

# **Feasibility of using abattoir generated data and BCMS records for carcass trait evaluations (Carcass Trait Evaluations)**

## **Summary Version**

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### Executive summary

Existing industry (abattoir) and government data were used to produce a consolidated dataset of carcass traits for beef and dairy cattle. The overall aim of this feasibility study was to assimilate, cleanse, salvage, validate and characterise abattoir and British Cattle Movement Service (BCMS) data followed by descriptive statistics for the resultant dataset. The subsequent use of these data is expected to be for genetic evaluations and so analyses undertaken in this study were designed to reveal information on the suitability of these data for genetic evaluations.

Initially, 3 million individual carcass abattoir records (from three abattoirs) and approximately 48 million BCMS animal records were made available for this project. Using intelligent string matching, 82% of the individual carcass records could be matched to a BCMS individual animal record, resulting in a dataset of 2,435,875 for further investigation. The three traits available from abattoir records were net carcass weight, conformation and fat class. Matching to BCMS data provided information on animal movements, breed, dates of birth and death, in addition to dam and sire identities. Sire, which is not compulsory to record, was recorded for approximately 23% of animal records and the level of recording was generally higher in more recent years (11% in 2001 and 23% in 2011). Dates on animal birth and death in BCMS enabled to determine age at slaughter, and the average daily gain for net carcass weight. Across all breeds, the averages for the slaughter population aged from 3 to 36 months for net carcass weight, days to slaughter, average net carcass weight daily gain, conformation and fat class were 323.7 kg, 743 days, 0.45 kg, -R, and +3 respectively.

A refreshed BCMS database was obtained which included movement records. The herd identity was encrypted which meant that no information was available on the holdings themselves although animals could be grouped by holding by time and contemporary groups formed. This was a significant improvement on the data expected to be available to the project in comparison to a previous extract which only included holding of birth and death and the number of movements. The average number of locations for an animal to be reared (for a period of at least two months) was 1.7.

Beef farming in the UK is extremely diverse with many breeds and crosses that are used to suit the many environments, systems, and markets. The major breeds present in the carcass population (with over 100,000 animals) were described as Limousin, Aberdeen Angus, Holstein Friesian, Charolais, Hereford, Simmental, and Belgian Blue, and these accounted for 92% of the animals present in the matched abattoir/BCMS dataset. A major proportion of animals described as beef breeds were cross-breeds and generally take the name of the sire breed. Dam breed records emphasise that dairy cows are a major component of beef production with Holstein Friesian being the most common dam breed accounting for 46% of the slaughter population.

A pedigree file was created for BCMS records by matching to other national data sources and to itself. This resulted in a (super) pedigree file of over 50 million animals going back a maximum of 13 generations, and sire was available for 25% of the slaughter population (an increase of 2.3%). The super pedigree tended to lead to greatest improvement in sire records for dairy breeds, which were generally low in BCMS. The across beef and dairy super pedigree can be used to explore additive and non-additive (heterosis, recombination losses) genetic effects for traits relevant across both breeds (where data exists), such as carcass and product quality and safety traits but also cattle health/disease traits.

Genetic analyses were performed on a subset of the data for animals with a Charolais sire, which consisted of 17,125 records after editing. Heritability estimates for net carcass weight, conformation and fat class were 0.31, 0.24, and 0.14. Similar results were seen in

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a within Limousin breed parameter estimation analysis. These results provide strong indication of the existence of genetic variation in the studied traits. This, in turn, suggests that improving carcass quality traits through genetic selection is entirely possible, thereby warranting more detailed investigation of their genetic background, particularly their relationship with other traits of importance and within, between and across breeds.

The results of this feasibility study indicate that genetic analysis for carcass traits is realistic, particularly for breeds which make up a major part of the carcass population and have sufficient information on the sire. Encouraging the recording of sire identity by farmers in BCMS would further improve the usefulness of future data.

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### Introduction

A number of national datasets contain information which could be used to produce estimated breeding values (EBVs) for carcass traits based on abattoir data. These include abattoirs, BASCO, breed societies, milk recording organisations and British Cattle Movement Service (BCMS). Work is needed to draw the relevant data together and to create a consolidated pedigree and performance file. Preliminary analyses of existing previous abattoir data revealed significant genetic variation and moderate heritability that could be used in selection (Coffey *et al.*, 2009<sup>1</sup>), with similar results in other studies (e.g., Hickey *et al.*, 2007<sup>2</sup>, Bertrand *et al.*, 2001<sup>3</sup>).

BCMS records have an increasing proportion of sires recorded in recent years. Also, abattoir records can be joined to BCMS and back to national milk recording and pedigree based databases and deeper and more complete pedigrees formed from the resulting merged datasets. This means all dairy and beef breeds represented in the abattoir data with sufficient records could have genetic evaluations calculated and, over time, (recorded) progeny group size will rise and accuracies improve even further.

### Objectives

The overall aim of this feasibility study was to assimilate, cleanse, salvage, validate and characterise abattoir and BCMS data and then produce descriptive statistics for the resultant dataset. The subsequent use of these data (in another follow on project) is expected to be for genetic evaluations for carcass traits when sufficient quality standards have been met.

#### Objective 1: Consolidate available data

Carcass data for all breeds from abattoirs will be collated into a single database. Animal identity will be reformatted where necessary and matched to BCMS to produce a national cross reference file. This will then be matched to other data sources which are available for national genetic evaluations. A datafile and pedigree file will be produced as a combination of data from all available data sources, for both beef and dairy bulls where data exists. The consolidated dataset will contain the 'best' data from different sources for the same animal (e.g. sire from one source and dam from another).

#### Objective 2: Characterise merged and validated data

Data produced in objective 1 will be validated, collated by cross referencing between all available and appropriate data sources and then extracted for analysis. The extraction processes will be automated and built into the national genetic evaluation systems with appropriate quality assurance tests, validation, logging and data salvaging. Reporting will include: 1) number of sires; 2) number of offspring per sire; 3) breakdown by breed; record counts for data salvaged / lost; 5) means for age, weight and carcass conformation at slaughter broken down into sire, breed, etc; and 6) estimates of efficiency differences between sires where possible.

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<sup>1</sup> Coffey MP, Wall, E, Banos G and Roehe R. 2009. Preliminary genetic analysis of beef carcass traits. Proceedings of the British Society of Animal Science, pg 58.

<sup>2</sup> Hickey JM, Keane MG, Kenny DA, Cromie AR and Veerkamp RF. 2007. Genetic parameters for EUROP carcass traits within different groups of cattle in Ireland. J. Anim. Sci. 85: 314-321.

<sup>3</sup> Bertrand, JK. Green, RD. Herring, WO and Moser DW. 2001. Genetic evaluation for beef carcass traits. J. Anim. Sci. 79(E. Suppl.):E190-E200.

## Description of data

### Sources of data

The carcass data was obtained from three abattoirs. For this study there was great willingness from each of the three sources to supply data, which was supplied free of charge for the sole purpose of this study. It was envisaged to also include Northern Ireland (DARDNI) abattoir data, however due to the data not being part of BCMS there were extra complications in addition to obtaining data in a similar file format. Files were not ready from DARDNI in time for the reporting of this project, but it is expected that this data will be available to use for following work. Initially though it was expected that data would only come from one abattoir in Britain, thus the two additional abattoirs, mitigate against the data not being yet available for reporting from DARDNI.

Automated procedures were developed to load and log the files received from the individual abattoirs and to put them into a common format. This should dovetail with current systems of genetic evaluation data and quality assurance. Carcass data for all breeds from abattoirs were collated into a single database. The raw data contained a total of 2,960,857 records from three abattoirs collected from 2001 to 2012 (Table 1). There were a very small number of duplicates due to errors in identities which were removed. Further validations of records were carried out and extraction procedures were modified where necessary.

**Table 1 Total number of records grouped by year of kill**

Year	Total number of records
NULL	1
2001	27108
2002	33792
2003	41562
2004	52029
2005	62302
2006	255145
2007	447088
2008	391823
2009	405619
2010	521917
2011	545538
2012	176933

The British Cattle Movement Service (BCMS) data was established in 1996 to trace births, deaths, and movements. A restricted version (i.e. location type, holding (CPH) number or address were not known) of BCMS data was obtained with a cut-off point of January 2012. All births, movements, and deaths of animals born up until this point were available.

### Abattoir data

#### Breeds

From the combined abattoir data there were 617 different entries for breed. Some entries could be grouped as there were different ways of recording the same breed type. For example, there were numerous different entries for a Limousin cross, such as LIMX, LIX, LIM\_X, LMX, L\_X, LIXX, \_LIMX, LIMRX, LIMBX. There were some animals which had no record for breed (240,777) in addition to some date entries entered by mistake. The 30 most recorded breed codes are shown in Table 2. It can be seen that the top five breed

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codes were Limousin cross (LIMX), Aberdeen Angus cross (AAX), Charolais cross (CHX), Holstein Friesian (HF) and Limousin (LIM).

**Table 2 Most common breed codes obtained from abattoir data**

	Breed code	Count		Breed code	Count		Breed code	Count
1	LIMX	404513	11	FR	83892	21	HFX	14880
2	AAX	401134	12	BF	59163	22	DAQ	12974
3	CHX	248862	13	BAX	48016	23	SAX	10734
4	HF	213824	14	BB	38232	24	HER	10372
5	LIM	178096	15	HO	30586	25	SDX	8526
6	HEX	161400	16	HE	22978	26	BFX	8276
7	SMX	154284	17	BRBX	21595	27	WB	7914
8	CH	143456	18	SIM	21386	28	SHOX	6465
9	BBX	116424	19	SM	21222	29	AY	6263
10	AA	110859	20	HOL	18204	30	MOX	5981

## Sex

A range of codes existed to describe sex as shown in Table 3. Not all animals had a record for sex or it was coded wrongly. H would indicate a heifer, C a cow, S a steer (bullock), YB a young bull, MB a mature bull, and V would denote a veal calf.

**Table 3 Codes available to describe sex**

Sex	Count	Sex	Count
NULL	1957154	S	579698
#	19	S BONNER C145	1
.	1	S V	1677
] ]	6	SA	14273
2	3	SB	1212
6	1	SF	176
C	25755	SS	35850
CF	5048	T	1
CL	1	V	1268
CLF	892	V H	13
F	1	V S	47
H	270814	wenlock om	1
H V	179	YB	19839
HA	6472	YBA	1169
HB	659	YBB	229
HF	314	YBO	805
HS	27603	YBS	8838
MB	394	YBV	442

## Conformation

There are five main classes for conformation: E, U, R, O, and P (where E=excellent and P=poor). In the UK EUROP scale the classes P, O, and U are further sub-divided into – and +. The 15 point scale however, divides each letter class into 3 subclasses e.g. +E, =E, -E. It appears that both the EUROP and 15 point scale and a combination of the two scales were used by the three abattoirs (Figure 4). It appears that some categories have been written in alternative ways e.g. –O and O-. In Table 5 the classes were collapsed and it can be seen that less than 1% make the top class, whereas the majority of carcasses are classified as either 'R' or 'O' (80%).



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**Table 4 Summary of conformation classes**

Conformation class	Count	Conversion to numerical scale on 15 point scale†	Conformation class	Count	Conversion to numerical scale on 15 point scale†
E+	19	45	O+	751751	18
E	17911	42	O+	1	18
E=	75	42	O	119971	15
E-	512	39	O=	9323	15
U+	54740	36	O	1	15
U	92339	33	-O	278974	12
U=	5722	33	O-	51827	12
U3	2	33	P+	79423	9
-U	278356	30	P	6688	6
U-	22115	30	P=	6110	6
R+	39499	27	-P	20432	3
R	990288	24	P-	12388	3
R=	15815	24	NC	9	NULL
-R	5	21	NULL	26	NULL
R-	106529	21	#NAME?	4	NULL

†See Appendix Table B1 for conversion of conformation and fat classes to numerical scale

**Table 5 Distribution of carcasses for conformation class categorised as E, U, R, O, and P**

Grade	Number of animals (%)
E	18,517 (0.63%)
U	453,274 (15.3%)
R	1,152,136 (38.9%)
O	1,211,848 (40.9%)
P	125,041 (4.2%)

## Fatness

**Table 6 Summary of fat classes**

Fat class	Count	Conversion to numerical scale on 15 point scale†	Fat class	Count	Conversion to numerical scale on 15 point scale†
NULL /0	2287	NULL	-4	567	30
1-	2660	3	4-	192330	30
1	42900	6	4L	934286	30
1=	1698	6	4M	1	33
1+	3482	9	4	153845	33
-2	5	12	4=	9061	33
2-	7607	12	4+	49414	36
2	232376	15	4H	270572	36
2=	7717	15	-5	12	39
2+	16234	18	5-	9086	39
-3	21	21	5L	26349	39
3-	26939	21	5=	245	42
3	865495	24	5	6282	42
3=	19499	24	5+	741	45
3+	74914	27	5H	4230	45

†See Appendix Table B1 for conversion of conformation and fat classes to numerical scale

For fatness classes there are five main classes ranging from 1 (very lean) to 5 (very fat). In the EUROP scale, classes 4 and 5 are sub-divided into L (leaner) and H (fatter). However, there were several forms of a single class as shown in Table 6, which indicates the use of

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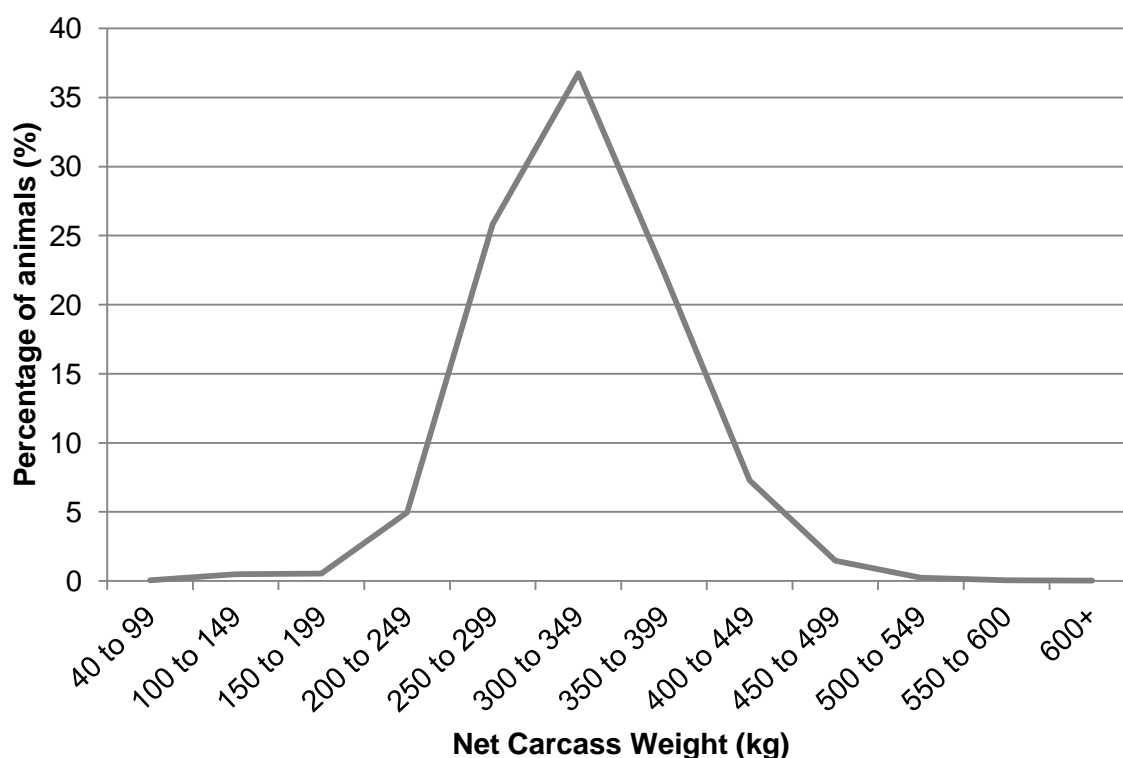
the 15 point scale. In Table 7 the classes were collapsed and it can be seen that 72% of carcasses fall into the desired categories 3 and 4L.

**Table 7 Distribution of carcasses for fat class**

Fat class	Number of animals (%)
1	50740 (1.7%)
2	263939 (8.9%)
3	986868 (33.4%)
4L	1146607 (38.6%)
4H	463469 (15.7%)
5L	33617 (1.14%)
5H	13328 (0.45%)

### Net Carcass Weight

There were 607 records (including negative values) that were less than 5 kg which were assumed to be mistakes when recording. Thus editing of weights, taking account of animal age, will be required prior to genetic analysis to establish suitable ranges. The weight data item is referred to as net carcass weight. Figure 1 shows a normal distribution for net weight with the largest proportion of carcasses weighing between 300 and 349 kg. Overall, the mean net carcass weight was 327 kg. Figure 2 shows that a wide range of slaughter ages exist, which includes mature cattle as well as prime beef.



**Figure 1 Distribution of net carcass weight at slaughter**

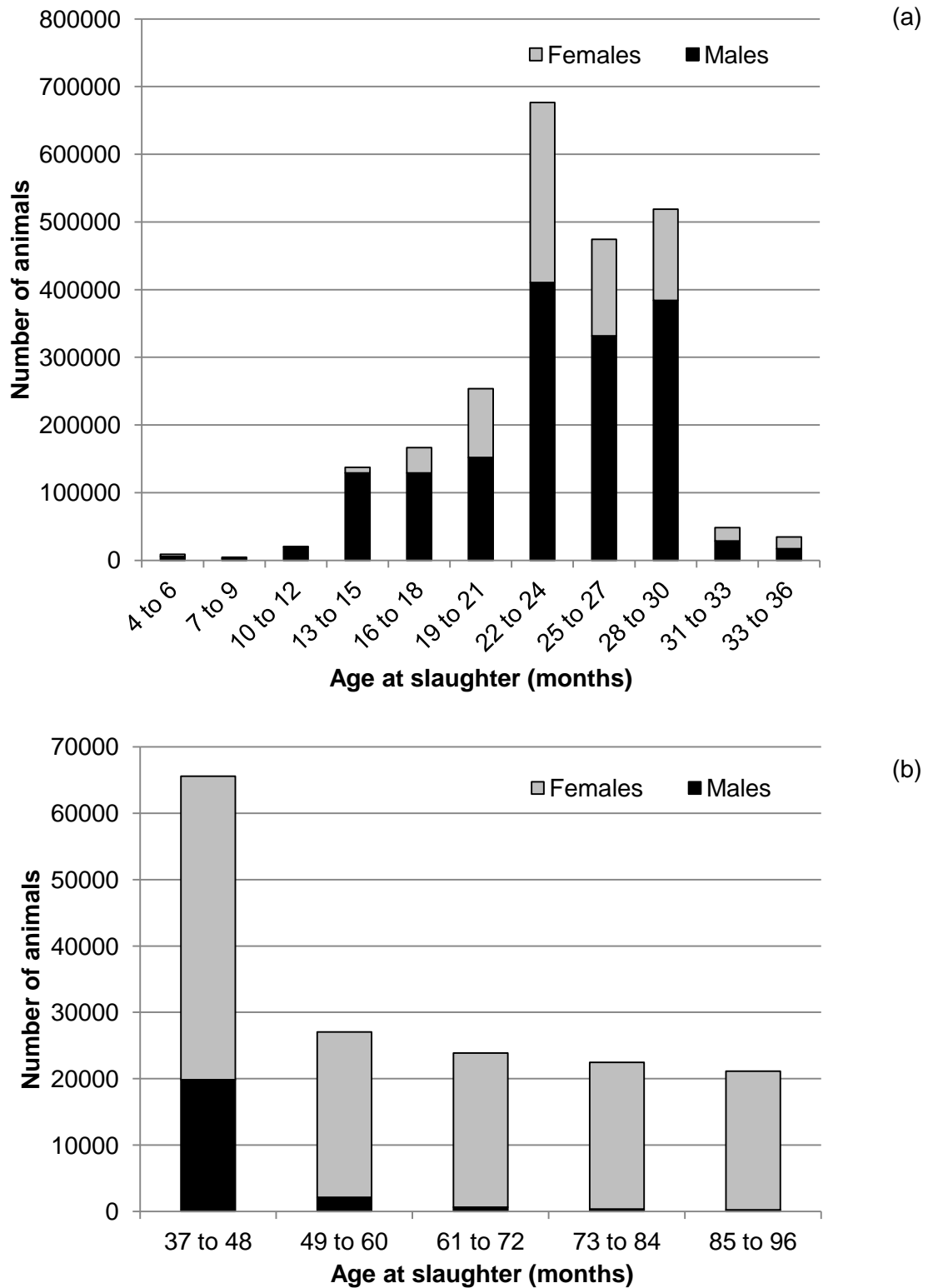


Figure 2 Distribution of age at slaughter for young (a) and old (b) animals

**Summary of abattoir data**

- Over 2.9 million records obtained from the three abattoirs
- The three most common breed types were Limousin cross, Aberdeen Angus cross, and Charolais cross.
- Slight differences in the scales used for classifying carcass conformation and fat across years and between data providers. Therefore, it would be suitable to add

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the effects of abattoir (location of death (individual abattoir) or source and the year-season of death for genetic analysis.

- Means for net carcass weight were similar between data providers but editing will be required to remove outliers/erroneous data.
- Data has been obtained from younger animals (specifically reared for beef) and mature animals (cull dairy cows, bulls and cows that have been bred from). These animals should be treated separately and a decision is needed to be made on the cut-off point (e.g. 24, 30 or 36 months), which may differ according to sex or breed type of the animal. Or different observation periods could be used if enough data is available (e.g. 12 to 18 months, 18 to 24 months, 24 to 30 months).

### **Matching abattoir data to BCMS**

The animal identity given in abattoir data was the UK eartag and this was reformatted if necessary (i.e. spaces, slashes removed) and matched to BCMS data. From a total of 2,960,857 animals with carcass records there were 2,437,365 that matched to BCMS data (82.3%). There were 523,491 animals that were not successfully matched to BCMS and of these 500,695 had no record for date of birth in abattoir data.

**Table 8 Additional information available from BCMS on date of birth**

Year of birth in abattoir records	Count in abattoir records	Count in BCMS records
NULL	2008510	
1899	245	
1990	1	
1994	6	6
1995	20	18
1996	645	3638
1997	2086	11943
1998	2269	18978
1999	5600	42911
2000	28957	51900
2001	40934	62282
2002	52038	75852
2003	64273	97409
2004	109820	211444
2005	128262	314387
2006	115675	336333
2007	116743	332495
2008	118944	358192
2009	115561	344524
2010	47031	166506
2011	3230	8546
2012	1	
2015	1	
2020	1	
2026	1	
2077	1	

There were 2,426,815 animals that had an exact match for date of death. Some animals do not have deaths recorded in BCMS because extraction of BCMS was up until January 2012, whereas some carcass data were obtained up until May 2012. In this case the abattoir date of death was used. The date of birth from abattoir data was not always known (e.g. 2,008,510 animals had date of birth recorded as NULL as well as input of erroneous data), thus data from BCMS can add to the information available as shown in Table 8. It can be seen that some of these missing values for date of birth have been solved once

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matched with BCMS, for example, an addition of 119,475 records for date of birth were extracted from BCMS for animals born in 2010.

There were 10,548 records where kill date from abattoir data and death date from BCMS were not the same (Table 9). Some of these records may indicate a mismatch, but for the majority the differences were minor indicating that the animal was matched correctly between both sources. There were 9,060 animals where the differences between sources for date of death were no more than 10 days. The majority of these differences were only one day (7,156 animals). Carcass records of 2,435,875 animals remained in the combined dataset by allowing dates of death records that had only a difference of 10 days.

**Table 9 Examples of differences between abattoir data and BCMS**

Id	Sex	Dob Abattoir <i>yymmdd</i>	Dob Bcms <i>Yymmdd</i>	Breed Abattoir	Breed Bcms	Death Abattoir <i>yymmdd</i>	Death Bcms <i>yymmdd</i>	Age diff (days)
1	F	NULL	03-04-12	AAX	ABANX	07-01-04	09-01-04	731
2	M	NULL	03-04-29	NULL	LIMOX	02-11-29	05-10-27	1063
3	F	04-11-04	04-11-04	BAX	BLONDAQX	06-11-14	09-11-14	1096
4	F	NULL	99-04-03	AYR	AYRSHIRE	12-01-30	00-09-01	-4168
5	F	06-01-23	06-01-23	SMX	SIMMX	08-07-22	08-01-22	-182
6	F	01-05-19	01-05-19	AAX	ABANX	03-05-22	03-05-23	1
7	M	NULL	09-07-24	BAX	BLONDAQX	11-09-26	11-09-16	-10

- 1) Appears to be correctly matched by id but there has been an error recording year of death
- 2) Death date at abattoir is before birth date in BCMS
- 3) Appears to be correctly matched by id but there has been an error recording year of death
- 4) Death date is very different – possibly mismatched
- 5) Appears to be correctly matched by id but there has been an error recording month of death
- 6) Correctly recorded but just 1 day difference between data sources for date of death
- 7) Appears to be correctly matched by id but there has been an error recording death due to 1 digit difference (10 days difference)

## Breeds

There were 168 BCMS breed codes (including crossbreds) in the abattoir/BCMS matched data (listed in Appendix Table C1). The five most numerous breed codes were Limousin cross (453,004), Aberdeen Angus cross (432,760), Charolais cross (274,452), Holstein Friesian (226354), and Hereford cross (180,584). There were slight differences between the matched data and Table 2, for instance Limousin was the 5<sup>th</sup> numerous breed code in Table 2 whereas it was the 10<sup>th</sup> numerous in the matched dataset. It appears that many animals that were described as Limousin in abattoir data were described as Limousin cross in BCMS. This was also observed in the Charolais breed.

Breed codes in BCMS were grouped into breed types, for example, limousin and limousin cross were categorised together and named LIMOUSIN, whereas black and white dairy breeds were categorised together and named HOLSFRIE. The top 25 breed codes (when matched to BCMS) are listed in Table 10. Seven breed types contained over 100,000 animals in the slaughter population, and these were Limousin, Aberdeen Angus, Holstein Friesian, Charolais, Hereford, Simmental and Belgian Blue. In Table 10 it can be seen that 15% of beef carcasses with breed type recorded were HOLSFRIE, which is not accounting for crossbred animals where the dairy component is not obvious in the breed type name. For instance, animal breed names generally take the sire breed name. It can be seen that a large proportion of animals from each breed type are cross-bred animals. The Limousin

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breed type is the most common of the carcass population, but about 90% are cross-bred animals. Further investigation showed that some animals which have not been recorded as a cross-bred in BCMS have a dam of a different breed to the animal breed type. Table 11 shows that at least 40% of animals that have been recorded as a 'LIMOUSIN' have a dam of a different breed, therefore indicating it is actually a cross-bred. Of those animals that were recorded as a 'LIMOUSIN CROSS' in BCMS the most common dam breed was Holstein Friesian breed type, followed by Limousin and other beef breeds. This was also observed in the Aberdeen Angus and it is also expected to be the case in other breeds. This emphasises that caution is required when analysing the data and that breed codes of sires and dams need to be checked to find whether they tie in with animal breed codes. Other data sources that are able to be matched with BCMS data (i.e. BASCO, milk recording organisations) would provide a further aid to determine animal breed.

**Table 10 Top 25 most common BCMS breed types of animals with abattoir records**

	Breed type	Number of animals	% of carcass population	of	Number of pure-bred animals†	Number of cross-bred animals†	% of breed type pure-bred	% of breed type cross-bred
1	LIMOUSIN	500047	21.083		53631	446416	10.73	89.27
2	ABERANGU	499458	21.058		77924	421534	15.60	84.40
3	HOLSFRIE	347051	14.633		319106	60623	91.95	17.47
4	CHAROLAIS	295021	12.439		22200	272821	7.52	92.48
5	HEREFORD	198362	8.363		24719	173643	12.46	87.54
6	SIMMENTAL	187147	7.891		21415	165732	11.44	88.56
7	BELGBLUE	159271	6.715		13020	146251	8.17	91.83
8	BLONDAQ	59581	2.512		5269	51971	8.84	87.23
9	SHORTHORN	17115	0.722		11860	5255	69.30	30.70
10	SOUTDEVO	15457	0.652		6143	9314	39.74	60.26
11	SALER	13335	0.562		2195	11140	16.46	83.54
12	WELSBLAC	12202	0.514		8809	3393	72.19	27.81
13	MONTBELIAR	7724	0.326		1322	6402	17.12	82.88
14	AYRSHIRE	7570	0.319		6795	775	89.76	10.24
15	STABILISER	7482	0.315		1483	5999	19.82	80.18
16	MRI	5377	0.227		2254	3123	41.92	58.08
17	LUING	3971	0.167		3118	853	78.52	21.48
18	SUSSEX	3517	0.148		1165	2352	33.12	66.88
19	DEVON	3419	0.144		1076	2343	31.47	68.53
20	BROWSWIS	3268	0.138		901	2367	27.57	72.43
21	GALLOWAY	3222	0.136		2229	993	69.18	30.82
22	HIGHLAND	2918	0.123		2566	352	87.94	12.06
23	JERSEY	2822	0.119		1359	1463	48.16	51.84
24	SWRE&WH	2421	0.102		379	2042	15.65	84.35
25	LINCRED	1638	0.069		686	952	41.88	58.12

† Assumed as purebred if no 'X' in breed code and crossbred if 'X' in code

**Table 11 Dam breed of animals recorded as either pure or cross-bred Limousin or Aberdeen Angus animals**

LIMOUSIN		LIMOUSIN CROSS		ABERDEEN ANGUS		ABERDEEN ANGUS CROSS	
Dam breed type	%	Dam breed type	%	Dam breed type	%	Dam breed type	%
LIMOUSIN	56.42	HOLSFRIE	31.10	ABERANGU	62.18	HOLSFRIE	44.66
HOLSFRIE	26.80	LIMOUSIN	30.76	HOLSFRIE	24.43	ABERANGU	18.38
BELGBLUE	3.24	SIMMENTAL	7.42	LIMOUSIN	3.19	LIMOUSIN	8.39
ABERANGU	2.65	BELGBLUE	7.24	HEREFORD	1.66	SIMMENTAL	7.43
SIMMENTAL	2.61	ABERANGU	6.92	SIMMENTAL	1.54	HEREFORD	4.11
HEREFORD	2.05	HEREFORD	4.61	BELGBLUE	1.27	BELGBLUE	3.49
CHAROLAIS	1.90	CHAROLAIS	3.44	CHAROLAIS	0.95	CHAROLAIS	2.74
BLONDAQ	0.93	BLONDAQ	1.58	SOUTDEVO	0.46	SHORTHORN	1.38
Null/other	3.41	Null/other	6.92	Null/other	4.33	Null/other	9.42

† Assumed as purebred if no 'X' in breed code and crossbred if 'X' in code

### Recording of parentage

Recording of dam is compulsory in BCMS therefore this is near to complete. However, some dam identities will not be accompanied by an animal record for earlier records. There is an entry for sire available when registering animals onto BCMS but this is not compulsory.

**Table 12 Recording of sire in BCMS**

Year of death	Total	Number with sire recorded	% with sire recorded
2001	26778	3051	11.39
2002	33607	6541	19.46
2003	41359	9734	23.54
2004	51926	13385	25.78
2005	61766	17727	28.70
2006	211759	49845	23.54
2007	327466	68365	20.88
2008	345907	76162	22.02
2009	342404	78122	22.82
2010	411389	93570	22.74
2011	441606	102677	23.25
2012	139908	30132	21.54

In BCMS data, overall 22.6% of animals had sire information recorded. The proportion of animals slaughtered with a sire identity increased up until 2005 to 28.7% but decreased in 2006 to 23.5% and remained at around 22% in following years (Table 12). It should be noted that the data included animals that were born prior to BCMS and these animals would be less likely to have sire recorded. It can be seen from Table 13 that sire was most recorded in the stabiliser breed, a relatively newly developed composite breed for use in the UK. In animals with dairy genotypes sire was least recorded. Editing on sire identity and sire breed would reduce the dataset considerably for the Holstein Friesian breed type (i.e. from 347051 to 19397). Of those animals that were described as Holstein Friesian breed type which had both dam and sire identity recorded 99.1% and 98.8% had dams and sires recorded as a dairy breed type, respectively.

**Table 13 The 25 most common BCMS breed codes ordered by percentage with sire records**

Breed type	count	% with sire record	Breed type	count	% with sire record
STABILISER	7482	59.60	BLONDAQ	59581	26.33
LUING	3971	57.34	SIMMENTAL	187147	25.41
HIGHLANDS	2918	57.23	CHAROLAIS	295021	21.93
SOUTDEVO	15457	53.92	LIMOUSIN	500047	20.01
LINCRED	1638	50.61	MRI	5377	14.28
GALLOWAY	3222	48.29	AYRSHIRE	7570	11.03
WELSBLAC	12202	44.39	MONTBELIAR	7724	7.52
SUSSEX	3517	41.97	BELGBLUE	159271	7.41
DEVON	3419	39.66	HOLSFRIE	347051	5.59
SALER	13335	38.10	BROWSWIS	3268	4.31
ABERANGU	499458	36.75	JERSEY	2822	4.29
SHORTHORN	17115	32.32	SWRE&WH	2421	1.03
HEREFORD	198362	30.02			

*Sire breed*

The most common sire breeds of the slaughter population are listed in Table 14. Beef sires dominate and these were Aberdeen Angus, Limousin, Charolais, Hereford and Simmental, which accounted for 83.5% of recorded sires.

**Table 14 Distribution of records by sire breed**

	Breed code	Count (no. sires)	%		Breed code	Count (no. sires)	%
1	ABERANGU	183037 (9511)	33.60	14	LUING	2324 (284)	0.43
2	LIMOUSIN	100433 (12117)	18.44	15	HIGHLAND	1616 (411)	0.30
3	CHAROLAIS	64394 (6257)	11.82	16	GALLOWAY	1528 (366)	0.28
4	HEREFORD	59402 (3896)	10.90	17	SUSSEX	1436 (241)	0.26
5	SIMMENTAL	47484 (5033)	8.72	18	DEVON	1263 (291)	0.23
6	HOLSFRIE	19555 (3530)	3.59	19	AYRSHIRE	817 (156)	0.15
7	BLONDAQ	14945 (1863)	2.74	20	LINCRED	809 (133)	0.15
8	BELGBLUE	11668 (1567)	2.14	21	MRI	782 (110)	0.14
9	SOUTDEVO	8443 (1108)	1.55	22	MONTBELIAR	581 (79)	0.11
10	SHORTHORN	5694 (1007)	1.05	23	LONGHORN	556 (170)	0.10
11	WELSBLAC	5390 (728)	0.99	24	GELBVIEWH	458 (59)	0.08
12	SALER	5123 (546)	0.94	25	RED_POLL	431 (67)	0.08
13	STABILISER	4461 (361)	0.82				

**Number of progeny per sire**

There were 50,682 sires recorded and the number of offspring recorded per sire ranged from 1 to 876. The mean number of progeny per sire was 10.8 (SD 20.8). Some sires have low progeny counts, some of which could possibly be due to misidentification or just not inputted into BCMS. It is possible that the same sire may have more than one sire ID in BCMS. When spaces were removed from the sire ID the number of sires reduced from 50,863 to 50,682, however this made virtually no difference to the mean number of progeny. Approximately 26% of sires had more than 10 progeny.

For genetic analysis edits will need to be made to omit animals of sires with few offspring in the dataset. It can be seen that in all sire breed types shown in Table 15 there were many sires with just one animal in the dataset and these would not be very informative for genetic analysis, and would also complicate analyses. In more common breeds such as Aberdeen Angus and Limousin the cut-off could be set higher i.e. at least 15 or 20 animals per sire, whereas in other breeds such as Hereford or Simmental at least 10 animals per sire might be more suitable, but the accuracy of EBV would be lower. In some breeds with fewer animals and low counts per sire, genetic analysis would be less feasible. Figure 3



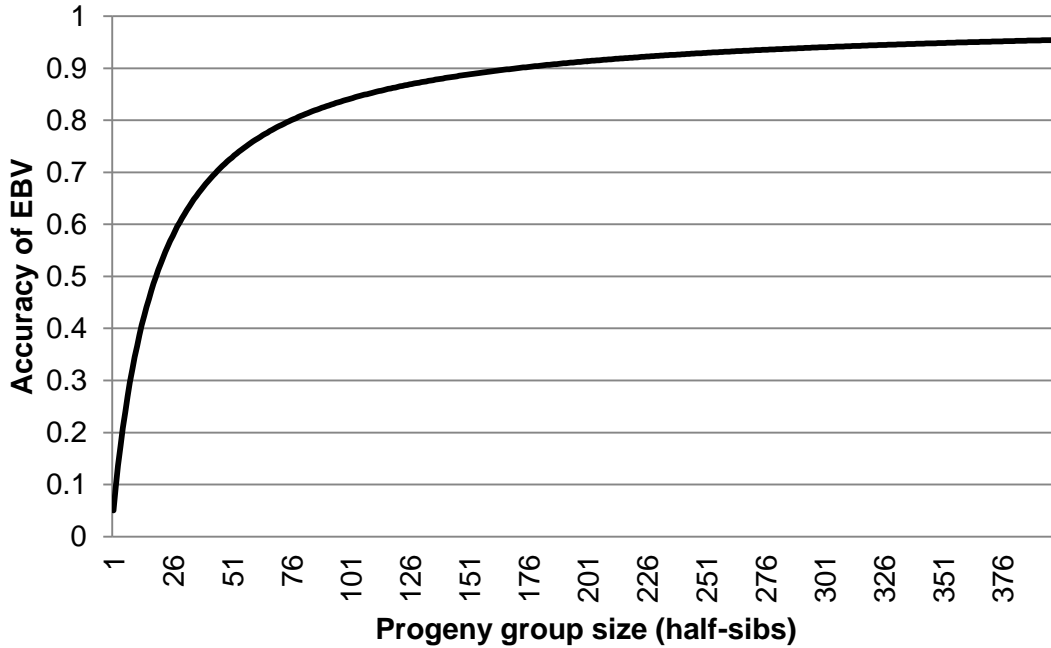
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shows how the accuracy of an EBV increases with increasing progeny size. The calculation for the graph takes the assumption that the trait in question had a heritability of 0.20 and that daughters were distributed across an equal number of contemporary groups. With a heritability of this magnitude 15 to 20 progeny would result in an accuracy from 0.44 to 0.51. However, if the heritability of a trait was lower, and comparison with offspring of other sires was limited, then more progeny would be required to achieve the same accuracy.

**Table 15 Number of offspring per sire by most populous sire breeds**

Number of offspring	Frequency						
	Overall	Aberdeen Angus	Limousin	Charolais	Hereford	Simmental	Holstein Friesian
1	12787	1547	3195	1470	728	1203	1537
2-5	16875	2432	4365	2072	1146	1792	1228
6-10	7851	1484	2001	1040	589	836	308
11-20	6280	1503	1411	846	580	621	231
21-30	2671	795	514	363	290	259	98
31-40	1447	494	255	179	192	123	47
41-50	849	316	135	96	113	60	33
51-60	539	231	61	59	73	41	25
61-70	371	171	54	27	52	24	7
71-80	287	125	39	24	38	27	8
81-90	167	80	17	22	24	10	2
91-100	126	55	20	20	11	6	2
101-150	321	176	37	25	43	22	4
151-200	104	67	8	9	10	4	0
201-250	36	18	3	5	3	4	0
251-300	10	5	2	0	1	1	0
>300	15	12	0	0	3	0	0
>=5	23648	5941	5242	3062	2218	2328	914
>=10	14323	4279	2813	1830	1533	1326	489
>=15	9843	3294	1762	1239	1151	869	331
>=20	7287	2650	1218	880	897	609	241

Prior to appropriate editing for genetic evaluations purposes all the above breeds (Table 15) with the exception of Holstein Friesian have over 20% of bulls with 10 or more progeny, with Aberdeen Angus at 45%, Limousin at 23% and Charolais at 29%. Given the likely added information coming from other related animals in the dataset (including the animal itself for older bulls) we could expect that a progeny group of 10 or more would yield a proof of accuracy of 34% or higher. This may be a reasonable cut-off for publication of such proofs and would equate to almost 14,000 bulls (across the above breeds) receiving proofs based on the date in this study. This is likely to be sufficient to meaningfully move forward with the majority/ all of these breeds. However, the less numerous breeds may require more careful considerations (e.g., breed specific editing, models, genetic grouping structure) before moving forward.



**Figure 3** The effect of progeny group size on the accuracy of EBV for a trait with 0.2 heritability and distribution over an equal number of contemporary groups

*Sires across herds*

Beef herds differ to dairy herds as more natural mating takes place when using beef sires rather than AI. Some farms will keep the same bull on the farm for many years and it may stay on the same farm and not used on any other herds in its lifetime. Also the number of bulls used in any one herd might be relatively few. This type of scenario would mean that there could be a confounding effect of sire and herd when fitted in a model (i.e. there is difficulty in disentangling the effects of both factors).

**Table 16** Summary of herds with more than one sire

	Birth herd	Finishing herd
Herds with > 1 sire	11913 (out of 22493)	9943 (out of 16892)
Herd-years with >1 sire	18815 (out of 71729)	20155 (out of 44930)
Herd-year-season with > 1 sire	23519 (out of 125529)	29338 (out of 75454)
Number of sires > 1 herd	5499	26090
Number of sires > 1 herd-year	25666	29941
Number of sires > 1 herd-year-season	30295	31201

After preliminary edits of the data (i.e. including movement data - see section Movement data) there were 22,943 birth herds, 16,892 finishing herds and 47,814 sires across all breeds. In Table 16 the following counts were obtained on herds and sires. Editing so that a sire is present in more than one herd and so that there would be a minimum of two sires per herd-year-season for genetic parameter estimation would be expected to reduce datasets for individual breeds considerably.

*Dam breed*

By joining records back to the BCMS database, information on the dam was retrieved and the dam identity obtained for some records. From the dam's own animal record, the dam's breed description was retrieved. The number of animals by dam breed is given in Table 17. It can be seen that dairy cows are a major component of producing offspring for beef production. The most common breed type was Holstein Friesian (black and white dairy cattle) accounting for 45.73% of offspring. Other dairy breed types listed in the top 25 were Ayrshire, Jersey, Brown Swiss, and Guernsey and together these breed types account for

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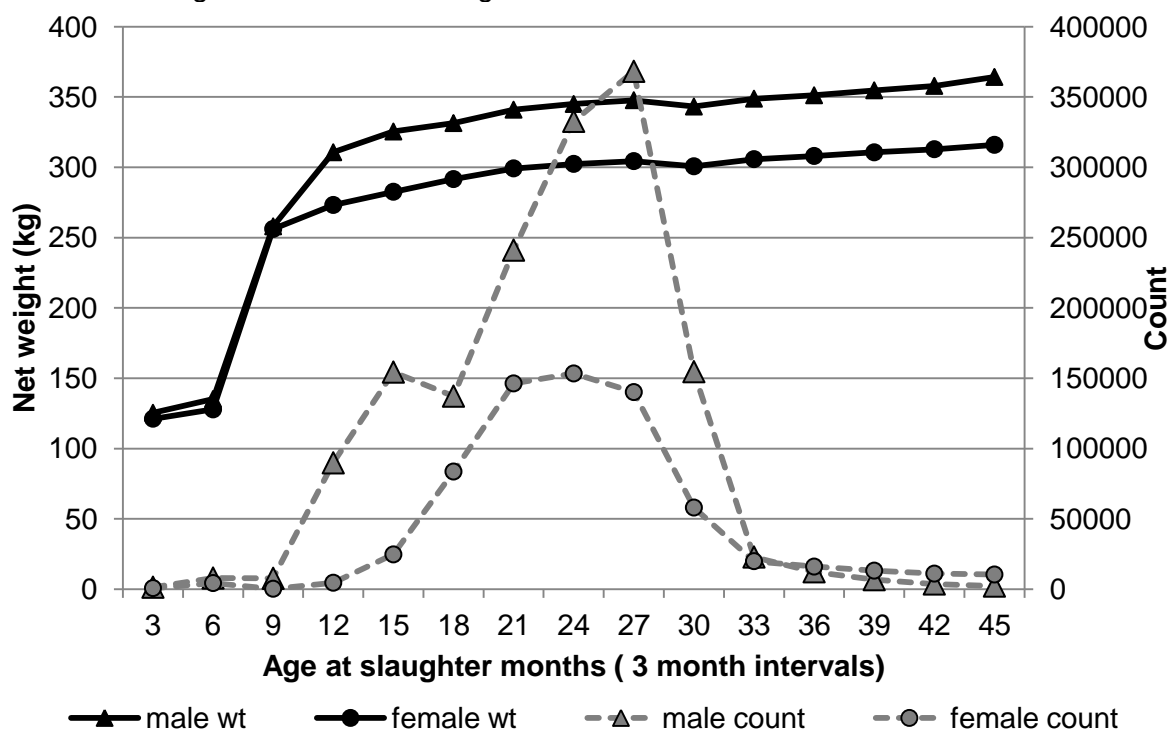
a further 1.76%. Meuse Rhine Issel (MRI), a dual purpose breed, accounts for 0.52% of dam breed types. The main beef breed types of dams were Limousin (14.48%), Aberdeen Angus (9.56%), Simmental (7.43%), Hereford (4.97%), Belgian Blue (3.84%), and Charolais (3.61%).

**Table 17 Distribution of records ordered by dam breed type for 25 most common breed types**

Dam Breed code	Count	%	Dam Breed code	Count	%
1 HOLSFRIE	1078469	45.73	14 MRI	12349	0.52
2 LIMOUSIN	341457	14.48	15 JERSEY	11312	0.48
3 ABERANGU	225330	9.56	16 GALLOWAY	9883	0.42
4 SIMMENTAL	175326	7.43	17 BROWSWIS	6357	0.27
5 HEREFORD	117247	4.97	18 LUING	6181	0.26
6 BELGBLUE	90459	3.84	19 MONTBELIAR	5653	0.24
7 CHAROLAIS	85118	3.61	20 HIGHLAND	5278	0.22
8 BLONDAQ	31778	1.35	21 DEVON	4074	0.17
9 SHORTHORN	29526	1.25	22 SUSSEX	3945	0.17
10 SALER	26363	1.12	23 BLUEGREY	3875	0.16
11 WELSBLAC	20928	0.89	24 STABILISER	3561	0.15
12 AYRSHIRE	20481	0.87	25 GUERNSEY	3263	0.14
13 SOUTDEVO	20064	0.85			

### Age at slaughter

Sex was taken from the BCMS record rather than abattoir record, which identified animals as either M or F. Figure 4 shows that (not surprisingly) a larger proportion of males than females go to slaughter under 48 months of age as more females are kept for breeding purposes. Also, the average net weight of male carcasses is higher than female carcasses slaughtered at the same age.



**Figure 4 Age at slaughter (in months) and average net weight (kg) of male and female carcasses, between 3 and 48 months of age**

It can be seen that there were records on mature animals which could be assumed to have been used for breeding (Table 18). From abattoir records some cows can be identified as they are recorded as 'C' in the column for sex, however this was not the case for all cows.

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In Table 20 there were 139,545 female animals that were slaughtered from 48 months onwards, but 20,093 (14.4%) were recorded as 'C' in abattoir records. For the purposes of genetic analysis we may want to concentrate on animals reared primarily for beef and not used for breeding. It might then be suitable to decide upon a cut-off point e.g. 36 months. However, for dairy breeds this may not be appropriate and different criteria may apply. Consideration should also be given to fit appropriate growth curves, rather than fitting linear age related growth rates.

**Table 18 Animals slaughtered from 48 months onwards**

Age slaughtered (mths)	Males		Females	
	Count	Net weight (kg)	Count	Net weight (kg)
>=48 <54	1792	379.41	14737	314.54
>=54 <60	781	407.57	13133	318.55
>=60 <66	454	432.89	12630	320.72
>=66 <72	295	455.53	12277	321.42
>=72 <78	215	489.40	11889	321.53
>=78 <84	176	489.91	11059	321.54
>=84 <90	101	493.60	10664	320.82
>=90 <96	124	497.93	9763	321.76
>=96	318	513.65	43393	320.72

### Net carcass weight

Tables 19 and 20 shows the average net carcass weight, average days to slaughter, and average daily gain for the 20 most numerous breed types for females and males. It was clear that abattoir data contained records on mature animals (i.e. suckler cows, cull dairy cows) as well as animals reared purely for beef production. This is shown clearly by the average days of life of the breed code Holstein Friesian (black and white dairy breeds) of 1950 days for female animals, whereas the average age at slaughter for the breed code Charolais was 797 days. Using average net daily gains to compare mature animals may therefore not be appropriate.

For male animals, the majority of animals would be reared purely for beef production rather than used for breeding, so we find that average age at slaughter is much lower for males than female animals as there is less influence of mature animals within the male subset. The number of bulls kept for breeding purposes prior to slaughter would be expected to be a very small proportion of the total within the male subset. The average age at slaughter of males and females for breed code Holstein Friesian is 674 days and 1950 days respectively, which clearly shows the influence of mature breeding animals in the female subset. The average weight and age at slaughter for Charolais males was 377.08 kg and 728 days, whereas for Charolais females the average weight and age at slaughter was 318.43 kg and 797 days. Also, differences are expected between castrated and entire males but these were not always clearly recorded.

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**Table 19 Average net carcass weight (kg) and days at slaughter of females by BCMS breed code**

	Breed type	Avg Wt	Std Wt	Avg Days	Std Days	Avg net carcass weight daily gain	Count
1	LIMOUSIN	308.62	42.43	982	680.59	0.31	192639
2	ABERANGU	284.46	38.88	889	579.87	0.32	157231
3	CHAROLAIS	318.43	42.40	797	436.36	0.40	122840
4	HOLSFRIE	300.54	50.61	1950	864.02	0.15	102462
5	SIMMENTAL	308.03	44.60	1063	770.11	0.29	72958
6	BELGBLUE	317.32	51.74	978	661.13	0.32	60206
7	HEREFORD	279.88	38.69	899	539.18	0.31	49656
8	BLONDAQ	320.60	47.68	901	596.97	0.36	24475
9	SOUTDEVO	317.42	54.73	1177	836.71	0.27	5586
10	SHORTHORN	292.31	50.78	1547	990.86	0.19	5568
11	SALER	313.35	44.96	1404	1065.86	0.22	5114
12	WELSBLAC	288.25	46.19	1392	929.13	0.21	4110
13	AYRSHIRE	270.87	43.05	1946	802.37	0.14	2918
14	STABILISER	283.71	35.62	888	486.02	0.32	2902
15	JERSEY	214.28	50.77	1817	821.04	0.12	1882
16	MRI	299.22	46.77	2049	978.91	0.15	1510
17	MONTBELIAR	299.95	47.62	1531	779.07	0.20	1429
18	SUSSEX	281.56	40.85	1132	855.75	0.25	1338
19	LUING	301.26	52.30	1706	1010.60	0.18	1318
20	GALLOWAY	268.98	42.55	1745	1059.40	0.15	1188

**Table 20 Average net carcass weight and days at slaughter of males by BCMS breed code**

	Breed code	Avg Wt	Std Wt	Avg Days	Std Days	Avg net carcass weight daily gain	Count
1	ABERANGU	325.50	38.94	748	135.80	0.44	342227
2	LIMOUSIN	359.12	49.37	739	186.66	0.49	307408
3	HOLSFRIE	299.70	51.54	674	227.99	0.44	244589
4	CHAROLAIS	377.08	50.40	728	180.38	0.52	172181
5	HEREFORD	320.38	38.09	778	145.57	0.41	148706
6	SIMMENTAL	351.92	46.60	708	193.62	0.50	114189
7	BELGBLUE	362.04	52.65	724	196.29	0.50	99065
8	BLONDAQ	370.56	53.99	701	201.78	0.53	35106
9	SHORTHORN	313.11	49.74	722	216.02	0.43	11547
10	SOUTDEVO	349.44	49.50	734	198.95	0.48	9871
11	SALER	356.14	45.87	727	199.11	0.49	8221
12	WELSBLAC	319.62	43.15	841	209.16	0.38	8092
13	MONTBELIAR	328.45	47.80	727	196.33	0.45	6295
14	AYRSHIRE	278.17	41.17	699	243.09	0.40	4652
15	STABILISER	324.45	40.08	604	168.20	0.54	4580
16	MRI	317.77	46.81	805	199.95	0.39	3867
17	LUING	320.12	45.03	700	243.06	0.46	2653
18	BROWSWIS	308.32	59.02	698	233.69	0.44	2394
19	DEVON	305.78	49.85	788	182.67	0.39	2260
20	HIGHLAND	253.00	41.51	1000	303.11	0.25	2210

Figure 5 and 6 show that there is seasonal variation in average net carcass weight and average daily carcass weight gain in both males and females. It was observed that for some animals there were average daily gains for carcass weight higher than expected (>1kg/ day). It was thought reasonable to remove animals with average daily gain for carcass weight >0.75. Higher daily gains may be seen in young animals so perhaps data

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edits should include gains for a given age, which might also vary depending upon sex (Figure 7 and Table 21) or breed (Figure 8) of the animal. Note that initial birth weight, which is unknown from this data, would be included in calculated average daily gain. Therefore, average daily gain might appear larger than expected, particularly in younger animals in which initial birth weight would contribute a larger proportion of net carcass weight.

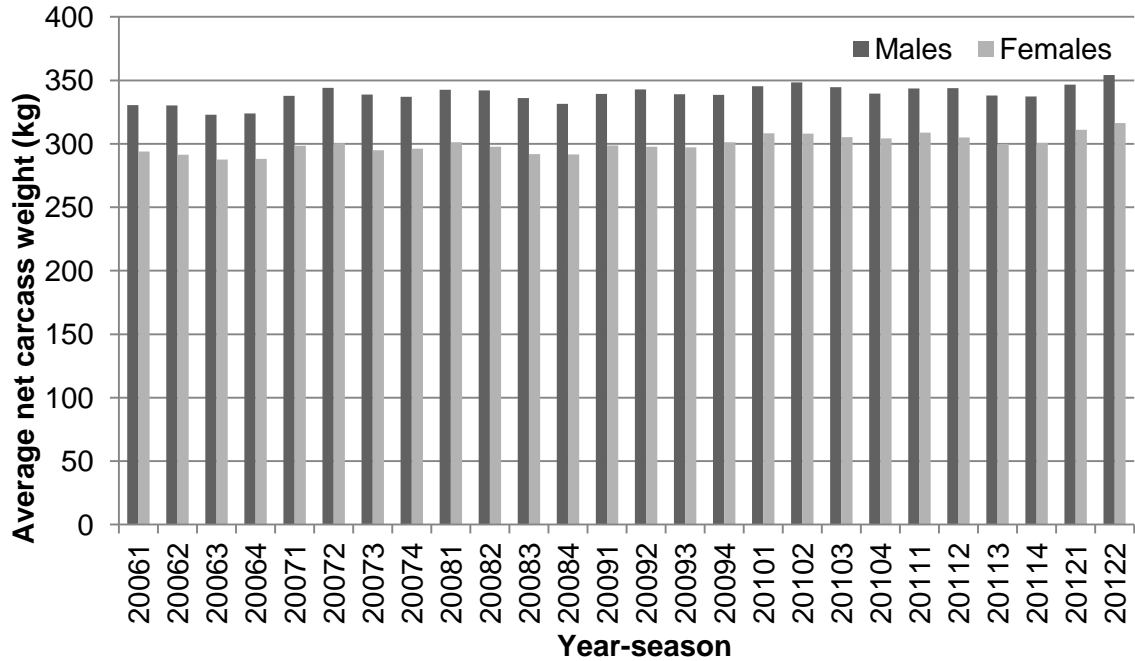


Figure 5 Average net weight of carcasses (slaughtered from 3 months to 36 months of age) from 2006 onwards grouped by Year-Season (Season: Jan, Feb, Mar = 1; Apr, May, Jun = 2; Jul, Aug, Sept = 3; Oct, Nov, Dec = 4)

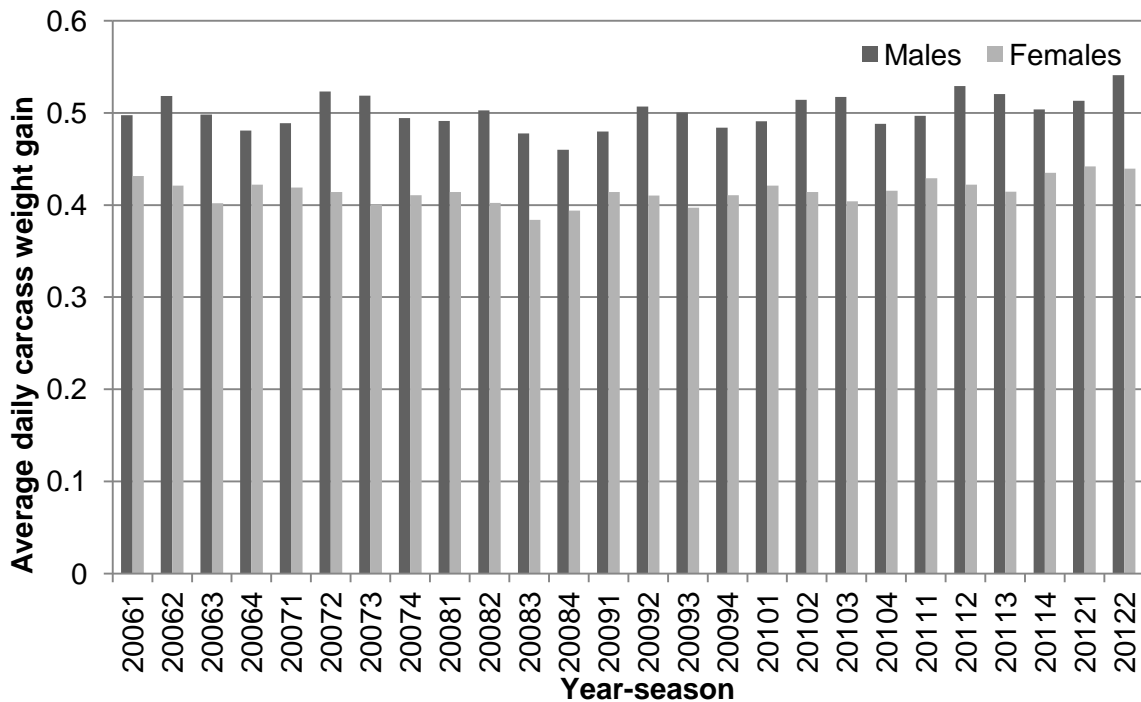


Figure 6 Average daily net gain of animals slaughtered from 3 months to 36 months of age grouped by Year-Season (Season: Jan, Feb, Mar = 1; Apr, May, Jun = 2; Jul, Aug, Sept = 3; Oct, Nov, Dec = 4)

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Figure 7 Average daily net carcass weight gain of females and males slaughtered at 4 to 36 months

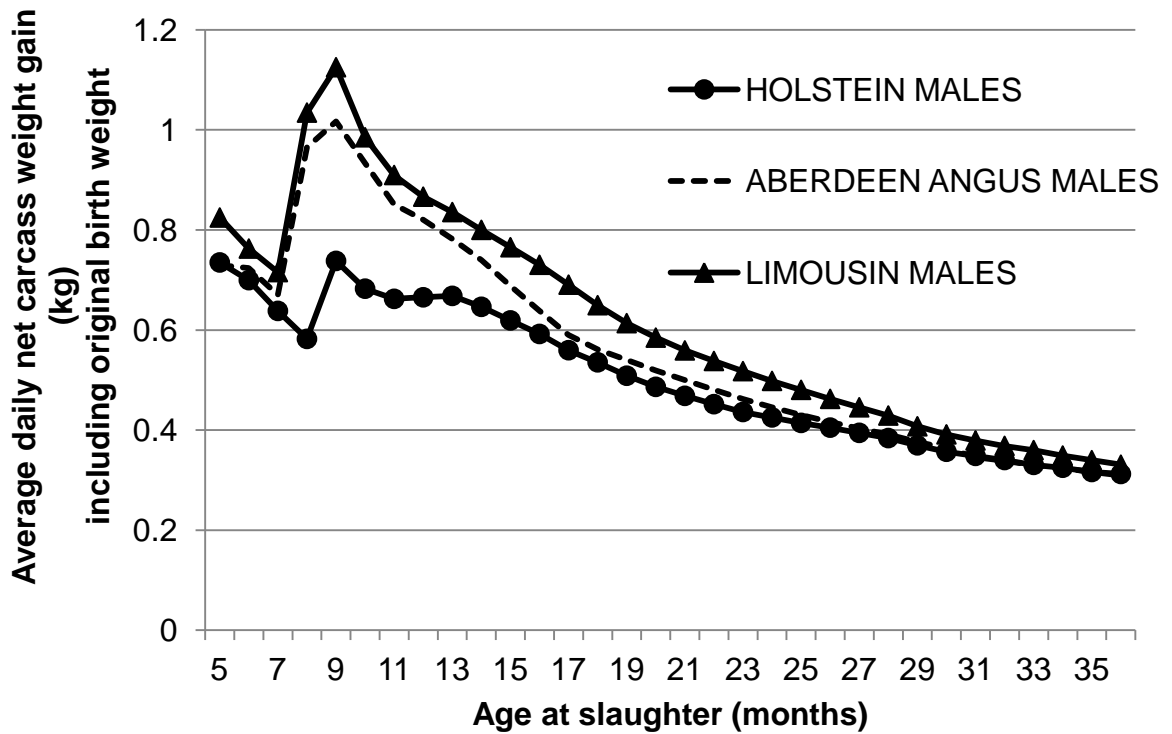


Figure 8 Average daily net carcass weight gain of males slaughtered at 5 to 36 months

**Table 21 Mean average daily net carcass weight gain grouped by age at slaughter and sex**

Age at slaughter	Females			Males		
	mean ADCWG	sd ADCWG	Count	mean ADCWG	sd ADCWG	Count
4 & 5 mths	0.51	0.12	1977	0.51	0.13	2036
6 & 7 mths	0.46	0.12	6946	0.48	0.13	8929
8 & 9 mths	0.70	0.27	492	0.59	0.28	968
10 & 11 mths	0.65	0.16	5816	0.65	0.17	7471
12 & 13 mths	0.67	0.13	29985	0.67	0.13	43771
14 & 15 mths	0.61	0.11	65778	0.63	0.12	110361
16 & 17 mths	0.53	0.10	58866	0.56	0.11	108357
18 & 19 mths	0.47	0.08	91548	0.49	0.09	111243
20 & 21 mths	0.43	0.07	144785	0.45	0.08	161801
22 & 23 mths	0.40	0.07	200195	0.42	0.07	229484
24 & 25 mths	0.38	0.06	215954	0.40	0.07	269528
26 & 27 mths	0.35	0.06	208320	0.37	0.06	273708
28 & 29 mths	0.33	0.06	235862	0.34	0.06	305028
30 & 31 mths	0.29	0.05	61702	0.33	0.06	151236
32 & 33 mths	0.28	0.06	23560	0.30	0.06	26689
34 & 35 mths	0.27	0.05	18985	0.28	0.06	19867

Table 22 summaries the carcass data across all breed types of over 1.9 million animals slaughtered from 3 to 36 months. The average net carcass weight of males and females were 335 and 298 kg respectively. Average conformation and fat converted to grades on the 15 point scale were -R and +3/-4 respectively. Overall, the mean number of days to slaughter and average net carcass weight daily gain were 743 days and 0.45 kg respectively.

**Table 22 Summary of means and standard deviations in parenthesis of net carcass weight (NCW), conformation (CONF), fat (FAT), days to slaughter (DTS), and average net carcass weight gain (NCWDG) for males and females slaughtered from 3 to 36 months of age**

Sex	NCW	CONF <sup>†</sup>	FAT <sup>†</sup>	DTS	NCWDG	Count
Males and Females	323.7 (51.14)	21 (5.7)	28 (5.5)	743 (146.9)	0.45 (0.10)	1,959,994
Males	335.3 (51.01)	21 (5.9)	27 (5.6)	741 (150.4)	0.46 (0.10)	1,355,229
Female	297.7 (40.82)	21 (5.0)	29 (5.1)	749 (138.6)	0.41 (0.09)	604,765

<sup>†</sup> Converted to numerical scale as shown in Appendix B

Breed types can be collapsed into three main categories, namely beef, dairy, or beef dairy cross. The breed code given in BCMS of an animal (which was assumed to be based upon the sire breed) and the breed code of the dam were used to create the categories above. Figure 9 illustrates the differences between net carcass weight for the above three categories at different ages. Figure 10 illustrates the differences between net carcass weight of males at different ages between the two most numerous beef breeds, Aberdeen Angus (a native UK breed) and Limousin (a continental breed), and dairy breeds together with their crosses. It can be seen that Limousin breed types tend to reach higher weights than Aberdeen Angus. Figure 11 shows that ages of slaughter differs between the different breed types.



Carcass Trait Evaluations

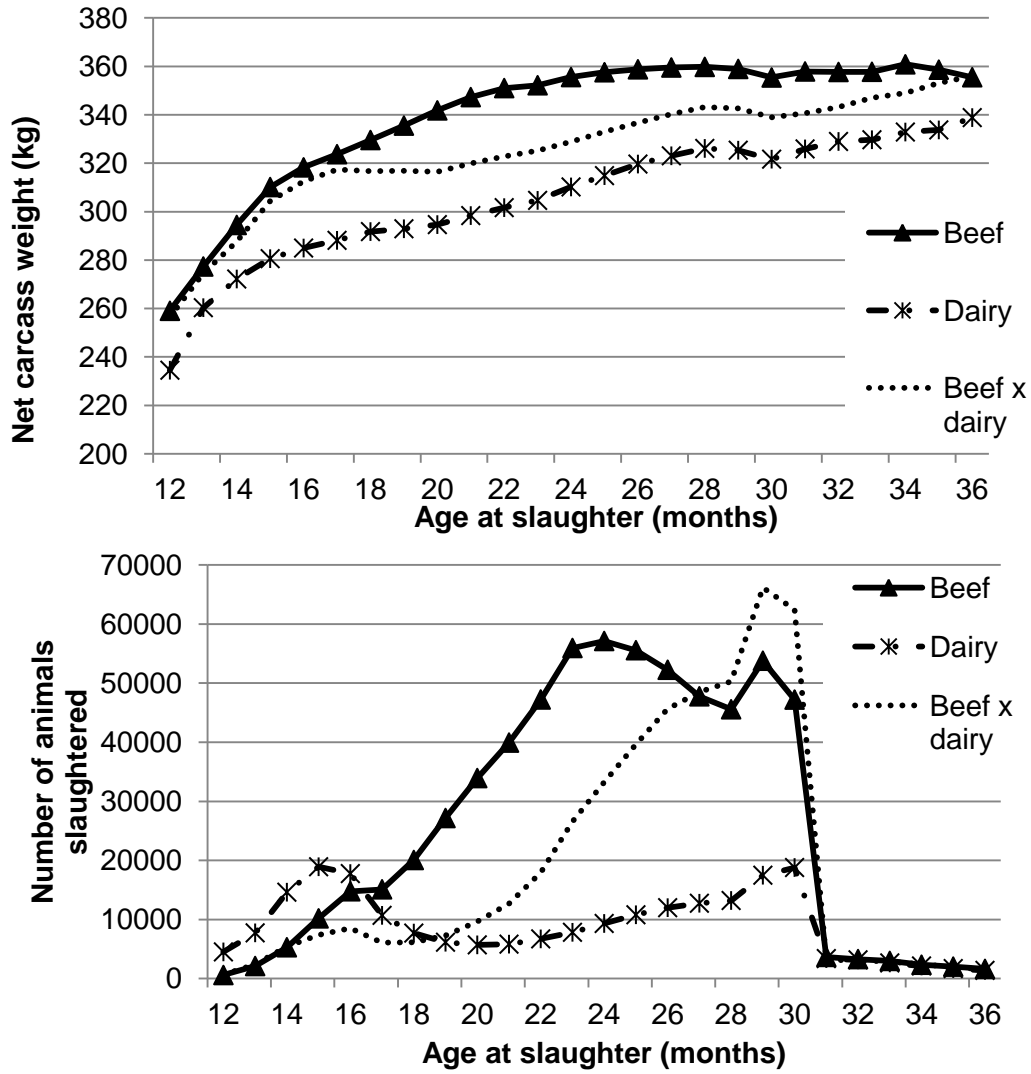


Figure 9 Average net carcass weight and number of animals slaughtered from 12 months of age for beef, dairy, and beef dairy cross breed types

Carcass Trait Evaluations

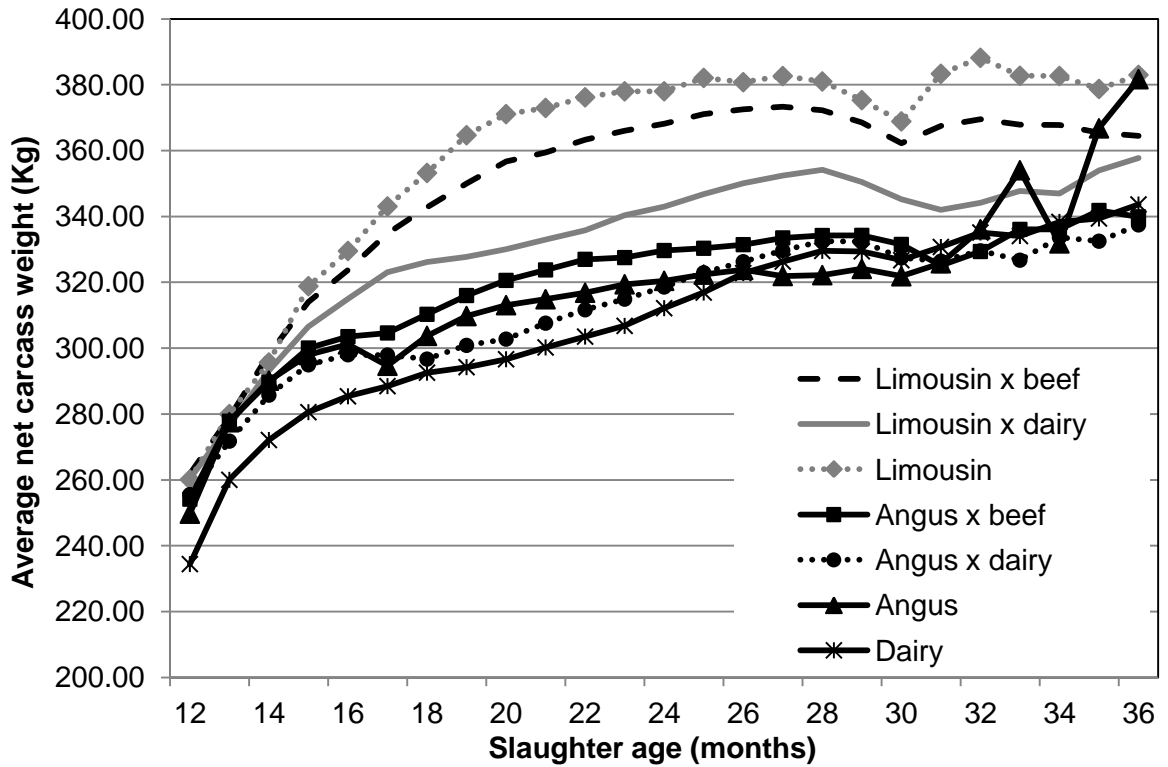


Figure 10 Average net carcass weight of male animals grouped by slaughter age for different breed types of cattle

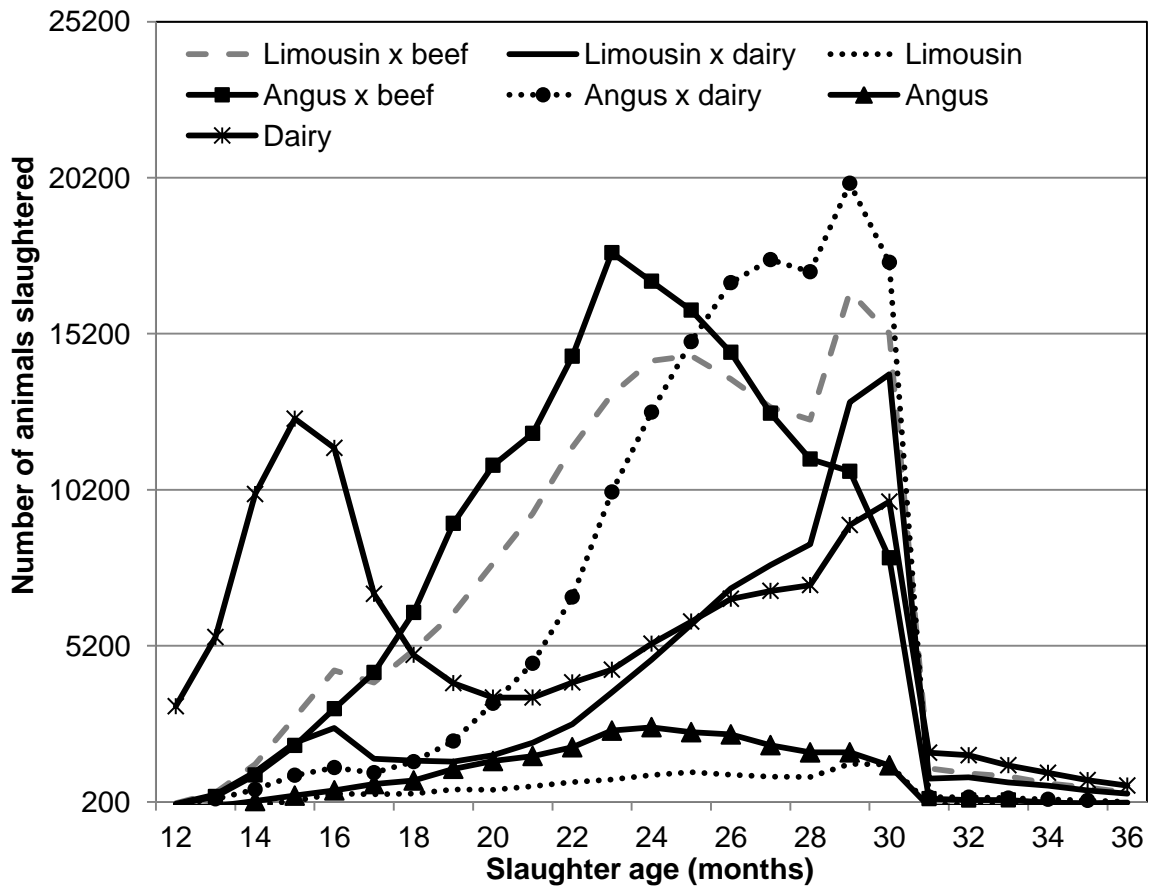


Figure 11 Number of male animals slaughtered from 12 months of age onwards for different breed types of cattle

**Table 23 Differences and averages for net carcass weight, days to slaughter, net carcass weight daily gain for progeny of Limousin sires**

Sire	Average NCW	Average DTS	Average NCWDG	Number of male progeny	Max – min NCW	Max – min DTS	Max – min NCWDG
1	456.22	762	0.60	36	129.5	331	0.22
2	426.31	748	0.57	29	127	274	0.26
3	423.22	876	0.48	70	204.3	319	0.27
4	417.45	842	0.50	29	142.9	128	0.14
5	414.48	759	0.55	52	161.4	236	0.24
6	404.51	801	0.51	26	107.1	317	0.18
7	404.21	685	0.59	47	145.4	357	0.31
8	403.99	781	0.52	25	85.9	338	0.27
9	400.40	786	0.52	27	133.4	315	0.25
10	399.96	789	0.51	25	147.6	232	0.21
11	399.61	829	0.49	39	135.3	340	0.22
12	398.22	708	0.56	37	143.4	269	0.24
13	397.94	765	0.52	50	111	156	0.20
14	396.93	818	0.49	43	110.2	285	0.18
15	394.95	786	0.50	32	113.7	233	0.14
16	392.56	786	0.50	47	138.8	195	0.17
17	390.28	782	0.50	40	202.4	215	0.27
18	389.58	648	0.60	32	107.4	101	0.19
19	389.23	724	0.54	30	121.4	354	0.27
20	387.69	821	0.47	30	141	246	0.17

NCW = net carcass weight (kg), DTS = days to slaughter, NCWDG = average net weight daily gain

There were differences between sires within the same breed for average net carcass weight, days to slaughter, and daily carcass gain of their progeny, and also a range exists between progeny of a single sire. In Table 23 the top 20 sires with highest net carcass weight are given for Limousin sires with at least 25 male progeny. The highest average carcass weight of a sire's male progeny was 456 kg. However, there was about 130 kg difference between the lightest and heaviest of it's progeny. Net carcass weight might not be the ideal trait if we want to compare the efficiency of sires as the average days to slaughter of an animal can differ greatly, thus the average net carcass weight daily gain would be more suitable.

### Conformation

For male carcasses it was observed that highest conformation tended to be in continental breeds (Belgian Blue, Blonde d'Aquitaine, Limousin, Charolais, and Simmental) (Table 24). Native British beef breeds tended to have lower conformation than continental breeds, and the lowest conformation were in dairy breeds. In Table 25 conformation classes were more simply categorised as E, U, R, O, and P where E commands highest value and P commands lowest value. Of the carcass population it can be seen that only a very small proportion of animals were scored as 'E.' Of the top 25 most numerous breed types Limousin, Charolais, Belgian Blue and Blonde d'Aquitaine had relatively more animals in the top two conformation classes 'E' and 'U.' Whereas, dairy breed types (Ayrshire, Holstein Friesian, Brown Swiss, Swedish Red and White) tended to be categorised in poorer conformation classes 'O' and 'P.'

## Carcass Trait Evaluations

**Table 24 Average conformation grade<sup>†</sup> of male carcasses grouped by sire breed (ordered by average conformation)**

Sire breed type	Average conformation	St dev conformation	Count (rank)
BELGBLUE	29.16	6.12	7288 (8)
BLONDAQ	27.32	5.73	8921 (7)
LIMOUSIN	27.07	5.30	62956 (2)
CHAROLAIS	26.42	4.58	37355 (4)
SIMMENTAL	24.95	4.44	30129 (5)
STABILISER	24.35	3.91	2747 (13)
SALER	24.12	3.64	3339 (12)
SOUTDEVO	23.78	4.53	5623 (9)
SUSSEX	23.41	4.17	916 (17)
LINCRED	22.39	3.89	608 (19)
LUING	21.97	4.08	1659 (14)
WELSBLAC	21.95	3.75	3752 (11)
SHORTHORN	21.29	4.27	3771 (10)
ABERANGU	21.16	3.80	123285 (1)
DEVON	20.84	4.18	880 (18)
GALLOWAY	20.80	3.56	995 (16)
RED_POLL	20.72	3.43	312 (24)
LONGHORN	19.81	3.90	363 (23)
MONTBELIAR	19.18	4.07	434 (22)
HEREFORD	18.99	3.44	44235 (3)
BRITWHIT	18.61	3.49	256 (25)
MRI	18.35	3.91	541 (20)
HIGHLAND	17.54	3.43	1294 (15)
HOLSFRIE	14.10	3.54	12534 (6)
AYRSHIRE	13.26	2.89	485 (21)

<sup>†</sup> Conformation converted to numerical scale

There were no sires of Holstein Friesian breed that had offspring with carcasses of conformation 'E' or 'U.' Table 26 shows the distribution of conformation scores of offspring from a subset of Holstein Friesian bulls. Few bulls had offspring with carcasses that were classified as 'R,' but one bull had 40% of its offspring in this category. Generally, it would be expected for a Holstein Friesian bull to be mated to a dairy cow and not a cow of a beef breed.

Carcass Trait Evaluations

**Table 25 Percentages of conformation class grouped by animal breed type**

Animal breed type	Count	% E	% U	% R	% O	% P
LIMOUSIN	500045	1.20	27.81	52.60	18.25	0.14
ABERANGU	499452	0.01	2.26	40.00	57.49	0.24
HOLSFRIE	347034	0.00	0.06	1.30	79.80	18.84
CHAROLAIS	295020	0.59	28.93	57.17	13.27	0.05
HEREFORD	198360	0.00	0.52	23.31	75.83	0.33
SIMMENTAL	187147	0.09	15.28	54.70	29.66	0.26
BELGBLUE	159270	2.45	25.43	52.95	18.98	0.19
BLONDAQ	59580	2.16	28.90	49.67	19.14	0.14
SHORTHORN	17115	0.04	4.05	37.19	56.31	2.42
SOUTDEVO	15457	0.21	14.00	54.74	30.78	0.28
SALER	13335	0.05	11.21	59.36	28.92	0.46
WELSBLAC	12202	0.03	4.45	48.61	46.08	0.82
MONTBELIAR	7724	0.00	0.80	23.95	72.90	2.34
AYRSHIRE	7569	0.00	0.04	0.82	82.72	16.42
STABILISER	7482	0.05	11.19	54.02	34.63	0.11
MRI	5377	0.00	0.60	19.75	75.82	3.83
LUING	3971	0.03	4.51	51.73	42.73	1.01
SUSSEX	3517	0.00	9.81	48.51	41.54	0.14
DEVON	3419	0.06	4.50	37.44	57.62	0.38
BROWSWIS	3268	0.00	0.18	6.70	85.31	7.80
GALLOWAY	3222	0.00	1.55	42.43	55.40	0.62
HIGHLAND	2918	0.00	0.24	17.99	80.43	1.34
JERSEY	2821	0.00	0.11	1.52	55.05	43.32
SWRE&WH	2421	0.00	0.21	3.92	85.21	10.66
LINCRED	1638	0.06	5.07	56.78	38.03	0.06

**Table 26 Distribution of conformation scores of offspring from a sample of Holstein Friesian bulls (with records on at least 50 offspring)**

Sire (recoded)	Sire breed	Total	% R	% O	% P
1	HOLSFRIE	60	40.00	60.00	0.00
2	HOLSFRIE	61	14.75	85.25	0.00
3	HOLSFRIE	55	9.09	90.91	0.00
4	HOLSFRIE	61	8.20	88.52	3.28
5	HOLSFRIE	81	4.94	95.06	0.00
6	HOLSFRIE	94	4.26	95.74	0.00
7	HOLSFRIE	109	3.67	96.33	0.00
8	HOLSFRIE	110	3.64	96.36	0.00
9	HOLSFRIE	67	1.49	50.75	47.76
10	HOLSFRIE	71	1.41	97.18	1.41
11	HOLSFRIE	51	0.00	100.00	0.00
12	HOLSFRIE	57	0.00	96.49	3.51
13	HOLSFRIE	54	0.00	96.30	3.70
14	HOLSFRIE	59	0.00	94.92	5.08
15	HOLSFRIE	57	0.00	71.93	28.07
16	HOLSFRIE	55	0.00	70.91	29.09
17	HOLSFRIE	77	0.00	63.64	36.36
18	HOLSFRIE	53	0.00	49.06	50.94
19	HOLSFRIE	91	0.00	41.76	58.24

## Carcass Trait Evaluations

### Fatness

Native British breeds tend to have higher fat grades (e.g. Aberdeen Angus and Hereford sired offspring) as shown in Tables 27 and 28. For the top five most numerous beef breed types the percentage of animals that were graded as 3 or 4L ranged from 76.8 to 81.97 and in Holstein Friesian it was 70.7%.

**Table 27 Average fat grade<sup>†</sup> of male carcasses grouped by sire breed (ordered by average fat grade)**

Count rank	Sire breed type	Average fat grade	St dev fat grade	Count
1	ABERANGU	30.84	3.78	123108
3	HEREFORD	30.83	3.99	44170
19	LINCRED	30.82	4.31	608
10	SHORTHORN	30.09	4.72	3768
14	LUING	29.90	4.84	1658
24	RED_POLL	29.53	4.53	311
16	GALLOWAY	29.09	5.15	994
18	DEVON	28.72	5.16	877
13	STABILISER	28.58	4.72	2747
17	SUSSEX	28.46	5.74	916
15	HIGHLAND	28.43	5.04	1294
5	SIMMENTAL	27.97	5.10	30102
12	SALER	27.88	4.90	3339
4	CHAROLAIS	27.49	5.29	37327
25	BRITWHIT	27.48	4.51	256
23	LONGHORN	27.23	5.63	363
2	LIMOUSIN	26.94	5.64	62921
20	MRI	26.72	4.65	541
22	MONTBELIAR	26.45	5.01	434
11	WELSBLAC	26.29	5.66	3751
9	SOUTDEVO	26.21	5.96	5613
6	HOLSFRIE	25.63	5.42	12534
8	BELGBLUE	24.56	6.46	7286
7	BLONDAQ	24.04	6.40	8919
21	AYRSHIRE	23.60	5.35	485

<sup>†</sup> Fat class converted to numerical scale

## Carcass Trait Evaluations

**Table 28 Percentages of fat grades grouped by animal breed type**

Animal breed type	Count	% 1	% 2	% 3	% 4L	% 4H	% 5L	% 5H	% 3+4L
1 LIMOUSIN	499643	0.56	7.27	32.18	47.39	11.41	1.07	0.11	79.58
2 ABERANGU	498598	0.10	0.93	12.88	64.56	18.31	2.90	0.32	77.43
3 HOLSFRIE	347028	5.50	18.70	41.31	29.35	4.73	0.36	0.05	70.66
4 CHAROLAIS	294778	0.39	5.04	28.95	53.03	11.88	0.66	0.06	81.97
5 HEREFORD	198035	0.08	1.14	13.37	63.42	18.10	3.47	0.42	76.79
6 SIMMENTAL	186960	0.57	5.42	30.18	49.86	12.95	0.91	0.11	80.05
7 BELGBLUE	159207	1.78	15.09	45.53	32.81	4.42	0.34	0.04	78.34
8 BLONDAQ	59519	1.54	14.79	40.61	36.73	5.74	0.51	0.07	77.35
9 SHORTHORN	17108	0.85	4.02	19.07	47.04	24.25	3.77	1.00	66.10
10 SOUTDEVO	15437	1.43	9.12	32.91	45.13	9.63	1.45	0.34	78.04
11 SALER	13325	0.68	6.56	31.74	48.10	11.83	0.92	0.17	79.84
12 WELSLAC	12194	1.06	10.20	36.38	43.32	7.78	0.93	0.33	79.70
13 MONTBELIAR	7724	1.97	13.57	43.90	35.44	4.69	0.36	0.08	79.34
14 AYRSHIRE	7569	4.40	21.64	47.21	22.50	3.96	0.28	0.01	69.71
15 STABILISER	7479	0.29	3.53	23.80	54.69	15.80	1.68	0.20	78.49
16 MRI	5376	1.90	12.05	44.36	36.38	4.72	0.50	0.07	80.75
17 LUING	3970	0.83	2.87	16.40	49.47	26.12	3.60	0.71	65.87
18 SUSSEX	3506	1.03	3.91	21.62	53.42	16.06	2.99	0.97	75.04
19 DEVON	3410	0.29	4.25	23.02	52.84	15.04	2.96	1.58	75.87
20 BROWSWIS	3268	3.64	17.99	40.51	31.55	5.60	0.67	0.03	72.06
21 GALLOWAY	3221	0.75	5.31	19.43	48.93	21.73	3.07	0.78	68.36
22 HIGHLAND	2918	0.45	5.28	25.60	50.14	16.14	1.92	0.48	75.74
23 JERSEY	2821	11.66	21.69	31.37	26.05	8.08	0.96	0.18	57.43
24 SWRE&WH	2421	2.81	13.88	43.78	35.03	4.01	0.41	0.08	78.81
25 LINCRED	1637	0.06	2.08	15.64	59.74	16.74	4.64	1.10	75.38

### Dairy beef

#### *Dairy crosses (animals slaughtered between 3 and 36 months)*

There were 99,909 animals with carcass data which were bred from a dairy dam and a beef sire. The most popular sire beef breed crosses were Aberdeen Angus (35,957), Hereford (32,119), Limousin (14,609), Simmental (9,109), and Charolais (3,610), and these five breeds accounted for 95% of the dairy cross animals.

**Table 29 Summary of carcass data of males (3 to 36 months at slaughter) grouped by sire breed**

	Average net carcass weight (kg)	Average age at slaughter (d)	Average net carcass weight daily gain (kg/d)	Average conformation score	Average fat class	Count
Aberdeen Angus	323.33	784.45	0.42	18.37	30.43	25440
Hereford	320.66	783.58	0.42	17.92	30.59	24914
Limousin	341.75	781.24	0.45	22.48	26.95	8734
Simmental	342.23	763.39	0.47	21.42	26.90	5440
Charolais	360.78	783.60	0.48	22.36	26.74	2021

Table 29 summarises male carcass averages of the most common beef sire crosses. British sire breeds, Aberdeen Angus and Hereford, were most common and accounted for 73% of male carcasses. On average heavier carcasses were obtained from crosses of continental sire breeds which also had higher average daily gain for net carcass weight. The average slaughter age was similar between sire breeds with the exception of the Simmental breed which was approximately 20 days earlier than the other four breeds. The average conformation of British sire breed crosses were +O, whereas the average

## Carcass Trait Evaluations

conformation of continental sire breeds were a grade higher (-R). Average fatness was higher in British sire breeds. However, average fat classes for both British (4L) and Continental (+3) sire breeds were within the most favourable (or valuable) fat classes.

**Table 30 Summary of carcass data of females (3 to 36 months at slaughter) grouped by sire breed**

	Average net carcass weight (kg)	Average age at slaughter (d)	Average net carcass weight daily gain (kg/d)	Average conformation score	Average fat class	Count
Aberdeen Angus	279.50	768.50	0.37	17.38	31.99	9656
Hereford	276.68	776.30	0.37	17.00	32.39	6320
Limousin	296.53	792.22	0.38	21.19	29.29	4664
Simmental	295.97	770.19	0.40	20.37	29.15	3083
Charolais	309.99	776.88	0.41	21.30	28.66	1434

Table 30 summarises female carcass averages of the most common beef sire crosses. Approximately 28% of dairy beef crossbred cattle slaughtered from 3 months to 36 months were female. As expected female carcasses were lighter than males and average conformation scores were lower (poorer) and average fat classes were higher. Similar to males, on average heavier carcasses were obtained from crosses of continental sire breeds, which also had slightly higher average daily gain for net carcass weight. Days to slaughter is lower in females than in males for British sire breeds and the Charolais sire breed, whereas days to slaughter was later in females with Limousin and Simmental sires. On average conformation was a grade higher (better) in females from continental sires, whereas on average females from British sires had a higher level of fatness.

### *Carcasses from dairy sire and dam*

**Table 31 Summary of carcass data (3 to 36 months at slaughter) from dairy sire and dam breeds**

	Average net carcass weight (kg)	Average age at slaughter (d)	Average net carcass weight daily gain (kg/d)	Average conformation score	Average fat class	Count
Female	277.57	901.54	0.31	13.11	26.18	993
Male	301.85	723.02	0.44	14.17	25.61	12969

Tables 30 and 31 show that the average net carcass weight of pure dairy females is similar to that of British sire breed crosses, yet the days to slaughter is approximately an extra 130 days in pure dairy females, thus resulting in lower daily gain. Average conformation score is lower compared to beef crosses, as well as fat level. The average net carcass weight of pure dairy males was lower than beef crosses, yet the mean days to slaughter was also lower with an average daily gain for net carcass weight of 0.44 which is comparable to male beef crosses. Similar to females, conformation is poorer in pure dairy males but the average level of fatness is within the most favourable fat classes. The average net weights of carcasses from the top 20 Holstein Friesian sires are shown in Tables 32 and 33 for males and females respectively.



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**Table 32 Top 20 Holstein Friesian sires for net weight (male carcasses)**

Sire identity (recoded)	Sire breed	Sex	Avg net weight (kg)	Avg days to slaughter	Avg daily net weight gain (kg)	Count
1	HOLSTEIN	M	383.12	958	0.40	18
2	HOLSFRIE	M	377.11	820	0.46	22
3	HOLSFRIE	M	365.05	896	0.41	13
4	FR_U	M	354.18	969	0.37	16
5	HOLSFRIE	M	348.97	943	0.37	27
6	HOLSFRIE	M	348.76	772	0.45	12
7	FR_U	M	347.59	823	0.42	16
8	HOLSFRIE	M	344.62	872	0.40	12
9	HOLSFRIE	M	344.51	852	0.40	57
10	HOLSTEIN	M	344.06	802	0.43	11
11	HOLSFRIE	M	343.98	820	0.42	15
12	HOLSFRIE	M	342.57	813	0.42	25
13	HOLSFRIE	M	342.34	875	0.39	10
14	HOLSFRIE	M	342.33	783	0.44	11
15	HOLSFRIE	M	341.92	815	0.42	11
16	HOLSFRIE	M	341.18	740	0.46	17
17	HOLSFRIE	M	340.24	844	0.40	11
18	BRITFRIE	M	338.51	800	0.42	14
19	HOLSFRIE	M	337.88	803	0.42	23
20	HOLSFRIE	M	337.34	902	0.37	11

**Table 33 Top 20 Holstein Friesian sires for net weight (female carcasses)**

Sire identity (recoded)	Sire breed	Sex	Avg net wt (kg)	Avg days to slaughter	Average daily net weight gain	Count
1	FR_U	F	340.69	1002	0.34	12
2	HOLSFRIE	F	307.32	1021	0.30	5
3	HOLSTEIN	F	305.90	763	0.40	6
4	HOLSTEIN	F	303.70	1058	0.29	5
5	BRITFRIE	F	303.36	1021	0.30	7
6	HOLSFRIE	F	301.46	941	0.32	5
7	HOLSTEIN	F	300.22	949	0.32	11
8	HOLSTEIN	F	299.33	901	0.33	9
9	HOLSFRIE	F	295.59	1011	0.29	13
10	BRITFRIE	F	294.58	862	0.34	6
11	HOLSTEIN	F	293.76	805	0.36	5
12	HOLSTEIN	F	293.57	948	0.31	10
13	HOLSTEIN	F	291.77	997	0.29	7
14	HOLSTEIN	F	286.28	975	0.29	5
15	HOLSFRIE	F	282.48	917	0.31	6
16	HOLSTEIN	F	279.22	941	0.30	11
17	BRITFRIE	F	278.96	836	0.33	5
18	BRITFRIE	F	277.20	905	0.31	5
19	HOLSTEIN	F	271.40	902	0.30	5
20	HOLSFRIE	F	270.35	1021	0.26	13

### **Summary of matched abattoir and BCMS data**

- 82.3% of abattoir data was successfully matched with BCMS data (~ 2.44 million out of 2.97 million animals)
- Recording of dam was almost complete in BCMS (97.4% ~2.37 million animals)
- In BCMS 22.6% of animals had sire information recorded (~0.55 million animals).
- BCMS data adds additional information such as date of birth which was commonly not recorded in abattoir data.
- Sex was not fully recorded in abattoir data but was recorded in BCMS. BCMS records either M/F thus distinction between steers and bulls could be difficult if not recorded in abattoir data.
- The five most common breed types (breed + breed crosses) were Limousin, Aberdeen Angus, Holstein Friesian, Charolais, and Hereford. Of these five breed types the majority of these animals were recorded as crossbreds with the exception of Holstein Friesian. Recording of breed types tend to favour the breed code of the sire but animals that were crossbreds were not always recorded as a 'X.'
- Dairy genetics are a major component of beef carcasses as a result of by-products of the dairy industry; male dairy calves and the production of crossbreds by a beef sire to produce a more valuable animal.
- The most common beef sires to produce a dairy cross included both British (Aberdeen Angus, Hereford) and Continental (Limousin, Hereford, Charolais) breeds.

### ***Movement data***

Movement data records the location that an animal is born on and from then on every movement on and off a holding until death. Some movements can be quite short, for example, in the event that an animal is brought and sold at a livestock market. It is quite normal for cattle for beef production to be reared on more than one holding. An animal might be born and reared in a suckler herd, then sold at weaning as a store animal and finished in another herd. Dairy calves destined for beef may be sold early in their lives as they are removed from their dam within a few days of birth.

There was a datafile in BCMS that provided location types of animal movements (e.g. agricultural holding, slaughterhouse, market, AI centre) but unfortunately for the data provided (for data security reasons) there was no link between location identity and the description of the location. Some of these location types can be deduced but it is far more time consuming without this link available and it leads to assumptions having to be made. It would be beneficial for a future extract of BCMS data to at least include a link between location (recoded) identity and location type. Location type would still give no identification for the actual holding and address which BCMS may prefer to be protected.

Market locations or collection centres could be deduced as those locations where an animal is moved on and off the holding on the same day, it is not the location of death, and where the location of an animal prior to market is different to the location afterwards. However, when using the above rules a number of locations were identified where just one animal had passed through, suggesting that not all locations were markets (or mistakes in recording holding were made). A large number of animals are expected to go through livestock markets to either get sold to other farms or to get sold for slaughter. There were 81 locations which had more than 1000 animals enter and leave on the same day indicating that these could be markets or collection centres.

Table 34 shows the frequency of animals grouped by location of birth and location of death. There were 23,511 different locations for birth. As all records matched to BCMS were abattoir records it would be expected that all the movements that result in death are location identities for abattoirs. There were 73 locations of death recorded but some of

these had few records (51 locations had 10 or fewer slaughter records). There were 8 abattoirs accounting for over 10,000 records. Data was received from different sources and it would be useful to have a unique abattoir identity allocated to separate abattoirs within a source and across sources as files were collated.

**Table 34 Frequency of animals by location of birth and location of death**

Location of birth		Location of death	
Number of animals	Frequency	Number of animals	Frequency
1	4387	1	37
2 to 5	6327	2 to 10	14
6 to 10	3567	11 to 50	2
11 to 50	6790	51 to 100	0
51 to 100	1401	101 to 1000	7
101 to 500	983	1001 to 10000	5
501 to 1000	42	10000+	8
1001+	14		

**Table 35 Frequency of the number of herds an animal has been reared**

Number of herds	Count (%)
1	191058 (39.2%)
2	238602 (48.9%)
3	50006 (10.3%)
4	6871 (1.4%)
5	876 (0.2%)
6	32 (<0.01%)
7	3 (<0.01%)

For animals slaughtered at 3 months to 36 months of age there were 37% that remained on the same herd at birth until finishing. This accounted for 31% of herds. For animals that were finished in a different herd than birth the average time spent at the herd of birth was 370 days (s.d. 214 days). In contrast, the average time spent on a finishing herd (when not the same as the birth herd) was 289 days (s.d. 179 days). Table 35 shows the number of herds an animal has been reared, with a minimum time spent of 2 months in each herd, up until slaughter (aged over 3 to 36 months of age). The edit of 2 months was the minimum time spent in a finishing herd used in the study of Hickey *et al.*, (2007<sup>4</sup>), which also analysed carcass data.

#### *Creation of contemporary groups*

Movement data is required to create contemporary groups. It is assumed that animals within the same contemporary group are managed similarly. Contemporary groups could be based upon either the herd at birth or the finishing herd. In some cases where the animal does not move herds the birth and finishing herd could be the same. In a subset of data of animals with Charolais sire breed type, the fixed effects based upon birth and finishing herds were compared to determine which had the greatest effect. Finishing herd had a greater effect than birth herd, and finishing herd-year (year based upon year of entry to finishing herd) had a greater effect than birth herd-year when included into a model for net-weight. Both birth herd-year-season and finishing herd-year-season (year-season based upon entry to finishing herd) were not significant, and of these effects finishing herd-year-season had least effect. In several studies investigating carcass traits the herd of finishing has been used to create contemporary groups (Hickey *et al.*, 2007; Mirzaei *et al.*, 2009<sup>5</sup>). If the finishing herd is used to create contemporary groups then it is more probable

<sup>4</sup> Hickey JM, Keane MG, Kenny DA, Cromie AR and Veerkamp RF. 2007. Genetic parameters for EUROP carcass traits within different groups of cattle in Ireland. *J. Anim. Sci.* 85: 314-321.

<sup>5</sup> Mirzaei HR, Verbyla AP, Deland MPB and Pitchford WS. 2009. Describing variation in carcass quality of crossbred cattle. *Pakistan Journal of Biological Sciences* 12: 222-230.

that contemporary groups will have offspring from a greater number of sires than if the birth herd is used, if the finishing herd acquires livestock from more than one farm. The study of Hickey *et al.*, (2007) used finishing herd-year-season based upon slaughter dates to define contemporary groups.

For genetic parameter estimation of dairy cattle the time span the contemporary group covers is often fixed and often a herd-year-season is used. However, in beef cattle herd sizes are generally smaller than in dairy cattle and fixed time spans could create smaller contemporary groups. Therefore, in beef cattle evaluations contemporary grouping may follow the algorithms of Crump *et al.*, (1997<sup>6</sup>), which allows more natural groupings and increases the time span if necessary to enable larger contemporary group size.

### Summary of movement data

- Location type could not be linked to movement record. Ideally this link could be provided in future extracts to add value to the data.
- Birth herd and finishing herd could be useful to base contemporary groups upon.
- Birth herd is easy to extract as it the first location an animal is given and it is coded by 'Birth.'
- Animals can be reared on more than one agricultural holding. Finishing herd is more difficult to define as an animal might have short time periods at various locations before it is slaughtered and is complicated by the fact that location type is not known. An animal should spend a reasonable time on a finishing herd if it is to be an effect to be considered in a model. Short time periods, such as when an animal is bought by a dealer and then sold quickly onwards, may not be useful. The question is how long is a reasonable time? In the paper of Hickey *et al.*, (2007) a minimum time period of 2 months in a finishing herd was required.

### Creating a (super) pedigree file

A database was developed to combine data from all available data sources for dairy and beef to provide as much pedigree information as possible. This resulted in a pedigree file containing 50,192,852 animal records with up to 13 generations. The pedigree contained 2,332,587 additional records from sources available for national genetic evaluations. The number of animals in the slaughter population with sire information increased from 22.6% (BCMS data) to 24.9% (super pedigree).

### Additional data on sire

Table 13 showed the percentage of records that could be matched to a sire identity in BCMS. As recording of sire is not compulsory in BCMS the proportion of sire records for some breed types were relatively low. In Table 36 it can be seen that the creation of a super pedigree has increased the number of animals in the slaughter population with a sire record. Using the super pedigree sire was recorded (proportionately) most in Highland cattle. For some breeds there was little change, particularly in the beef breeds (e.g. Luining), whereas increases tended to be greatest in dairy breeds, which were initially low in BCMS. Sire records for Ayrshire, Holstein Friesian, and Jersey breeds increased by 6.1%, 8.4%, and 16.5%. This should mean that during data editing for genetic parameter estimation fewer records would be removed due to missing sire information and it would be likely higher progeny counts would be obtained per sire.

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<sup>6</sup> Crump RE, Wray NR, Thompson R and Simm G. 1997. Assigning pedigree beef performance records to contemporary groups taking account of within-herd calving patterns. *Animal Science* 65:193-198.

## Carcass Trait Evaluations

**Table 36 Percentage increase in sire records using a super pedigree**

Breed	Count	No. of sires in super pedigree	% sire records abattoir/BCMS	% sire records super pedigree	% difference
HIGHLAND0S	2918	1950	57.23	66.83	9.60
STABILIS0R	7482	4951	59.6	66.17	6.57
LUING	3971	2278	57.34	57.37	0.03
SOUTDEVO	15457	8479	53.92	54.86	0.94
LINCRED_U	1638	831	50.61	50.73	0.12
GALLOWAY	3222	1558	48.29	48.36	0.07
WELSBLAC	12202	5503	44.39	45.10	0.71
SUSSEX	3517	1557	41.97	44.27	2.30
DEVON	3419	1371	39.66	40.10	0.44
SALER	13335	5115	38.1	38.36	0.26
ABERANGU	499458	185935	36.75	37.23	0.48
SHORTHORN	17115	5802	32.32	33.90	1.58
HEREFORD	198362	60196	30.02	30.35	0.33
BLONDAQ	59581	15892	26.33	26.67	0.34
SIMMENTAL	187147	48263	25.41	25.79	0.38
CHAROLAIS	295021	65889	21.93	22.33	0.40
LIMOUSIN	500047	104330	20.01	20.86	0.85
JERSEY	2822	586	4.29	20.77	16.48
AYRSHIRE	7570	1298	11.03	17.15	6.12
MERHIS_U	5377	881	14.28	16.38	2.10
HOLSFRIE	347051	48526	5.59	13.98	8.39
SWRE&WH_U	2421	337	1.03	13.92	12.89
BROWSWIS	3268	381	4.31	11.66	7.35
MONTBELIAR	7724	839	7.52	10.86	3.34
BELGBLUE_U	159271	13277	7.41	8.34	0.93

It should be noted that we would expect the super pedigree to be further enhanced if other breed society pedigree information were to be available. This would allow us to validate the portions of the pedigree for these breeds that has been built through BCMS data only, add older generations of pedigree as well as potentially filling pedigree “holes” across time.

In summary, the creation of a super pedigree has allowed us to link dairy and beef genetics through crossbred slaughter progeny, as well as grand progeny on the maternal and paternal side. This opens up an opportunity to tackle a true across cattle genetic analysis for traits in the commercial populations, likely to have multiple breeds and crosses represented. The most obvious of these traits are carcass traits, including any future developments in recording of “meat” quality. However, this merging of pedigree information also provides opportunities for traits that are affecting both populations such as traits around calving and potentially disease traits such as Johnes and TB.

### *Holstein Friesian*

In total there were 7887 Holstein sires with slaughter progeny in the super pedigree. The super pedigree is an improvement for extracting additional sire records as shown in Table 37 but the progeny count for the majority of sires is low. Sires with most progeny in the slaughter population are shown in Table 38. Table 17 showed that Holstein Friesian was the most common dam breed of the slaughter population so we would expect a larger number of Holstein Friesian maternal grand-sires. There were 325,074 dams that had a Holstein Friesian sire (the maternal grand-sire) recorded, which totalled 20,892 sires.

**Table 37 The frequency of number of offspring for Holstein Friesian sires in BCMS and the super pedigree**

Number of offspring	Super pedigree	BCMS
>=5	1839	914
>=10	996	489
>=15	677	331
>=20	504	241

The top 20 Holstein Friesian maternal grand-sires with the highest number of dams are shown in Table 39. Although the number of Holstein Friesian sires with reasonable progeny counts were low (even using the super pedigree (Table 37)) it was found that maternal grand-sires have much higher grand-progeny counts in the slaughter population (Table 38). Table 39 also shows the proportion of grand progeny from Holstein Friesian maternal grand-sires that are recorded themselves as Holstein Friesian, indicating that a beef sire is often used on a Holstein Friesian dam to produce cross-bred dairy beef. For example, the grand-progeny of one Holstein bull were recorded as 34.7% Holstein Friesian, 25.4% Aberdeen Angus, 11.4% Hereford, 10.1% Limousin, 3.2% Simmental, 1.9% Charolais and 13.4% other breeds. It is expected that the super pedigree could be further improved to obtain more information on male dairy animals by linking the dam recorded in BCMS to its calving and insemination records in milk records to obtain the service sire.

**Table 38 Top 20 Holstein Friesian sires for highest progeny count in slaughter population**

Sire Name (recoded)	No. progeny in slaughter generation
1	544
2	430
3	358
4	356
5	329
6	329
7	301
8	283
9	278
10	249
11	244
12	235
13	234
14	228
15	211
16	207
17	201
18	190
19	180
20	175

**Table 39 Top 20 Holstein Friesian maternal grand-sires with highest no of progeny (dams) and grand-progeny (slaughter population)**

Sire name (recoded)	No. dams (progeny)	No. slaughter population (grand-progeny)	% grand progeny Holstein Friesian breed
1	3549	4079	34.67
2	2846	3408	25.97
3	2765	3419	22.76
4	2728	3217	29.38
5	2521	2877	30.90
6	2154	2614	18.40
7	2008	2502	16.75
8	1935	2294	28.42
9	1906	2273	22.66
10	1897	2335	19.74
11	1895	2193	43.46
12	1853	2100	31.95
13	1825	2216	23.19
14	1777	2166	21.70
15	1722	2210	17.78
16	1596	1833	28.70
17	1571	1989	14.28
18	1568	1780	25.39
19	1556	1705	46.16
20	1545	1807	27.06

**Table 40 Number of grand-maternal sires with 5+, 10+, 15+, 20+, 30+, 40+, 50+ progeny (dams) /slaughter population (grand-progeny)**

Number	Dams (progeny)	Slaughter population (grand-progeny)
>=5	7521	8314
>=10	4280	4967
>=15	2908	3511
>=20	2086	2665
>=30	1322	1676
>=40	1011	1239
>=50	840	1015

### **Preliminary genetic parameter estimation of carcass traits**

#### ***Editing data for genetic parameter estimation***

A subset of the abattoir/BCMS matched data was extracted for all slaughter animals with Charolais as a sire breed (the third most popular sire breed). The edits listed in Table 41 were then carried out to create a file for genetic parameter estimation and the number of animals remaining after each edit is shown. The edits reduced the size of the dataset considerably (as expected) and 28% of the animals remained. The pedigree was extracted for 6 generations and consisted of 43,069 animals.

**Table 41 Summary of edits (in order) to create datasets for genetic parameter estimation**

Edits	Count
Sire breed	61014
Days at slaughter from 3 to 36 months	58698
Dam breed is not null	58399
Average daily gain net carcass wt <=0.75	54096
Sire has at least 10 offspring	40814
Average daily gain (>3 sd removed)	40801
At least 25 animals per abattoir	40744
At least 5 animals per finishing herd yr	29625
At least 5 animals per abattoir herd yr	29621
Sire in at least two finishing herds	19560
At least two sires in a finishing herd-year-season	17125

**Model**

Genetic analyses were conducted for the traits net carcass weight, conformation and fat carcass grades using ASReml. In each case the fixed effects; sex, dam breed, birth herd, birth-year-season, location of death, finishing herd-year-season, the covariates; linear and quadratic of age at slaughter and the random effect of the animal were accounted for in the model. A year consisted of two seasons for the definition year-season due to relatively small contemporary group size.

Maternal effects (genetic and environmental) were not considered as maternal effects and are generally considered to be low among carcass traits as development of carcass tissues occur in later development when the diet relies less upon the dam's milk.

**Results from genetic analysis**

Heritability estimates for net carcass weight, conformation, and fat class were 0.31 (0.04), 0.24 (0.04), and 0.14 (0.03) respectively using an animal model (Table 42). Genetic correlations between net carcass weight and conformation, net carcass weight and fat, and conformation and fat were 0.38 (0.09), -0.54 (0.12), and -0.67 (0.11). Estimated breeding values (EBVs) were obtained for each animal in the pedigree file. The minimum, maximum and mean EBV for net carcass weight was -32.15 kg, 46.9 kg and 0.16 kg respectively. Figure 9 shows that EBVs were normally distributed for net carcass weight and that genetic variation exists.

**Table 42 Genetic parameter estimates of carcass traits in Charolais using an animal model**

	Animal variance	Residual variance	Phenotypic variance (s.e.)	Heritability (se)
Net carcass weight	196.80	447.07	643.9 (9.89)	0.31 (0.04)
Conformation	2.29	7.20	9.48 (0.14)	0.24 (0.04)
Fat	1.72	10.48	12.21 (0.17)	0.14 (0.03)

It should be noted that these results are preliminary and are only presented for one breed. However, these results provide strong indication of the existence of genetic variation in the studied traits. This, in turn, suggests that improving carcass quality traits through genetic selection is entirely possible, thereby warranting more detailed investigation of their genetic background.



## Carcass Trait Evaluations

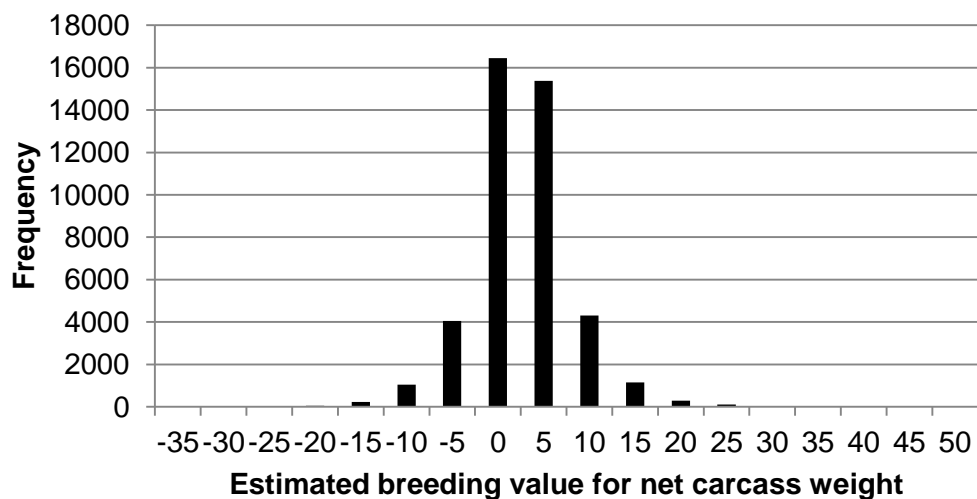


Figure 12 Distribution of net carcass weight EBV's for all animals in the pedigree file

### ***Summary of creating pedigree file and genetic parameter estimation***

- A super pedigree file containing 50,192,852 animal records with up to 13 generations can be produced from abattoir, BCMS and performance recording databases.
- Additions of over 2.3 million pedigree records were obtained from sources available for national genetic evaluations.
- Using the super pedigree resulted in an increased number of sire records, particularly for dairy breeds.
- Heritability estimates for net weight, conformation, and fat class were 0.31, 0.24, and 0.14 (0.03) respectively using an animal model for the Charolais sire breed
- EBVs were normally distributed and indicate that genetic variation exists.
- Data is considered sufficiently voluminous to enable EBVs to be produced.

## Appendix A: Preliminary genetic analysis of Limousin data

### *Editing data for genetic parameter estimation*

A subset of the abattoir/BCMS matched data was extracted for all slaughter animals with Limousin as a sire breed (the second most popular sire breed). Edits were then carried out to create a file for genetic parameter estimation and 27,038 animals remained in the dataset (Table A1). The pedigree was extracted for 6 generations and consisted of 72,140 animals.

### *Model*

Genetic analyses were conducted for the traits net carcass weight, conformation and fat carcass grades using ASReml. In each case the fixed effects; sex, dam breed, birth herd, birth-year-season, location of death finishing herd-year-season, the covariates; linear and quadratic of age at slaughter and the random effect of the animal were accounted for in the model. A year consisted of two seasons for the definition year-season due to relatively small contemporary group size.

**Table A 1 Summary of edits (in order) to create datasets for genetic parameter estimation**

Edits	Count
Sire breed	96273
Days at slaughter from 3 to 36 months	89913
Dam breed is not null	89442
Average daily gain net carcass wt $\leq 0.75$	82051
Average daily gain ( $>3$ sd removed)	82040
Sire has at least 10 offspring	55857
At least 25 animals per abattoir	55812
At least 5 animals per finishing herd yr	46268
At least 5 animals per abattoir herd yr	46244
Sire in at least two finishing herds	33018
At least two sires in a finishing herd-year-season	27038

### *Results from genetic analysis*

**Table A2 Genetic parameter estimates of carcass traits in Limousin using an animal model**

	Animal variance	Residual variance	Phenotypic variance (s.e.)	Heritability (se)
Net weight	136.90	511.64	648.5 (8.42)	0.21 (0.03)
Conformation	1.77	9.05	10.8 (0.14)	0.16 (0.03)
Fat	2.69	11.55	14.2 (0.18)	0.19 (0.03)

Heritability estimates are shown in Table A2. EBVs from traditional genetic evaluations were obtained for all animals in the pedigree file for the carcass traits net carcass weight, conformation and fat class. About 60% of sires had at least 10 progeny in the dataset after strict edits. Figure A1 shows that some sires with high accuracy had few progeny in the data. Whereas, some sires with lower accuracy had higher progeny counts in the slaughter population, which would mean that carcass data could improve the information available on some sires.

Sires in the pedigree file that were Limousin and had progeny with carcass data were matched to results from Beef Genetic Evaluations (1379 out of 1728) and EBVs were obtained for 400 day weight, ultrasonic muscle depth and ultrasonic fat depth. There were approximately 100 sires that had at least 25 slaughter progeny with accuracies of at least 0.55 for live beef measurements. The correlations between EBVs of net carcass weight and 400 day weight, carcass conformation and ultrasonic muscle depth, and carcass fat

## Carcass Trait Evaluations

and ultrasonic fat depth were 0.14, 0.0, and 0.32. This suggests that further investigation is required as it is concerning that current predictors appear to be lowly correlated with net carcass weight, conformation and fat class.

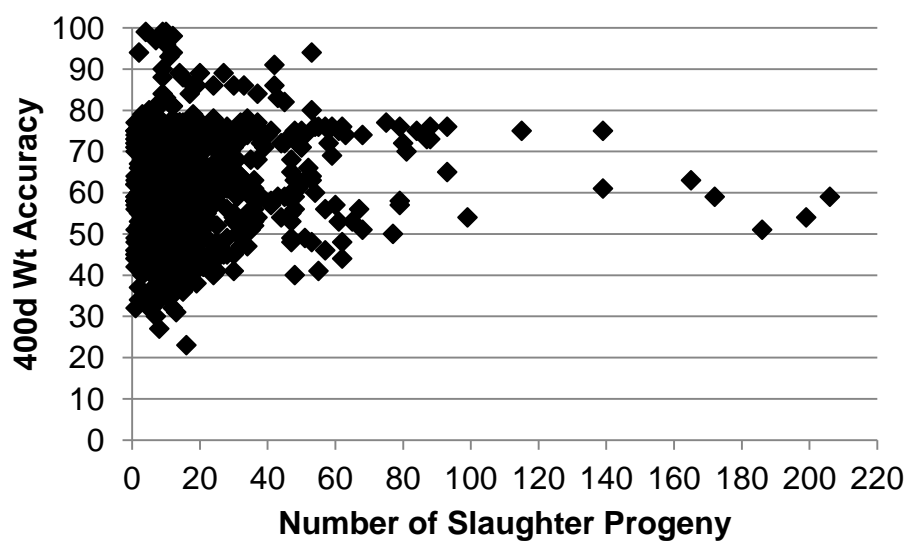


Figure A1 Sire 400d weight accuracy versus number of slaughter progeny

## Appendix B

Table B1 Carcass trait transformation table

### Conformation

	Improved conformation														
EUROP Numerical scale Conformation	E	E	E	+U	U	R	R	R	+O	-O	+P	-P			
	42	42	42	35	31	24	24	24	17	13	8	4			
15 point scale Numerical scale Conformation	+E	E	-E	+U	U	-U	+R	R	-R	+O	O	-O	+P	P	-P
	45	42	39	36	33	30	27	24	21	18	15	12	9	6	3

### Fatness

	Increased fatness														
EUROP Numerical scale Fatness	1	1	1	2	2	2	3	3	3	4L	4H	5L	5H		
	6	6	6	15	15	15	24	24	24	31	35	40	44		
15 point scale Numerical scale Fatness	-1	1	+1	-2	2	+2	-3	3	+3	-4	4	+4	-5	5	+5
	3	6	9	12	15	18	21	24	27	30	33	36	39	42	45

The conversion table was provided by Signet

**Appendix C: Breed codes in BCMS****Table C1 Summary of breed codes, breed names and the number of animals from abattoir/BCMS matched data**

Breed code	Breed name	n	Crossbred	Dairy	Upland	Lowland
LIMOX	Limousin Cross	453004	1	0	0	1
ABANX	Aberdeen Angus Cross	432760	1	0	0	1
CHARX	Charolais Cross	274452	1	0	0	1
HOLSFRIE	Holstein Friesian	226354	0	1	0	0
HEREX	Hereford Cross	180584	1	0	0	1
SIMMX	Simmental Cross	169572	1	0	0	1
BELBLUX_U	British Blue Cross.	147927	1	0	0	1
ABERANGU	Aberdeen Angus	83884	0	0	0	1
BRITFRIE	British Friesian	63424	0	1	0	0
LIMOUSIN	Limousin	56080	0	0	0	1
BLONDAQX	Blonde D'Aquitaine Cross	52565	1	0	0	1
HOLSTEIN	Holstein	33867	0	1	0	0
HEREFORD	Hereford	26034	0	0	0	1
CHAROLAIS	Charolais	23385	0	0	0	1
SIMMENTAL	Simmental	22334	0	0	0	1
HOLFRIX	Holstein Friesian Cross	15860	1	1	0	0
BELBLUE_U	British Blue.	13647	0	0	0	1
SALEX	Saler Cross	11614	1	0	0	1
FR_U	Friesian.	10240	0	1	0	0
SODEX	South Devon Cross	9481	1	0	0	1
WELSBLAC	Welsh Black	9150	0	0	1	0
BRFRX	British Friesian Cross	8573	1	1	0	0
AYRSHIRE	Ayrshire	7141	0	1	0	0
SHORTHORNX	Shorthorn Cross	7122	1	0	0	1
MONTX	Montbeliarde Cross	6445	1	0	0	1
SOUTDEVO	South Devon	6322	0	0	0	1
STABX_U	Stabiliser Cross.	6003	1	0	0	1
BLONDAQ	Blonde D'Aquitaine	5520	0	0	0	1
BEESHOX	Beef Shorthorn Cross	4387	1	0	0	1
HOLSX	Holstein Cross	3847	1	1	0	0
WELBLAX	Welsh Black Cross	3473	1	0	1	0
LUING	Luing	3314	0	0	1	0
MERHISX_U	Meuse Rhine Issel Cross	3246	1	1	0	0
HIGHLAND0S	Highland.	2642	0	0	1	0
BROWSIX	Brown Swiss Cross	2389	1	1	0	0
DEVONX	Devon Cross	2375	1	0	0	1
SUSSEXX	Sussex Cross	2370	1	0	0	1
MERHIS_U	Meuse Rhine Issel.	2360	0	1	0	0
BAZADAISEX	Bazadaise Cross	2350	1	0	0	0
SALER	Saler	2342	0	0	0	1
SHORTHORN	Shorthorn	2279	0	0	0	1
BEEFSHOR	Beef Shorthorn	2263	0	0	0	1
SWEREDX_U	Swedish Red and White Cross	2053	1	1	0	0
GALLOWAY	Galloway	1834	0	0	1	0
JERSEY	Jersey	1602	0	1	0	0
STABILIS0R	Stabiliser.	1513	0	0	0	1
JERSX	Jersey Cross	1475	1	1	0	0
MONTBELIAR	Montbeliarde	1395	0	0	0	1
GELBVIEH0X	Gelbvieh Cross.	1269	1	0	0	1
SUSSEX	Sussex	1190	0	0	0	1
DEVON	Devon	1102	0	0	0	1

## Carcass Trait Evaluations

Breed code	Breed name	n	Crossbred	Dairy	Upland	Lowland
PIEMX	Piemontese Cross	1098	1	0	0	1
LINREDX_U	Lincoln Red Cross	971	1	0	0	1
BROWSWIS	Brown Swiss	942	0	1	0	0
NORREDX_U	Norwegian Red Cross.	904	1	1	0	0
SWERX_U	SWEDISH RED CROSS.	899	1	1	0	0
LONGHORNX	Longhorn Cross	887	1	0	0	1
LUINGX	Luing Cross	883	1	0	1	0
DAIRSHOR	Dairy Shorthorn	791	0	1	0	0
AYRSHIREX	Ayrshire Cross	784	1	1	0	0
GALLX	Galloway Cross	743	1	0	1	0
LINCRED_U	Lincoln Red.	696	0	0	0	1
LONGHORN	Longhorn	615	0	0	0	1
PARTX	Parthenais Cross	557	1	0	0	1
BRITWHIT	British White	496	0	0	0	1
BELTGALL	Belted Galloway	484	0	0	1	0
DAISHOX	Dairy Shorthorn Cross	481	1	1	0	0
BLUEGREY_U	Blue Grey.	474	0	0	1	0
WHSOX	Whitebred Shorthorn Cross	445	1	0	1	0
REDPOLLX	Red Poll Cross	435	1	0	0	1
SWRE&WH_U	Swedish Red and White.	387	0	1	0	0
HIGHLAND0X	Highland Cross.	370	1	0	1	0
RED_POLL	Red Poll	348	0	0	0	1
BELGALX	Belted Galloway Cross	347	1	0	1	0
BRIWHIX	British White Cross	346	0	0	0	1
MURRGREY_U	Murray Grey.	342	0	0	0	0
GUERNSEY	Guernsey	328	0	1	0	0
CROBRED0I	Unspecified Dairy Cross.	300	0	1	0	0
MURGREX_U	Murray Grey Cross.	290	1	0	0	1
FRIEX_U	Friesian Cross.	237	1	1	0	0
PIEMONTESE	Piemontese	230	0	0	0	0
GELBVIEW_U	Gelbvieh.	228	0	0	0	1
DEXTER	Dexter	204	0	0	1	1
WAGYUCRO0S	Wagyu Cross.	204	1	0	0	1
WHITEPARK	White Park	202	0	0	0	1
DANISHRE0X	Danish Red Cross.	172	1	1	0	0
CROBREBE0E	Unspecified Beef Cross.	171	1	0	0	1
NORMANDEX	Normande Cross	165	1	0	0	0
BAZADAISE	Bazadaise	149	0	0	0	0
SHETLAND_U	Shetland.	138	0	0	1	0
GLOUX_U	Gloucester Cross.	134	1	0	0	0
SWER_U	SWEDISH RED.	106	0	1	0	0
GLOUCEST0R	Gloucester.	101	0	0	0	0
PARTHENAIS	Parthenais	95	0	0	0	1
OTHERBEE0F	Unspecified Beef.	89	0	0	0	1
ROMAGNOLAX	Romagnola Cross	87	1	0	0	1
WHITEPARKX	White Park Cross	86	1	0	0	1
CHIANINAX	Chianina Cross	83	1	0	0	1
FLCKVIEWHX	Fleckvieh Cross	83	1	0	0	0
BLUEGREY0X	Blue Grey Cross.	81	1	0	1	0
SHETLAND0X	Shetland Cross.	79	1	0	1	0
WHITGALL_U	White Galloway.	79	0	0	1	0
DEXTERX	Dexter Cross	65	1	0	1	0
MAIANJX_U	Maine Anjou Cross.	61	1	0	0	1

## Carcass Trait Evaluations

Breed code	Breed name	n	Crossbred	Dairy	Upland	Lowland
IRIMOIX	Irish Moiled Cross	59	1	0	0	1
IRISMOIL	Irish Moiled	54	0	0	0	1
BLUALBX_U	Blue Albion Cross.	52	1	0	0	1
DANISHRE0D	Danish Red.	50	0	1	0	0
MARCX	Marchigiana Cross	50	1	0	0	1
NORMANDE	Normande	50	0	0	0	0
NORWRED_U	Norwegian Red.	46	0	1	0	0
GASCONNEX	Gasconne Cross	45	1	0	1	0
ANGROTX_U	Angeln Cross.	44	1	1	0	0
WHBRSH	Whitebred Shorthorn	43	0	0	1	0
BLUEALBION	Blue Albion.	42	0	0	0	1
GUERNSEYX	Guernsey Cross	41	1	1	0	0
WELSHWHITE	Welsh White	34	0	0	1	0
UNAVAILA0L	Unknown.	31	0	0	0	1
BELWELBL0A	Belted Welsh Black.	27	0	0	1	0
ANGLROTV_U	Angeln.	21	0	1	0	0
BRAHMANX_U	Brahman Cross.	21	1	0	0	1
FLCKVIEH	Flekvieh	18	0	0	0	0
GROBLAX_U	Groningen Whiteheaded Cross.	18	1	1	0	0
MARCHIGIAN	Marchigiana	17	0	0	0	1
ROTEBUND0X	Rotebunde Cross.	17	1	1	0	0
AUBRAC_U	Aubrac.	16	0	0	0	0
OTHERDAI0Y	Unspecified Dairy.	14	0	1	0	0
BEWEBLX_U	Belted Welsh Black Cross.	13	1	0	1	0
ROMAGNOLA	Romagnola	12	0	0	0	1
SWIBRAX_U	Braunvieh Cross.	10	1	0	0	1
WAGYU_U	Wagyu.	10	0	0	0	1
KERRY	Kerry	9	1	0	0	0
WELWHIX	Welsh White Cross	9	1	0	1	0
CHIL_U	Chillingham.	8	0	0	1	0
CHILX	Chillingham Cross	8	1	0	1	0
BEEFALO	Beefalo	7	0	0	0	1
GRONBLAA_U	Groningen Whiteheaded.	7	0	1	0	0
WHIGALX_U	White Galloway Cross.	7	1	0	1	0
BRAHMAN_U	Brahman.	6	0	0	0	1
GASCONNEX	Gasconne	6	0	0	1	0
SWISBRAU_U	Braunvieh.	5	0	0	0	1
ARMORICA0N	Armoricaine.	4	0	1	0	0
MAINANJO_U	Maine Anjou.	4	0	0	0	1
OLDENGX_U	Old English Cross.	4	1	0	0	1
PINZGAUERX	Pinzgauer Cross	4	1	0	0	0
ANKOLE_U	Ankole.	3	0	0	0	0
CHIANINA	Chianina	3	0	0	0	1
KERRYX	Kerry Cross	3	1	1	0	0
ARMOX_U	Armoricaine Cross.	2	1	1	0	0
AUBRACX_U	Aubrac Cross.	2	1	0	0	1
ENGPARG	English Park Cross	2	1	0	0	1
NORDAIRSH	Northern Dairy Shorthorn	2	0	1	0	0
ROTEBUND0E	Rotebunde.	2	0	1	0	0
SWERP_U	SWEDISH RED POLLED.	2	0	1	0	0
BISON_U	Bison.	1	0	0	0	1
BRPINOX_U	Bretonne Pie-Noire Cross.	1	1	1	0	0
CONTINEN0A	Unspecified Continental.	1	0	0	0	1
EASFINBR0O	East Finnish Brown.	1	0	0	0	0

## Carcass Trait Evaluations

Breed code	Breed name	n	Crossbred	Dairy	Upland	Lowland
ENGLPARK	English Park	1	0	0	0	1
ESTRED	Estonian Red	1	0	1	0	0
FRIESPX	Frisona Espagnola Cross	1	1	1	0	0
FRISESPA	Frisona Espagnola	1	0	1	0	0
SWISSGRE0X	Swiss Grey Cross.	1	1	1	0	0
SWISSGRE0Y	Swiss Grey.	1	0	1	0	0
TYRBLAX_U	Tyrone Black Cross.	1	1	0	0	0
VAYNOL_U	Vaynol.	1	0	0	0	1
WATEBUFF_U	Water Buffalo.	1	0	0	0	1
ZEBU_U	Zebu.	1	0	0	0	1

n = number of animals with Breed code in matched abattoir/BCMS data. Breeds were categorised as Crossbred, Dairy, Beef Upland, or Beef Lowland where 1 = true and 0 = false.