Beef Feed Efficiency Final Milestone Report
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Summary

- This project was led by AHDB (The Agriculture and Horticulture Development Board) and SRUC (Scotland's Rural College) with the aim of bringing together an industry-wide consortium to deliver a lasting infrastructure for the measurement of feed efficiency in beef cattle and its incorporation into breed improvement programmes. The final element of the project was to determine genetic parameters for efficiency traits and to predict the impact on the beef industry with the inclusion of feed efficiency into breeding goals.

- Data from feed efficiency trials on Limousin and Aberdeen Angus sired males were collated from Easter Howgate Beef Research Farm and five commercial farms in the UK between 2015 and 2019. In total 2,529 male cattle started the trials and were fed ad libitum with feed intakes measured for 63 days. Cattle were weighed weekly throughout the trial.

- Overall the mean age of cattle starting the trial were 337.3 days (~11 months) and the mean weight was 384.9 kg. During the trial period the mean weight gain was 81.2 kg or 1.3kg per day. Electronic feeders were employed that allowed the individual intakes of each animal to be measured and daily dry matter intakes were calculated. The mean daily dry matter intake was 8.3kg and the mean feed conversion ratio was 6.7kg which means that on average for every 6.7kg of dry matter an animal will put on 1kg liveweight. Residual feed intake (RFI) is the difference between actual feed intake and expected feed intake required for maintenance of body weight and weight gain. Calculation of expected feed intake was based upon measures of average daily gain and the animal's liveweight. RFI ranged from -3.93 to 8.10 kg/d and had a mean of 0 kg/d ($\pm$ 1.34 sd). A lower value for RFI is preferable in terms of efficiency as it means an animal requires less feed than anticipated based upon their level of production and maintenance requirements.

- The weekly weights were checked for linear growth which resulted in the analysis of 2,434 male cattle to estimate feed intake measurements and estimate genetic parameters. Despite a relatively small dataset with low progeny group sizes it has been demonstrated that feed efficiency traits were heritable and should respond to selection provided that there is enough phenotypic data. From the combined breed dataset heritability estimates were moderate in magnitude for the feed intake traits with estimates of 0.23, 0.35, and 0.39 for residual feed intake, growth rate and dry matter intake, respectively. These estimates were also within the ranges found in similar feed intake studies. Estimates using a trivariate sire model were similar and genetic correlations were moderate to high (0.56 to 0.92) between the feed intake traits.

- In addition to the project aims we explored the genetic associations between feed intake traits and carcase traits. Limousin bulls that had progeny on the feed intake trial also had their progeny traced in the abattoir data collated by SRUC. A dataset of 6,162 Limousin cattle was created that included heifers, steers and young bulls between 12 and 36 months. The mean net carcase weight was 365.1 kg and the mean age at slaughter was 664.7 days. Multivariate sire models were run and heritability estimates of net carcase weight, conformation, and fat were 0.15, 0.31, and 0.27 respectively. Residual feed intake in this multivariate setting had a lower heritability of 0.11 but growth rate and dry matter intake were very similar to previous estimates. However, due to limitations of dataset size and structure standard errors of the genetic correlations between feed intake traits and carcase traits were large in magnitude and not significantly different from zero. This project would benefit by future work involving the collection of more data that would enhance data structure and achieve more robust estimates to further confirm the results of this work and also to correlate with other traits in the breeding goal.

- The accuracy of data and ultimately genetic parameter estimates are reduced when trial days or animals need to be removed and decrease the size of the dataset. For all further trials care needs to be taken that suitable animals are used, electronic feeders are working properly, and filled appropriately.

- Feed is a major cost in all beef production systems and by taking steps to improve feed efficiency will improve margins together with reducing the environmental impact. The potential industry benefits of introducing feed efficiency into routine beef breeding programmes was expressed over 20 year horizon assuming 10 years of continued selection. Including records of RFI in the breeding goal was estimated to increase that economic response by 40% to £43.4 million (compared to £30.9 million) and GHG savings of 27% reduction over the same time period.

Introduction

Many traits that are directly and immediately related to **production efficiency**, such as daily weight gain or milk yield and feed conversion ratio, have long been part of breeding programmes and this has no doubt resulted in correlated genetic changes in **nutrient utilisation efficiency**. Selection for these direct production traits has generally resulted in an increase in feed intake relative to maintenance requirements and, as a result, an increase in the proportion of feed energy and nutrients that is utilised directly to synthesise consumable animal product. This in itself has a direct beneficial effect on emissions intensity of meat production. In addition, other, frequently longer-term, traits can be part of broader breeding goals that have also been shown to reduce the emission intensity of a unit of livestock product.

Due to the nature of many ruminant production systems, where there is less opportunity for individual feed intake recording, the use of feed intake traits in selection has been limited although there have been some examples (GRA White Paper, 2011[1]). Direct selection for efficiency of utilisation of the different components of the diet is difficult to achieve as many animal and feed parameters need to be collected. Work on these types of traits has mainly been at an experimental level, but have shown direct impact on reduced individual animal methane emissions (e.g., Hegarty et al, 2007[2]) and indirect in terms of overall reduction in emissions intensity per unit of product. *A review of the potential role of selection for* **nutrient**

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[1] Mitigating Livestock Greenhouse Gas Emissions Intensity through Animal Selection, Genetics and Genomics. A 'white paper' outlining stage 2 of establishing a Global Research Network

[2] Hegarty RS Goopy JP, Herd RM and B McCorkell 2007. Cattle selection for lower residual feed intake have reduced daily methane production. Journal of Animal Science 85: 1479-1486.

utilisation efficiency (in beef and sheep) is given in the final reports to Defra for projects IF0183[3] and IF0149[4].

In the UK there is a limited amount of feed intake data and the associated performance efficiency traits (e.g., growth rate, final carcase weight/characteristics, body fat), to allow the industry examine the genetic control of **nutrient utilisation efficiency** under UK production scenarios and with UK industry relevant genotypes. There are "pockets" of experimental hypothesis driven data (e.g., Defra project IF0169[5], the GHG Platform[6]) available in the UK which has some potential value to provide an indication of genetic control for traits related to feed efficiency, but limited value for data to provide estimated breeding values by which the industry could begin to actively select for such traits. Until very recently there were very few drivers for the industry to directly record (and select for) these traits and the economics of production were "perturbed" via payment schemes. However, the policy push to reduce the emissions intensity of ruminant agriculture is such that there is now traction in the industry for such traits. This is coupled with a clearer expression of the economic benefit of reduced costs of production now that the industry is exposed to market prices due to the changes in payment schemes. This is reflected, in part, in the industry roadmaps.
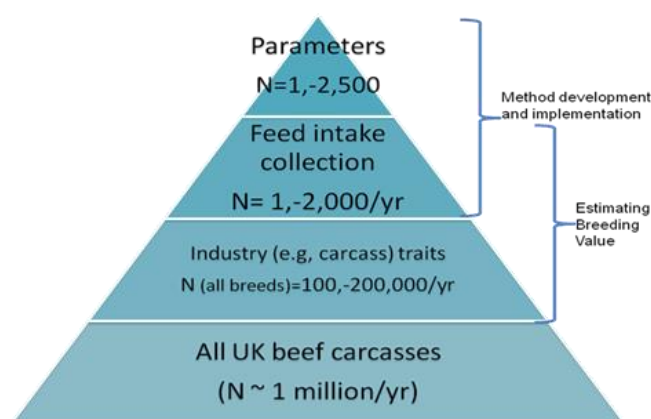
Although feed intake is the main trait associated with feeding costs, we have not yet been able to incorporate it in our national breeding goals, in part due to the lack of available data given the costs of directly recording feed efficiency in cattle. This project aimed to work with the industry to establish a key data resource for the development of base information for the inclusion of feed efficiency in our beef breeding goals.

Figure 1 Phenotyping pyramid

To maximise the potential industry relevance of the data, in terms of delivering sufficient data to estimate meaningful genetic parameters and correlation between the target traits (i.e., feed intake and derived efficiency traits) and wider industry traits (i.e., growth rates to slaughter) it is essential that the data are collected on a structured subset of the population that is connected to the final target population. The diagram in Figure 1 describes the "pyramid" of depth of phenotyping that was deployed in this project. In the "perfect" design the animals at each phenotyping stage will be strongly connected to the animals lower down the phenotyping pyramid. This is important so that meaningful (and significant) genetic correlations can be estimated and therefore wider industry data on correlated traits could be harnessed to increase the accuracy of estimated breeding values for the "expensive to record" traits.

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[3] Review of nutrient efficiency in different breeds of farm livestock, 2010

[4] Determining strategies for delivering environmentally sustainable production in the UK ruminant industry through genetic improvement, 2010

[5] Underpinning tools to be utilised by the ruminant GIN, 2011

[6] http://www.ghgplatform.org.uk/

Materials and Methods

Sources of animals

Data from feed efficiency trials on Limousin and Aberdeen Angus sired males were collated from Easter Howgate Beef Research Farm and five commercial farms in the UK between 2015 and 2019. It is important to note that the trial included crossbreds from the two sire breeds and not just purebred animals, thus reflecting the nature of the commercial sector. The sire breed crosses could be either from another beef breed or a dairy breed. At the trial start there were 504 Limousin sired steers at Easter Howgate, and 39 Limousin sired young bulls and 1,986 steers (comprising of 1,489 Limousin sired steers and 497 Aberdeen Angus sired steers). The Limousin and Angus breeds and their crosses numerically have the largest populations registered in the UK and represent a continental late maturing breed and a native early maturing breed. The number of batches per farm ranged from 1 to 7. Two electronic feed systems were employed that allowed the individual intakes of each animal to be measured. The trials conducted at Easter Howgate Beef Research Farm employed the Hoko electronic feeders (HOKO, Insentec, Marknesse, The Netherlands) whereas the commercial farms employed the GrowSafe system (GrowSafe, Calgary, Alberta, Canada). The experiment was approved by the Animal Experiment Committee of SRUC and was conducted in accordance with the requirements of the UK Animals (Scientific Procedures) Act 1986, although recording intake on commercial farms is not subject to such regulation.

Pilot trial Easter Howgate

From November 2015 onwards 504 animals had completed the trial over 5 batches held at Easter Howgate (Table 1). Within batches 1, 2, 3 and 5 the animals were split up into 4 pens, whereas batch 4 had 1 pen only. Summary statistics for age and weight at initial and final scans for batches 1 to 5 are given in Table 2.

Table 1 Summary of trial batches at Easter Howgate

Batch ID	Training start	Trial start	Trial end	n	n sires	n farms
1	20/08/2015	11/09/2015	13/11/2015	93	13	10
2	23/12/2015	22/01/2016	25/03/2016	119	15	8
3	04/04/2016	29/04/2016	01/07/2016	127	17	12
4	11/07/2016	19/08/2016	21/10/2016	39	6	4
5	09/12/2016	18/01/2017	21/03/2017	126	4	11

Table 2 Summary of age and weights by batch and pen at Easter Howgate

Batch	Pen	Count	N sires	N farms	Age at trial start		Initial weight		Final weight	
					Mean (s.d.)	Range	Mean (s.d.)	Range	Mean (s.d.)	Range
1	1	24	8	6	378.3 (21.50)	336-407	495.1 (40.10)	442-594	592.9 (45.61)	528-708
1	2	23	10	9	363.2 (31.86)	299-410	424.9 (29.41)	373-488	521.4 (34.86)	458-578
1	3	23	8	6	362.1 (34.19)	301-403	368.3 (23.83)	330-424	464.6 (26.37)	410-508
1	4	23	8	6	339.5 (34.62)	275-402	320.4 (41.75)	228-411	413.9 (52.15)	315-532
2	1	30	9	6	276.1 (19.65)	232-307	283.0 (30.73)	215-338	358.6 (42.59)	254-432
2	2	30	11	7	280.5 (22.50)	238-333	313.9 (22.80)	255-356	391.7 (28.63)	334-447
2	3	30	12	6	295.5 (21.09)	248-327	340.0 (20.50)	299-376	413.5 (28.13)	369-463
2	4	29	10	7	305.9 (24.31)	211-359	375.2 (23.71)	327-425	451.4 (31.19)	395-526
3	1	32	8	7	310.1 (34.25)	258-394	271.2 (33.05)	211-350	368.7 (41.63)	304-473
3	2	31	11	9	355.5 (41.67)	292-422	330.0 (25.51)	281-374	433.4 (34.27)	369-488
3	3	32	10	8	376.0 (31.09)	322-427	372.2 (23.09)	317-422	476.0 (27.94)	404-524
3	4	32	9	7	388.5 (25.32)	319-421	426.2 (28.71)	360-475	530.5 (29.59)	461-582
4	1	39	6	4	321.3 (48.62)	260-433	308.4 (78.38)	204-483	395.9 (86.84)	256-578
5	1	32	8	8	277.2 (18.06)	233-320	291.2 (36.22)	198-345	384.3 (44.62)	276-454
5	2	31	9	8	288.4 (18.80)	259-322	314.4 (41.49)	201-380	401.5 (55.13)	257-485
5	3	32	10	7	283.3 (16.82)	251-311	342.0 (26.62)	291-395	436.8 (31.71)	372-495
5	4	31	9	6	294.3 (12.00)	270-313	372.2 (32.15)	297-427	469.2 (44.50)	316-532
1	overall	93	13	10	361.0 (33.46)	275-410	403.2 (74.18)	228-594	499.2 (78.48)	315-708
2	overall	119	15	8	289.4 (24.70)	211-359	327.6 (41.81)	215-425	403.4 (47.00)	254-526
3	overall	127	17	12	357.5 (44.74)	258-427	350.0 (63.50)	211-475	452.3 (68.38)	304-582
4	overall	39	6	4	321.3 (48.62)	260-433	308.4 (78.38)	204-483	395.9 (86.84)	256-578
5	overall	126	19	14	285.7 (17.63)	233-322	329.7 (45.69)	198-427	422.7 (54.99)	257-532

Commercial Farms

Feed intake data was collated from 22 batches across 5 farms (located in Dorset, Yorkshire, Angus, Flintshire and County Durham) between 2016 and 2019. Table 3 provides a summary for trial dates and Table 4 provides an overall summary of age, weight, and scanning measurements on the commercial farms.

Table 3 Summary of commercial farm trial dates

Farm Id	Batch	Training start	Trial start	Trial end	n
1	1	14/09/2016	19/10/2016	20/12/2016	46
1	2	27/12/2016	24/01/2017	28/03/2017	113
1	3	12/04/2017	10/05/2017	11/07/2017	98
1	4	01/08/2017	05/09/2017	07/11/2017	89
1	5	21/11/2017	19/12/2017	20/02/2018	107
1	6	13/03/2018	10/04/2018	12/06/2018	86
1	7	06/11/2018	04/12/2018	05/02/2019	88
2	1	14/09/2016	12/10/2016	13/12/2016	79
2	2	22/12/2016	19/01/2017	22/03/2017	118
3	1	14/07/2017	14/08/2017	16/10/2017	136
3	2	27/10/2017	24/11/2017	26/01/2018	165
3	3	02/02/2018	02/03/2018	04/05/2018	165
3	4	08/05/2018	05/06/2018	07/08/2018	121
3	5	18/09/2018	30/10/2018	11/01/2019	134
4	1	11/12/2017	08/01/2018	12/03/2018	62
4	2	19/03/2018	16/04/2018	18/06/2018	64
4	3	25/06/2018	23/07/2018	24/09/2018	57
4	4	14/11/2018	11/12/2018	12/02/2019	62
5	1	05/01/2018	02/02/2018	06/04/2018	58
5	2	13/04/2018	11/05/2018	13/07/2018	61
5	3	27/07/2018	24/08/2018	26/10/2018	61
5	4	14/11/2018	12/12/2018	12/02/2019	55

Table 4 Summary of scanning measurements across all commercial farms and batches

| | Initial Scan | | Final Scan | |
	Mean	Range	Mean	Range
Age (d)	321 ± 46.8	216-431	387 ± 45.2	286-498
Weight (kg)	310 ± 148.2	167-566	458 ± 77.4	212-654
EMD (mm)	56.8 ± 9.29	34-82	64.3 ± 9.06	40.5–95
Rib fat (mm)	1.3 ± 1.04	0-7.6	2.8 ± 1.54	0-8.3
Lum fat (mm)	1.3 ± 1.04	0-7	2.9 ± 1.63	0-11.3

Measurements

The cattle were housed indoors and fed a total mixed ration (TMR) using a diet mixing wagon. The diet varied between farms but was formulated within the ranges of the feed protocol based upon a growing ration typical of UK commercial diets. The ration was formulated based upon the quality of the silage on farm and was fed at all times during the acclimatisation and recording periods of the programme. The TMR specification was 11.8 (11.5-12.2) MJME/kg dry matter (DM), 15% crude protein (CP) on a DM basis. The maximum forage proportion in the diet was 70% (acceptable range 50-70% forage in DM according to silage quality). All ingredients were mixed thoroughly to avoid diet selection and the feed loading data was provided to calculate diet composition. Samples from each ration ingredient were tested for their dry matter content which was then used to calculate total DM content of the ration on a weekly basis. The main ingredient types are given in Table 5.

Table 5 Ingredients contributing to the ration

Forage	
Rations must be consistent as possible over a batch – no change of basal forage type, minimise changes of quality due to different cuts/fields etc	
Grass silage	Aim for 10.5-11.5 MJ ME/kg DM
Maize silage or wholecrop	It is acceptable to include up to 50% of the forage DM as maize silage or wholecrop cereal silage as long as this remains consistent during a batch and between batches.
Concentrate	
The specification of the concentrate/blend part of the ration will depend on the quality of the silage.	
Other	
Vitamins and minerals	A standard beef grower mineral/vitamin premix appropriate to the farm/area should be included in the blend – providing vitamins A, D, E and B12 plus Fe, Mn, Zn, I, Co, Cu and Se as is appropriate to local conditions

Each morning at the same time everyday feed bins were emptied and then provided with fresh feed. The ration was provided ad libitum using electronic feeders together with fresh water. The bedding comprised of non-edible wood fibre to ensure consumption of bedding did not contribute to the diet. Each batch of animals were separated into pens that ranged from 18 to 55 animals (mean = 33.2 animals). The number of feeders per pen ranged from 4 to 8 (minimum, maximum, and mean were 2.5, 4.8, 6.9 animals per feeder) when they were all fully functioning. Each batch comprised of an acclimatisation period of 28 days, for animals to adapt to their diet and environment, followed by a trial period of 63 days (91 total days on trial). Previous studies have come to the agreement that an individual's intake is recorded for at least 45 days to give an adequate estimate of daily intake but a longer period is required to allow for any failures which lead to removal of data on days where for example an individual has not had ad libitum access, and to ensure robust estimate of weight gain. Individual intakes were recorded for each animal using the electronic feeding equipment and converted to dry matter intakes. Total daily feed intake was summed for each animal and converted to total dry matter intake.

Weekly body weights (BW) of the male cattle were measured using a calibrated weigh scale throughout the trial and were taken at the same time of day for each farm. At the beginning and the end of the trial all cattle were ultrasonically scanned by a trained scanner using an industry-standard Aloka 500 machine (BCF technology Europe Ltd, Middlesex, UK) for fat depth at the 13th rib and the 3rd lumbar comprising of four measures at each site. The first fat depth measurement, at both sites, was taken above the deepest muscle point and the following three measurements were taken at 2cm intervals from this point further from the backbone. Muscle depth was also measured at the third lumbar at the deepest point. Overall (combining both Easter Howgate and commercial farm data) the average age of the cattle at the start of the testing period was 337.2 days (± 53.47 days SD) and the initial and final body weights were 384.9 kg (± 81.58 kg SD) and 466.1 (± 82.87 kg SD) respectively.

**Statistical analysis**

Growth rates (Average daily gain)
Animals were weighed weekly and individual growth was modelled by linear regression of weekly body weight (BW) against time (days on test) as

$$bw_{it} = a_{it} + b_{it}X_t + e_{it}$$

where bw_{it} is the observed weekly BW of animal i measured on day t during the test, a_{it} is the estimated initial BW of animal i on day t, b_{it} is the estimated regression coefficient that is equal to the estimated ADG of animal i on day t, x_t is the weekly BW measurement on day t, and e_{it} is the

residual error associated with each observed weekly body weight bw_{it} which provided average daily gain (ADG), mid-test BW (mid-BW) and mid-test metabolic BW (mid-MBW = BW0.75). Any cattle not eating or growing normally were removed from the trial data. The majority of animals that completed the trial had a correlation coefficient of 0.90[7] or higher indicating that they had grown normally, exhibiting the linear growth phase, therefore indicating that a linear regression model was appropriate (e.g. Figure 2). However, animals that had a regression coefficient with a R^2 value < 0.90 on the commercial farm trial or <0.95 on the Easter Howgate trial had their plots of weight versus trial day checked and if one of the weights appeared erroneous it was removed from the dataset and linear regression was re-analysed allowing some records to be salvaged (Figure 3). Figure 2 illustrates linear growth of one animal during trial with a correlation coefficient of 0.97 whereas Figure 4 shows the growth of one animal with a correlation coefficient of 0.61. The animal in Figure 4 was reported to have had a low intake during the last week of the trial.

There were 68 animals with a R^2 value less than 0.90 that were omitted from further analysis on the commercial farm trial which left 1,941 animals (mean R^2 = 0.987). Whereas on the Easter Howgate trial 6 animals with a R^2 value less than 0.95 were omitted which left 498 animals (mean R^2 = 0.991). These animals were generally reported as ill during the trial. An animal at Easter Howgate with a correlation coefficient of 0.395 was reported to have had chronic pneumonia. Two further animals (leaving 496 animals) were removed from the Easter Howgate trial as their feed intake was suspected to be underestimated and were possibly associated with double entries[8].
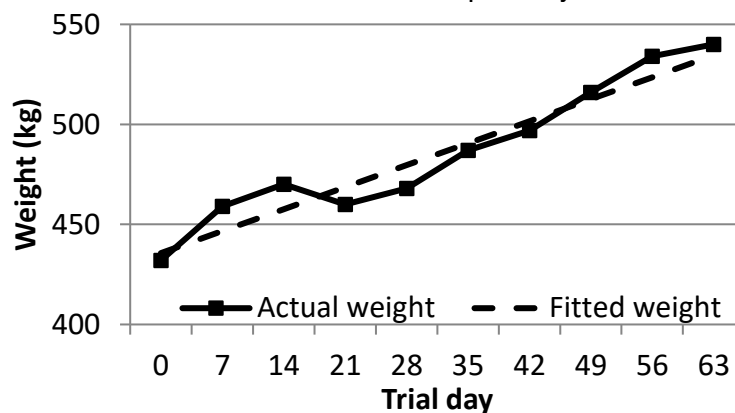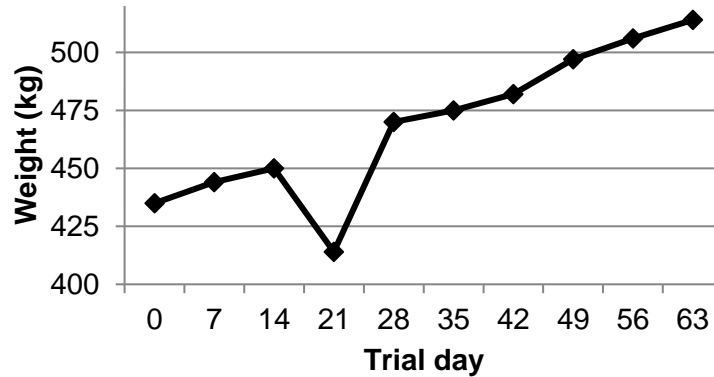

Figure 2 Individual animal example of actual and fitted weights with correlation coefficient >0.90

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[7] Note that for the trials at Easter Howgate a correlation coefficient (R squared value) of the weights for each animal was at least 0.95. However, for commercial trials the value was 0.90 as in BREEDPLAN protocols (http://breedplan.une.edu.au/tips/Collecting%20Feed%20Intake%20Information.pdf)

[8] Double entries took place generally when there were smaller animals on trial. Double entries arose when one animal would be feeding at an electronic feed bin and another animal would squeeze in and push the animal out of the bin and continue feeding in its place. The electronic feeder would continue registering the intake from the first animal although it had already left. This was only picked up if the first animal (the one that was pushed out) goes to feed at another bin. (i.e. it is apparently feeding at two feed bins at the same time).

Figure 3 Plot of weight versus trial day to show a probable erroneous value at day 21
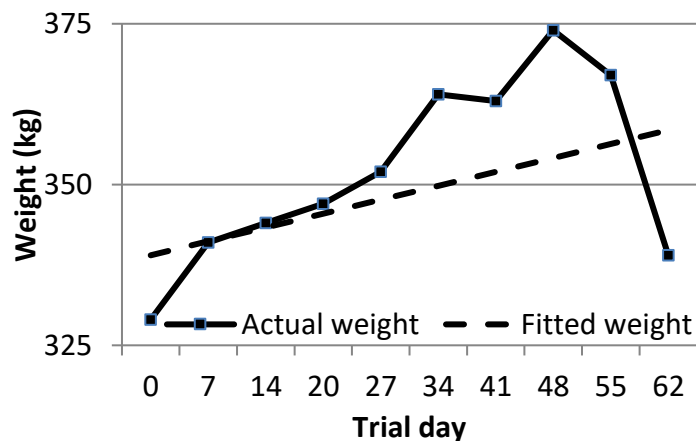
Figure 4 Individual animal example of actual and fitted weights with correlation coefficient <

Data cleaning led to the exclusion of a day's intake for an animal, pen, or the whole batch if 1) an animal was reported ill 2) an animal had lost its EID, 3) a pen had no feed for an extended period (i.e. not Ad libitum), or 4) there was a loss of power or a fault with the equipment. Animals that became ill during the trial for over 5 days were removed completely from the trial. The average daily intake was calculated with the remaining data over the test period for each animal.

Definition of fixed effects, covariates, and possible traits
There were 38 young bulls and 2,396 steers on the trial. As the young bulls were only in one pen during one batch on one farm and were not mixed with steers there was no need to include the fixed effect of category (bull/steer). Table 6 provides a description of traits and effects considered for analysis.

Mean dry matter intake (DMI) over the 63-day period was expressed as kg per day or as a proportion of mid-BW and mid-MBW. Feed conversion ratio (FCR) was calculated as average DMI per day (kg/day)/ADG. Residual feed intake (RFI) is defined as the difference between an animal's actual feed consumed and predicted feed requirements based upon its body weight and liveweight gain during the trial period. A negative RFI is when an animal eats less than predicted (i.e. more efficient) whereas a positive RFI is when an animal eats more than expected (i.e. less efficient). RFI was calculated as the deviation of actual DMI (kg/day) from DMI predicted based on linear regression of actual DMI on ADG (average daily liveweight gain), mid-metabolic body

weight (midMBW) and fat depth (UFD2_LR). The model used to predict feed requirements was as follows:

Predicted mean daily DMI ~ midMBW + ADG + UFD2_LR

Table 6 Definition of traits, covariates and fixed effects

Effect / Trait	Abbreviation	Description
Breed group	BGrp	Main breed of animal given in BCMS (Limousin (includes Limousin cross) , Aberdeen Angus (includes Aberdeen Angus crosses)
Sire breed group	SGrp	Breed name given to the sire
Farm_batch_pen	FBP	The combined grouping of farm (7), batch (7), and pen (4)
Birth location	BLoc	Recoded herd number given in BCMS for animal's location of birth
Age at trial start	AgeStart	Age of animal in days at the start of the trial
Weight at trial start	BW1	Weight of animal in kgs at the start of the trial
Back fat change	FD_DIFF	Difference between average fat measurements in mm at start and end of the trial (UFD2_LR -UFD1_LR)
Weight at trial end	BW2	Weight of animal in kgs at the end of the trial
Mean growth rate/ Average daily gain	ADG	Mean daily growth (kg/day) during the length of the trial
Mean daily dry matter intake	DDMI	Daily dry matter intake in kgs averaged over the whole trial period
Residual Feed Intake	RFI	calculated as deviation of actual DMI (kg/day) from DMI predicted based on linear regression of actual DMI on ADG, mid-MBW and ultrasonically scanned fat depth (UFD)
Feed Conversion Ratio	FCR	calculated as average DMI per day/ADG
Mid-metabolic body weight	MidMBW	BW75 at mid-test
Ultrasonically scanned fat depth combined at trial start	UFD1_LR	Mean of 4 measurements each at 13th rib and the 3rd lumbar at first scan
Ultrasonically scanned fat depth combined at trial end	UFD2_LR	Mean of 4 measurements each at 13th rib and the 3rd lumbar at final scan
Ultrasonically scanned fat depth (lumbar)	UFD2_L	Mean of 4 measurements at 3rd lumbar at final scan
Ultrasonically scanned fat depth (rib)	UFD2_R	Mean of 4 measurements each at 13th rib at final scan
Ultrasonically scanned muscle depth	UEMD2	Muscle depth measurement at final scan
Heterosis	Het	Heterosis calculated from breed proportions of dam and sire (Equation 1)
Recombination	Rec	Recombination calculated from breed proportions of sire and dam (Equation 2)
Dam breed	damBreed	Breed of dam given in BCMS
Dam age class	damAge	Age of dam grouped into 4 age classes
Dairy dam percentage	DairyDam	Percentage of dairy breed component of the dam

The significance of fixed effects was initially tested using the statistical package SAS (version 9.2; SAS Institute Inc., Cary, NC) to aid the construction of appropriate statistical models (Summary of effects chosen in Table 7). Genetic parameters of beef efficiency and carcase traits were estimated in ASReml (version Release 3.0; Gilmour et al., 2009) by initially running univariate animal models for each trait followed by bivariate and multitrait models where possible between combinations of traits. Employing a multitrait model makes use of phenotypic and genetic

correlations between the traits, which means that adjustments using (co)variables would not be necessary (such as for carcase traits which are adjusted for age or weight).

The traits available from the beef efficiency trial were average daily gain ADG (also referred as growth rate), mean fat depth at the end of the trial (UFD2_LR), daily dry matter intake (DDMI), feed conversion ratio (FCR), and residual feed intake (RFI). Animals that completed the trial were linked to any abattoir data that had been collated by SRUC. In total there were 1,339 animals with data on net carcase weight (CCW), conformation class (CONF) and fat class (FAT) measurements. For analysis, conformation and fat scales were transformed to a numerical classification (1 to 15) as given in Table 8. Two additional traits; age at slaughter (AGE) and average daily carcase gain (ADCG (ADCG = CCW/AGE)) were made available through merging abattoir data with BCMS data where date of birth and date of death was validated against kill date provided by the abattoir. A dataset was also created to provide a larger dataset of carcase traits to obtain more robust genetic correlation estimates. This was achieved by extraction of all progeny from the sires of trial animals from abattoir records.

Table 7 Summary of fixed effects and covariates used in analysis

Factors	Trait					
	DDMI	UFD[a]	UEMD2	ADG	RFI	AGE
Farm-batch-pen	x	x	x	x	x	x
Birth location	x	x	x	x	x	x
MidMBW	x		x			
Heterosis and recombination effects	x	x	x	x	x	x
Weight at end of trial		x				x
Age start						
Dam breed						
Dam age class						
Percent dairy dam			x			
Fat change				x		

[a] UFD incorporates model for all ultrasonically scanned fat depth measurements

Table 8 Transformation of carcase conformation and fat classes to numerical scale

Conformation class scale			Fat class scale		
15-point scale	5-point scale	Numerical scale	15-point scale	7-point scale	Numerical scale
E+		15	1-		1
E	E	14	1	1	2
E-		13	1+		3
U+		12	2-		4
U	U	11	2	2	5
U-		10	2+		6
R+		9	3-		7
R	R	8	3	3	8
R-		7	3+		9
O+		6	4-	4L	10
O-	O	5	4		11
O-		4	4+	4H	12
P+		3	5-	5L	13
P	P	2	5		14
P-		1	5+	5H	15

Sire breeds were either Limousin or Angus however dam breeds could vary therefore heterosis and recombination coefficients were calculated for combinations of four breed types; dairy, native beef, continental beef, and indicus/other breeds. The heterosis/recombination coefficients (In this case 6 different coefficients for each animal) were included in the model as covariates. Heterosis and recombination coefficients were calculated from the breed type proportions of the animal's sire and dam and are shown by formulae 2 and 3 respectively:

$$\text{heterosis}_{ij} = \frac{(\text{sire}_i * \text{dam}_j) + (\text{sire}_j * \text{dam}_i)}{100} \quad (2)$$

$$\text{recombination}_{ij} = \frac{(\text{sire}_i * \text{sire}_j) + (\text{dam}_i * \text{dam}_j)}{100} \quad (3)$$

where i and j correspond to two different breed types.

Combined dataset with Easter Howgate and Commercial trials

On the Commercial farms trial 2,025 animals started the trial from which 16 were removed before the trial finished. Of the 2,009 remaining animals 1,939 had RFI calculated that had exhibited linear growth during the trial.

Table 9 Animal records collected from HOKO (H) and GrowSafe (G) systems (remaining animals)

Farm	Feeder	Batch 1	2	3	4	5	6	7	Total
1	G	45	107	90	88	105	84	83	602
2	G	77	115						192
3	G	134	158	163	119	125			699
4	G	62	64	56	61				243
5	G	48	59	49	46				202
6	H	91	117	126	39	122			496
Total									2434

A combined dataset comprising of Easter Howgate and the Commercial farm beef feed efficiency data was created with 2,434 animals after editing (Table 9). All animals on the trials were recorded in BCMS and a pedigree file was created by matching animals to other national data sources and breed societies to provide as much pedigree information as possible. The pedigrees of the trial animals were traced up to five generations back, resulting in a pedigree file that comprised of 24,411 animals.

Results

Limousin sire breed genetic parameter estimation

The majority of the feed intake data came from progeny of Limousin sires. The aim of the project was to collect feed intake data from 1,800 cattle and for the Limousin breed this was surpassed with a total of 1,949 animals. The pilot trial at Easter Howgate provided feed intake data from 496 steers across 5 batches whereas five commercial farms across 21 batches provided 1,911 steers and 38 young bulls in the final edited dataset. The cattle on trial were traced to 301 Limousin sires and the number of progeny per sire ranged from 1 to 23. There were 179 sires that had at least 5 progeny on the trial. A summary of descriptive statistics are given in Table 10. Please note that for RFI a mean value is expected to be close to zero because it is based upon deviations from expected feed intake.

Table 10 Summary of descriptive statistics for Limousin sired steers and bulls

Measurement	Steers Min, Max	Mean, sd	Bulls Min, Max	Mean, sd
Age at trial start (days)	172, 500	335.3, 53.39	272, 389	349.7, 32.85
Weight at trial start (kg)	147, 710	383.1, 83.24	358, 550	477.2, 44.17
Weight at trial end (kg)	197, 782	463.4, 83.82	455, 654	574.5, 50.96
Back Fat Scan start (mm)	0.0, 8.8	1.7, 1.16	0.3, 2.0	0.8, 0.43
Back Fat Scan end (mm)	0.0, 13.1	3.1, 1.67	0.9, 4.6	2.1, 0.69
Final Eye muscle depth (mm)	38.0, 92.0	66.1, 8.51	63.0, 95.0	80.2, 5.98
Feed conversion ratio	3.1, 16.9	6.6, 1.85	5.8, 8.8	7.0, 0.71
Residual feed intake	-3.9, 8.1	-0.1, 1.22	-0.5, 1.4	0.5, 0.43
Mean growth rate (kg/d)	0.3, 2.3	1.3, 0.30	1.1, 1.8	1.4, 0.18
Mean daily dry matter (kg/d)	3.5, 16.7	8.1, 1.56	7.9, 11.4	9.8, 0.80

Table 11 Genetic parameter estimates of bodyweight, ultrasonically scanned, feed efficiency and carcase traits for Limousin sired cattle using an animal model

	Animal variance	Residual variance	Heritability
Final mean fat depth (rib and lumbar)	0.05 (0.109)	0. 99 (0.094)	0.05 (0.104)
Final mean fat depth (rib)	0.08 (0.110)	0.95 (0.094)	0.08 (0.105)
Final mean fat depth (lumbar)	0.02 (0.151)	1.41 (0.131)	0.02 (0.105)
Final muscle depth	8.19 (3.606)	13.33 (2.824)	0.38 (0.153)
Residual Feed Intake	0.02(0.037)	0.30 (0.031)	0.07 (0.115)
Growth Rate	0.01 (0.006)	0.025 (0.004)	0.35 (0.135)
Dry matter Intake	0.17 (0.072)	0.26 (0.056)	0.40 (0.152)

For the Limousin breed heritability estimates derived from an animal model are given in Table 11. Heritability estimates for eye muscle depth, growth rate and dry matter intake were moderate (0.35 to 0.40) whereas the remaining fat depth traits and RFI were low (<0.10) and lower than expected. Estimates were similar when a sire model was employed (Table 12). From the sire model estimates for net carcase weight and age at slaughter were 0.40 and 0.30, respectively.

Table 12 Genetic parameter estimates of bodyweight, ultrasonically scanned, feed efficiency and carcase traits using a sire model

	Sire variance	Residual variance	Heritability
Final mean fat depth (rib and lumbar)	Did not run successfully		
Final muscle depth	1.70 (0.878)	19.43 (0.698)	0.08 (0.039)
Residual Feed Intake	0.01	0.31	0.06 (0.116)
Average daily gain	0.002	0.03	0.24 (0.150)
Dry matter Intake	0.04	0.39	0.39 (0.162)
Feed conversion ratio	Not estimable		
Net Carcase Weight	40.96	368.23	0.40 (0.221)
Age at slaughter	181.10	2263.2	0.30 (0.205)
Conformation	Did not run successfully		
Fat Class	Did not run successfully		

Aberdeen Angus sire breed genetic parameter estimation

Part-way into the commercial farm trials a second sire breed, the Aberdeen Angus, had feed intake data collected. Collecting a second breed allowed the feeder systems to be fully utilised as it was sometimes difficult to source animals of the same breed. Although, the number of Aberdeen Angus sired steers were fewer it was envisaged that the second breed could give an indication of possible differences between breeds in addition to adding to the number of animals for a

combined sire-breed analysis for genetic parameter estimation. In total there were 485 Aberdeen Angus steers in the final dataset from 95 Angus sires with feed intake data derived from two commercial farms and 10 batches. The number of progeny per sire ranged from 1 to 20. There were 40 sires that had at least 5 progeny in the trial. A summary of descriptive statistics are given in Table 13. The dataset was considered to be too small at this stage to estimate genetic parameters accurately.

Table 13 Summary of descriptive statistics for Aberdeen Angus steers

Measurement	Min, Max	Mean, sd	Count
Age at trial start (days)	233, 480	344.0, 54.51	485
Weight at trial start (kg)	168, 608	385.0, 72.66	485
Weight at trial end (kg)	209, 690	468.3, 75.09	485
Back fat scan start (mm)	0.0, 9.4	2.4, 1.42	485
Back fat scan end (mm)	0.3, 12.3	4.3, 1.91	485
Final eye muscle depth (mm)	39.4, 78.0	59.4, 6.58	485
Eye muscle difference (mm)	-9.7, 18.4	6.4, 3.58	485
Feed conversion ratio	3.4, 16.8	6.9, 1.97	485
Residual feed intake	-3.4, 6.5	0.4, 1.67	485
Average daily gain	0.4, 2.2	1.3, 0.29	485
Mean daily dry matter	4.7, 16.4	9.0, 2.05	485

Combined Limousin and Angus sire breed genetic parameter estimation

The Limousin and Aberdeen Angus breeds are the two most numerous beef breeds registered in the UK. A combined breed analysis of Limousin and Aberdeen Angus sired progeny was conducted to estimate genetic parameters with a dataset comprising of animals that were progeny from 396 Limousin and Angus sires with feed intake data derived from 6 farms (Pilot trial at Easter Howgate and 5 commercial farms) with 2 to 7 batches each. The number of progeny per sire ranged from 1 to 23. There were 219 sires that had at least 5 progeny in the dataset. A summary of descriptive statistics for combined sire-breed dataset is shown in Table 14.

Table 14 Descriptive statistics for age, weight, ultrasonic, feed efficiency and carcase measurements

Trait/covariates	Min	Max	Mean	s.d	Count
Age at trial start (days)	172	500	337.3	53.47	2434
Weight at trial start (kg)	147	710	384.9	81.58	2434
Weight at trial end (kg)	197	782	466.1	82.87	2434
Initial mean fat depth (rib and lumbar) (mm)	0	9.375	1.8	1.25	2431
Final mean fat depth (rib and lumbar) (mm)	0	13.125	3.3	1.80	2434
Final eye muscle depth (mm)	38	95	64.9	8.76	2432
Mean dry matter intake (kg)	3.5	16.7	8.3	1.71	2434
Feed conversion ratio	3.14	16.89	6.7	1.87	2434
Residual feed intake	-3.93	8.10	0.00	1.34	2434
Average daily gain (kg/day)	0.322	2.255	1.30	0.30	2434
Net weight (kg)	247.4	518.03	346.5	39.66	1339
Conformation (1-15)	4	14	8.4	1.96	1339
Fat (1-15)	2	13	9.1	1.65	1339

Genetic parameter estimates from combined sire-breed dataset

Results from univariate analysis employing animal and sire models are shown in Tables 15 and 16. Variance components of these were used as starting values to build models up to bivariate and multivariate models.

Table 15 Genetic parameter estimates of bodyweight, ultrasonically scanned and feed efficiency traits using an animal model

	Animal variance	Residual variance	Heritability
Final mean fat depth (rib and lumbar)	0.223 (0.1441)	0.949 (0.1177)	0.19 (0.118)
Final mean fat depth (rib)	0.151 (0.1241)	1.013 (0.1030)	0.13 (0.104)
Final mean fat depth (lumbar)	0.329 (0.2106)	1.312 (0.1704)	0.20 (0.123)
Final muscle depth	5.754 (2.749)	14.409 (2.1885)	0.29 (0.128)
Residual Feed Intake	0.087 (0.0460)	0.290 (0.0371)	0.23 (0.116)
Average daily gain	0.013 (0.0056)	0.025 (0.0044)	0.35 (0.135)
Dry matter Intake	0.236 (0.0821)	0.306 (0.0639)	0.39 (0.132)

Heritability estimates derived from univariate analysis and an animal model were moderate for eye muscle depth and feed efficiency traits (0.23 to 0.39) and low to moderate for fat depth traits (<=0.20). Using a sire model the heritability estimates for feed efficiency traits RFI, ADG, and DMI were moderate (0.24 to 0.46) and are given in Table 16. Genetic correlations between RFI, ADG, and DMI were moderate to high (0.56 to 0.92). A trivariate sire model was employed to estimate genetic parameters of carcase traits for those animals on trial with abattoir records. The heritability of net weight was within the expected range but the results for conformation and fat class were lower than expected. For the analysis of liveweight and ultrasonically scanned muscle and fat depth at the end of the trial the heritability estimates were higher than results from univariate analysis (Table 17 and 18).

Table 16 Heritability estimates on diagonal and genetic correlations below the diagonal for feed efficiency traits

	RFI	ADG	DMI
RFI	**0.24 (0.117)**		
ADG	0.56 (0.310)	**0.35 (0.132)**	
DMI	0.85 (0.090)	0.92 (0.11)	**0.46 (0.14)**

Table 17 Genetic parameter estimates of net carcase weight, conformation and fat class using a trivariate sire model

	Sire variance	Residual variance	Heritability
Net Carcase Weight	34.4	362.289	0.35 (0.198)
Conformation	0.032	1.193	0.06 (0.157)
Fat Class	0.011	1.676	0.03 (0.163)

Table 18 Heritability estimates on diagonal and genetic correlations below the diagonal for liveweight and ultrasonically scanned traits at the end of the trial using a trivariate sire model

	BW2	UEMD2	UFD2_LR
BW2	**0.90 (0.145)**		
UEMD2	0.66 (0.138)	**0.43 (0.137)**	
UFD2_LR	0.85 (0.119)	0.28 (0.244)	**0.43 (0.130)**

Creation of a dataset combining abattoir and feed intake data

Limousin bulls that had progeny on the feed intake trial (FIT) also had their progeny traced in the abattoir data collated by SRUC. The final dataset had in total 6,162 progeny from 293 sires. Of these 5,355 progeny had abattoir data, 1,889 progeny had FIT data and 1,082 progeny had both abattoir and FIT data. Editing was not as stringent on contemporary groupings as used generally when creating a dataset for genetic parameter estimation as the dataset was already small. The

dataset was restricted to the first 300 progeny (including those with FIT data) born on the same farm as FIT animals, and to farms of birth and finishing with 3 or more animals. The descriptive statistics for traits or covariates from the resultant dataset are shown in Table 19.

Table 19 Descriptive statistics for traits and covariates

Trait / Covariate	Min, Max	Mean	Stdev	Count
Net carcase weight (kg)	228.6, 680.9	365.1	45.039	5355
Conformation class (numerical scale 1-15)	3, 15	9.36	1.862	5355
Fat class (numerical scale 1-15)	1, 13	8.76	1.961	5355
Age at slaughter (days)	352, 1095	664.69	137.302	5853†
Average daily carcase gain (kg/day)	0.24, 1.15	0.56	0.133	5280
Weight at trial start (kg)	147, 710	383.8	83.417	1889
Weight at trial end (kg)	197, 782	464.8	84.627	1889
Residual feed intake	3.93, 8.10	-0.11	1.216	1891
Feed conversion ratio	3.14, 16.89	6.56	1.805	1891
Dry matter intake	3.49, 16.72	8.09	1.567	1891

† There were more age at slaughter records available than other carcase traits because age at slaughter can be extracted from BCMS records in addition to abattoir records. However, the data collated from SRUC do not contain data from all UK abattoirs which is the reason why 573 animals have age at slaughter records but are without abattoir measurements.

Table 20 Summary of models employed for genetic parameter estimation

Trait	Category	
NCW, CON, FAT, AGE	Category + damAgeClass + damBreedGrp + percDairyDam + DLOC + BLOC+ FHYS	Run four traits as multivariate
DMI	Category + damAgeClass + damBreedGrp + percDairyDam + metab + FBP	Run with NCW, CON, FAT (carcase trait were analysed with AGE in model)
RFI	Category + damAgeClass + damBreedGrp + percDairyDam + FBP	Run with NCW, CON, FAT
ADG	Category + damAgeClass + damBreedGrp + percDairyDam + FBP	Run with NCW, CON, FAT

Abbreviations and definitions in model: Category = 3 classes (Young bulls, Steers, heifers); damAgeClass is age of dam at birth of progeny in dataset (4 classes); damBreedGroup is the breed of the dam (breed code given in BCMS); percDairyDam is the percentage of dairy breed of the dam (covariate); DLOC is the location of death (abattoir as given in BCMS); BLOC is the location of birth (farm as given in BCMS); FHYS is the finishing herd – year and season of slaughter; Metab is the estimated mid-metabolic body weight (covariate); FBP is the grouping of farm, batch and pen of a FIT animal; AGES is the age of an animal in days at slaughter (covariate); NCW = net carcase weight; CON = conformation; FAT = fat; AGE = age at slaughter; DMI = mean daily dry matter intake; RFI = Residual Feed Intake, ADG = Growth rate.

A sire model was employed in all analyses and the model for each trait is given in Table 20. A Five trait model with traits net carcase weight (NCW), conformation class (CON), fat class (FAT), average daily carcase gain (ADCG) and age at slaughter (AGE) was run however it was not successful. A Four trait model without ADCG was then run and converged successfully however the heritability of AGE was much higher than expected (> 0.9). For the analysis of carcase traits with FI a four trait model with the traits NCW, CON and FAT were run together with age at slaughter as a covariate and one FI trait (DMI, RFI, GR) at a time. Analyses with more than one FI trait were unsuccessful with both the Limousin FI dataset and the Limousin combined FI and carcase dataset. Variance component results are given in Tables 21, 22 and 23. The analysis would benefit from a larger dataset. Even for those analyses that did converge and appear to run successfully the standard errors were still very large. Some editing of the data was done but this was kept to a minimum in order not to reduce the dataset size further. Including Limousin sired progeny from a previous trial at Easter Howgate in 2011 could increase the dataset by 84 animals

however not all the same information was available (ultrasonic scanning and a comprehensive trial diary).

Table 21 Variance component estimates from a sire model

	NCW	CON	FAT	AGE	RFI	DMI	ADG
Residual variances							
NCW	615.040						
CON	10.705	1.190					
FAT	2.824	-0.171	1.785				
AGE	245.156	-0.467	3.317	2425.860			
RFI	-0.727	-0.048	a		0.309		
DMI	0.190	-0.085	0.072			0.437	
ADG	1.237	-0.022	0.030				0.037
Sire variances							
NCW	23.254						
CON	1.046	0.101					
FAT	0.676	0.011	0.129				
AGE	-1.123	-4.042	3.198	743.153			
RFI	0.228	0.012	a		0.008		
DMI	0.700	0.030	0.057			0.048	
ADG	0.140	0.012	0.008				0.003
Phenotypic variances							
NCW	638.290						
CON	11.751	1.291					
FAT	3.500	-0.160	1.914				
AGE	244.030	-4.509	6.514	3169.000			
RFI	-0.499	-0.036	a		0.318		
DMI	0.890	-0.153	-0.055			0.129	
ADG	1.377	-0.010	0.039				0.040

a The model converged with traits NCW, CON, FAT, and RFI but the warning was given that variances were liable to change. Variances were different compared to the model without FAT.

Table 22 Heritability (on diagonal) and genetic correlation estimates (below the diagonal with standard errors in parenthesis)

	NCW	CON	FAT	AGE	RFI	DMI	ADG
NCW	**0.15±0.108**						
CON	0.68±0.282	**0.31±0.137**					
FAT	0.39±0.433	0.09±0.365	**0.27±0.142**				
AGE	-0.01±0.344	-0.47±0.237	0.33±0.264	**0.94±0.191**			
RFI	0.51±0.822	0.42±0.665			**0.11±0.125**		
DMI	0.68±0.448	0.43±0.354	0.76±0.310			**0.40±0.161**	
ADG	0.48±0.431	0.64±0.361	0.43±0.404				**0.35±0.161**

Shown in the table are results from the 4 trait model NCW, CON, FAT, DMI. Without FAT the heritability estimate of DMI was 0.35 (0.155) and genetic correlations with NCW and CON were 0.56 (0.481) and 0.44 (0.381) respectively.

Table 23 Residual correlations (below the diagonal) and phenotypic correlations (above the diagonal) with standard errors in parenthesis

	NCW	CON	FAT	AGE	RFI	DMI	ADG
NCW		0.41 (0.022)	0.10 (0.027)	0.17 (0.034)	-0.04 (0.042)	0.04 (0.042)	0.28 (0.040)
CON	0.40 (0.015)		-0.10 (0.030)	-0.07 (0.038)	-0.06 (0.042)	-0.08 (0.043)	-0.05 (0.044)
FAT	0.09 (0.018)	-0.12 (0.018)		0.08 (0.037)		0.13 (0.040)	0.14 (0.041)
AGE	0.20 (0.017)	-0.01 (0.018)	0.20 (0.017)				
RFI	-0.05 (0.037)	-0.01 (0.034)					
DMI	0.01 (0.037)	-0.12 (0.034)	0.01 (0.037)				

ADG │ 0.27 (0.035)   -0.11 (0.034)   0.27 (0.035)

Summary of EBV solutions (both breeds)
A summary of EBV solutions for RFI, DMI, and GR from pedigree animals are shown in Table 24. Figure 6 shows the normal distribution of EBV's for RFI on trial animals and trial sires.

Table 24 Distribution of estimated breeding values

Trait	Min	Max	Mean	Standard deviation
RFI	-0.66	0.75	0	0.04
DMI	-1.36	1.19	-0.01	0.08
GR	-0.28	0.2	0	0.02
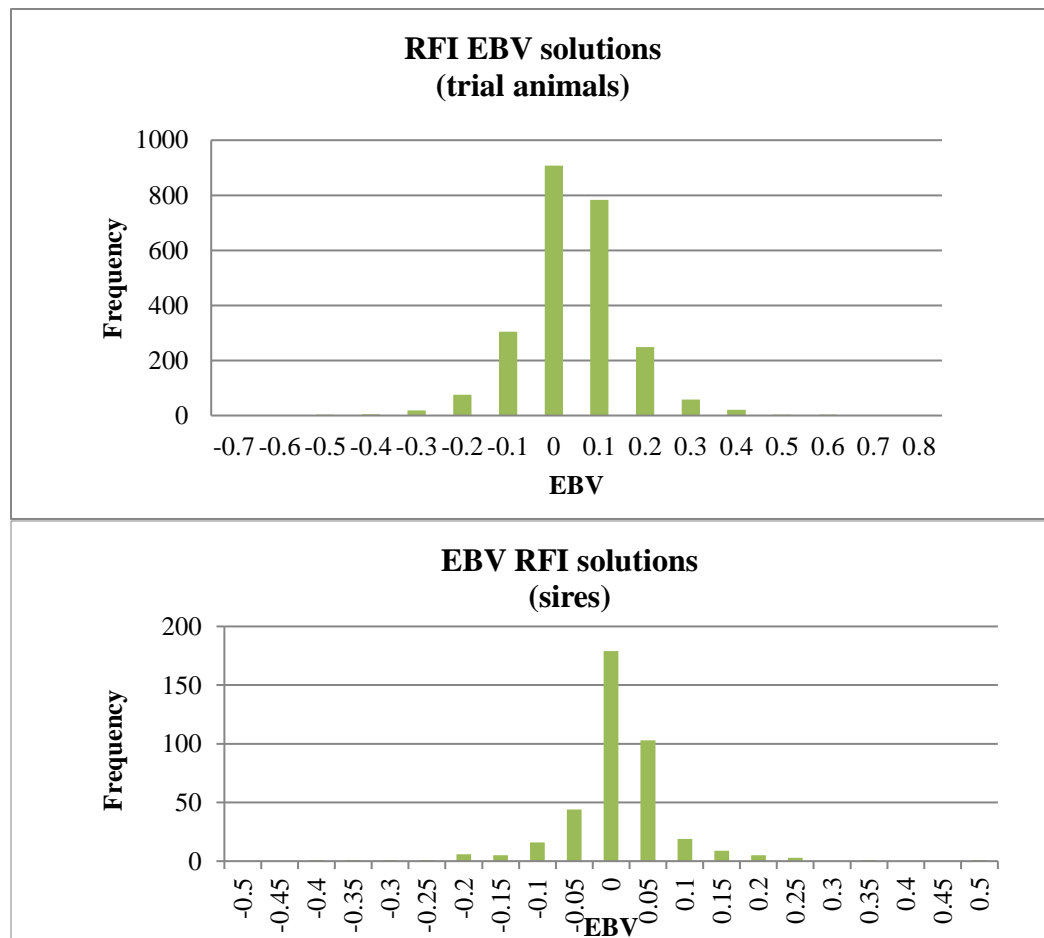
Figure 5 Distribution of EBV's for trial animals and sires

Expected responses to selection with the inclusion of feed efficiency in beef breeding goals

Sustainable and efficient beef production depends on several traits and Figure 6 diagrammatically lists the traits and the interactions between them. These traits include reproduction, growth, feed intake and carcase quality. Due to the structure of the beef industry, production systems can be divided in general terms into two systems. These are the breeding cow herds and the growing and finishing systems, in which pre-weaning and post-weaning performances are the more

relevant traits, respectively. Even though they have different breeding goals, the productivity and efficiency of both systems determine the global efficiency of the beef industry.
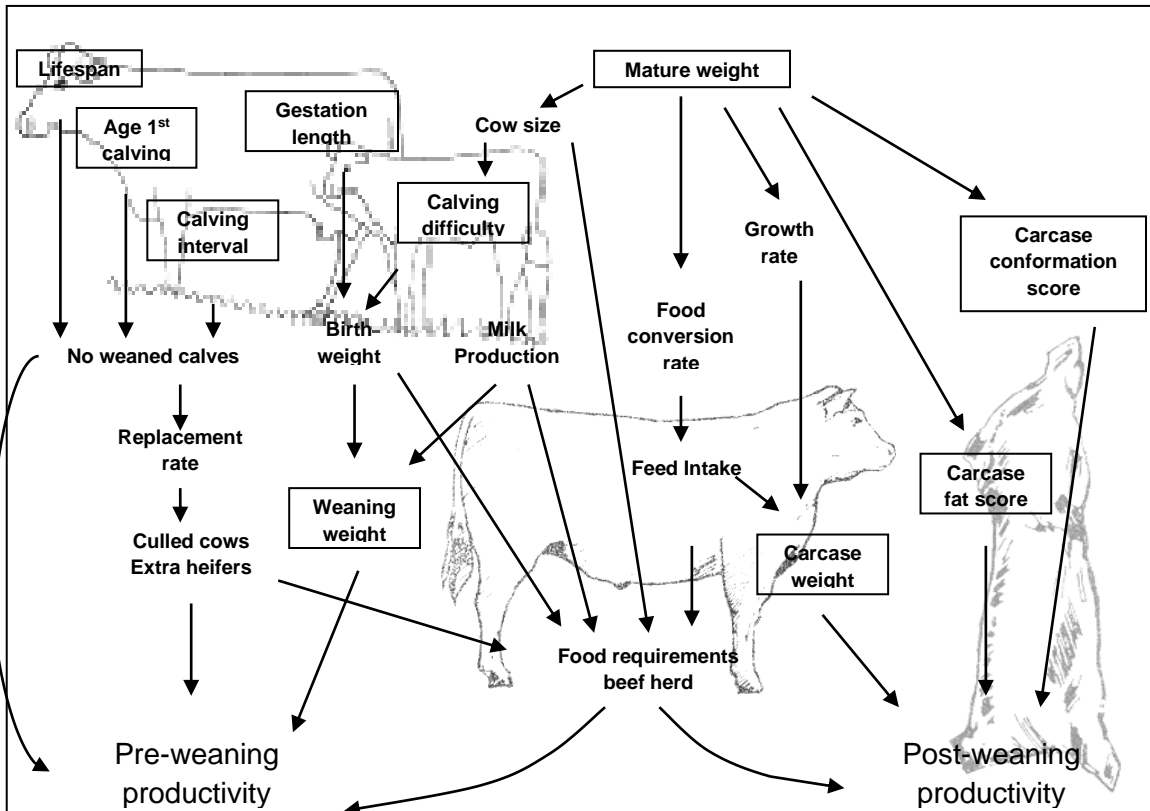
Figure 6 Diagram of the association between the economically relevant traits of beef production systems

The selection indexes and Estimated Breeding Values (EBV) available in the UK provide the information for the selection of both terminal sire and maternal traits. Examples of the traits in the breeding goals for beef breeds evaluated in the UK are summarised in Table 25. This list includes reproduction, growth performance and carcase quality traits which are economically important to the UK beef production systems. Table 26 shows the EBVs available in the UK underlying the breeding goals and their interpretation.

Currently genetic evaluations arre concentrated on optimising carcase merit at minimum cost. The estimations of genetic merits were focused towards growth and carcase quality traits: birth weight, 200-day weight, 400-day weight, muscle score and ultrasonic fat and muscle depths with some breeds also incorporating traits related to maternal performance and female fertility (Table 27).

Table 25 Current beef breeding goals traits and indices in the UK

Trait type	Index	Current traits
GROWTH	Maternal Value	Maternal weaning weight
		Calving interval
		Age at first calving
		Lifespan
REPRODUCTION	Calving Value	Maternal calving ease
		Direct calving ease

		Gestation length
CARCASE	Beef Value	Carcase weight
		Carcase fat score
		Carcase conformation score

Table 26 Estimated breeding values for selection of beef cattle in UK – some/all of these being included to many terminal beef selection indices.

TRAIT	DESCRIPTION
400-day weight (WT400)	To improve post-weaning growth rates of calves. Selection for high growth rates also tends to result in an overall increase in mature size.
Muscle score (MSC)	Selection on high scores will increase the amount of visual muscle leading to better progeny conformation.
Ultrasonic fat depth (FD)	Selection on low fat depth EBVs will result in less carcase fat. A 0.2 mm change in fat depth is approximately equivalent to one fat class.
Ultrasonic muscle depth (MD)	Selecting animals with high muscle depth EBVs will increase muscle depth at 400 days and hence the lean meat content of the carcase.
Gestation length (GL)	The direct component indicates the gestation lengths of a sire's calves. The maternal component indicates the cow influence on gestation length.
Birth weight (BWT)	Selection for optimised birth weights which results in fewer calving difficulties.
Calving ease (CE) – direct	The higher the scores the greater the percentage of a sire's calves which will be born without difficulty, i.e. +3 is preferable to –3.
Calving ease (CE) – maternal	Predicts the ease with which a cow will calve. For sires it predicts ease of calving of their female offsprings.
Calving interval (CI)	Predicts reproductive success. For sires, it predicts the reproductive success of female offspring (-ve values = cows that will get back in calf more quickly).
Age first calving (AFC)	Predicts the ability to first calve at a young age, given the opportunity. For sires, it predicts their female progenies ability to first calve at a young age, given the opportunity.
Lifespan (LS)	Predicts the length of a cow's breeding life in calf parities. For sires it predicts the breeding life of his female offspring.
200-day milk	To improve maternal characteristics (e.g. milking ability, milk yield, mothering ability). This is the maternal component of 200 day weight.

Methods: Modelling Selection Response

The base index was constructed to mimic the current terminal sire index using information available from the UK national genetic evaluations data. Current recorded traits include: birth weight, weight at 200 and 400 days, muscle score, fat depth, muscle depth, gestation length and calving difficulty. A second index was created by adding the new trait of interest RFI (during the growing period) to the goal trait. Estimates of genetic and phenotypic parameters for current recorded traits were obtained from UK national genetic evaluations data based on data from the Limousin breed, where parameter estimates were not available, further information was obtained from Roughsedge *et al.* (2005). Genetic and phenotypic parameters for the new traits were based on estimates reported in the literature and estimated earlier in this report. Estimates of heritability, phenotypic variance and repeatability for the current and new traits in the selection criteria are presented in Table 28.

Table 27: Terminal breed trait description

Abbreviation	Trait Name	Description and Units
CW	Carcase weight	Kg carcase weight
WT200	Weaning weight at 200days of age	kg live weight
WT-400	Weight at 400 days of age	kg live weight
BWT-D	Birth weight of offspring	kg live weight
RFI- grow.	Residual feed intake	1kg DM reduction in the dry matter intake of growing animals each year while maintaining production
FD	Fat Depth	Millimetres
MD	Muscle Depth	Millimetres
CFS	Carcase fat score	Units (1-15)
CCS	Carcase condition score	Units (1-15)
GL-D	Gestation length- direct	Days
CD-D/M	Calving difficulty- direct	CD units
LS	Lifespan	Years at time of disposal
SF	Shear Force	Kg
BSV	Birth survival	0 or 1
DS	Docility score	(1-6)
MSC	Muscle score	(1-15)

Profit (or breeding goal) traits incorporated in the base index include carcase weight, carcase fat score, carcase conformation score, gestation length and calving difficulty.

The summary of the economic weights derived in previous project report (July, 2018, Table 29). The breeding objective is made of four sub-indexes. The maternal index is derived from the calving and maternal trait sub-indexes, while the terminal index is made of sub-indexes for growth and carcase traits. The sub-indexes have been given draft names and can be added together to constitute an overall index.

Table 28. Heritabilities (diagonal), genetic (above the diagonal) and phenotypic (below) parameters traits in the selection index and breeding goal modelled

	BWT	WT200	WT400	MSC	FD	MD	GL-direct	CD-direct	RFI	CW	CFS	CCS
BWT	**0.23**	0.27	0.19	0.10	0.05	0.10	0.20	0.31	0	0.05	0	0
WT200	0.27	**0.33**	0.85	0.42	0.22	0.60	0.10	0.29	-0.16	0.50	0.80	0.18
WT400	0.19	0.85	**0.40**	0.53	0.12	0.55	0.05	0.10	-0.07	0.60	0.10	0.20
MSC	0.10	0.48	0.43	**0.27**	0	0.63	0.19	0.07	0	0.30	0	0.60
FD	0.05	0.17	0.22	0.16	**0.29**	0.18	0	0.05	0	0.10	0.40	0.10
MD	0.10	0.32	0.43	0.49	0.16	**0.26**	0.20	0.10	0	0.30	0.10	0.60
GL-direct	0.20	0.07	-0.00	0.12	0	-0.01	**0.29**	0.21	0	0.10	0	0.10
CD-direct	0.31	0.02	0.03	0.01	0	0	0.11	**0.12**	-0.02	0.10	0	0.10
RFI	0	0	-0.02	0	0	0	0	0	**0.24**	0	0	0
CW	0.05	0.30	0.50	0	0	0	0	0	0	**0.14**	0	0
CFS	0	0	0	0	0.30	0	0	0	0	0	**0.31**	0
CCS	0	0	0	0.30	0	0.30	0	0	0	0	0	**0.27**

Table 29. Economic weights calculated for beef breeding goals

Sub-Index	Trait	EW
Growth	Carcase weight[1] (kg)	**5.98**
	Carcase weight[2] (kg)	**2.64**
	Daily feed intake (kgDM/day)	**0.20**
Carcase	Carcase conformation (underlying EBV scale)	**9.18**
	Fat score (underlying EBV scale)	**-6.94**
	Dressing percentage (%)	**37.73**
Calving	Gestation length (days)	
	Direct offspring	**-5.98**
	Descendants of daughters	**-0.39**
	Calving difficulty (% difficult)	
	Direct offspring	**-9.16**
	Descendants of daughters	**-3.13**
Maternal	Maternal weaning weight (kg)	**0.75**
	Age at first calving (days)	**-0.35**
	Lifespan (years)	**4.22**
	Calving interval (days)	**3.94**
	Mature weight (kg)	**-1.46**
	body condition score (BCS units 1 – 5 scale)	**51.03**

[1] CW trait definition assumes that the feed intake EBV and breeding objective trait are defined as total daily feed intake.

[2] CW trait definition assumes that the feed intake EBV and breeding objective trait are defined as residual daily feed intake.

The breeding goal scenario that was largely the base scenario was akin to the current breeding programme where selection is based on approximately 40% young sires (generation interval <3 years) and 60% of older sire (sires which are still breeding at 4 years of age). Sources of information for each breeding structure and proportions of males/female candidates for selection were calculated from UK national genetic evaluations data based on the Limousin breed. It should be noted that other breeds of similar size would have similar structure of breeding programme design and information recorded and therefore the results can act as a template.

Given the pyramid structure of performance recording and genetic improvement dissemination in the beef industry we can assume that genetic improvement that occurs in the pinnacle of the breeding structure will disseminate through the purchase of the improved stock by commercial producers. Based on the analysis of national data we can assume that currently approximately 40-50% of cows that produce progeny destined for slaughter are mated to bulls that flow from pedigree populations undergoing genetic improvement. This could be considered a conservative estimate as it does not account for genetic improvement that could be occurring, even at a lower rate, in the bulls used over the rest of the population (e.g., those bulls could be the sons of improved sires).

The results from the genetic improvement in the pedigree population is used as a steady state of the pedigree population. In reality, for new goals that would include RFI we would require time for this impact to be realised for sufficient data to be collected to achieve this. Assuming that only a proportion of the pedigree population are undergoing recording for the both current and new traits

we must assume that the genetic improvement within all pedigree animals will result in a genetic lag in **all** pedigree sires could achieve thisand how it flows across **all** commercial farms. A conservative estimate would be 2 generations of bull improvement (sires and grandsires) and would take 10 years under current scenarios. This could be reduced significantly (maybe as little as 4 years) if intensive recording and industry co-operation in planning could occur. Returns at the whole industry level were calculated assuming genetic improvement results described.

Discounted incomes were calculated for each of the goal traits based on the annual genetic gain in the trait units and their economic values discounted by the specific genetic expression coefficients considering time and number of expressions of the genetic progress, and the number of bulls from the breeding programmes required to mate the industry females, assuming a 100% adoption of the technology. A discount rate of 7% was used when discounting genetic expressions of goal traits over time. Cumulative marginal net discounted return from 10 years of selection (at a steady state) with benefits considered over a 20-year horizon were calculated, including farmer profitability and societal economic benefit from reduction in GHG emissions.

Results

Table 30 shows the potential benefit from selection on alternative combinations and breeding goals and trait recording using results generated in this project. Key results generated to derive this table for UK beef production included
- trait definition for feed efficiency,
- feed efficiency data including recording protocols,
- genetic parameter estimates for feed efficiency traits in UK crossbred cattle
- genetic correlations between feed efficiency traits and other beef traits including carcase traits
- derivation of new economic weights for UK terminal beef production indices including the generation of economic weights for carcase traits and feed efficiency traits for the first time.

Combining these data we can model the potential impact of selection following UK beef structures. Including RFI as a trait in the breeding goal and the selection index (i.e., with recording data) showed that the annual economic response per breeding cow increased £0.85 (£2.10 to £2.95) in comparison to the current industry standard goal/traits. It should be remembered that this is cumulative over time and benefits will be additive year on year. The accuracy of selection increases with the inclusion of more data in the index increasing from 0.56 to 0.67 by adding feed efficiency records and to 0.85 with the additional inclusion of carcase traits data.

Scaling the potential industry impact of widespread and continued recording on feed intake and uptake by the industry we also modelled the benefit across the industry assuming similar penetration rates seen today. The benefits are expressed over 20 year horizon assuming 10 years of continued selection and all benefits are discounted according to UK treasury methodology for economic and GHG benefits. It can be estimated the current breeding goal has a potential approximate value to the industry of £30.9 million. Beginning to include records of RFI in the breeding goal was estimated to increase that economic response by 40% to £43.4 million. Building on previous work we also can show that the GHG savings was 27% reduction over the same time period.

Table 30: The impact of the "current" breeding programme without and with records on RFI for a range of breeding goals when selection intensity is 0.1

	Without RFI records		With RFI records		
	Current Goal	Current + RFI	Current Goal	Current + RFI	Current + RFI + Carcase
BWT-direct	0.06	0.08	0.06	0.07	0.05
WT200	1.66	1.74	1.42	1.37	1.08
WT400	3.11	3.34	2.78	2.44	2.16
MSC	0.04	0.05	0.04	0.03	0.03
FD	0.3	0.16	0.05	0.09	0.45
MD	1.76	1.93	1.63	1.35	1.34
CW	1.54	1.55	1.55	1.48	2.67
CFS	0	0	-0.02	-0.01	0
CCS	0.04	0.03	0.04	0.03	0.02
GL-direct	0.02	0.01	0.01	0.01	0.03
CD-direct	0.01	0	0.01	0	0
RFI-growing	-0.79	-3	-5.73	-15.02	-13.47
Annual Economic Response (£/cow)	2.1	2.23	2.65	2.95	3.76
Index Accuracy	0.56	0.5	0.61	0.69	0.85
Industry (Farm Profit)	£30,916,867	£32,830,768	£39,014,142	£43,430,837	£55,355,914
GHG (t CO2e)	-725,621	-749,011	-811,342	-917,998	-1,306,470
Profit (% change from current)	0%	6%	26%	40%	79%
GHG (% change from current)	0%	3%	12%	27%	80%

Discussion

This study has made it possible to test out protocols and to collect feed intake data on two breeds of cattle. The aim of the project was to collect feed intake data from 1,800 cattle and for the Limousin breed this was surpassed with a total of 1,949 animals. The data has made it possible to test out models and to provide preliminary estimates for feed efficiency traits in Limousin male cattle.

A difficulty that arose in the project was sourcing suitable animals for the trial. This meant that a wider age range and weight range were used on the trial than what was anticipated. In some cases animals were too small which led to problems such as 'double entries.' Also, some animals were older and heavier when they started the trial and some may no longer be on the linear part of the growth curve so their data would have to be removed. There were 396 sires in the analysed dataset (Angus and Limousin). For genetic parameter estimation some data editing is generally required such as a minimum number of progeny per sire. However as the dataset was relatively small editing on contemporary group size or the number of progeny per sire was not carried out. The number of progeny per sire ranged from 1 to 23 and over half of the sires had 5 or fewer progeny. Low progeny sizes are not very informative for genetic analysis, complicate the analysis, and the accuracy of genetic parameters and from the estimated breeding values (EBV's) produced would have low reliability. The accuracy of an EBV increases with progeny size and it is also associated with the heritability of the trait (a trait with lower heritability requires more progeny to achieve the same accuracy than a trait that has a higher heritability). If we edited upon the number of progeny per sire then we would have 1961 and 1079 animals in the final dataset for a combined breed analysis with the minimum number of 5 and 10 progeny per sire, respectively. Whereas, we would have 1594 and 859 animals in the final dataset for the Limousin breed with the minimum number of 5 and 10 progeny per sire, respectively.

Despite a relatively small dataset with low progeny group sizes it has been demonstrated that feed efficiency traits are heritable and should respond to selection provided that there is enough phenotypic data. The analyses produced heritability estimates which were within the ranges in literature from other studies. In this study heritability estimates were moderate in magnitude for RFI, ADG, and DMI ranging from 0.24 to 0.46. Although wide ranging estimates have been given in previous studies the estimates of heritability reported for RFI, ADG, and DMI in general have been moderate (0.2 to 0.5) as summarised by a meta-analysis that combined results from a range of studies from different countries and breeds[9]. The meta-analysis reported wide ranging estimates across studies for genetic correlations between feed efficiency traits and carcase traits. The mean genetic correlation across studies for RFI with carcase fat, RFI with conformation, and RFI with carcase weight were 0.06 (0.06), -0.30 (0.05), and -0.11 (0.06) respectively, but correlation estimates did vary from negative to positive in individual studies. In the present study genetic correlations between RFI with net carcase weight, fat and conformation were positive, however standard errors were high leading to non-significant results. Again, it is important to emphasise that this project dealt with crossbred animals including beef-beef crossbreds and beef-dairy crossbreds. Previously, it has been found that the direction of genetic correlations between some carcase traits differ between dairy breeds and beef breeds therefore we would expect some differences when comparing results to literature using beef breeds only.

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[9] Berry, D.P. and Crowley, J.J. 2013. Genetics of feed efficiency in dairy and beef cattle. J. Anim. Sci. 91:1594-1613.

Feed is a major cost in all beef production systems and by taking steps to improve feed efficiency will improve margins together with reducing the environmental impact. The potential industry benefits of introducing feed efficiency into routine beef breeding programmes (terminal sires cross commercial crossbred suckler cows) was expressed over 20 year horizon assuming 10 years of continued selection. Including records of RFI in the breeding goal was estimated to increase that economic response by 40% to £43.4 million (compared to £30.9 million) and GHG savings of 27% reduction over the same time period. It should be noted that sires and semen from terminal beef breeds is also used in the dairy herd and this will lead to additional economic and environmental benefits from the crossbred progeny from those matings. This will be dependent on the focus of "improved" beef semen for use in the dairy herd in terms of which triats take priority in the breeding goal, with a current focus around cavling ease.

This investigation would benefit from the collection of more data and an improved data structure to confirm the results of this work. If there were to be a continuation of collecting feed intake data then it would be expected that over time the progeny numbers per sire could be further built upon. Possibly a more targeted approach could be achieved in obtaining progeny from specific sires. However, at the same time sourcing the animals at the right age and their other requirements can already be challenging and electronic feeders are hoped to be used to their full capacity. As part of this study we did not specify any further protocols for after the trial period such as finishing of the animal and its sale for slaughter. However, fortunately we were able to extract slaughter data for some of the animals on the trial from data we collect from specific abattoirs at SRUC. Nevertheless, data on some animals is missing on carcase traits and although recording of sire is on the increase in British Cattle Movement Service (BCMS) it is still a weakness that it leads to many animals being dropped from an analysis, particularly on studies in the commercial sector.

The trials are costly and whatever can be done to reduce costs without compromising data quality should be considered. Several studies have investigated the length of the trial period [10][11]. It would be advantageous to reduce the trial length to enable more animals to go through the trials within a given time thus providing more phenotypes and therefore improving the accuracy of genetic parameter estimates and resultant estimated breeding values. However, the current trial length of 63 days was chosen to allow days to be excluded if problems occurred, such as power failures or equipment needing repairs. These extra days were required for the current trials but some of the reasons could be avoidable with tighter control such as under filling or over filling the feed bins. An automatic weighing unit that weighs cattle such as when they are at a water trough could benefit the trial by reducing the staff time for weighing, eliminate human error, and reduce associated stress on the animals if the technology is reliable. An automatic weigh unit would also provide several measurements daily rather than a weekly manually recorded weight. Reducing the number of manual weighings were investigated by removing weights from alternate weeks (i.e. fortnightly weights rather than weekly). This did not effect the accuracy of the data for 'non-

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[10] Manafiazar et al. 2017. Optimizing feed intake recording and feed efficiency estimation to increase the rate of genetic gain for feed efficiency in beef cattle. Can. J. Anim. Sci. 97:456-465

[11] Wang et al. 2006. Test duration for growth, feed intake, and feed efficiency in beef cattle using the GrowSafe System. J.Anim. Sci. 84:2289-2298.

problem animals' that grew linearly but it may lead to overlooking animals that appear to grow linearly with half their weights but their weight has actually fluctuated in between.