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**Luing Cattle
Breed Society**

Investigating the Potential use of Estimated Breeding Values for Luing Cattle

By

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Executive Summary

The Luing cattle breed was established as a composite of the Beef Shorthorn and Highland cattle breeds approximately 60 years ago. The society breeding objective is to produce sustainable commercial upland or hill cow breed. This goal has not been supported comprehensively by the traits for which EBV are produced by UK beef evaluations. Recently an expanded range of maternal traits have been included in the UK evaluations. This combined with an in house type evaluation scheme has led the Luing breed towards considering engaging in genetic evaluations.

The report identifies the advantages of moving towards genetic evaluations to undertake selection decisions compared to the use of phenotypic information alone. The primary reason is that genetic evaluations separate the underlying genetic component of the variation seen between animals from that variation caused by environmental factors. It is only the genetic component that is transmitted from one generation to the next.

An overview is provided of the full set of UK genetic evaluations currently provided. The report also summarises the recording process that a breeder must undertake in order to generate meaningful EBVs.

The set of recorded data held by the Luing society was assessed in terms of data structure, effects recorded and pedigree structure to establish its suitability for genetic evaluations. Records utilised in the maternal traits pertaining to reproduction and longevity can be established from the data currently held. However, it is recommended that 200 day weight recording is established in the breed and also that calving ease should be formally recorded.

The linear type scoring system was assessed and a number of recommendations are provided in order that the scheme can be used to generate meaningful EBVs. This includes some guidance on establishing robust objective definitions for the scoring system. The data is not currently suitable for genetic evaluation.

The society has been engaged in a scheme that scores genetic markers for a number of commercial traits. Some advice with regard to marker assisted selection is provided within the report. The primary advice to the society is to concentrate on establishing wider phenotype recording in order to be in a strong position for future genetic evaluation innovations.

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1. Introduction

The Luing cattle breed was established in the late nineteen forties as a composite breed based on Shorthorn and Highland cattle. The Luing breed society have a breeding goal to produce a sustainable commercial either hill or upland cow breed. This goal has in the past been seen to be at odds with the genetic evaluation services offered in the UK, which were focused on terminal sire trait improvement. Genetic evaluation service providers now estimate breeding values for a number of “maternal” traits. Maternal traits place a focus on the genetics of the cow and align with a sustainable maternal breeding goal. In 2003 the Luing Cattle Society introduced an innovative in-house cow classification scheme based on assessing a number of functional type traits in cows that are dams of sale bulls. The scheme has been successful within the breed which is mainly attributed to the simplicity of the information presentation. This information is currently presented in the form of raw phenotypic scores but multiple generations of cow data are now being presented with some bulls. In addition information about the cow’s calving interval is also presented.

The Luing cattle breed has grown in numbers of pure bred cows. The number of females registered has more than doubled in the last seven years (currently over 7,000 females are registered). The growth of the breed has exposed a difficulty in the ability of the cow-classification scheme to convey all the necessary information held within the database to buyers. This project will consider the opportunities available to the Luing Cattle Society for adopting a more formalised recording and evaluation system. The potential benefits and drawbacks of such a move will also be considered. The future direction of genetic evaluations will also be explored briefly.

2. Why Should Genetic Evaluations Be Used?

The phenotype of an animal, i.e. the performance and type of the animal is a result of both the genetics and the environment. The genetics we measure by the “estimated breeding value” (EBV) of the animal. The environment is a catch all term for the non-genetic aspects that contribute to phenotype including the nutrition available, the disease status of the farm and the farm geography. We will look later at how environment is accounted for in calculating the EBV. Only the genetic component of the phenotype is passed on to the animal’s offspring and therefore in a breeding animal the genetic component is what we are interested in. This is especially important when a breed has the goal of sustainable production in an extensive environment. In the light of this it is important that selection decisions are made using the best information about genetic value available. By recording traits of cows the first step on the journey towards generating EBVs is being made. The next logical step is to separate these phenotypic measures into their genetic and environmental components using a procedure such as BLUP which utilises information about pedigree and management to estimate breeding values. For this procedure to work effectively it is necessary to have good genetic linkages over time and space. By this we mean related animals exist across farms and related animals exist through time. These related animals act as a benchmark for the different environments they live in.

3. UK Beef Evaluations

The UK beef evaluation system "Beefbreeder" is based on the statistical approach called BLUP. The implementation of this methodology allows the resulting breeding values to be compared across herds and years provided that sufficient genetic "connections" exist. An outline of the data recording protocols can be found in Tables 3.1 and 3.2.

3.1 Recommended Data Recording Protocols for Beefbreeder

Table 3.1 Traits and recording protocols

Goal[1]	Recorded trait	Notes
Easy Calving	Gestation length	To maximise accuracy only gestation length records from AI matings are used in calculations
Easy Calving	Calving ease	Recorded subjectively by breeder using 5 categories related to calving difficulty
Easy Calving	Birthweight	Calf weight is recorded by breeder within 48 hours of the animal's birth
Cow Efficiency	Age First Calving	Considers age categories 2, 2.5 and 3 years of age at first calving and then uses herd information to account for management effects
Cow Efficiency	Calving Interval	Measure of first calving interval
Cow Efficiency	Lifespan	Measures the number of parities achieved by cows accounting for data censorship
Cow Efficiency	Calf growth to weaning (Maternal)	Weight at 200 days recorded by breeder
Carcass	400-day weight	Based on at least two measures of weight between 270 and 500 days of age
Carcass	Muscling score	Visual assessment of animal's conformation at around 400 days of age.
Carcass	Ultrasonic muscle depth	Measured at about 400 days of age (between 350 and 500) by technician at 3rd lumbar. Depth defined as the vertical distance from deepest point of eye muscle up to fat interface
Carcass	Ultrasonic fat depth	Measured at about 400 days of age (between 350 and 500) by technician at 13th rib and 3rd lumbar.

[1] N.B. This is the primary goal. Traits are correlated so a trait can contribute information to more than one goal. For example 400 day weight is highly correlated with mature weight and therefore provides some indication of cow size which is an important aspect of cow efficiency.

Table 3.2 Calving ease classification

Score	Description
1	No assistance
2	Slight assistance by hand
3	Severe assistance (e.g. mechanical)
4	Non-surgical veterinary assistance
5	Veterinary assistance, surgery

3.2 “Environment” Information Recorded

In order for a genetic evaluation to take account of the management and environmental effects that animals experience it is essential that all of the following factors are recorded accurately.

- Herd of birth
- Calf date of birth
- Calf sex
- Insemination service dates where applicable
- Multiple birth (Y or N)
- Transplant status
    - If Transplant:
        - breed of recipient
        - Date of birth of recipient
        - Identity of recipient
        - Flushing date
        - Implantation date
- Foster status
    - If Foster:
        - breed of foster dam
        - Date of birth of foster dam
        - Identity of foster dam
- Dates of all measurements such as weights.
- Breed (if crossbred proportion of breeds in 16ths)
- Management code at 200 and 400 days to indicate which groups of animals are being managed together
- Management code for cows at weaning
- Date of exposure to bull (currently optional)
- Calf disposal code
    - R = retained in herd but no records available
    - D = died
    - S = sold for slaughter
    - B = sold for breeding
    - T = transferred to breeding herd

- Cow disposal details
    - R = retained but not calved
    - D = died
    - S = sold for slaughter
    - B = sold for breeding

3.2.1 Contemporary Groups

In the BLUP statistical model the environmental effects to be accounted for are defined. One important definition is the contemporary group which is used to account for feeding and management environment.

Contemporaries are animals that have been treated in a similar way – e.g. born over a relatively short period of time, on the same farm, and fed and managed similarly – and the groups they belong to are contemporary groups. Within these groups the animals are compared with each other.

The accuracy of selection can be improved by:

a) ensuring that animals in contemporary groups get managed in the same way.

b) maximising the size of contemporary groups (herd size can constrain this).

Different groups are formed for each trait as different factors are involved. For example before weaning sex is not used in forming the contemporary group as there is very little management difference between calf sexes at this stage.

3.3 EBVs

The EBVs produced are a measure of the genetic worth of the animal for the recorded traits. Most of the EBVs are classed as “direct” which means that they refer to the potential of that animal’s own genes for performance. There are however a number of traits of interest in livestock breeding where the performance of an animal is not only affected by its own genes and environment, but also by the maternal characteristics of its mother. For example weaning weight is affected not only by the growth genes of the calf but also by its mother’s genes for maternal characteristics such as uterine capacity and milk production. It is useful to think of such traits as having direct and maternal genetic merit. Another good example is calving ease which has a direct genetic component in the genes of the calf for size, shape and influence on gestation length, and also a maternal genetic component which varies the cow’s pelvic size and shape and control of gestation length by the cow.

3.3.1 EBV Accuracy

The accuracy of an EBV is a very useful tool in the interpretation of EBVs. The accuracy is essentially a measure of confidence in the estimation process. A very high accuracy associated with an EBV indicates that there is a great deal of confidence that the estimated breeding value is close to the “true” underlying breeding value of the animal. Two factors are key in the accuracy of EBVs. The first is the number of records of both the individual and its relatives that contribute to the calculation of the EBV. The second factor is the heritability of the trait. The EBVs of traits with low heritabilities have lower accuracies than those with high heritabilities given the same recorded information. This is because if a trait has a low heritability then the information from a single trait record for an animal is less correlated with its breeding value than if the trait had a high heritability, i.e. the variation observed in the phenotype is heavily influenced by environment and only to a small degree by genetics. If the accuracy is low then the confidence we can have in an EBV being the "true" value is low. EBVs with low accuracy are likely to change in the future as more information is included in the evaluation process. If we look at Figure 3.1 we see a trait that has an EBV of +40kg but 9 different accuracies. The thick black bar represents the range of the underlying true breeding value as the accuracy changes.

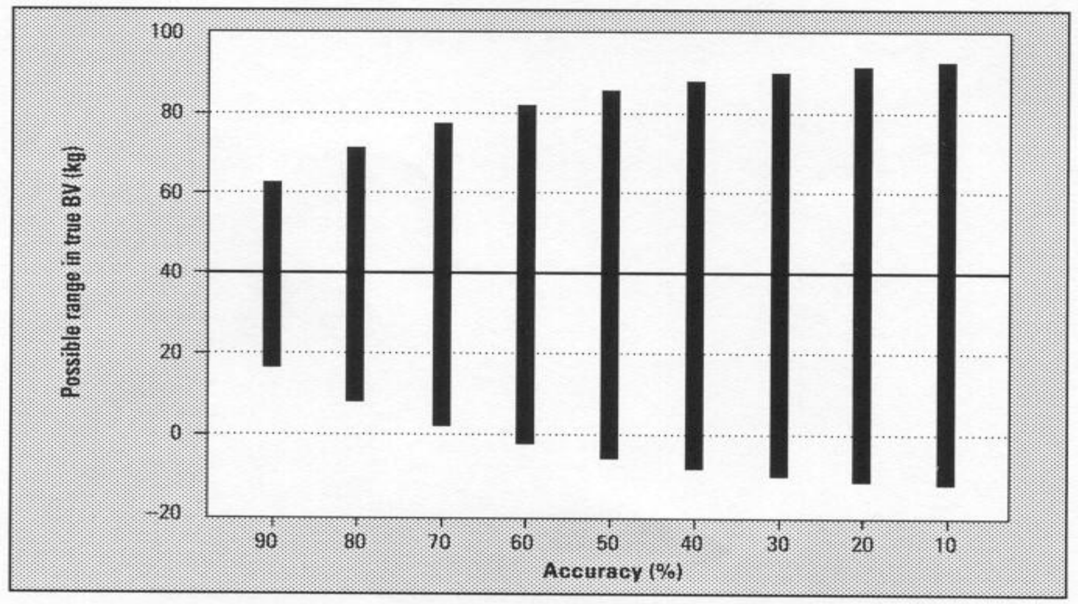

Figure 3.1. Illustration of accuracy in EBVs.

The message that we can take from Figure 1 is that "the higher the accuracy, the less a 'gamble' is being made in selection decision".

4. Luing Data Recorded

4.1 Type Classification

The Luing breed society has over recent years implemented a cow type classification system based on linear measures which they feel reflect good maternal type. The classification is undertaken on the dams of bulls to be presented for sale. At present the dams are scored whenever their sons are presented for sale and at no other time. If a cow has previously been scored then she is scored again and her new scores are presented and recorded to the database. This score information is presented with sale bulls and the age of the bull's dam is also indicated. In terms of adapting this system and existing recorded data to one which could be used in a genetic evaluation a number of issues need to be addressed.

The traits to be scored should be defined in objective and non-emotive terms. The use of words like good and bad should be avoided as such terms are open to wide interpretation. In Appendix 1 a selection of examples of clear scoring guidelines are presented based on information produced for the dairy herd. An approach such as the one they have implemented should be considered. This will enhance the repeatability of the system across multiple operators. The distribution of the scores currently recorded is in Appendix II.

The following guidelines are taken again from the dairy world but all of the messages are equally valid in applying linear type scoring to beef cows. There are a few issues with the current Luing system of type scoring that limit their immediate adaptability for genetic evaluations that are underlined in the guidelines.

4.1.1 Recommended Guidelines for a type classification system to be successfully utilised by genetic evaluation procedures in order to generate meaningful EBVs.

- There should be a head-classifier in charge of training and supervising other classifiers within the evaluating system to achieve and maintain a uniform level of classification.
- Ideally classification should be completed by individual full time professionals, though for a single beef breed this is unlikely to be practical.
- Ideally classifiers should be independent of commercial interest in the breed.
- Genetic evaluations should be based on the classification of first calvers. If the evaluating system is modified, repeat classifications can be added.
- Classification should be undertaken for all contemporary first calving females for a successful genetic evaluation to be undertaken.
- A minimum of 5 first calvers must be inspected at the same visit.
- Scoring should be done on a well defined scale suitable for the classification of the breed. This ensures that animals are well distributed in all classes of the scale.

Recommendation 1

In order that the type data can eventually be used to generate EBVs it is recommended that the type recording scheme should be expanded following the guidelines provided in section 4.1.1 of this report. The type traits being recorded are useful as early indicators of longevity. The existing national beef evaluations do not currently include type trait evaluations and in order to generate EBVs for these traits an investment would be required in research and development.

4.2 Luing Data Evaluation

The following is based on data supplied to SAC by Grassroots and is to our knowledge the complete recorded pedigree and data set of the Luing breed. The data were processed to investigate the potential for undertaking genetic evaluations.

4.2.1 Age at first calving

Data Used: Luing records of first calvings.

Trait: Age at first calving (AFC).

Ages defined according to Table 4.1.

Table 4.1. Age at first calving as aged 2, 2.5 or 3 years definitions

Age category	Minimum age (yr)	Maximum age (yr)
2	1.5	2.25
2.5	2.25	2.75
3	2.75	3.5

A total of 10188 raw first calving records were identified.
5193 of these records fall in the age category 3.5 years old or less.

Table 4.2. Luing Age at first calving data

Age category	Average age within category (days)	Number of records
2	751	390
2.5	921	743
3	1110	4060

Contemporary Group:
The principle contemporary group for age at first calving is Herd_Year_Season of birth:

- 290 contemporary groups have only one record.
- Mean contemporary group size is 6
- Median contemporary group size is 2 indicating that the majority of groups are small.

4.2.2 Lifespan

Data Used: Beefbreeder records of calvings.

Trait: Lifespan.

Approach: Analysis of records of lifespan accounting for censorship of data. This is due to the nature of the trait. Young cows only have early parity information and hence would be unfairly treated, i.e. their records would be censored. An adjustment of their record occurs to remove this bias based on average survival rate for the breed. Lifespan is calculated as parity of cow attained, or predicted if censored, following a set of rules developed in the dairy sector (Brotherstone et al, 1997; Lubber et al, 2000). This figure gives us a measure of the age and parity that the cow reaches as a final productive event.

Definition: Number of calvings a cow completes, or is expected to complete prior to culling. If the actual final calving is known, i.e. cow calved at parity n but did not calve at parity n+1 then the lifespan is n. The rules for parity reached are in Table 4.3. For cows deemed to be still in the herd, having had time for calving n but not n+1, the lifespan figure must reflect the parity that is expected to be reached. This information can be assigned to censored cows based on average survival probabilities from parity to parity in the population (Table 4.4). In this way all cows in the population that have a valid first calving recorded are assigned a lifespan figure.

Table 4.3 Rules for assigning longevity value to animals utilising calving appearances

Parity[1]	**Minimum Age (yr)**	**Maximum Age (yr)**
1	1.8	3.5
2	3	5.5
3	4	7.5
4	5	9.5
5	6	11.5

[1] In the Beefbreeder evaluation only 5 parities are used in the lifespan calculation.

Table 4.4 Survival results for Luing dataset considering cows born before 1998 to avoid censored animals.

Calving Event	**Records**	**Survival Probability**
First Calving	1160	1
First to Second	781	0.67
Second to Third	648	0.83
Third to Fourth	534	0.82
Fourth to Fifth	411	0.77
Fifth to Sixth	325	0.79

The focus of the breeding goal is to reduce the number of cows which drop out at early parities. The aim of breeding is to move the population towards improvement by removing the animals with poor breeding values from the system.

Contemporary Group:
The principle contemporary group for lifespan is Herd_Year_Season of first calving:

- 365 contemporary groups have only one record.
- Mean contemporary group size is 4.6.
- Median contemporary group size is 2 indicating that the majority of groups are small.

4.2.3 Calving interval

Data Used: Beefbreeder records of calvings.

Trait: Calving Interval First to Second Calving.

Approach: Utilising the same data used to investigate longevity the interval between first calving and second calving was determined. If no second calving appeared in the data the record was set as missing.
Definition: The same rules were applied to define first and second calving as in Table 3. If no second calving, as defined by the rules in Table 3, was found then the record was assigned missing. The distribution of first calving interval data can be seen in Figure 4.2.

Contemporary Group:
The principle contemporary group for lifespan is Herd_Year_Season of first calving:

- 365 contemporary groups have only one record.
- Mean contemporary group size is 4.6.
- Median contemporary group size is 2 indicating that the majority of groups are small.

Table 4.5 Unadjusted average calving interval data with different data restrictions

	Data Record Restriction[1]										
Measure[2]	**All**	**>1 Calf**	**>2 Calf**	**>3 Calf**	**>4 Calf**	**>5 Calf**	**>6 Calf**	**>7 Calf**	**>8 Calf**	**>9 Calf**	**>10 Calf**
AFC	1045	1050	1057	1057	1055	1047	1034	1014	1010	991	946
CI1	434	434	427	432	430	434	447	438	432	418	403
CI2	414	414	414	411	408	408	407	395	386	378	376
CI3	413	413	413	413	415	411	414	416	408	387	369
CI4	404	404	404	404	404	400	403	405	412	400	405
CI5	395	395	395	395	395	395	391	395	389	385	371
CI6	393	393	393	393	393	393	393	388	380	377	374
CI7	392	392	392	392	392	392	392	392	386	372	362
CI8	385	385	385	385	385	385	385	385	385	377	366
CI9	374	374	374	374	374	374	374	374	374	374	363

CI10	396	396	396	396	396	396	396	396	396	396	396
CI11	388	388	388	388	388	388	388	388	388	388	388
CI12	351	351	351	351	351	351	351	351	351	351	351
CI13	371	371	371	371	371	371	371	371	371	371	371
CI14	359	359	359	359	359	359	359	359	359	359	359

[1] In the table the data records used to measure the average calving intervals is restricted according to the qualifier, i.e. >1 Calf means that only cows with 2 or more calving events contribute to the mean calving intervals.

[2] AFC = Age at first calving, CI1 = calving interval from calf 1 to 2.

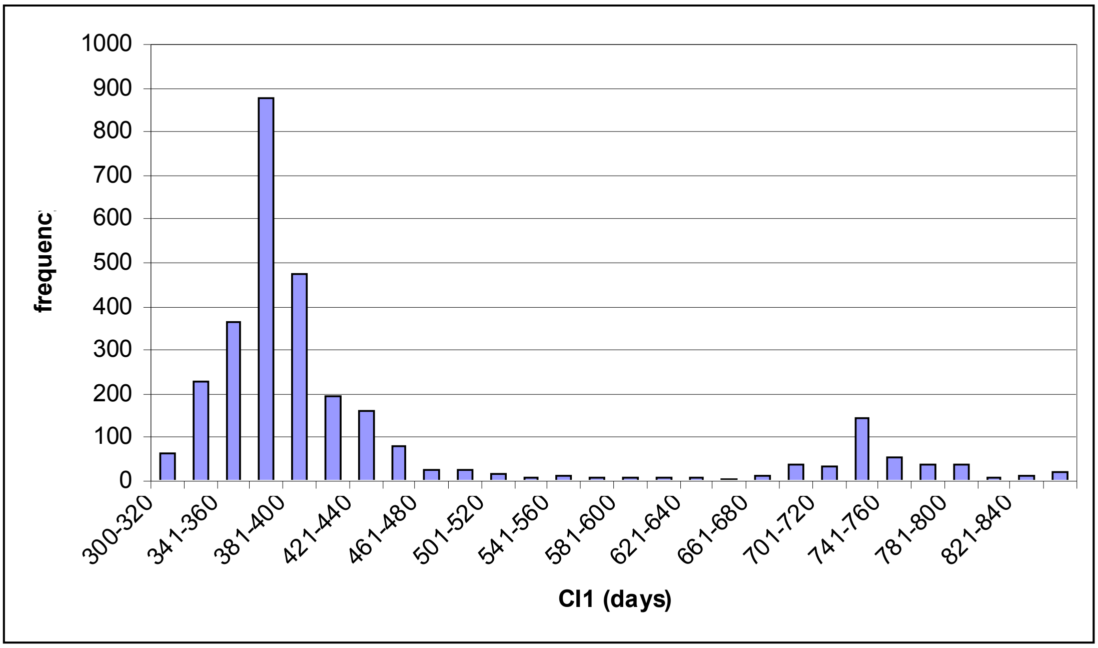

Figure 4.2 Phenotypic data first calving interval distribution

4.3 Pedigree Structure For Validated Data Records

The essential component for a successful BLUP genetic evaluation of a trait for a population is that an adequate pedigree structure exists in the data to both allow the trait phenotype to be separated into its genetic and management components and the comparison of EBVs across the population. The pedigree structure for the main trait groupings (reproductive and type) are shown in Tables 4.6 and 4.7. For the reproductive traits a data structure exists that has good potential for a genetic evaluation. As expected the principle linkages lay in the sire and paternal grandsire categories. The important number is the median here as the average group size tends to be skewed upwards by one or two individuals with large group sizes. The story is different for the type scores (Table 4.7). Here the number of records is very small which presents a problem and this problem is further compounded by the nature of the pedigree. Because the animals score are only selected based on a bull being for sale rather than picking a few herds and scoring all first calvers the pedigree structure is dissipated across the whole breed with small representations of key sires.

Table 4.6 Pedigree structure associated with records on reproductive and survival traits in the Luing breed

Relative in animals pedigree	Total unique individuals	Mean number records per relative	Median number of records per relative
Animal	4335	1	1
Sire	447	9.7	6
Dam	2869	1.5	1
Paternal Grandsire	186	23	10
Paternal Granddam	364	11.8	11.8
Maternal Sire	468	9.3	4
Maternal Granddam	2139	2	1

Table 4.7 Pedigree structure associated with records on type traits in the Luing breed

Relative in animals pedigree	Total unique individuals	Mean number records per relative	Median number of records per relative
Animal	311	1	1
Sire	113	2.6	2
Dam	253	1.1	1
Paternal Grandsire	70	4.2	2
Paternal Granddam	103	2.9	2
Maternal Sire	112	2.6	1
Maternal Granddam	225	1.3	1

Recommendation 2
The Luing breed has sufficient data to generate the EBVs currently produced for some of the maternal traits. However, currently weight data is a requirement of undertaking genetic evaluations. A dialogue would need to be established with both Signet and EGENES to reconcile this issue.

Recommendation 3
It is recommended that the Luing breed start recording weights around weaning in order to establish 200 day weight (2 weights required) and that they adopt official recording of calving ease. These two traits will provide information on which contribute to the primary maternal breed goals.

5. Marker Assisted Selection

The Luing breed have utilised a number of commercially available marker tests. I would urge the elite sector of the breed to focus on phenotypic recording activity and aim to utilise genetic evaluations as a primary objective. The use of markers to identify trait genetic indicators is a worthy activity but focus should rest primarily on breeding values in the first instance with markers being used as an added indicator. The same argument can be used as that often used by breeders that breeding values do not provide a total substitute for the stockman being able to identify sound breeding animals. So markers need a well phenotyped seedstock/elite population in order to be utilised accurately and be validated. The new genomic selection approaches on the horizon for beef producers make this truer than ever before.

5.1 Economics of gene markers

The following is extracted from an American extension review paper looking at the economics of gene testing in cattle (DeVuyst, 2009) but is very applicable to beef genetic markers in a UK context.

There is a great deal of buzz in the beef cattle industry regarding the genetic testing of bulls, beef cows and even finisher calves. The services being offered commercially now include parentage testing and testing for markers associated with economically relevant traits. However, there is very little unbiased published information on the value provided by these genetic markers to a producer’s bottom-line. Appendix III outlines the basis for genetic marker technology.

Economics of genetic information is in its infancy with only a few peer reviewed economic studies published. The main reasons for information on the economic analysis of markers being scarce are the cost of undertaking a trial/validation study and also the lack of genetic training. The review cites three studies that have considered the Leptin SNP marker, two on finishing cattle and one on a cow-calf operation. Here I will concentrate on the cow calf operation.

Leptin is a hormone secreted by white fat cells and the marker discovered is connected with fat deposition and energy metabolism. The SNP is due to a C to T switch at Exon 2, SNP 305. Heavier weaning weights have been reported for TT and CT cows than CC (DeVuyst et al. 2008). This effect was significant in crossbred (mostly Angus) cows, but weaker in other breeds. There was however a general tendency for TT cows to wean heavier cows than CC. Mitchell et al. (2008) considered the economic differences due to Leptin genotype for cow-calf production. They found that TT and CT genotypes were more profitable due to higher weaning weights and longer cow productive life. The trial was however small and their results should not be viewed as definitive. For the many other SNP panels being introduced commercially the economic value has not been evaluated by independent researchers.

5.1.1 What does the future hold for marker tests?

It is important to consider what the market currently rewards producers for and this often varies by sector. For example higher weaning weights may be important in cow-calf production but feed efficiency is key in finishing. At the present time there is not a market reward system for meat quality, e.g. tenderness. This issue of reward makes it difficult for nucleus breeders to make choices about markers for such traits. This is not to say that future markets will not change and there is likely to be a time when selection for such traits is rewarded.

Recommendation 4

It is recommended that the use of markers to identify genetic values of traits should not be given priority over establishing a good recording regime within the breed. That is not to say that markers are not useful but that they should be used along with EBVs in making selection decisions at this time. The markers may however have a marketing value to the breed at the present time.

6. References

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Appendix I: Linear Type Classification

Linear classification is based on measurements of individual type traits instead of opinions. It describes the degree of trait not the desirability.

Advantages of linear scoring are:
- traits are scored individually
- scores cover a biological range
- variation within traits is identifiable
- degree rather than desirability is recorded

Feet

Angle at the front of the rear hoof measured from the floor to the hairline at the right hoof.
1 – 3 Very low angle
4 – 6 Intermediate angle
7 – 9 Very steep

1

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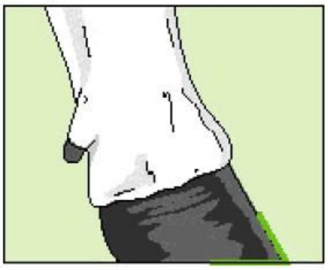

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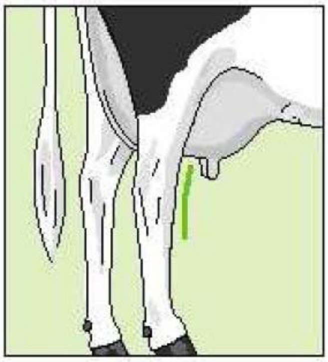
Hind Legs

Angle measured at the front of the hock.
1 – 3 Straight (160 degrees)
4 – 6 Intermediate (147 degrees)
7 – 9 Sickle (134 degrees)



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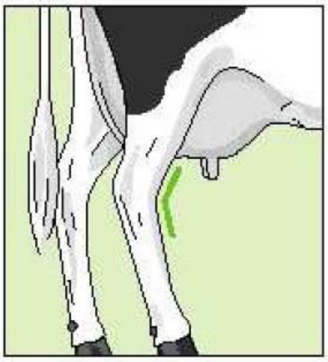

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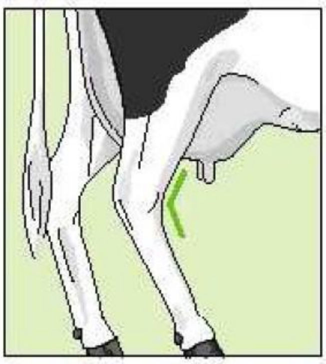

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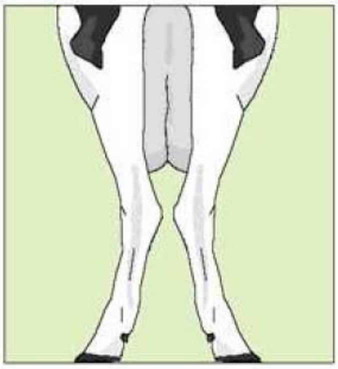
Direction of feet when view from the rear.
1 Extreme toe-out
5 Intermediate; slight toe-out
9 Parallel feet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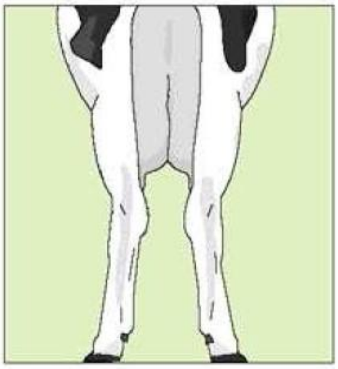
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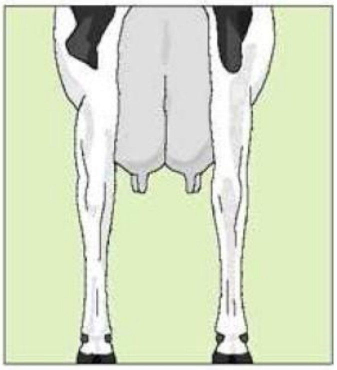
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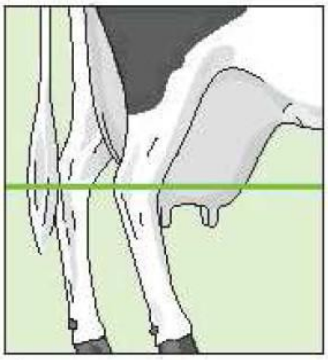
Udder

The distance from the lowest part of the udder floor to the hock.
1 Below hock
2 Level with hock
5 Intermediate
9 Shallow
Reference scale: level=2 (0 cm); 3 per point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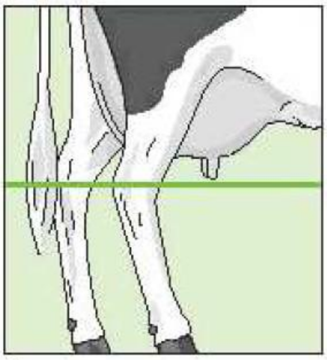
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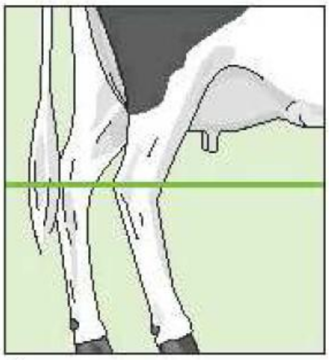
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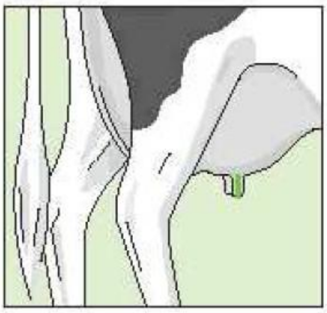
Teats

The length of the front teat.
1 – 3 Short
4 – 6 Intermediate
7 – 9 Long
Reference scale: 1-9 cm; 1 cm per point


1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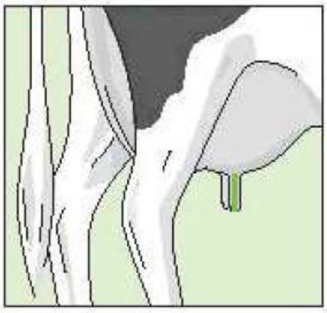
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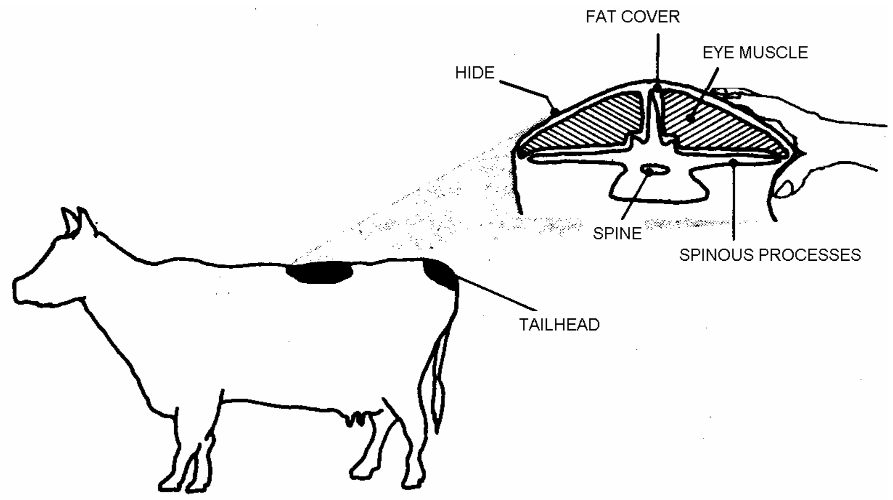
Condition Score

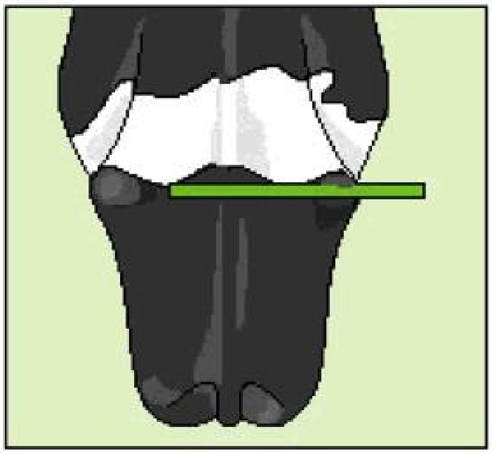
Score*	Description
1	The individual transverse processes are sharp to the touch and easily distinguished. There is no fat around the tail head.
2	The transverse process can be identified individually but feel rounded rather than sharp. There is some fat cover at the tails head.
3	The transverse processes can only be felt with firm pressure and the areas on each side of the tail head have some fat cover
4	Fat cover around the tail head is easily seen as slight mounds and is soft to the touch. The transverse processes cannot be felt, even with firm pressure.
5	The bone structure of the animal is no longer noticeable and the tail head is almost buried in fatty tissue

*The condition scoring system is based on handling two areas of the cow to assess the level of fat cover – the loin area and around the tail head. The fat cover over the loin is the major area for condition scoring, particularly thin animals. Above a condition score of 3, however, the bones around the loin can no longer be felt and the amount of fat cover around the tail head is also used.

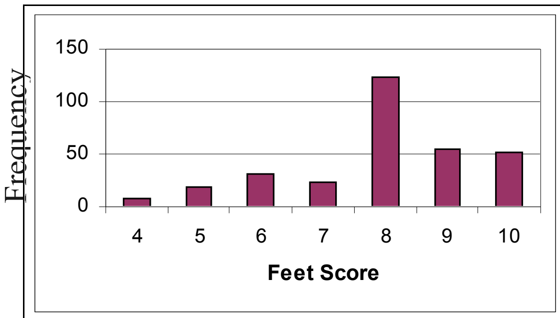


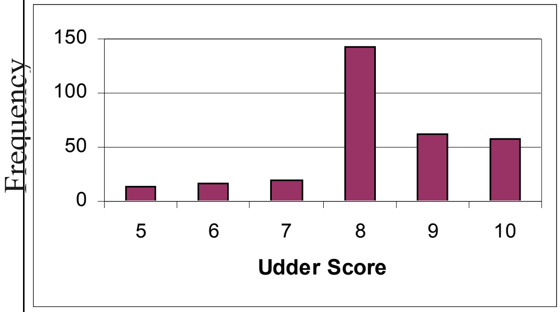
Skeletal Size

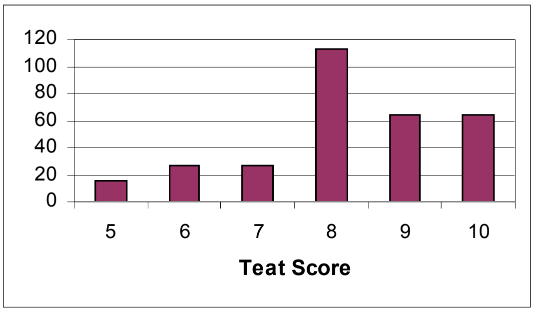
Measured from top of the spine in between hips to ground.
Precise measurement in centimetres or inches, or linear scale.
1 Short (1.30 cm)
5 Intermediate (1.42 cm)
9 Tall (1.54 cm)
Reference scale: 1.30 cm – 1.54 cm; 3 cm per point

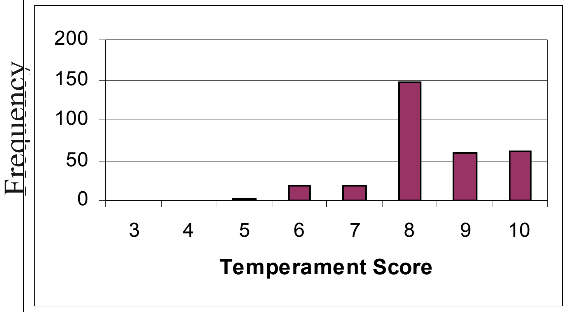


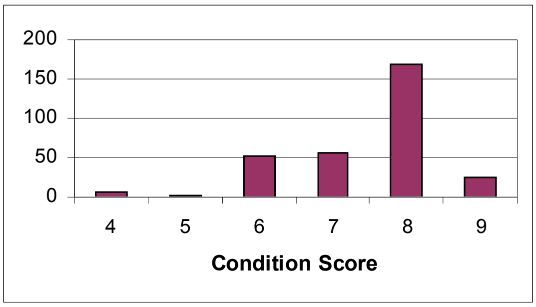
Appendix II: Distribution of Luing Type Scores

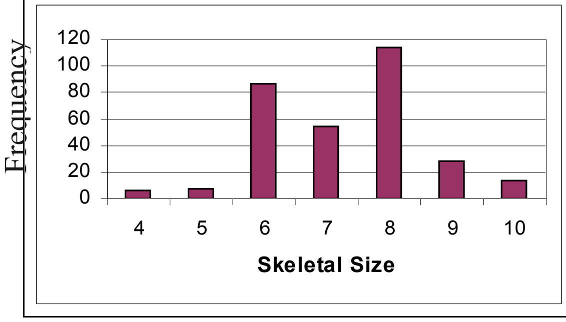












Appendix III: A Basic Understanding of Genetics

Extracted from "DeVuyst (2009) The economics of gene testing cattle"

Along with management and environment, genes determine the biology of an animal. Genes also determine, in part, the economics of animal agriculture. There are two general types of characteristics to be considered. A qualitative trait describes a trait that is either present or not. For example, a beef animal is either polled or not. So polled is called a qualitative trait. Similarly hide colour in Angus cattle is a qualitative trait. A red beef animal carries two copies of the recessive red gene where a black-hided beef animal carries at most one copy. In general, management and environment do not affect qualitative traits.

Other characteristics are quantitative. They vary in a continuum from one animal to another. Traits such as marbling, tenderness, weight, and fat cover are quantitative traits and are affected by genetics, management and environment. These traits are typically influenced by numerous genes and this where gene testing comes in.

A gene is a strand of DNA. Genes are further divided into exons and introns. Exons and introns alternate along a gene. Each exon is followed by an intron (and vice versa). Introns act essentially as spacers between exons. Subdividing even further, both exons and introns are made of strings of nucleotides. When one of these nucleotides is replaced by another nucleotide, a genetic mutation has occurred. In the terminology of geneticists, a Single Nucleotide Polymorphism (SNP) is present. (The abbreviation SNP is pronounced as "snip.") An SNP can also occur due the insertion or deletion of a nucleotide.

To a layperson, the terminology can be confusing. It helps to think of a chromosome as a city, a gene as a city street, exons and introns as blocks on that street and nucleotides as specific houses in that block. So, given a chromosome (city), a gene (street), an exon (block) and a nucleotide (house), we can "drive" up to a given location and observe the specific type of nucleotide (house) present. Note, there is also genetic code located in between genes (i.e., rural houses), called microsatellites, that can also influence biology.

As the previous analogy implies, there are different types of houses (nucleotides) that can be found at a given location. Four different nucleotides, cytosine, guanine, adenine, and thymine, make up DNA. These acids are abbreviated with the letters C, G, A, and T.

While most SNPs have no association with changes in biology, some SNPs are important because they are associated with quantitative traits. Those SNPs that are associated with biological variability typically explain less than 5% of biological variability. So, for many economically relevant traits, we may need to look at dozens of SNPs to explain a significant portion of biological and economic variability between animals.

Geneticists also refer to "alleles." An allele is used to describe differences between gene pairs. For example, if at a given position a C-nucleotide is found on a gene and a T-nucleotide is found on its paired gene, we would refer to C-allele and T-allele to denote the differences between the gene pair. It is possible that the gene might have nucleotide differences in multiple locations. For example, a CT-allele and a GA-allele. The allele pair is called a genotype. Animals with two different nucleotides are called heterozygous, for example a CT genotype. If the animal has the same nucleotide on the gene pair, it is called homozygous, for example, "homozygous T," or TT genotype. Also, note if more than one nucleotide or microsatellite is tested, the resulting information is called a haplotype.

Several genotyping/haplotyping testing services are available. These include parentage, hide colour, polled, feed efficiency, tenderness, some reproductive traits, marbling, and several other carcass traits (Garrick and Van Eenennaam 2008). What is not well known at this time is the value to the producer of most of this genetic knowledge.