obtained directly from Sheep Genetics data (A Swan, pers. comm.)*
  - *Obtained directly from BREEDOBJECT data (B Walmsley, pers. comm.), with the assumption of the same Standard deviation of Objective across the 3 beef sectors (this is a simplification, but not major)*
- *e.* *i/L is the ratio of selection intensity to generation length, across sexes. It is derived here from the R value (response per year) and the index standard deviation, but has been cross-checked with estimates from simulated breeding programs and data from Sheep Genetics (A Swan, pers. comm.)*

For calculating the value of additional data, the index accuracy is derived from R, i/L and Index Standard deviation, and then modified to reflect the additional data (see below).

The underlying logic here is that response is being calculated as:

$$R = i/L \,.\, \delta_{IT}$$

with $\delta_{IT} = r_{IT} \,.\, \delta_{T}$

r_{IT} = accuracy of Index,

and δ_{T} = standard deviation of Objective

For each sector, two rates of genetic progress (or response) were modelled:

- the base or current rate
- a higher rate, there the accuracy was increased by either 20% (*i.e*. x 1.2) or 35% (*i.e*. x 1.35), reflecting approximately 4,500 and 10,000 additional useful records per year per sector (see below).

Modelling industry value of genetic gain

For each sector, the following steps were completed:

1. Genetic merit of the seedstock or stud sector was modelled by incrementing the merit by the base rate of genetic progress, and the increased rate of progress
2. The merit of the sires being used in the commercial sector was modelled as the average merit of the 3 previous year drops (so that sires are modelled to have first progeny at 2 years old, and to have progeny over 3 years, and progeny express their merit at 1 year old)
3. Numbers of commercial progeny were calculated based on number of females evaluated x number of sires per female evaluated x number of females (in the commercial sector) mated per sire lifetime
4. The British and European modelling results are combined as weighted totals
5. The industry value of the increase in accuracy is then simply the difference in total commercial merit with increased accuracy – base or current accuracy. The commercial sector is modelled as simply tracking seedstock sector merit, but lagged.
6. To calculate the annual value of the two levels of rate of genetic progress:
    - The model was run over a 15 year period
    - No discounting was applied for time
    - Total value across the 15 years was obtained by summing
    - And the total value across 15 years was divided by 15 to get an "annuity" value

The results for additional value (faster rate of genetic progress, compared to the current rate) are as shown in Table A3.3.

Table A3.3. Industry value from faster genetic progress

	Beef		**Sheep**			**Total Annuity Value ($m p.a.), beef**
Accuracy increment	**Northern**	**Southern**	**Terminal**	**Maternal**	**Merino**	
+ 20%	$0.83	$18.35	$14.79	$8.28	$25.73	$19.18
+ 35%	$1.45	$32.12	$25.88	$14.48	$45.03	$33.57

This shows that total industry value from a 35% increase in accuracy of selection (due to additional data) is estimated at $33.57m p.a. over 15 years for the beef sector, above that obtained if genetic progress continues at the current rates. If such data became available at some point in the future, and the current rate of genetic progress was higher at that point, the benefit of the increase in accuracy would also be higher.

A note concerning the contribution of additional wealth from the northern industry, which is low by comparison with the other sectors, and in particular with southern beef. This reflects two points not modelled here:

1. There is a considerable but imprecisely-known multiplier effect operating across the northern beef industry: larger operations commonly buy or breed bulls that are evaluated through BREEDPLAN, but which are then used to breed sons for use across large commercial operations. The modelling here, based on BREEDPLAN throughput, does not account for this multiplier effect. The real contribution made by genetic improvement in the north, and a corresponding impact of increased accuracy, is almost certainly very much larger than the results here suggest.

2. It is very likely that both the rate of genetic progress in the northern industry, and the scale of impact, are likely to increase rapidly in the next decade, as genomics is taken up rapidly, in part driven by projects such as Repronomics.

The modelling here does not include any changes in scale of evaluations *i.e.* animals going through BREEDPLAN and Sheep Genetics: there is reason to be cautiously optimistic that this will rise, and potentially that i/L will rise too, as enterprises make more use of reproductive technologies such as AI to harvest the value of elite genetics.

The estimates of additional industry value from faster genetic improvement, resulting from additional data becoming available through genotyping of recorded commercial animals, are almost certainly conservative. Anything that increases scale of evaluation and/or rate of genetic progress will mean larger returns from that data capture.

Appendix 4. Modelling genomic screening for management

If we know the variance and standard deviation of some trait or economic parameter of commercial animals, then we can define the performance of sub-sets of any cohort. Then if we assume a proportion that will be culled/retained conditional on a test, and we assume an accuracy of the genomic test for such animals, then we can calculate the change in returns from testing *n* animals and retaining (or treating, or supplementing *etc*.) *n-r* animals.

The example used here is for screening long-fed steers, using 2019 prices and costs. The parameters are as shown in Table A4.1.

Table A4.1. Assumptions used to model the value of genotypes to predict performance in the cattle.

Trait	**Mean**	**Genetic standard deviation**	**Value per unit**	**Days on Feed**	**Mean feed consumed**	**Standard deviation of feed cost**
Carcase weight at constant age (kg)	425	17	$5.60			
AUS-MEAT marble score at slaughter (score)	7.5	0.52	$0.67			
Feed intake (kg/day)	12.6	0.70	$0.35	400	$1,764.00	$97.64

The basic principle is that knowing the genetic standard deviation for each trait makes it easy to define the expected performance of (for example) the top and bottom half of the cohort for each trait, and if there are 3 uncorrelated traits we are focussed on, that means we can define the expected performance of each 1/8th of the cohort.

For this example the performance levels of each 1/8th of a cohort are as shown in Table A4.2. From this, if we assume that we will cull the bottom quarter (the two rows shaded), we can predict the merit of the remaining ¾ and hence their difference from the overall average. In this case that difference is + $64. Accordingly, if we want 100 animals to enter this production system, we should genomically test 133, and cull the bottom 33 (Table A4.2).

Table A4.2. Example of calculated performance of long-fed steers, by 1/8th of the cohort.

Carcase weight	AUS-MEAT MS	Feed intake	Cwt	Average AUS MS	FI	Carcase Value	Carcase value less feed cost	Difference from average
Relative to average			**kg**	**Score**	**Kg/day**			
Above	Above	Below	442	8.02	11.90	$2,629	$963	$347
Above	Below	Below	442	6.98	11.90	$2,321	$655	$39
Above	Above	Above	442	8.02	13.30	$2,629	$768	$152
Below	Above	Below	408	8.02	11.90	$2,427	$761	$145
Above	Below	Above	442	6.98	13.30	$2,321	$460	-$156
Below	Below	Below	408	6.98	11.90	$2,143	$476	-$140
Below	Above	Above	408	8.02	13.30	$2,427	$565	-$51
Below	Below	Above	408	6.98	13.30	$2,143	$281	-$335
Average	**Average**	**Average**	**425**	**7.5**	**12.6**	**$2,380**	**$616**	**$0**

In most cases (including this example), the traits will not be uncorrelated and there will not be an expectation of equal numbers in each cell. This, however, does not affect the differential between each level.

The final value of the selection/culling decision depends on the accuracy of the genomic test used. For example, if the test has an accuracy of 50% for the 3 traits included here, then the predicted economic gain is $64 x 50% = $32.

The procedure used for estimating the benefits of using genomic information to aid culling decisions as follows:

1. The principle outlined above was applied across three potential applications –culling short-fed steers, long-fed steers (Waygu) and heifers.
2. For heifers, the three traits involved were carcase weight, marble score and weaning rate. Each of these three had a different base value (or cohort average merit), being $1230, $2002 and $5,520, respectively; and
3. respective standard deviations of profitability indices of $134, $258 and $356.
4. For steers, assumed culling rates based on genomic predictions were 25% and for heifers were 50%.
5. The resulting values were then discounted in proportion to (1-prediction accuracy), leading to greater profitability when prediction accuracy is 60%, compared with 45%; or in the case of no additional genomic information, 20%.
6. This provided an estimate of the per head benefits, which were then scaled to a national benefit by applying them to the total number of animals tested, which was set at 33.3% of the potential maximum (this means approx. 550k animals when half the herd is genotyped and 1.1m animals when all animals are genotyped).

Appendix 5. A possible framework for using Flock Profiling for traceability

1. If an unknown animal or mob is found, it would be genotyped, and the genotype submitted to a sheep genomic traceability database
2. This database would then be used to calculate the genomic relationship of that sample to all other genotypes currently held
3. The sample would have highest relationship (or similarity) to animals or samples previously taken from that flock.
4. The relationship would not be unity (*i.e.* 100%), but the parameters for the probability of an animal coming from a flock based on its genomic relationship to a flock profile would need to be established. It would be expected to be a high number (close to, but less than unity unless that particular animal was itself included in the genomic traceability database)
5. The distribution of such values could be investigated using the existing sheep genomic information (such as the Sheep Genetics database) – for example by simulating animals from a particular flock profile and determining the calculated relationship.
6. This R&D would establish "confidence bands" for the values that would be expected – basically to assist in identifying the level of relationship which would be accepted as indicating that an animal was likely to be from a particular flock, with a known precision.
7. The "traceability accuracy" of this approach would be defined by the structure of genetic relationships among flocks in the industry, which as discussed above, could be defined by R&D using the existing Sheep Genetics database.

The amount of work required to establish this approach – how many flocks would be needed to sample, can be determined from the current level of testing for Flock Profile. However, in the worst case, we could assume that every flock would need to be sampled – assuming 50,000 flocks[71], and $700 per flock as the genotyping cost, that would be an implementation cost of 50,000 x $700 = $35m p.a. (This is of similar magnitude to the estimated implementation cost of EID-NLIS in cattle).

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[71] ABARE actually estimates the number of active sheep producers at around 25,000. We have doubled this number to allow for sub-populations within many flocks.

Appendix 6. Making use of genomic information in the Irish cattle industry

The following notes were recorded during an interview with colleagues in Ireland. They illustrate that ICBF is essentially building (or already delivering) the functions identified in our report as "ancillary benefits", with the reasonable expectation that as these benefits become more apparent, then 100% genotyping (or close to it), will be achieved almost by default. The accompanying presentation (pp 98-101) was kindly provided by Dr A Cromie. It illustrates how the Irish use ID and DNA databases in conjunction with other forms of data to provide information services.

Overview

Total of c. 2.5m cows, or cattle:
  - 900,000 beef (suckler) cows
  - 1.6m dairy cows

Genotyping
  - C. 600,000 beef cows enrolled in the ICBF Genomics program, which means c. 300,000 female beef cows genotyped per year (the herds are referred to as suckler herds)
  - Much lower rate of female genotyping in dairy – about 10,000 male calves genotyped per year, to identify c. 150 candidates
  - About 500 dairy herds doing some genotyping – a total of about 70,000 females per year
- The focus for R&D funding around genotyping is on production – would struggle to get funding solely for climate-related issues:
  - The focus of policy has moved to mitigation – Ireland has to reduce methane output by 25%, and genetic improvement can contribute. So it's not just increase production and slow methane – its reduce methane
- Genotyping in beef started out as focussed on increasing accuracy – c. 20% lift – but is now being used increasingly for characterising animals at a young age (stimulated by increasing focus on dairy-beef pathways):
  - ICBF delivers the tools for this early age screening – straight out of routine genetic evaluations
  - Increasing push from government, processors, milk co-ops, around carbon footprint, aiming to reduce age at slaughter (currently 26-28 months), and increasing use of contracts from processors or co-ops for calves, backed by assistance with feeding for contracted calves
- Still a challenge getting phenotypic data, esp. more than weaning weights, alongside genotyping

Databases, governance etc
- Databases in use have developed and grown over last 10 years ie didn't get designed in one big step
- Strong links between ICBF database (for breeding, so contains ID, pedigree, phenotype, and more recently genotype), and Dept. of Ag database, which is for legislative purpose including calf registration, animal movements, health testing (eg compulsory BBD testing every calf) – so this holds 100% of calves.
- Dept of Ag database starting to make use of ICBF database, but they are managed and funded separately – Dept of Ag have a seat on the ICBF Board. ICBF database adds functionality accessible to the Dept of Ag database: comment at this point that at least some of the functionality and linkage has grown via individual projects, as stakeholders (government, industry, research etc) have seen opportunities
- The genetic evaluation service delivered by ICBF, which includes genotyping, is costing €18 per animal, and is for a 50k genotype
- Animals getting genotyped via ICBF programs and services still need two tags – "NLIS" (ie via Dept of Ag) and "genotype" tag
- ICBF (but this may be a gov't-ICBF shared goal) aiming to get cost down to €15 per animal, with €5 from each of farmer, gov't and industry – this is focussed on the national methane mitigation goal
- Breeds (ie societies) are shareholders in ICBF, but this does not mean that every is completely smooth – breeds are reported to 2-3 times per year, each breed seeking best service possible
  - This "herdbook-based" model (ie herd-book=breed society) is coming under increasing pressure as coops, genotyping companies, processors are moving to "control" or manage genetics better and better, so potentially including proprietary genetics

Ireland is a currently some distance from having universal genotyping, but they have:
- An integrated or central "coordination" body (ICBF) with strong working links with government
- Very strong push to tackle methane
- Discussions happening at the moment that could ensure that starts in 2023, with then a 3 year roll-out plan to have it in place by 2026. Broad farmer, govt, industry support is key, as they need to have the funding then committed on an annual basis thereafter (target €15/animal, all costs). Having a model that is now working on the ground (i.e. 500 herds & 50k calves per year), which could be rapidly scaled up as/when required, is crucial to that.

icbf

The role of the ICBF/AHI database in helping provide better supports for vets & farmers.

Andrew Cromie (ICBF), Natascha Meunier & David Graham (AHI).

AgTech - it's in our DNA

The ICBF/AHI Database.

- **ICBF's Approach => Working with partners** to build data flows, that will; (i) support our core objective (i.e., genetic gain), and in doing so, (ii) help support their service needs, e.g., AHI, vets etc.

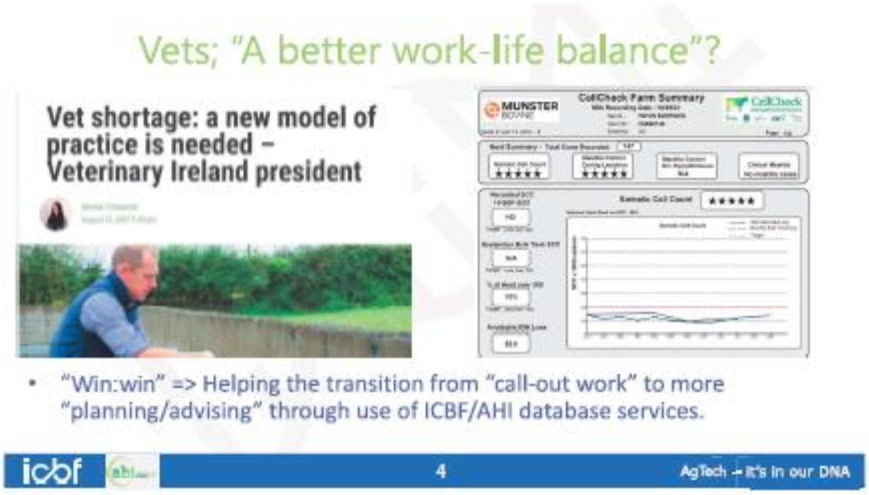
icbf 2 AgTech - it's in our DNA

Working with partners to meet our shared objectives.

Figure 1. Liver diagnosed with liver fluke at slaughter (Source: AHI)

Breeding for reduced liver fluke infection

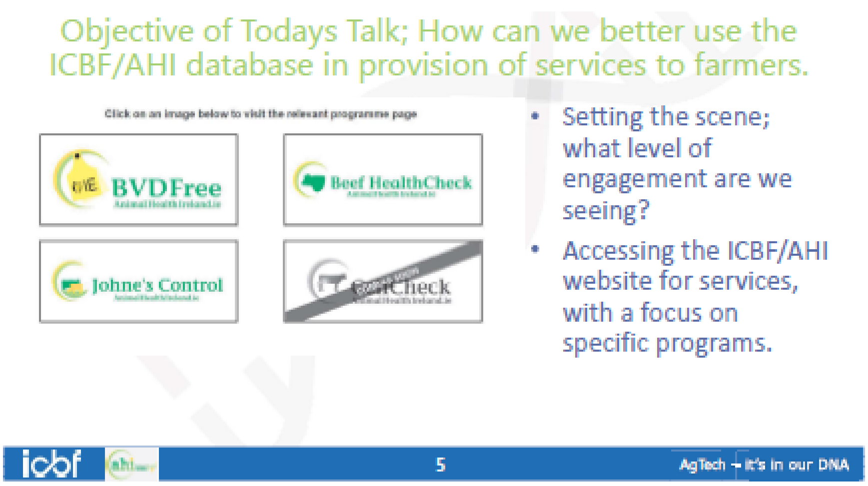
- Liver-fluke => a great example of working together to meet our shared objective.
- Can we build on this for the future, e.g., other traits?
- Can we create win:win's for other services?



Vets; "A better work-life balance"?

Vet shortage: a new model of practice is needed – Veterinary Ireland president

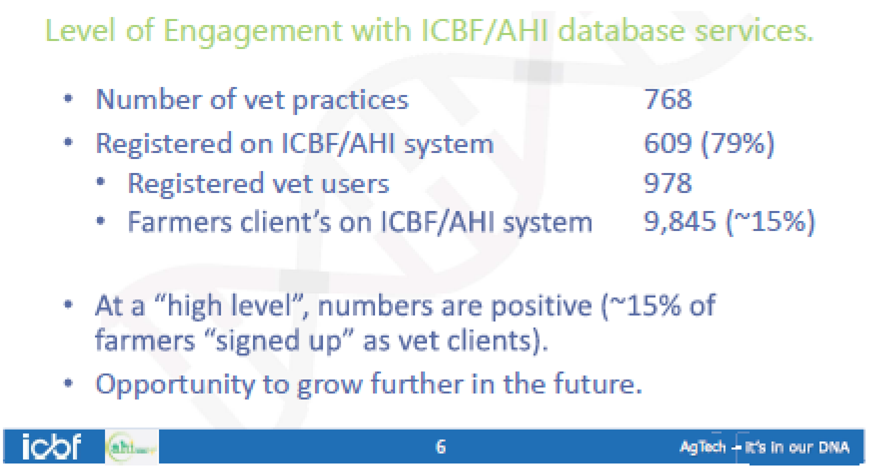
- "Win:win" => Helping the transition from "call-out work" to more "planning/advising" through use of ICBF/AHI database services.



Objective of Todays Talk; How can we better use the ICBF/AHI database in provision of services to farmers.

Click on an image below to visit the relevant programme page

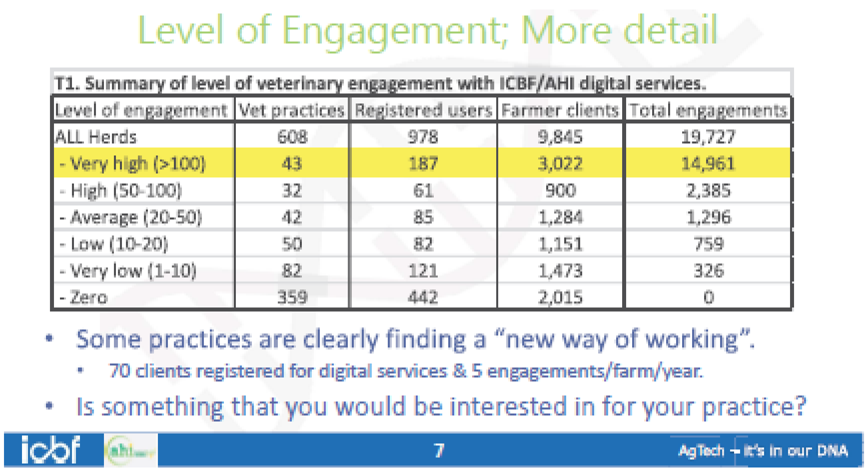
- Setting the scene; what level of engagement are we seeing?
- Accessing the ICBF/AHI website for services, with a focus on specific programs.



Level of Engagement with ICBF/AHI database services.

• Number of vet practices	768
• Registered on ICBF/AHI system	609 (79%)
• Registered vet users	978
• Farmers client's on ICBF/AHI system	9,845 (~15%)

- At a "high level", numbers are positive (~15% of farmers "signed up" as vet clients).
- Opportunity to grow further in the future.

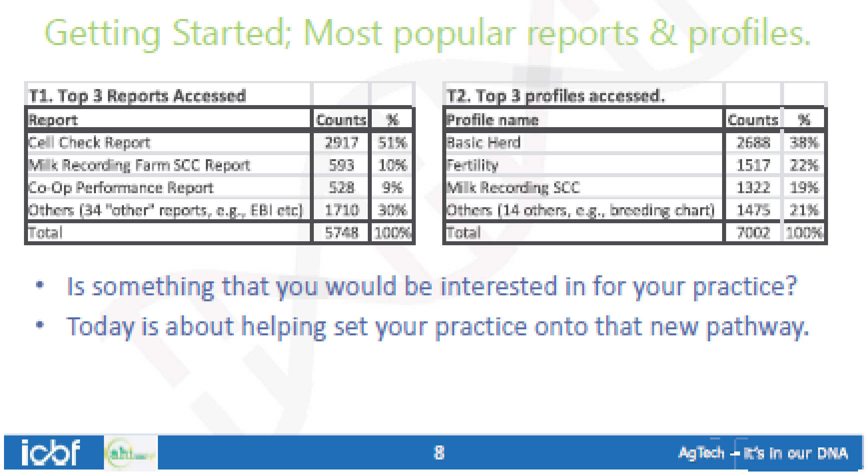


Level of Engagement; More detail

T1. Summary of level of veterinary engagement with ICBF/AHI digital services.

Level of engagement	Vet practices	Registered users	Farmer clients	Total engagements
ALL Herds	608	978	9,845	19,727
- Very high (>100)	43	187	3,022	14,961
- High (50-100)	32	61	900	2,385
- Average (20-50)	42	85	1,284	1,296
- Low (10-20)	50	82	1,151	759
- Very low (1-10)	82	121	1,473	326
- Zero	359	442	2,015	0

- Some practices are clearly finding a "new way of working".
  - 70 clients registered for digital services & 5 engagements/farm/year.
- Is something that you would be interested in for your practice?



Getting Started; Most popular reports & profiles.

T1. Top 3 Reports Accessed

Report	Counts	%
Cell Check Report	2917	51%
Milk Recording Farm SCC Report	593	10%
Co-Op Performance Report	528	9%
Others (34 "other" reports, e.g., EBI etc)	1710	30%
Total	5748	100%

T2. Top 3 profiles accessed.

Profile name	Counts	%
Basic Herd	2688	38%
Fertility	1517	22%
Milk Recording SCC	1322	19%
Others (14 others, e.g., breeding chart)	1475	21%
Total	7002	100%

- Is something that you would be interested in for your practice?
- Today is about helping set your practice onto that new pathway.