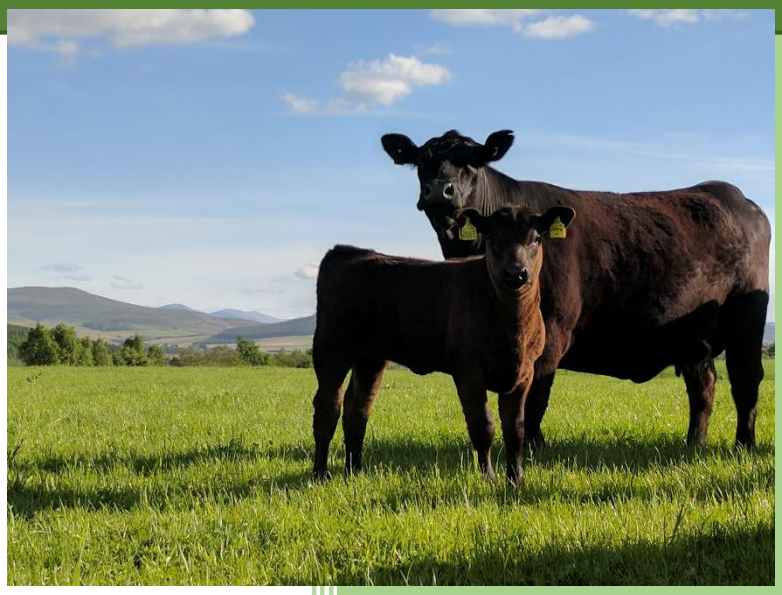
2021

Scotch Beef PGI Traceability and Performance Project



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1. Introduction

Beef farming in Scotland is currently not fulfilling its potential, based on a number of KPIs, in terms of performance. For example, in 2019 on average 82.4 calves were reared per 100 cows, considerably less than the rest of the UK and Ireland. However, with improved performance this opportunity could be maximised and the potential for additional profitability is significant. The need to change is urgent as the industry faces a range of challenges which will impact ongoing sustainability. These include changing farm support systems, environmental targets, increased market competition, changing consumer demand, and the requirement to improve product quality and consistency.

This project has identified that one of the most effective ways to combat the challenges in the beef sector is through the utilisation of DNA profiling of maternal DNA and utilising the information through analysis to create a suite of key performance indicators which can guide management decisions on farm and importantly, can guarantee full effective traceability from finished product back to animal and farm of origin.

This pilot project aims to test a system which could be used to address these challenges whilst highlighting the benefits of introducing DNA traceability to the Scotch Beef PGI supply Chain. The pilot project will make recommendations for an industry wide performance enhancement programme to provide a platform on which a sustainable Scottish beef industry can be built.

A long term, advanced genetics and traceability programme could deliver the following benefits for Scotch beef:

1. Scotland having world leading traceability and integrity levels for beef, through comparison of a product against an already existing database of DNA from dams in Scotland.
2. Scotland having a world leading beef production system, driven by advanced technology to deliver animals with very high genetic potential.
3. Scotch beef having superior and more consistent eating quality delivered through a combination of genetic improvement and appropriate industry targets.
4. Scottish beef production having the lowest incidence of disease, with animals being selected for disease resistance.
5. Scottish beef production having the lowest environmental footprint by selecting for the higher performing, more efficient animals, reducing energy expenditure on maintenance requirements and reducing the output of methane.
6. Scottish farmers having access to recommended, across breed, sire lists to choose sires which are proven to be the highest performing for a range of different functions (terminal and maternal traits).
7. Ultimately, Scotch beef being recognised as the ‘Ultimate Beef Product’, with high global consumer demand.

The pilot study was established to test two aspects of this; the use of genomic analysis of maternal DNA to optimise traceability within the Scottish beef supply chain, and the use of genomic analysis of maternal DNA in predicting performance of offspring.

2. Executive Summary

This project was operated as a proof-of-concept study to test the concepts which may be applied in a larger rollout programme. The main questions posed by this project were:

1. Can maternal DNA samples be lifted accurately enough at farm level to drive a traceability programme?
2. Can maternal DNA samples be lifted accurately enough at farm level to drive a DNA led herd improvement programme?
3. Can enough accurate phenotype data be lifted at farm level to drive an advanced genetic improvement programme?

The pilot programme was able to answer each of the above questions, allowing effective preparation to make recommendations for an industry wide scheme.

DNA sample accuracy

The pilot programme showed that farmers could collect DNA samples which were of high enough quality to enable both accurate traceability and the use of DNA to drive a herd development programme.

Accuracy of data from farm level

The pilot programme revealed a number of technical difficulties around the collection of phenotype data from farm level. The timely collection of consistent data sets proved difficult: the accuracy was, in some instances questionable and the format of data was different from each farm, leading to challenges in comparability and interoperability. The findings from the pilot programme clearly showed that the initial data used in the rollout programme cannot be drawn from farm. The data used to drive the DNA programme must come from sources which are accurate, meaning that the initial data used for the programme will be sourced from factories and external sources (such as Scot EID and BCMS). Additional data can be gathered from small subsets of farms which can be relied on to provide proven data in the correct format.

Use of maternal DNA

The pilot programme demonstrated that maternal DNA can provide very accurate traceability when used in conjunction with BCMS and will be able to provide full assurance to Scotch Beef consumers. The work in the project also showed that maternal DNA can be used to guide breeding decisions across the Scottish Herd.

Conclusion

The pilot programme concluded that:

- Maternal DNA samples can be lifted accurately enough at farm level to drive a traceability programme.
- Maternal DNA samples can be lifted at farm level to drive a DNA led herd improvement programme.
- Phenotype data can be lifted at farm level in order to drive an advanced genetic improvement programme however the accuracy and consistency of the data needs to improve to capitalise on all of its potential benefits.
- Provided that a large-scale project is carefully designed, maternal DNA can underpin the development of the national herd and Scotch Beef brand.

The project also demonstrated that it is feasible to develop a project that is not only effective but can provide a significant cost benefit to the national herd and with limited additional burden to be placed on individual farming businesses.

The programme also has the potential to supply Scotland with a world leading database of maternal DNA proving guaranteed traceability and virtually eliminating fraud from the beef meat sector while also providing farming businesses with a suite of key performance indicators which can allow them to make management decisions that can improve their performance, sustainability, and profitability.

3. Context

Ruminant agriculture is under severe pressure, economically and environmentally.

Scottish beef has a higher cost of production than what is potentially possible. This is driven by sub-optimal livestock performance, made worse primarily by reduced fertility, poorer growth rates, health challenges, inefficient utilisation of feedstuffs etc. These factors raise both the economic cost of production and the environmental costs through low resource use efficiency.

Genetic development is one of the most significant influencers in addressing the above challenges.

A number of factors can be implemented to address the challenges in the Scottish beef herd. Genetic improvement is one of the most important, offering the ability to be more resource efficient, improving herd fertility, improving growth rates, improving feed conversion ratio, and reducing the economic and environmental costs associated with beef production.

A range of other benefits can be delivered through genetic enhancement, including increased eating quality, reduced use of antibiotics and enhanced resistance to disease – all desirable traits.

The Scotch Beef supply chain has the potential to deliver significant social and economic benefits.

These benefits include environmental enhancement, carbon sequestration, increased Scottish exports and tailored customer-specific programmes.

The delivery of these market benefits requires high-level product traceability delivering total integrity to underpin the sales of this enhanced Scotch Beef.

Sampling and analysis of breeding herd and sire DNA can offer the ability to make fast genetic progress whilst providing rapid and full traceability. The use of maternal DNA is a world first for Scotland and would enable significant steps towards protecting two of Scotland's natural assets, namely agriculture and the scenic landscape and environment. This would bring significant brand benefits for QMS.

The proposed programme is unique because it links traceability to productivity and environmental improvement through use of maternal and sire DNA to guide herd breeding decisions.

4. Objective of Project

This project aimed to prove two principal concepts and establish the feasibility of rolling these principles out into a larger nationally focused programme. The two key aims of the project were as follows:

1. Proving that meat traceability can take place commercially through the use of maternal DNA.
2. DNA analysis of over 500 dams who have produced calves finished through two finishers, in depth DNA analysis and the indication of potential to identify markers linked to positive maternal or terminal traits.

Through the process of this proof-of-concept study, there were a number of key milestones:

1. Identification of the suckler breeding herds that work with the two finishers within the operational group.
2. Collection and submission of DNA samples from each female who has bred a calf who has gone through the finishers.
3. Analysis of each Maternal DNA sample to identify key SNPs linked to performance by the genetic partner.
4. Obtaining from the 2 finishers, and the abattoir partner, full health, feeding and slaughter records of all finished stock linked to each dam.
5. Obtaining from the breeder's full health, feeding and output records for dams linked to each finished animal.
6. Identification from the breeder of sire data from each finished animal.
7. Establishment of data flow from the meat processor.
8. Parental analysis of 100 samples from meat products derived from slaughtered animals from the sampled dams to prove concept of commercial traceability.
9. Evaluation of this methodology against the Beef Efficiency Scheme and a quantification of the additional benefits to industry from having a method of DNA traceability within the Beef Efficiency Scheme.
10. Production of conclusions about traceability using maternal DNA.
11. Production of conclusions about performance prediction.

5. Project Group

Quality Meat Scotland were the lead organisation with overall responsibility, covering management, administration and reporting of the Scotch Traceability and Performance pilot project. An operational group was established for the duration of the pilot project containing all partners involved at the various stages of the process.

The Operational Group included:

Quality Meat Scotland

Non-departmental public body for the Scottish Red Meat Sector. QMS undertakes a programme of work to promote, protect, develop, and communicate the Scottish Red Meat sector.

Birnie Consultancy

Led by Dr Jonathan Birnie, the team at Birnie Consultancy has extensive knowledge of agricultural supply chains, having worked in both research and development and commercial business for over 15 years. Jonathan is an experienced project manager and has successfully developed a number of projects of over £1,000,000 in value. Jonathan has been working with the QMS DNA Working group to develop a solution that delivers multiple wins for the Scottish beef industry.

Identigen Ltd

Identigen are world leaders in delivering DNA-based solutions which shape the future of food trust.

AK Stoddart

Stoddart's was founded in 1959 as a multi-species butchery supplier located in the municipal abattoir in Edinburgh. By 1993 the business had expanded to a level that saw the addition of a state-of-the-art boning plant being opened at Broxburn. In 2000 the group added its own abattoir at Ayr with the capacity to process over 1,000 head of cattle per week. Stoddart pride themselves in developing long standing relationships with Scotland’s best cattle farmers, delivering an exceptional end product to the consumer.

Kingan Farms

Kingan Farms is approximately 1,080 acres beef finishing unit in Dumfriesshire and is run by The Kingan Family. They finish 1,400 cattle a year purchased through a mix of private deals with specific breeder units, and through auction markets. This business will support around 23 suckler breeder farms through the purchasing of their store calves. All stock is sold deadweight through AK Stoddart.

WJ Henderson

WJ Henderson and sons is a 1,000-acre beef finishing unit in Dumfriesshire. They finish 1,100 cattle annually, purchased through a mix of private deals with specific breeder units, and through the auction markets. WJ Henderson and Sons is run by Scott Henderson and his wife Susan, and son Neil. This business will support around 18 suckler breeder farms through the purchasing of their store calves. All stock is sold deadweight through AK Stoddart.

Harbro Ltd

A member of the Harbro Group, Harbro Ltd provides innovative high quality livestock solutions, focused on improving animal performance and its customers' profitability. Harbro will be involved on the on-farm data collection specifically around feed conversion and feed efficiency.

Moredun Research Institute

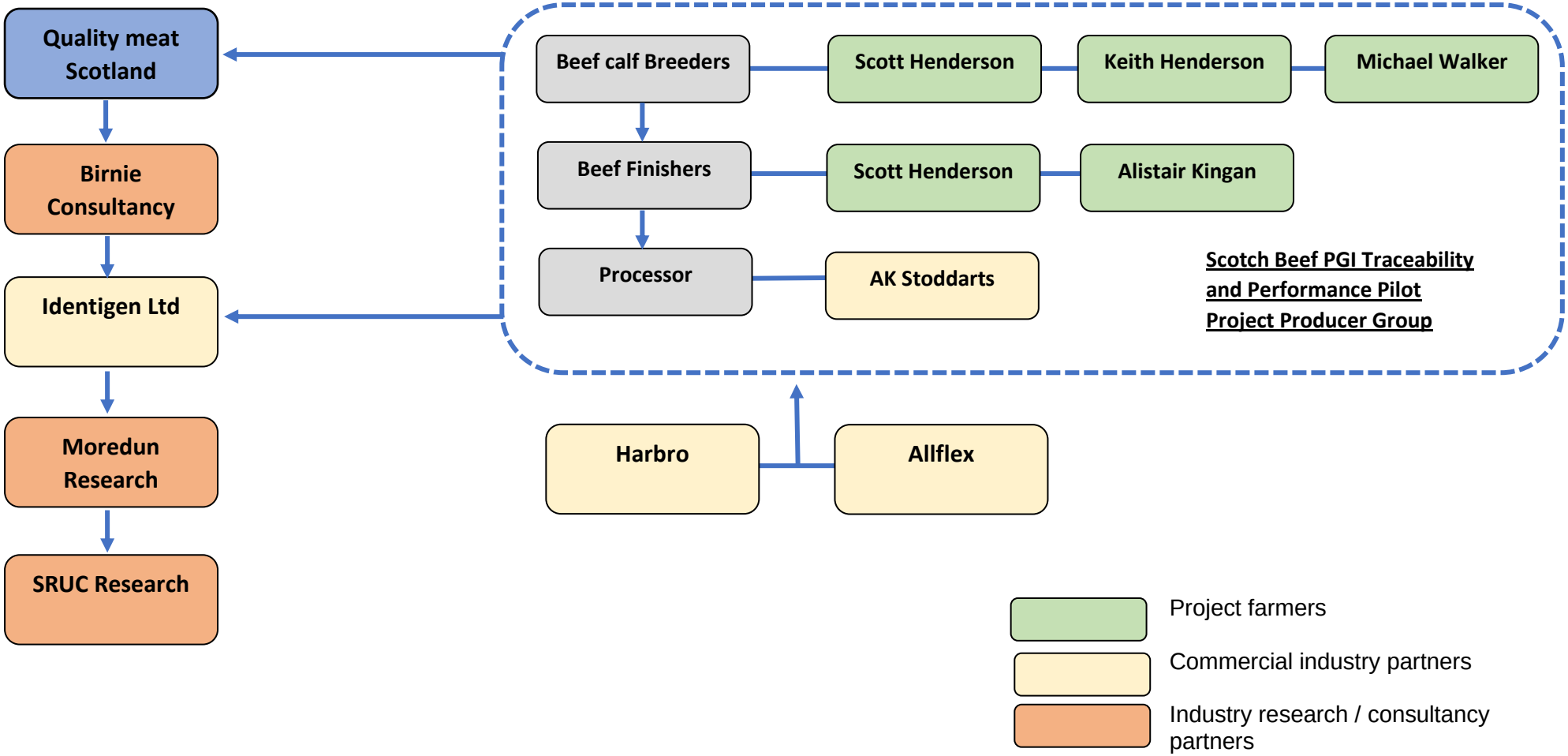
The Moredun Research Institute (MRI) is a world leader in endemic disease research, focusing on the health, welfare and productivity of livestock through the development of novel vaccines, diagnostics and management systems for disease control. This research is supported by state-of-the-art laboratory and animal facilities, which include purpose-built laboratories for the different pathogen groups, high containment accommodation for livestock and small animals (BSL-3) and full Home Office approval. Quality of scientific output is a mainstay for MRI's Strategic Plan, and this is reflected by consistent publication rates in high impact journals relevant to the institute's research focus. The institute is quality assured and works under ISO 9001, GLP and GvCP accreditation. An ongoing training programme for scientific and administrative staff ensures skills development to ensure MRI's research remains at the forefront of infectious disease research.

SRUC Research

Professor Eileen Wall is researcher in livestock genetics and systems within the Animal & Veterinary Sciences Group at SRUC. She has extensive experience in animal breeding, genetics, modelling and biostatistics, with a focus on BES genomic work.

Delivery of the project will involve members of the operational group at various stages following the methodology.

Figure 1. Flow Diagram showing Project Group, Producer Group and Project Partners



6. Process

The following 8 step methodology was used to guide the project under the direction of project manager Dr Jonathan Birnie. Operational group members were involved at various stages:

1. Scott Henderson and Kingan Farms to identify breeder farm units that provide them with over 500 store calves per year.
2. Sample of DNA taken from up to 700 mothers from the breeder units' herd that have produced a calf or calves in the last 3 years, that have been finished through either of the finishers, and that have now been slaughtered through the processor AK Stoddart.
3. DNA sample sent to Identigen to identify SNPs of importance. Data set of DNA SNP's collated.
4. Obtain all slaughter records (provided by abattoir), and animal health records from the mothers, and slaughtered progeny from which a DNA sample has been taken (including details on calving patterns, fertility, mobility and disease outbreaks).
5. All DNA analysis, slaughter records and health records sent to research partner for analysis.
6. Swab taken to obtain DNA sample from slaughtered progeny from dams sampled during step 2.
7. Traceability from DNA taken at step 6 tested against DNA taken during step 2 to prove concept of traceability and performance benefit.
8. Final report compiled and blueprint developed for wider pilot scheme.

6.1. Establish a Producer group

Scott Henderson and Alistair Kingan had been selected as the cattle finishers with AK Stoddarts the processor for the pilot project. To complete the supply chain from farm to finished product we needed to identify suckler cow producers which supplied calves to these finishers.

They identified two local suckler producers who supply them with cattle regularly, these were Michael Walker and Keith Henderson. Michael supplies cattle to both Scott and Alistair. Keith supplies cattle to Scott as part of a longstanding business arrangement.

Scott Henderson also runs a suckler heard and finishes his own cattle, so he was included as a breeder finisher

Keith Henderson, Breconside

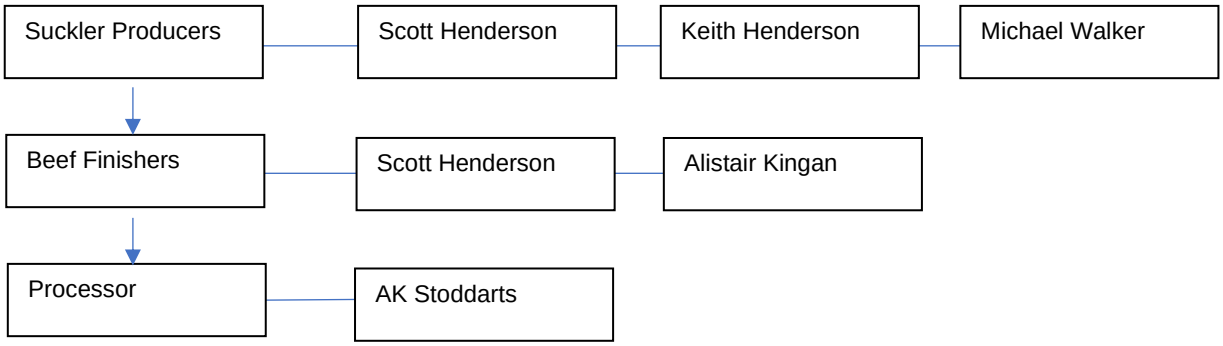
Breconside is a 900 acre hill farm in south west Scotland. They are a family partnership, Keith and Annette Henderson and their son Stuart. The farm has a suckler herd of 250 angus cross cows and a ewe flock of 500 Texel / Lleyn cross ewes. They specialise in producing high-quality, grass-fed beef and sheep. The sheep are all sold finished through local auction outlets. Whereas the cattle are sold on as forward stores either privately to a specialist finisher or through their local auction market. Recently they have however dipped their toe into finishing the high end of their calves and these have been sold deadweight to AK Stoddart.

Michael Walker, Drumbuie

Drumbuie Farm is a 1,500 Ha farm in Sanquhar in South-East Scotland. The farm business is a family partnership. The livestock enterprise consists of 650 majority Aberdeen-Angus Cross suckler cows, their followers, 80-100 replacement heifers, 32 bulls and over 2500 Scottish blackface and mule breeding ewes. Calves are sold store, privately, while heifers are retained for breeding or finished at home.

In recent years, brothers Stuart and Michael have increased their breeding cattle, built a state-of-the-art winter housing unit, a designated calving shed and implemented EID throughout the herd.

Figure 2: Scotch Beef PGI Traceability and Performance Pilot Project Producer Group



Milestone 1:

Identification of the suckler breeding herds that work with the two finishers within the operational group.

Keith Henderson, Michael Walker, and Scott Henderson

6.2. On Farm DNA Sampling

A DNA tissue tag was selected to be the method of collecting DNA samples from the cows in the breeding herds. After researching the main tag manufacturers Allflex were selected as they had experience of producing tags for the Aberdeen-Angus Breed Society and the Beef Efficiency Scheme. Identigen, the lab used to carry out the testing, had also worked with Allflex tags. Crucially, Allflex were happy to print the whole herd mark and individual number on each tag (minus the crown) and their tags used 2d barcodes for scanning in the lab, increasing the reliability of tracing the samples through the process.

Allflex UK Group Ltd

The Allflex Group is a world leader in the design, manufacture and delivery of animal identification technology – helping livestock producers use individual animal identification as a key management tool.

Figure 3: Example of Allflex DNA sample tag including sample tube and 2d barcode.

DNA sampling was to be carried out for cows which calved in 2018 using ear tag tissue sampling. Animal tag lists were collated for 2018 calving cows and supplied to Allflex to produce the tags which were then distributed to the project farmers. Tagging commenced in January 2020 and was completed in May 2020. QMS staff were involved on farm in the tagging operation and oversaw the tagging of Scott Henderson and Keith Henderson's cattle, the collation of the samples, and packaging for sending to Identigen. Due to unforeseen circumstances and the COVID lockdown restrictions, Michael Walker carried the sampling process on farm without QMS staff assistance.

Once batches of tags were collected they were sent to Identigen for analysis.

Date	**Location**	**Number of animals**
29/1/2020	Carswadda Farm, Dumfries (Scott Henderson)	59
10/3/2020	Breconside Farm, Dumfries (Keith Henderson)	164
31/5/2020	Drumbuie, Tower, and Knockenjig Farms, Dumfries (Michael Walker)	318
	Total	**541**

Milestone 2:

Collection and submission of DNA samples from each female who has bred a calf who has gone through the finishers

Collection and Submission of 541 DNA samples to Identigen

6.3. Maternal DNA quality analysis

Once received by Identigen the DNA samples were firstly given a quality check before being stored ahead of use.

Dam Analysis:

- A total of 541* samples were received and analysed on a chip.
- 13 samples did not return data of sufficient quality for parentage analysis, compatible with the finished product parentage SNP panel.
- 7 samples did not return chip data.

*one sample received did not have an associated dam ear tag and could therefore not be linked to the individual dam of origin

Milestone 3:

Analysis of each Maternal DNA sample to identify key SNPs linked to performance by the genetic partner.

541 Maternal DNA Samples Analysed by Identigen – 96.3% Success rate

6.4. Obtain slaughter, performance, health and nutrition records

Animals

Over 500 dams were sampled in the trial and phenotype data was collected from the dams and their progeny. The phenotypic data was derived from two sources and focussed on the calves of the genotyped dams. The first set of data is referred to as “breeder” data and comes from 3 suckler producers and the second is referred to as the “finisher” data and comes from 2 grower-finishers. Slaughter data was collected direct from the abattoir as a means of establishing and testing this as a data flow.

Measurements

Measurements were collected throughout the supply chain using the pilot project producer group and included:

Breeder data

Breeder data		
Dam (cow data)	**Calf Data**	
Dam ear tag number	Calf ear tag number	Weaning weight
Dam age	Calf date of birth	Daily liveweight gain to weaning
Dam weight	Calf sex	Sale weight
Age at first calving	Calf breed	Sale date
Calving interval	Birth weight	Daily liveweight gain to sale
Cow efficiency	First weight	
	200-day weight	

Finisher data

Finisher data		
Calf Data		**Sale Data**
Dam ear tag number	Daily liveweight gain at purchase	Carcass weight
Calf ear tag number	Date sold finished	Carcass fat classification
Calf date of birth	Age at finished	Kill out percentage
Calf sex	Sale weight	
Calf breed	Daily liveweight gain to sale	
Purchase source		
Purchase date		
Weight at purchase		

Abattoir Data

Abattoir Data	
Kill date	Age (months)
Producer code	Breed ID
Category (H/C/S/YB)	
Kill number	
Net weight	
Ear tag	
Grade	
Date of birth	

Health and treatment records

Health and treatment records were collected for treatments administered to the project cattle and their progeny.

Health and treatment records	
Name of medicine	**Treatment reason**
Date of treatment	Source of medicine
Animal ear tag	Date of birth
Person administering treatment	Days meat withdrawn
Date treatment finished	Dam
End of meat with drawl period	
Quantity of medicine	
Batch number	

Nutritional data

In addition to gathering data on farm management systems information was also gathered on nutrition and diet for different classes of cattle throughout the production cycle and included.

Nutritional data	
Stock classes and specific points in production cycle	**Ration details**
Suckler cows at grass	Forage details including analysis
Suckler cows up to calving	Mineral and supplement details
Suckler cows during calving	Water
In calf heifers	Accommodation details
Young stock	Group sizes
Finishing cattle	Any additional management practices relating to nutrition

This information was gathered by specialists from Harbro and put into a suitable format by QMS staff, then passed to Moredun for further analysis. Due to the large number of variables per stock class and ration a referencing system was used to

relate the nutritional information to the breeder and finishing data. Below is an example:

Figure 4: Extract showing Breeder data including nutritional referencing.

	Dam Information								
	Herd number	Individual number	Age (months)	Weight (Kg)	Age at first calving (months)	Date calved in 2019	Calving interval (days)	Cow efficiency (%)	Cow Nutrition Reference
1	UK540635	202179	88	671	24	20/04/2019	405.00	35%	2,3,5,6
2	UK561466	201946	87	671	24	10/04/2019	394.00	30%	2,3,5,6
3	UK582636	606105	52	671	24	28/03/2019	379.00	36%	7
4	UK540663	501496	51	671	24	02/05/2019	411.00	33%	
5	UK540663	101506	52	671	24	27/04/2019	404.00	29%	7
6	UK560446	501239	75	671	24	31/03/2019	376.00	36%	2,3,5,6
7	UK540663	701351	74	671	24	09/04/2019	385.00	33%	2,3,5,6
8	UK540618	501329	51	671	24			31%	7
9	UK582636	406278	51	671	24	22/03/2019	365.00	33%	7
10	UK540618	301278	42	671	24			27%	7
11	UK582636	606196	51	671	24	19/04/2019	392.00	32%	7
12	UK582636	405718	64	671	24	29/03/2019	371.00	40%	2,3,5,6
13	UK540635	602043	99	671	24	01/05/2019	408.00	26%	2,3,5,6
14	UK561466	401927	87	671	24	04/04/2019	377.00	39%	2,3,5,6
15	UK582636	104077	112	671	24	10/04/2019	383.00	39%	2,3,5,6
16	UK561459	703512	93	671	24	28/03/2019	369.00	33%	2,3,5,6
17	UK561459	703512	93	671	24			28%	2,3,5,6
18	UK582636	705840	63	671	24	28/04/2019	400.00	29%	2,3,5,6
19	UK582636	305724	64	671	24	13/05/2019	415.00	32%	2,3,5,6
20	UK540635	301935	100	671	24	01/05/2019	403.00	34%	2,3,5,6
21	UK560446	401007	100	671	24	14/04/2019	386.00	41%	2,3,5,6

From the breeder data set we can see that cow 1&2 ration is referenced as 2,3,5,6. Cow number 3 in the list was referenced as 7 and therefore fed differently.

Nutritional data referencing system	
Nutrition Reference	**Ration details**
1	Supplemented with colostrum
2	Grass (summer grazing)
3	Grass (winter grazing)
4	Kale
5	Cow ration
6	Cow ration
7	2.5 kg cereal mix + silage

The original project plan had been for project staff to visit the farmers and work with them to extract and collect the required data from various on farm data sources. This process became more complex, due to Covid-19 restrictions, meaning that all farm management data had to be collected and worked on remotely, significantly increasing the workload for both QMS staff and the farm business. This was unavoidable, and we would anticipate this to be a significantly smoother process were this project to be run without Covid -19 restrictions.

Issues in gathering farm management data have nevertheless highlighted a potential issue in scaling up this project as there were found to be inconsistencies in farm management software leading to inconsistencies in data as well as inconsistencies in the formatting of the data making them less comparable for analysis.

Milestone 4:

Obtaining from the 2 finishers, and the abattoir partner, full health, feeding and slaughter records of all finished stock linked to each dam.

Milestone 5:

Obtaining from the breeder's full health, feeding and output records for dams linked to each finished animal.

Milestone 6:

Collection and submission of DNA samples from each female who has bred a calf who has gone through the finishers.

Milestone 7:

Establishment of data flow from the meat processor.

Collection of breeder, finisher, abattoir, health, and nutritional data from producer group.

6.5. Collation of data for analysis by research partner

Genomic Modelling - To determine the existence of relationships, genomic and phenotypic data were collated prior to analysis.

Genomic Data

Genotype data was provided by Identigen Ltd for 533 dams genotyped at 46,111 SNPs. Prior to testing for associations between these SNPs and traits of interest, the project team used the check.marker() function in GenABEL to perform quality control. The project team removed all SNPs and individuals with a call rate of <0.95 (i.e. removed SNPs that <95% of individuals were typed at and individuals that were typed at <95% of the SNPs), removed all SNPs with a minor allele frequency of <0.05, removed all individuals with identity by state with another individual of <0.95, and removed all SNPs that did not adhere to Hardy-Weinberg equilibrium (HWE) with a false discovery rate of 0.2.

586 SNPs were removed because of low call rate; 9891 had low MA; and 440 were out of HWE. In addition, 17 individuals were removed because of low call rate and 4 were removed because of unacceptably high individual heterozygosity.

The final genomic data set consisted of 512 individuals typed at 35,194 SNPs.

Phenotypic Data

The dataset was provided by QMS staff and included breeder data, finisher data, abattoir data, nutritional data and health records. The combination of these data sets resulted a very large number of variables. For this reason, the pilot study analysis focussed only on breeder and finisher traits.

The phenotypic data used in the analysis included: breeder data with information on dam age, dam calving interval, calf sex and calf breed, and data on calf weight and daily live weight gain (DLWG) measured at various intervals (a first weight, 200 days, weaning, sale). The breeder dataset contained information on 782 calves, but data are missing in all of the phenotype columns, ranging from 56 missing values for sale weight to 331 missing values for the “first weight”, which was measured between days 6 and 98. The finisher data includes more information on weights and DLWG at various time points, including at transfer and finishing, as well as information on carcass weight and age at finishing. This is a smaller data set on 458 calves, with missing data ranging from just 5 for weight at transfer to 51 for weight at finishing. During the pilot programme it was concluded that phenotypic data on health and nutrition was too inaccurate/vague or had too many variables to form part of the analysis. In the rollout programme an alternative method of obtaining genomic information around these variables is laid out.

The calf phenotypic traits that were analysed in relation to maternal genotype are:

- First weight
- 200-day weight
- Weaning weight
- DLWG to weaning
- Sale weight
- DLWG to sale
- Age at finishing
- Weight at finishing
- DLWG at finishing
- Carcass weight

These were broadly normally-distributed and unsurprisingly they are broadly positively correlated, with the exception of finishing age, which is negatively associated with the weight traits (Figure 5). It should be noted that not all traits will correlate positively so there may be some negative correlation in further work.

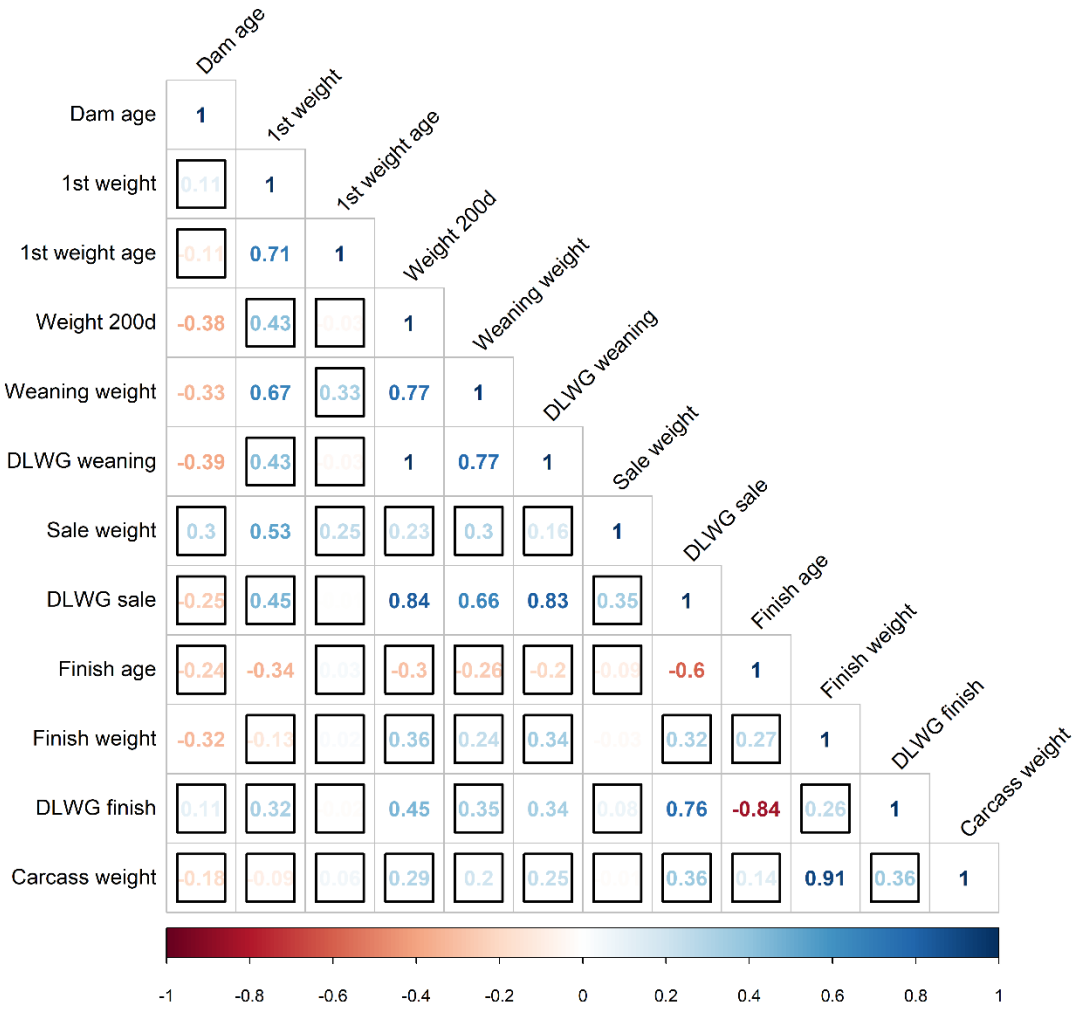


Figure 5: Correlation plot showing the pairwise Pearson correlation coefficients between pairs of continuous variables. Higher absolute values indicate stronger correlations; positive correlations are in blue and negative ones in red. Those marked with a black square are non-significant (P>0.05).

Genome-wide association analysis

We used the genome-wide rapid analysis using mixed models and regression (GRAMMAR) approach in GenABEL to perform genome-wide association analysis (GWAA) on the ten traits listed above. First, we created a kinship matrix to determine the pairwise relatedness of all individuals in the study based on identity by state at the >35,000 SNPs (**Figure 6**). We used a polygenic model to account for the influence of relatedness when estimating the influence of SNPs on all traits. Thus, we essentially ran mixed-effects models where the fixed effect of interest is each SNP, and the random effect is the relatedness matrix. For each of the calf traits (1-6 above) we fitted calf sex, calf breed and dam age as additional fixed effects) and for each of the finisher traits (7-10 above) we fitted calf sex, calf breed, dam age, breeder identity and finisher identity.

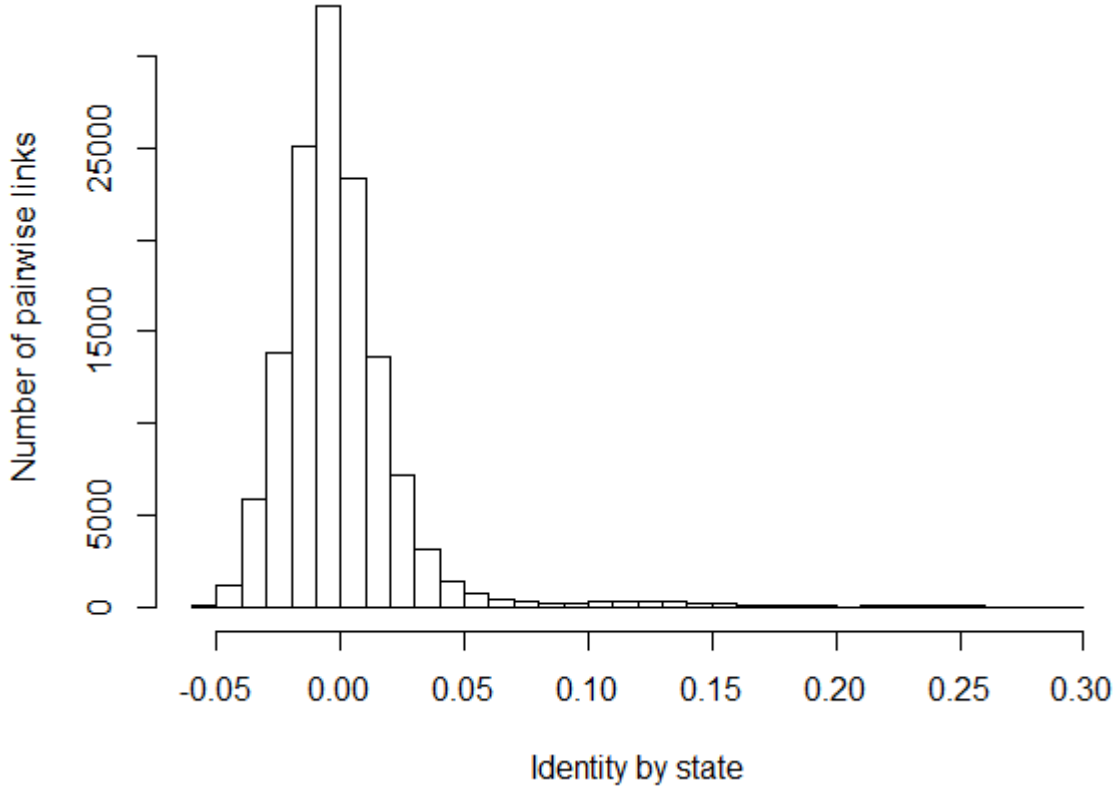


Figure 6. *Histogram of frequency of identity-by-state for the 512 individuals included in the final data set. Values closer to zero represent individuals that share fewer alleles.*

We then estimated genome-wide significance of each SNP using the qtscore() function on the residuals from the polygenic model, accounting for the fixed effects and relatedness. No SNPs were genome-wide significant for any of the traits examined (**Table 1**), and indeed the value majority of genome-wide P-values were near 1. This is no doubt a function of the small size of the data set.

Table 1. *Summary of GWAA for ten production traits in calves of genotyped dams. 'N' shows the number of calves that were phenotyped for a given trait; 'h²' indicates heritability estimated from the relatedness matrix; the remaining information corresponds to the identity of the SNP with the highest genome-wide significance, its chromosome, and the genome-wide p-value.*

Trait	N	h²	Top hit	Chromosome	GW P value
First weight	280	0.45	AX-106734619	3	0.360
200d weight	483	0.72	AX-106722404	0	0.935
Weaning weight	437	0.42	AX-115099909	4	0.375
Weaning DLWG	437	0.81	AX-124377692	18	0.700
Sale weight	486	0.28	AX-124386054	7	0.740
Sale DLWG	476	0.64	AX-106733023	6	0.585
Finishing age	286	0.22	AX-106757280	29	0.235
Finishing weight	282	0.44	AX-106722726	8	0.330
Finishing DLWG	282	0.27	AX-185122107	7	0.495
Carcass weight	283	0.54	AX-185122631	8	0.080

Milestone 3:

Analysis of each Maternal DNA sample to identify key SNPs linked to performance by the genetic partner.

Collation and preparation of genotype and phenotype data for analysis

6.6. Abattoir Sampling

Sampling was carried out by AK. Stoddarts at two production sites. Carcass sampling took place at Ayr, whereas product sampling was carried out at their Broxburn site.

Maternal Traceability – Carcass Sampling

As a method of testing the DNA traceability element of the project the project team aimed to sample 100 slaughtered animals on the line at the abattoir and trace these back to their dams using a low - level DNA parentage test. The following process was carried out to prove the concept of traceability by comparison against maternal DNA samples collected in stage 2.

- Finishers notified QMS staff they had animals going away to slaughter at AK Stoddarts and supplied a list of animal tag numbers
- Cattle tag numbers were then linked back to corresponding dam tag number to confirm a tissue tag sample had been previously taken
- List of carcasses to be sampled was supplied to staff at AK Stoddarts

Ayr Protocol – Carcass Sampling

1. Samples are taken at the grader station using the blue swabs. The samples are taken using the IdentiGEN DNA blue devices to scrape a small piece of lean meat the size of a grain of rice. Each unique carcass are sampled only once, but in duplicates.
2. Operator puts in a bag with a carcass label. The duplicate blue devices from each primal are placed in a small poly bag. Each small bag is identified, with the duplicate samples for each of the carcass, with an unique ID (e.g. 1 -60).
3. Samples are scanned on to carcass detail report.
4. Samples are immediately stored in a freezer. All the samples collected are stored in a freezer at -20°C or below prior to shipment.
5. Reports are emailed once a week to IdentiGEN and samples sent out on the same day.

*Maternal Traceability – Primal and Mince Sampling*DNA traceback was also used to test product samples taken once the carcass had undergone further processing. To do this meat samples were taken from primals (prime cuts of meat) and mince samples.

Broxburn Protocol – Primal Sampling

1. Samples are taken at the liberator station using the blue swabs once the carcass has been broken down. The carcass to be swabbed is labelled with a pink label which was used to identify the carcass selected for the QMS Project. The samples are taken using the IdentiGEN DNA blue devices to scrape a small piece of lean meat the size of a grain of rice.
   A total of 60 primal samples in duplicates are collected across different batches to complete the total of 20 samples. Each unique primals are

sampled only once, but in duplicates. The primal to be swabbed was selected at random.
2. Operator puts in a bag with a label. The duplicate blue devices from each primal are placed in a small poly bag. Each small bag is identified, with the duplicate samples for each of the carcass, with an unique ID (e.g. 1 -60).
3. Samples are recorded on a report
4. Samples are immediately stored in a freezer. All the samples collected are stored in a freezer at -20°C or below prior to shipment
5. Reports are emailed to IdentiGEN and samples sent out when enough samples taken.

Broxburn Protocol – Mince Sampling

1. Trims coming from selected QMS Scotch carcasses and from not selected QMS Scotch carcasses were stored in a stainless steel bin. Once the bin is full, the content is transferred into the hopper of a Vemag to be minced.
2. Samples are taken at the outfeed of the Vemag using a sample bag. For sampling reason, the first 5kg were not used for the sampling in order to avoid any risk of contamination from the previous batch. 3 handful/burger size grabs from each batch of mince are taken. For each of the 4 separate mince batches, the grab samples are collected in a bag, vacuum packed and dip tanked (keeping the mince batches separate). Label with the information below. Each of the outer bags containing the grab sample are identified with an unique ID (e.g. A to D).
3. Samples are recorded on a report.
4. Samples are immediately stored in a freezer. All the samples collected are stored in a freezer at -20°C or below prior to shipment.
5. Reports are emailed to IdentiGEN and samples sent out when enough samples taken.

For the Scotch Mince samples, a dilution was applied with the aim of mixing five trial animals with 25 non-trial animals.

Trim from five trial carcasses was minced and mixed with minced trim from circa 20 non-trial carcasses. There were four batches of mince containing the following dilution:

Batch A

2 QMS trial carcasses mixed in batch with approximately 20 non-trial carcasses.

Batch B

3 QMS trial carcasses mixed in batch with approximately 20 non-trial carcasses.

Batch C

1 QMS trial carcass mixed in batch with approximately 20 non-trial carcasses.

Batch D

3 QMS trial carcasses mixed in batch with approximately 20 non-trial carcasses.

From these batches, three samples were collected from each batch and mixed to yield one sample per batch. Samples from different batches were kept separately and labelled as above (A-D).

The samples were then sent to Identigen for testing.

Figure 7: Identigen's blue abattoir sampling device.

Milestone 8:

Parental analysis of 100 samples from meat products derived from slaughtered animals from the sampled dams to prove concept of commercial traceability.

Collection of 116 carcass SAMPLES and 64 product samples

6.7 Identigen low - level maternal parentage analysis

Maternal Traceability

For maternal traceability, Identigen extracted the DNA and conducted a DNA TraceBack for primal and diluted minced samples.

For maternal traceability from the carcass sample, the DNA TraceBack method identified 10 animals from 110 samples as being Not Assigned which indicates that maternity was not assigned to a dam in identified population. Maternity was however assigned to 100 animals from the sample pool of 110, yielding a 90.9% success rate. (omit 6 results)

A total of 116 carcasses were sampled and analysed.

- 100 carcasses assigned to a dam – 86.2%
- 10 samples not assigned to a dam – 8.6%
- 6 samples did not return a suitable DNA profile – 5.2%

It is worth noting that non assigned samples are a result of working with a small population of sampled Dams and the resulting administration errors. If the entire national herd were to be DNA sampled and information contained within a databased then any carcass could be sampled at random on the line and linked directly to the dam which would simplify the above process

Regarding the minced samples, as expected none of the samples were within specification. Table 2. details the results of the sample analysis for maternity assignment.

Primal results returned 95% in specification.

Table 2: Bovine Maternity Test Results

Task ID	Product	Result	Assignment
2305	Mince Sample A	70%	Out of Specification
2306	Mince Sample B	89%	Observation
2307	Mince Sample C	35%	Out of Specification
2308	Mince Sample D	31%	Out of Specification
2310	Primal Samples	95%	In Specification

Definitions

- In specification
  - ≥ 95% samples assigned to a dam in identified population.
- Observation
  - ≥ 80%, < 95% samples assigned to a dam in identified population.
- Out of Specification
  - < 80% samples assigned to a dam in identified population.

Milestone 8:

Parental analysis of 100 samples from meat products derived from slaughtered animals from the sampled dams to prove concept of commercial traceability.

Carcass traceback returned 90.9% in spec

Primals returned 95% in spec

7. Potential of utilising DNA in the Scottish Beef Herd

Delivering Traceability

Dam verification and identification requires approximately 200 and 800 SNP's respectively, and was well within the scope of the project. Identigen use a two-tier analytical system within DNA TraceBack to validate parentage and any animal with a "Not Assigned" status verifies dam is not in reference population. The work within the pilot project demonstrated that a full traceability system can be driven through the use of maternal DNA, opening up the possibility of implementation of a full traceability and performance improvement programme for the Scottish Beef Herd.

In order to confirm the operational accuracy of mince traceability on a commercial scale, more samples of mince require testing, with controls in place. For example, a DNA TraceBack could be applied to mince samples with the following mix:

- 100% trial animals
- 90% trial animals
- 80% trial animals
- 75% trial animals
- 25% trial animals
- 0% trial animals

Multiple repeats, 20 per test level, are required to test the validity of the process and also to deliver a level of confidence that the process is commercially applicable.

Genetic Gain

To achieve desired output of the project in terms of genetic gain; specific traits are required, and detailed phenotypic data must be collected. For genomic breeding values / predictions, a reference population is required whereby both genotypic and phenotypic data is collected in each individual animal (a quantitative geneticist is required to oversee this process). Growth traits are very heritable so performance of the dam is a good indicator of future potential and mass selection could be used whereby selection of an animal is based on its own data. This would be a less effective approach for fertility traits due to the low level of heritability.

The sampling of maternal DNA will enable linkages between traits in the offspring and the dam genetics. However, in the rollout programme it is recommended that the initial genomic maps are produced from groups of animals (30-60,000 in size) from the DNA of the actual animal. The reason for this is that it takes many fewer animals (and much less time) to accurately link DNA to phenotype. The Genomic maps produced can then be used to assess the presence of desirable traits in the breeding herd; decreasing the time taken to communicate useful breeding advice to farmers.

Identifying Markers for Improved Performance

Given the initial scope of the pilot study, sample size was too small to yield any significant results in terms of genomic markers for improved performance. In such a

small sample it is extremely difficult to account for variation between samples, this was demonstrated in the results. The pilot study did successfully demonstrate the process required to carry out DNA based performance analysis. Additional data points and reduced relatedness are needed to provide meaningful outputs. To use maternal DNA to correlate maternal genomic SNP data to progeny phenotypic data would need >1,000,000 data points per trait. This is within the scope of the long term programme, but there are methods of accelerating progress which are discussed in the second half of this document.

Knowledge Transfer/Technology Transfer

Much more work is required to develop the understanding of beef breeders and commercial breeders of the potential genomic technology could offer. This could include a more extensive knowledge transfer exercise and incentivising breeders and commercial farmers in integrating this technology in their breeding programs.

Milestone 10:

Production of conclusions about traceability using maternal DNA.

Milestone 11:

Production of conclusions about performance prediction.

DNA can be effectively utilised to guarantee traceability and improve performance in the Scottish beef herd

8. Challenges uncovered by the Project

During the proof-of-concept project several operational challenges were identified. Collection of high quality on farm performance data (phenotype data) was challenging. This is due to the fact that all farm businesses, systems and strategies are different. In some cases, the project team were also looking to collect data from 2 years previously. In order for accurate recording of information, and analysis, data has to be objective and comparable in standard format.

Main challenges

- Collecting consistent and accurate on farm performance data (phenotype data)
- Collection of historical on farm data
- Differing on farm priorities result in differently recorded data sets
- Data formats
- Changes to business structures
- Changes in farm management software packages and difficulty carrying over historical data
- Collating and comparing data from differing sources
- Covid – 19 restrictions remote working practice

Some of the above challenges were a direct result of Covid-19 restrictions imposed on Scotland and the rest of the UK. These were unavoidable and cannot be considered as obstacles to any national roll out.

Due to Covid-19, the operation of the project had to be carried out almost entirely remotely by members of QMS staff and project partners which proved a reliable test as to how much information can be practically extracted in a large-scale industry rollout from farms in a consistent format for analysis.

As a result of the challenges in on-farm data capture it was concluded that for a larger project or national rollout data should be sourced from existing objective, standardised databases.

9. Successes identified by the project

During this proof-of-concept study several operational successes were identified. Most have been described in more detail in their respective sections within this document, but the principal success of this project was that it established that DNA gathered on farm can be utilised to guarantee traceability from the finished product, back to the maternal animal. This was proven through a comprehensive suite of tests over a large sample of maternal animals and their finished progeny.

Main successes

This project aimed to establish that maternal DNA can underpin a highly robust traceability system in Scotland. As this report demonstrates, this was done effectively and proven in conditions that would likely replicate that of a full, or national rollout.

Assembling the main project group was one of the most important successes of the project, as it demonstrated that effective utilisation of data and communication of data from, and to, all parts of the red meat supply chain could be beneficial to each of the individual businesses involved, this helps to establish how essential it is that data can be harnessed to best serve Scottish beef producers moving forward.

An extensive cost-benefit-analysis is presented in the rollout proposal document.

Data flow from abattoir back to producer was highlighted as particularly beneficial, and when combined with data gathered from other, objective sources, could be an extremely useful management tool.

The project also, demonstrates that carcass traceback systems, using established protocols in place between the abattoir and the laboratory conducting the testing, was successful and scalable with little complexity.

Testament to the skillsets of the farmers involved, it was also proven that the ease and success of the on-farm DNA collection using sampling tags was evident, demonstrating that this project can utilise existing industry practices and a larger scale, or national rollout can be successful.

As discussed in the analysis element of this document, there were more phenotypic traits gathered from on farm management information that could be properly utilised, this was intended to establish the identification of data which can and cannot be accurately collected and analysed to create effective Genomic maps.

Critically, this report confirms that the data received by the Moredun Institute for analysis, was of good quality and would have permitted the development of genomic maps if this data had been received from a much larger sample of animals, as is illustrated in the rollout document.

10. Recommendations for rolling out on a larger scale

Based on the summary of conclusions from the proof-of-concept study a suite of recommendations has been made by QMS under the recommendations of Dr Jonathan Birnie.

A separate document accompanying this technical report makes recommendations and outlines proposals for a national system to utilise maternal DNA testing to both reinforce traceability and improve the genetic performance of the Scottish beef herd.

The report contains comprehensive cost benefit analysis on the likely cost of administering such a scheme with the potential industry benefit outlined.

The report also describes additional benefits that may come from utilising maternal DNA for traceability and performance. In particular, a potential improvement in farm business profitability, in addition to a reduction in greenhouse gas emissions and general improvement in environmental sustainability, as well as potential benefits for eating quality of Scotch Beef.

11. Comparison with the Beef Efficiency Scheme

[SRUC critical evaluation will be presented here when complete]

Milestone 9:

Evaluation of this methodology against the Beef Efficiency Scheme and a quantification of the additional benefits to industry from having a method of DNA traceability within the Beef Efficiency Scheme.

Evaluation conducted by Professor Eileen Wall, Head of Animal and Vet Science, Integrative Animal Sciences, SRUC

12. Summary of Conclusions

This project was developed by the Project steering group to be a pilot study to test concepts which may be applied in a larger, potentially national rollout programme that could be tied into Scottish Government farm support and climate change targets.

The project aimed to determine the following points, with a view to establishing a larger, potentially national rollout.

1. Can maternal DNA samples be lifted accurately enough at farm level to drive a traceability programme?
2. Can maternal DNA samples be lifted accurately enough at farm level to drive a DNA led herd improvement programme?
3. Can enough accurate phenotype data be lifted at farm level to drive an advanced genetic improvement programme?

In order to accurately assess the effectiveness of this project, these questions have been covered by the following questions and their respective answers.

Q: Can full traceability be achieved through use of maternal DNA?

A: Yes, a full traceability programme could be operated using only maternal DNA

Q: Can farmers take and deliver accurate DNA samples?

A: On-farm DNA collection using sampling tags was carried out extremely successfully, showing that industry rollout can be successful.

Q: Can Accurate Phenotypic data be collected on-farm at a large scale?

A: There were large gaps in some of the farm data, and other data had too much variation to enable accurate Genomic mapping. This suggests that phenotypic data collection from all farms in the programme is not appropriate.

Data used to create the initial genomic maps should initially only be collected from sources which are known to be accurate.

Sub-sets of farms could be used later in the main programme to collect specific types of data (e.g. health, fertility, feed efficiency), using DNA from the animals from which the phenotypic data has been collected. This is described in detail in the main rollout document.

Q: Can maternal DNA be used to drive high performance in the Scottish Beef Industry?

A: Yes, maternal DNA is a tool which can be used to accelerate genetic gain in the Scotch Beef Industry but some “ground truthing” work is required to develop models to fast-track progress.

Q: Is there a way of accelerating the process of this project, if it were to be scaled up?

A: The identification of associated genetic markers can be accelerated by starting the project by sampling slaughtered animals and linking direct phenotypic data to the DNA. Once the ground-truthing models are established and associated correlations between genomic markers and phenotypes, maternal DNA can be analysed for these traits.

Q: Can a group of farm businesses work together to deliver an effective DNA traceability and performance improvement programme?

A: The group of farm businesses in this pilot project worked well with each other and the other project partners, showing that effective joint working is possible and will enable benefits to be delivered across Scotland. This project has also demonstrated that collaboration across the full extent of the supply chain is not only possible but can be advantageous to all involved.

Q: Can data transfer be effectively achieved up, down and across the supply chain?

A: The pilot programme demonstrated that effective data flow up, down and across the supply chain was not only possible, but less challenging than expected. On a larger, or national scale this could provide significant food security, profitability, and sustainability improvements to the National Beef Herd. These potential benefits are laid out in greater detail in the rollout proposal document.

Q: Was the data collected suitable for developing genomic maps for the Scottish Beef herd.

A: The data received by Moredun was of good quality and would have permitted the development of genomic maps if this data had been received from a much larger sample of animals.