

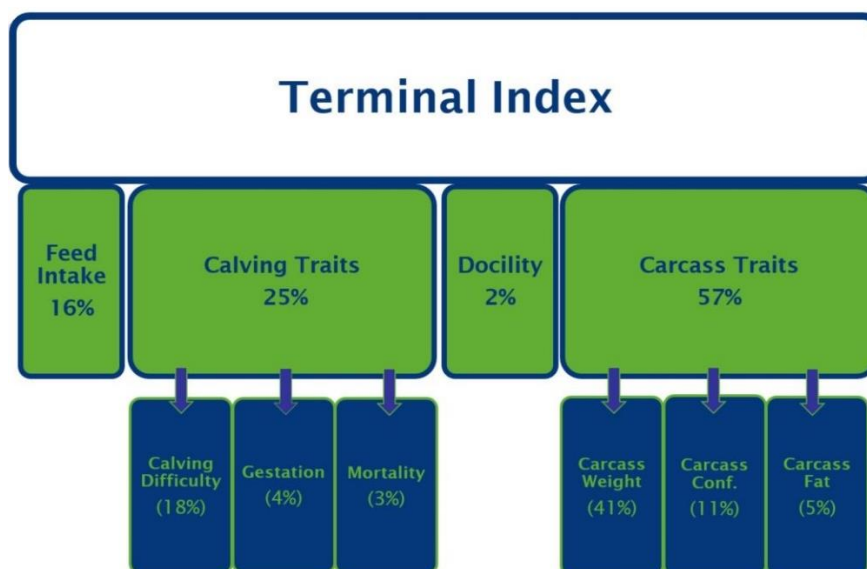


Beef Evaluations

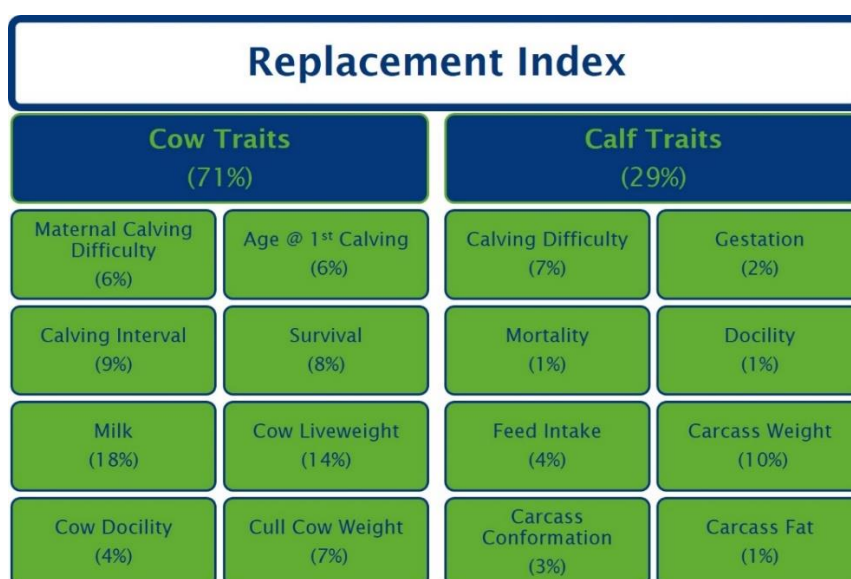
Supporting Document

The Eurostar Index is a profit focused index designed for Ireland's beef sector. The Eurostar Index is divided into the Terminal and Replacement indexes, with traits grouped together according to their importance to achieving the overall goal.

The principle of the Terminal Index is based on low costs of production, *i.e.* low cost associated with calving, low mortality, short gestation, less feed consumed per kilogram of carcass and as high a return on the carcass as possible. In short, the Terminal Index estimates how profitable an animal's progeny will be with regards to live weight, carcass conformation and being finished for slaughter.



The Replacement Index estimates how suitable an animal's daughters will be for calving ability, milk, fertility, and ultimately being low maintenance suckler cows. Cow Contribution accounts for the performance of direct daughters for Milk, Calving Interval, Cull Cow Weight, etc. Calf Contribution reflects the performance of the progeny of daughters for traits such as Feed Intake, Carcass Weight, Carcass Conformation, etc.



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1.0. Glossary of Terms

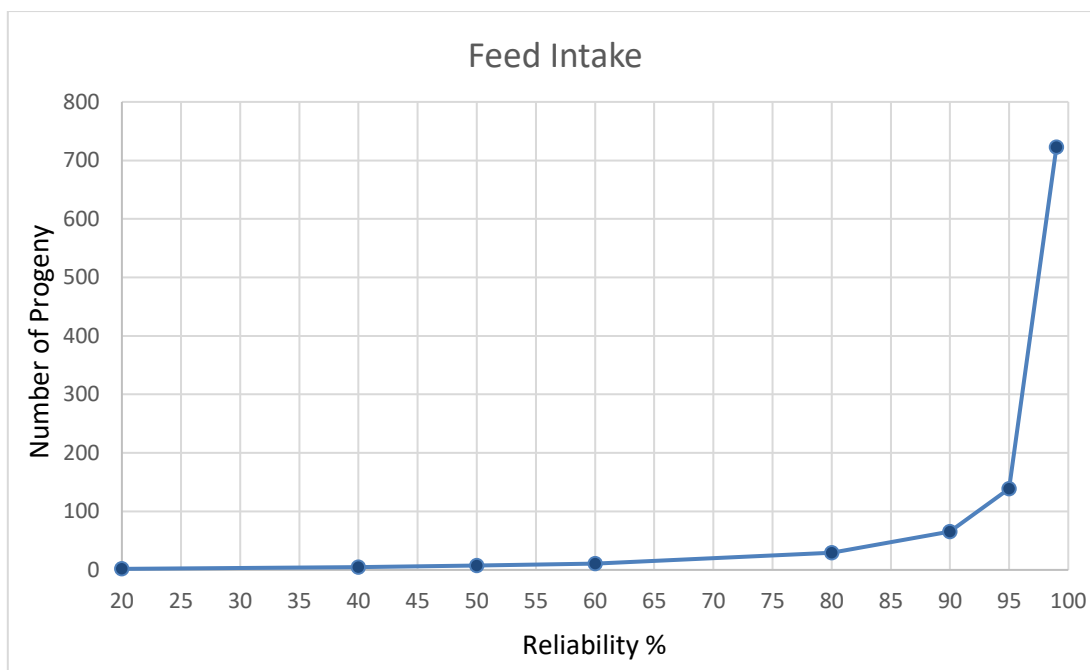
1.1. Breeding Value

Breeding value refers to the value of an animal in a breeding program for a particular trait. An animal's breeding value is estimated to be twice the expected performance of its progeny. The expected progeny performance is called transmitting ability and is, therefore, half of the breeding value. In other words, transmitting ability is the genetic advantage an individual transmits to its offspring. Breeding values can be estimated based on the animal's own records and the performance of known relatives. These estimated breeding values (EBV) divided by two may be used to predict the performance of future offspring and are termed **Predicted Transmitting Ability** or **PTA**. For example, the daughters of a bull with a PTA of 18 kg for milk yield would be expected to produce, on average, 8 kg more milk per lactation than the daughters of a bull with a PTA of 10 kg for milk yield if their dams have equal genetic merit. The actual difference will not be exact for comparing individual daughters because no two daughters would get the exact same combination of genes or be exposed to the exact same environment. Thus, daughters of the same sire may have widely varying performance.

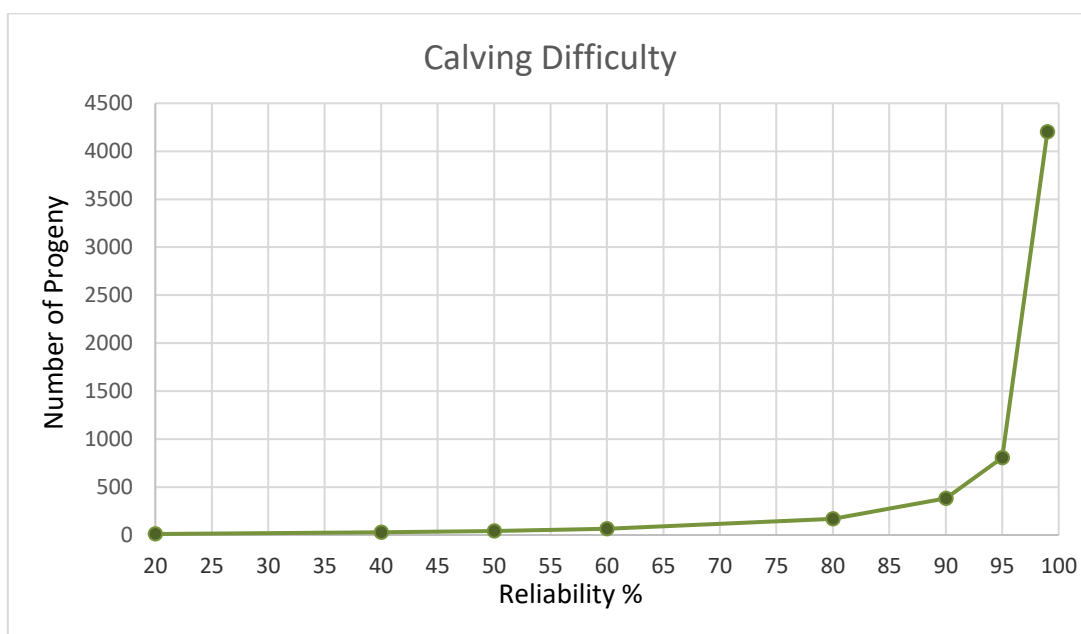
1.2. Reliability

The measure of accuracy or degree of confidence in a PTA is called reliability, which is defined as the squared correlation between an animal's true transmitting ability and PTA. Often, in practice, this value is approximated rather than calculated directly. Essentially, reliability for PTA of a trait is a function of the heritability of that trait and the amount of information available. That information may come from the animal's own performance, from the performance of offspring, or from information for parents. As heritability and amount of information increase, reliability also increases. Thus, an animal has a higher reliability for carcass weight than for reproductive efficiency (even if the same number of records are available from the animal and its relatives) because carcass weight is under greater genetic control. Also, a bull with many daughters has a more reliable PTA for any given trait than a bull with few daughters.

The number of progeny records required to achieve certain levels of reliability depends on the heritability of the trait. For example, Feed Intake has a heritability of 43%, whereas Calving Difficulty has a heritability of 9%. The number of records required to achieve high reliability in these two traits is very different. To reach 90% reliability for Feed Intake, 66 progeny performance records are required.



To have the same level of reliability for Calving Difficulty, 382 progeny calving records are required.



1.3. 95% Confidence Interval

When looking at reliabilities, high or low, it's important to know how much a trait PTA can change by from one evaluation to the next. We do this by calculating the 95% Confidence Interval. Essentially, what it does is say you can be 95% certain that the true value falls within the limits of a specific range. It can be easily calculated for the overall index or individual traits with a small amount of information.

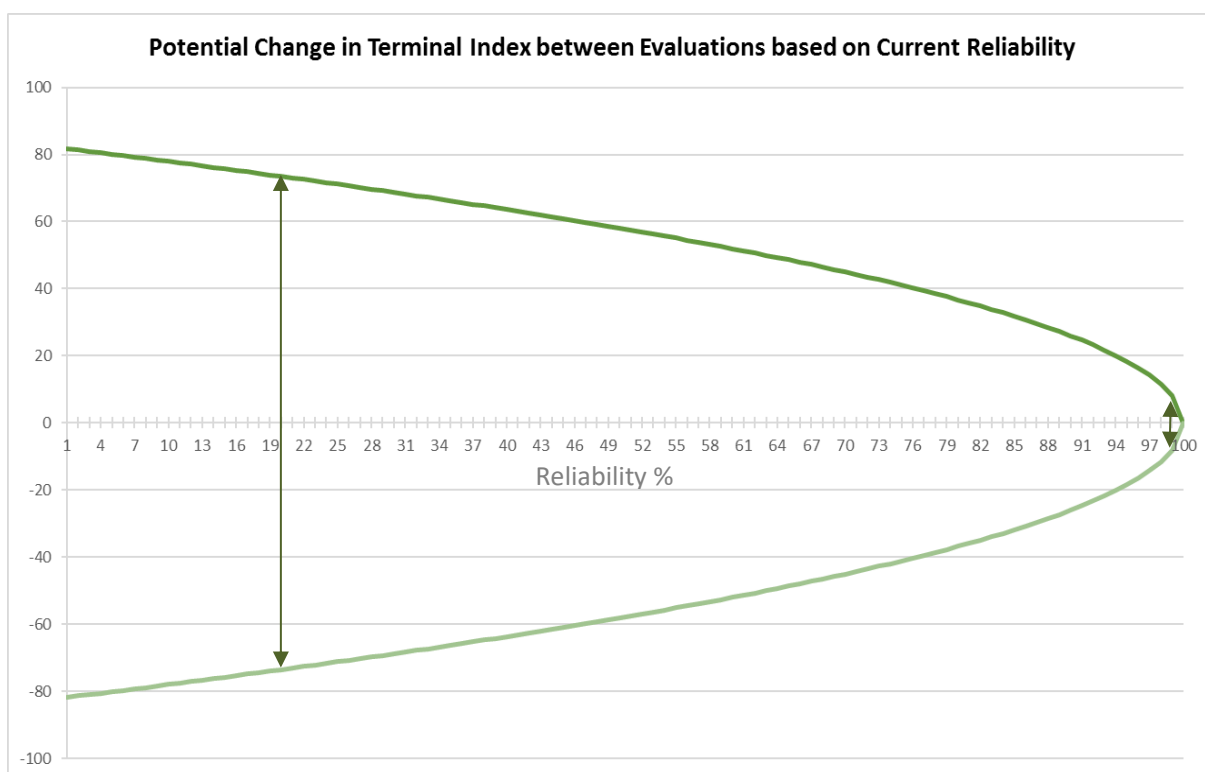
$$95\% \text{ Confidence Interval} = \text{Index Value} \pm (1.96)(\text{Std Dev}) \left(\sqrt{\frac{(100 - \text{Reliability})}{100}} \right)$$

Standard deviation reflects the variation across the population, and 1.96 is a standard value used to calculate the 95% confidence interval. This equation will work for any trait, as long as you have the standard deviation for that trait, in the most recent evaluation run.

e.g. if a bull has a Terminal Index of €140 at 92% reliability, you can be 95% sure that the true Terminal Index value falls between €117 and €163 (December 2017 Evaluation).

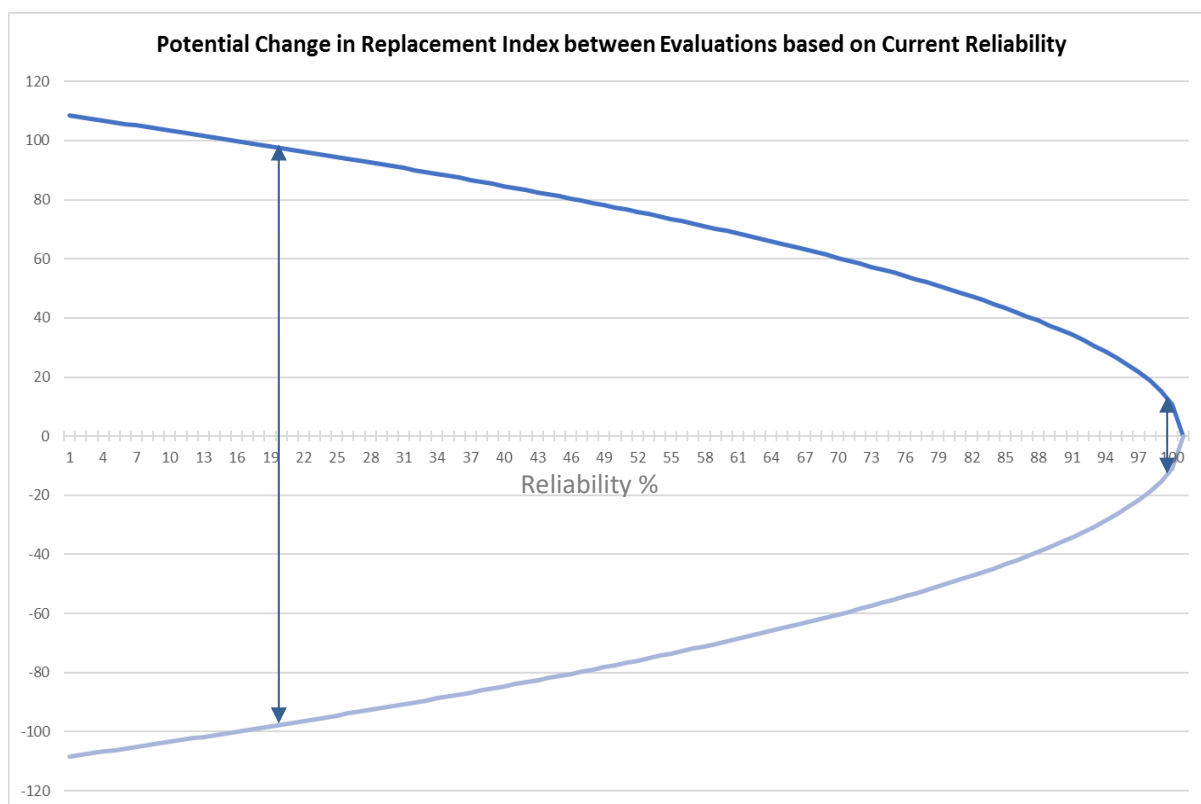
$$95\% \text{ Confidence Interval} = \text{€}140 \pm (1.96)(41.903) \left(\sqrt{\frac{(100-92)}{100}} \right) = \text{€}140 \pm \text{€}23$$

Below are visual representations of the 95% Confidence Interval for both indexes, with the standard deviation coming from AI bulls with 60%+ reliability (representative of the population). The standard deviation changes at each evaluation.



Reliability is on the horizontal axis, with the magnitude of potential change on the vertical axis. From the above graph you can see that the Terminal Index of a sire at 20% reliability can change by ±€73

as indicated by the larger arrow (December 2017 Evaluation). Conversely, at 99% reliability, the Terminal Index can only change by $\pm\text{€}8$ (December 2017 Evaluation).



Above is the 95% Confidence Interval graph for the Replacement Index. At 20% reliability, the Replacement Index of a sire can change by $\pm\text{€}97$ as indicated by the larger arrow (December 2017 Evaluation). Conversely, at 99% reliability, the Replacement Index can only change by $\pm\text{€}11$ (December 2017 Evaluation).

The 95% Confidence Interval for each trait is included in this document, using the standard deviations of AI bulls with 60%+ reliability from the December 2017 Evaluation.

1.4. Contemporary group

A contemporary group comprises of animals of similar age range kept under the same or at least similar management conditions. Contemporary groups allow us to account for variation in animals that is due to external factors, giving a clearer view of the genetic merit of an animal to help accurately predict its breeding value. Examples of these external factors include Herd-Year-Season, Calving month, etc.

1.5. Genetic Correlation

The correlation between breeding values for two traits is called genetic correlation and indicates to what extent the two traits are influenced by the same genes. For example, the genetic correlation between Cow Live Weight and Cull Cow Weight is high (0.74). Many of the same genes that influence Cow Live Weight also influence Cull Cow Weight, and a bull with daughters that have high mean Cow Live Weight almost always will sire daughters that have high mean Cull Cow Weight. As with any correlation, the larger the magnitude (*i.e.* the further from 0), the greater is the relationship between the traits. For a heritable trait, selection of genetically superior animals to be parents (*i.e.*, genetic selection) will produce offspring that are genetically better on average for that trait. This result is called response to selection. Genetic selection on such a trait will also affect any genetically correlated traits; this is called correlated response to selection.

1.6. Heritability

Heritability is the extent to which genetics influences a trait or characteristic. Unlike breeding values and predicted transmitting abilities, which are estimated for individuals, heritability is a population parameter. Strictly defined, heritability is the ratio of additive genetic variance to phenotypic variance. Additive genetic variance is the true variance among breeding values of animals in a population. Hence, heritability is a ratio of the variance of breeding values to the variance of phenotypes. The possible range of values for heritability is from 0 to 1.0, because additive genetic variance is a part of phenotypic variance. Phenotypes are what is observed or measured about a particular trait; phenotypes are influenced by genetic and environmental effects. In measuring heritability, phenotypic variances are taken to be the total of random sources of variation after adjusting for systematic sources of variability, such as herd/year, age, month of calving, or stage of lactation. The extent of genetic control is different for each trait. The higher the heritability, the greater the genetic control on the trait, and the more rapidly selection will result in genetic progress. In general, yield traits and overall type tend to be moderately heritable; size has higher heritability, and reproductive efficiency has lower heritability. Mastitis resistance has a heritability of about 0.10. In other words, genetics accounts for 10% of the variation in cows' capacity to resist mastitis infection, and environment accounts for the remaining 90%.

1.7. Genetic Variation

Individuals of a species have similar characteristics, but they are rarely identical, the difference between them is called variation. Genetic variation describes the genotypic differences between individuals in a population, and between populations. This variation arises through genetic mutation and is important as it provides the diversity within and between populations required for selection. It is a measure of the variation that exists in the genetic makeup of animals within the population. The genetic variation of an entire species is often called genetic diversity. Genetic variations are the differences in DNA segments or genes between individuals and each variation of a gene is called an

allele. If you remove environmental variation from phenotypes, what you have left is the genetic variation.

For example, a population with many different alleles at a single chromosome locus has a high amount of genetic variation. Genetic variation is essential for selection because selection can increase or decrease frequency of alleles that already exist in the population.

Genetic variation is caused by:

1. Mutation
2. Random mating between animals
3. Random fertilization
4. Recombination during meiosis

The last three of these factors reshuffle alleles within a population, giving offspring combinations which differ from their parents and from others.

1.8. Edits

Edits refer to the tidying up of data before using it for evaluation. It is used when data is deemed not useful, *i.e.* a known abortion record is not useful in calculating Calving Difficulty or Calving Interval of an animal. Editing also occurs on improbable records, *i.e.* lack of variation in a record like milk ability and errors in recording leading to records outside of biological limitations.

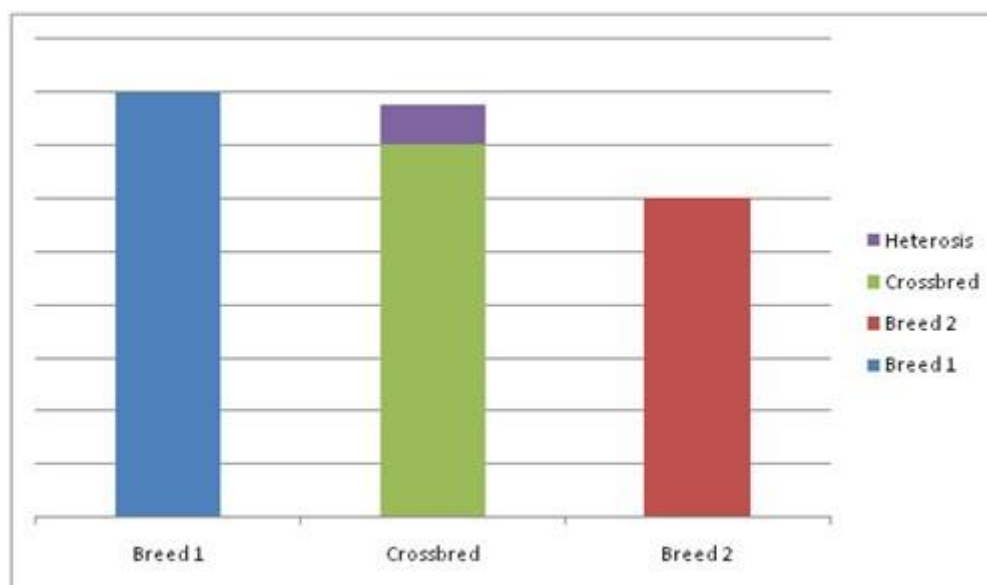
1.9. Genomics

Genomics is the study of an animal's DNA or 'Genotype' collected from tissue, blood or hair sample. Genotypes are made up of Single Nucleotide Polymorphisms (SNPs). These are a DNA sequence variation occurring commonly within a population and each SNP represents a difference in a single DNA building block, called a nucleotide. Chips used in genomic testing can vary in size and can have various numbers of SNPs. DNA is transmitted in chunks and genomic testing then identifies which DNA chunks have been passed from the parents to its offspring. The genotype is studied to check parentage to confirm that the dam and sire recorded are correct. The second thing that genomics looks at are the SNPs an animal has which can account for the variation in an animal's traits (carcass weight, milk ability etc.). The genomic sample is essentially compared to the genomic samples of proven animals (called the Training Population). The Training Population for animals for beef evaluations is made up of many cows, stock bulls, along with well proven AI sires. Having a greater the number of well proven animals in the Training Population results in more accurate genomic evaluations. It also varies between traits, *i.e.* the number of animals in the training population for carcass weight is over 227,000 animals, whereas calving difficulty is just over 106,000 animals (December 2017 Evaluation). The number of animals in the Training Population changes with each evaluation.

1.10. Heterosis

The increased productivity or superiority over the parental average is known as heterosis or hybrid vigour. Heterosis can be defined as the superiority of a hybrid or crossbred over both the parents in terms of yield and some other characteristic.

Heterosis, hybrid vigour, or outbreeding enhancement, is the improved or increased function of any biological quality in a hybrid offspring. An offspring exhibits heterosis/hybrid vigour if its traits are enhanced as a result of mixing the genetic contributions of its parents.



1.11. Recombination

Recombination is a process by which pieces of DNA are broken and recombined to produce new combinations of alleles. This recombination process creates genetic diversity at gene level that reflects differences in the DNA sequences of different organisms.

In eukaryotic cells, which are cells with a nucleus and organelles, recombination typically occurs during meiosis. Meiosis is a form of cell division that produces gametes, or egg and sperm cells (haploid cells). During the first phase of meiosis, the homologous pairs of maternal and paternal chromosomes align. During the alignment, the arms of the chromosomes can overlap and temporarily fuse, causing a crossover. Crossovers result in recombination and the exchange of genetic material between the maternal and paternal chromosomes. As a result, offspring can have different combinations of genes than their parents. Genes that are located farther apart on the same chromosome have a greater likelihood of undergoing recombination, which means they have a greater recombination frequency.

1.12. Blending

Blending is the process of amalgamating two sources of trait information. This occurs for all traits where an animal has been genotyped, where the genotype (SNP) information is amalgamated with the domestic proof for an animal. Blending also occurs in the Milk trait, whereby Cow Milk Scores and Maternal Weaning Weight are combined, with the weighting of each dependent on source reliability. Where the reliability of records is higher for one trait or the other, more emphasis is given to the trait with higher reliability. This becomes very relevant for animals with an imbalance in the data for the two traits.

1.13. Direct Effects

Direct effects are the traits of the animal that are solely influenced by the genes of the animal. Direct effects are what is coming directly from the animal's own genotype. These are not influenced by the animal's environment or the mothering ability of the animal's dam (See: 1.14. Maternal Effects).

1.14. Maternal Effects

Maternal genetic effects occur when genes expressed in the dam affect the phenotype of her offspring. Maternal genetic effects are arguably the most common example of indirect genetic effects, wherein the genes in one individual affect the phenotype of another. However, maternal effects (genetic and non-genetic) also arise from a range of scenarios in which mothers provide a component of the environment experienced by offspring, such as through nutritional provisioning (milk).

Two traits where maternal effects have a large role are Calving Difficulty (Maternal Calving Difficulty) and Weaning Weight (Maternal Weaning Weight). Maternal Calving Difficulty is derived from the maternal effect of Calving Difficulty. This is because the dam's phenotype plays a role in the calving ease of a calf. If the dam has expressed genes resulting in a smaller pelvis, there will be increased difficulty in the birth of progeny. Similarly, weight at weaning can be, in part, attributed to the dam. The dam provides nutrition for the calf, but the calf's own genes will impact growth rate.

1.15. Predictor Traits

Predictor Traits, or Indicator Traits as they are also known, signal what an animal may be like for another trait. An example of this is the inclusion of Carcass Fat in the Fertility evaluation. Fat is known to adversely affect female fertility. Another common example of this is birthweight being an indicator of Calving Difficulty, as heavier calves have more difficult births.

1.16. Economic Values

Economic Values are determined by Teagasc and are routinely updated. These are derived from data collected from beef farms and from the National Farm Economic Model. The Economic Value factors in the associated costs and income for a specific trait; *i.e.* for milk, it accounts for cows producing more milk consuming more feedstuffs (Cost) but returning a heavier weanling (Income). Economic Values are crucial in the calculation of the index, as PTAs are multiplied by the economic weight for each trait, and when summed, amount to give the Index Value.

1.17. Publication

Beef proofs are released six times annually, and the publication dates are available under the *Genetic Evaluations* tab on www.icbf.com. All proofs of pedigree males are available through the ICBF Animal Search, also located on the website and new proofs can be found in online profiles for HerdPlus customers. Where a genotype has been received prior to the extract date (available under the *Genetic Evaluations* tab on www.icbf.com, approximately 6 weeks before the publication date), a blended genomic and domestic will be published. Where a genotype has not been received prior to this date, a non-genomic domestic proof is published in the new evaluation.

1.18. Eurostars

€urostars make the Index value easy to understand by providing a visual component. They show where an animal's genetic index ranks within the population. €urostars are formed on a percentile basis from the Index Value. Five stars means the animal is in the top 20% of the population, with each star representing 20% of the population.

<i>Across Breed</i>	<i>€urostar Rankings</i>	
★★★★★	5 Stars	<i>Index Value is in top 20% of all animals</i>
★★★★	4 Stars	<i>Index Value is in top 40% of all animals</i>
★★★	3 Stars	<i>Average Index Value</i>
★★	2 Stars	<i>Index Value is in bottom 40% of all animals</i>
★	1 Star	<i>Index Value is in bottom 20% of all animals</i>

The Index is calculated prior to a Star Rating being applied. The cut offs for each star rating change with each evaluation as they are reflective of the entire population. A document (*Breed Percentiles*) with the current breed specific percentiles for €urostar cut-offs has been included with this document.

Within Breed stars are for ranking purebred animals from the same breed. Across Breed stars show where the animal's index ranks against animals across all other breeds. For example, a bull may be 5 stars for a trait Within Breed, but 1 star Across Breeds, if the bull's breed has a lower Breed Average than the All Breeds Average for that trait.

E.g. NEX – Nelson - (December 2017 Evaluation)

Star Rating (within Charolais breed)	Key profit traits	Index value	Trait reliability	Star Rating (across all beef breeds)
★★★★★	Daughter milk (kg) Breed ave: -4.61kg. All breeds ave: 2.09kg	-2.30kg	97% (V High)	★☆☆☆☆

2.0. Foreign Data

Foreign Estimated Breeding Values (EBVs) are included in Irish evaluations, where available, for 10 major breeds. Currently data from both France and the UK are included. The relationship between Foreign EBVs and our evaluations is set at 0.85, with the respective Irish trait. The correlation is due to differences in trait definition and subsequently trait measurement. We currently receive foreign EBVs for Calving Difficulty, Maternal Calving Difficulty, Maternal Weaning Weight, Linears and Carcass Weight. We do not receive the actual data recorded from foreign countries, so we incorporate the EBVs after our domestic evaluations have taken place.

2.1. Foreign Data Inclusion

Foreign data inclusion is summarised in the document, *Incorporation of Foreign EBVs*, included with this document. This document outlines how ICBF incorporates foreign EBVs into the genetic evaluations.

3.0. Beef Performance Traits

3.1. Traits in Model

There are three multi-trait models used to calculate the six beef performance traits. These are split into Carcass Weight, Conformation and Feed Intake models.

The 12 traits included in the Carcass Weight model are: Carcass Weight, 150-250 day weight, 250-350 day weight, 350-450 day weight, 450-550 day weight, 550-700 day weight, Cow Live Weight, Cull Cow Weight, Skeletal Score, Foreign Weaning Weight EBV, Foreign Skeletal EBV and Foreign Carcass Weight EBV.

The 9 traits included in the Conformation model are: Carcass Conformation, Cow Conformation, Muscle Score, Calf Quality, Calf Price, Weanling Price, Post Weanling Price, Foreign Muscle EBV and Foreign Skeletal EBV.

The 11 traits included in the Feed Intake model are: Feed Intake, Carcass Weight, Carcass Conformation, Carcass Fat, 350-450 day weight, 450-550 day weight, 550-700 day weight, Skeletal score, Foreign Weaning Weight EBV, Foreign Carcass Weight EBV and Foreign Carcass Conformation EBV.

3.2. Contemporary Groups

Slaughtered animals: Bullocks, cows, heifers and bulls are all compared in separate groups. Show animals and ET animals are grouped into separate contemporary groups. Linear scored animals are compared to their own contemporary groups. Crossbred and pedigree animals are compared in separate contemporary groups. Animals in groups of less than 5 animals are included for each trait. Maximum contemporary group size is 30. Slaughtered animals are compared to contemporary groups in herd at time of slaughter and their herd of longest residency prior to that (usually herd of birth). Contemporary groups are random, which helps account for environmental variation and helps estimate breeding values for smaller breeds.

3.3. Edits

Animals with invalid sires and dams have progeny excluded. Show herds are separated from commercial herds. There is editing on weights within the evaluation. Outside of the ranges below, weights are excluded from the evaluation.

Weight Type	Less than	Greater than	ADG less than	ADG greater than
0-10 day weight	25	115	-	-
10-50 day weight	30	130	-	-
50-150 day weight	55	350	0.4	2.0
150-250 day weight	105	600	0.4	2.0
250-350 day weight	145	870	0.4	2.0
350-450 day weight	185	1003	0.4	2.2
450-550 day weight	225	1100	0.4	2.2
550-700 day weight	265	1200	0.4	2.2

If animals were linear scored and weighed, then 75% of eligible animals need to be scored to be included in the evaluation. The number of eligible animals is calculated as follows:

$$\frac{\text{Number of Animals Scored} + \text{Number of Sick Animals} + \text{Number Previously Scored}}{\text{Total Number of Animals Eligible to be Scored}}$$

Mart prices are adjusted for sale effect and age. Only mart weights of single animals are included in the evaluation. Sale prices of pedigree animals are excluded. Calf Quality scores where there is no variation within herd are excluded.

3.4. Carcass Weight

3.4.1. Definition

Carcass Weight is defined as the weight of both half carcasses after being bled, eviscerated and after removal of skin, removal of external genitalia, the limbs at the carpus and tarsus, head, tail, kidneys and kidney fats and the udder.

3.4.2. Trait Explanation

Carcass Weight as a trait comes from the recorded factory carcass weights of a bull's progeny. This information comes from the Department of Agriculture. Along with this, Carcass Weight is highly correlated with many other traits. Live weights can be very good predictors for Carcass Weight.

3.4.3. Heritability

The heritability of Carcass Weight is 38%, meaning it is a trait where we can actively breed for improvement, and make significant, cumulative gains. There is a huge amount of genetic variation in Carcass Weight, with PTAs of AI bulls over 60% reliability ranging from -56kg to 57kg.

3.4.4. Correlations

Carcass Weight is positively correlated to many live weight traits. This is useful for predicting the slaughter attributes of an animal's progeny while they are still alive. Carcass Weight is also a good indicator of Cow Live Weight and Cull Cow Weight. These correlations are useful in gathering data on animals early in life, resulting in more accurate breeding values.

Trait	Genetic Correlation
150-250 Day Weight	0.57
250-350 Day Weight	0.61
350-450 Day Weight	0.65
450-550 Day Weight	0.67
550-650 Day Weight	0.70
Cow Live Weight	0.50
Skeletal Composite	0.38
Cull Cow Carcass Weight	0.60

3.4.5. Base

93,711 animals (in the current beef evaluation with a carcass record & born in the 2000 to 2002 period) across varying breeds define the base Carcass Weight as 315kg. These same animals set the bases for Carcass Conformation and Carcass Fat.

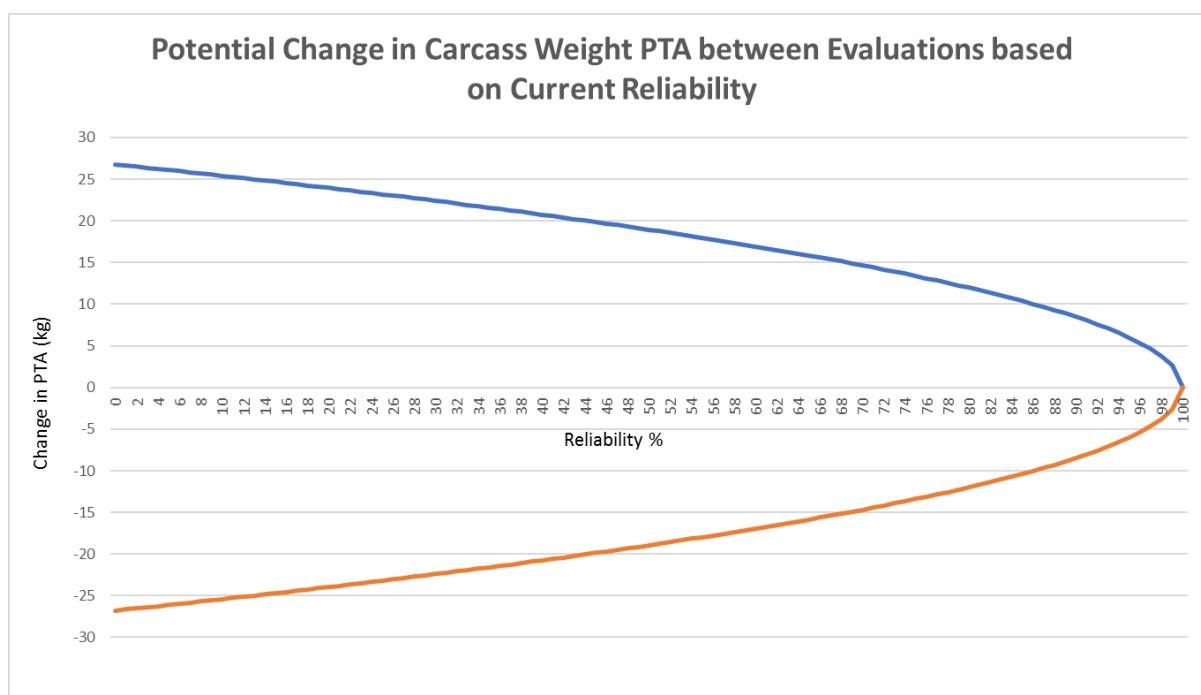
Primary Breed	Number of Records	Carcass Weight (kg)
HO	52,103	320
BB	9,236	333
AA	8,691	303
FR	6,634	318
LM	6,139	327
HE	4,857	311
SI	3,227	325
CH	2,966	353
MO	1,045	333
12 other dairy breeds	1,244	322
9 other beef breeds	145	327
Total Number Slaughtered	96,287	315kg Weighted Average

3.4.6. Economic Weight & Relative Emphasis

Trait	Terminal Index		Replacement Index	
	Trait Emphasis	Economic Weight	Trait Emphasis	Economic Weight
Carcass Weight	41%	€3.14	10%	€2.10

See section 1.16 – Economic Values

3.4.7. 95% Confidence Interval



3.5. Carcass Conformation

3.5.1. Definition

Carcass Conformation is the shape and development of the carcass. It is denoted by the letters E, U, R, O, P with E being the best and P the poorest and subsequently divided into a 15-point scale with the use of +, =, and – for each letter grade.

3.5.2. Trait Explanation

Carcass Conformation is derived from recorded carcass grades from the slaughter plants across Ireland. Over 90% of carcasses are classified by machine. Machine classification makes use of Video Image Analysis (VIA) to carry out various measurements of the carcass. The determination of classification in this case is objective. In smaller plants, classification is carried out by factory employees who have been licensed by the Department of Agriculture, Fisheries and Food. As the EUROP scale is used across Europe which facilitates the use of foreign EBVs being incorporated into our evaluations.

3.5.3. Heritability

The heritability of Carcass Conformation is 33%, meaning it is a trait where we can actively breed for improvement, and make significant, cumulative gains. There is a huge amount of genetic variation in Conformation, with PTAs of AI bulls over 60% reliability ranging from -1.39 to 3.48 (Grade in 15 point scale).

3.5.4. Correlations

Carcass Conformation is correlated to a number of traits which can be recorded when animals are still alive, making them good predictors for Carcass Conformation.

<i>Trait</i>	<i>Genetic Correlation</i>
Cow Conformation	0.57
Muscle Composite	0.47
Weanling Quality	0.30
Weanling Price	0.36
Post Weanling Price	0.51

3.5.5. Base

93,711 animals (in the current beef evaluation with a carcass record & born in the 2000 to 2002 period) across varying breeds define the base Carcass Conformation as between an O = & an O+, on the 15-point scale. The breed breakdown of these animals is listed below.

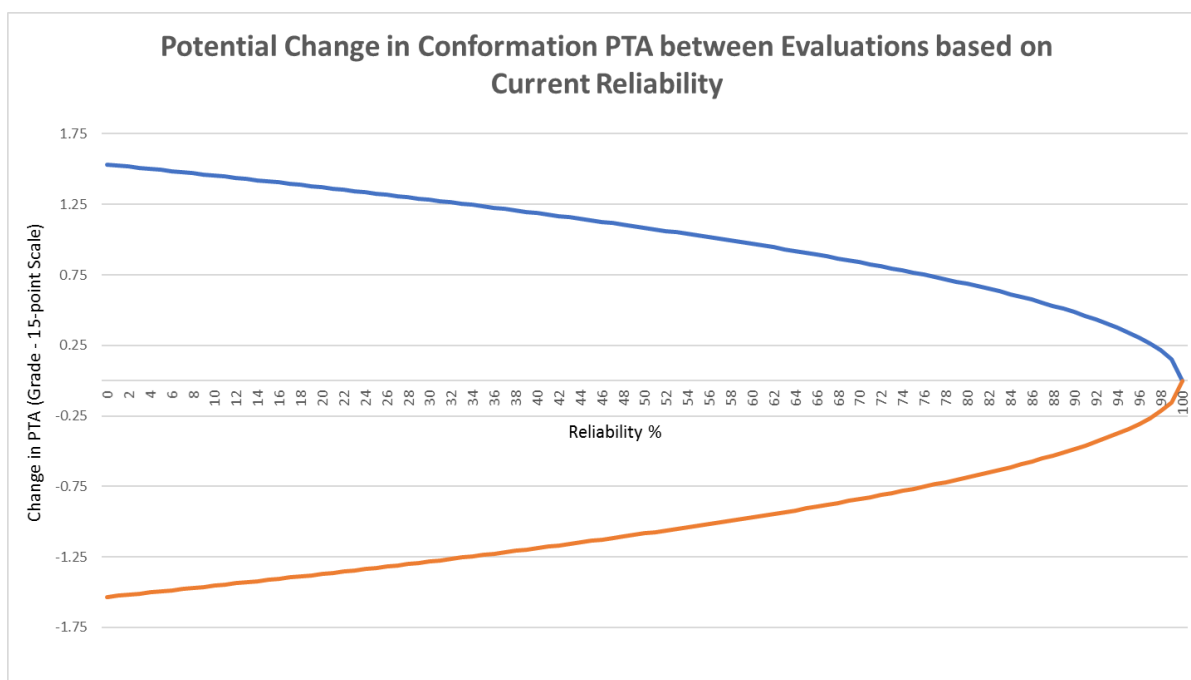
Primary Breed	Number of Records	Carcass Weight (kg)
HO	52,103	320
BB	9,236	333
AA	8,691	303
FR	6,634	318
LM	6,139	327
HE	4,857	311
SI	3,227	325
CH	2,966	353
MO	1,045	333
12 other dairy breeds	1,244	322
9 other beef breeds	145	327
Total Number Slaughtered	96,287	315kg Weighted Average

3.5.6. Economic Weight & Relative Emphasis

Trait	Terminal Index		Replacement Index	
	Trait Emphasis	Economic Weight	Trait Emphasis	Economic Weight
Carcass Conformation	11%	€14.77	3%	€10.22

See section 1.16 – Economic Values

3.5.7. 95% Confidence Interval



3.6. Carcass Fat

3.6.1. Definition

Carcass Fat is the level of fat covering on the carcass. It is denoted by a scale from 1 to 5 (1 being lean and 5 being fattest) and subsequently divided into a 15-point scale with the use of +, =, and – for each fat score.

3.6.2. Trait Explanation

Carcass Fat is derived from recorded carcass fat scores from the slaughter plants across Ireland. Over 90% of carcasses are classified by machine. Machine classification makes use of Video Image Analysis (VIA) to carry out various measurements of the carcass. The determination of classification in this case is objective. In smaller plants, classification is carried out by factory employees who have been licensed by the Department of Agriculture, Fisheries and Food.

3.6.3. Heritability

The heritability of Carcass Fat is 30%, meaning it is a trait where we can actively breed for improvement, and make significant, cumulative gains. There is a huge amount of genetic variation in Carcass Fat, with PTAs of AI bulls over 60% reliability ranging from -1.49 to 1.41 (Fat Score in 15 point scale).

3.6.4. Correlations

Trait	Genetic Correlation
Carcass Weight	0.10
Carcass Conformation	-0.05
Skeletal Composite	-0.20
350-450 Day Weight	-0.15
450-550 Day Weight	-0.15
550-650 Day Weight	-0.15
Weanling Price	-0.34
Post Weanling Price	-0.28

3.6.5. Base

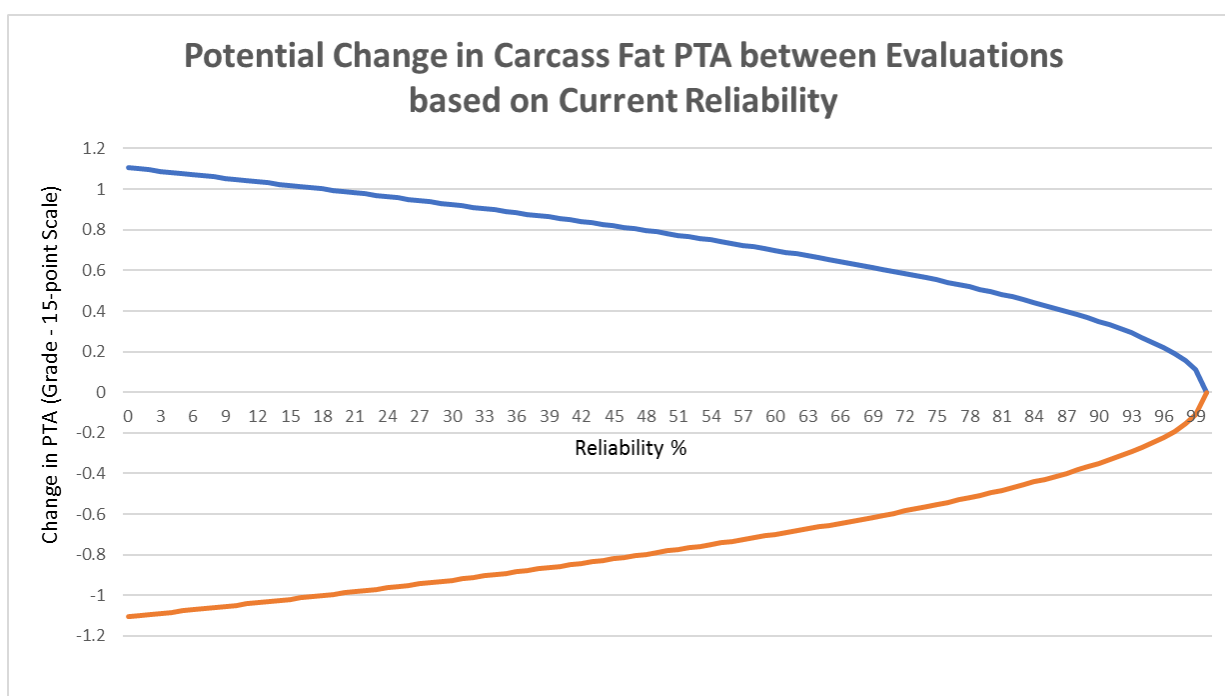
The average Carcass Fat score from the same 93,711 base animals (in the current beef evaluation with a carcass record & born in the 2000 to 2002 period) as Carcass Weight is between a 3 = & a 3 +, on the 15-point scale. The breed breakdown is below.

Primary Breed	Number of Records	Carcass Weight (kg)
HO	52,103	320
BB	9,236	333
AA	8,691	303
FR	6,634	318
LM	6,139	327
HE	4,857	311
SI	3,227	325
CH	2,966	353
MO	1,045	333
12 other dairy breeds	1,244	322
9 other beef breeds	145	327
Total Number Slaughtered	96,287	315kg Weighted Average

3.6.6. Economic Weight & Relative Emphasis

Trait	Terminal Index		Replacement Index	
	Trait Emphasis	Economic Weight	Trait Emphasis	Economic Weight
Carcass Fat	5%	-€7.86	1%	-€5.44
See section 1.16 – Economic Values				

3.6.7. 95% Confidence Interval



3.7. Feed Intake

3.7.1. Definition

Feed Intake is the amount of feed consumed by a young growing animal for the duration of the finishing period.

3.7.2. Trait Explanation

Feed Intake as a trait is difficult and costly to measure, however, progeny have feed intake measured in the Tully Performance Test Centre in Kildare. The trait evaluated is feed consumed per day on test. The PTA is used in the Terminal and the Replacement Index. In the Terminal Index it is the measure of feed consumed per slaughtered animal. In the Replacement Index it is also the measure of feed consumed per slaughtered progeny from a suckler cow.

3.7.3. Heritability

Feed Intake has a heritability of 43% meaning it is a trait where we can actively breed for improvement, and make significant, cumulative gains. There is a huge amount of genetic variation in Feed Intake, with PTAs of AI bulls over 60% reliability ranging from -1.17kg and 1.2kg.

3.7.4. Correlations

Feed Intake is also correlated to many traits which are more easily recorded, and information for other traits also comes from these sources.

<i>Trait</i>	<i>Genetic Correlation</i>
Cold Carcass Weight	0.37
Cold Carcass Grade	-0.22
Cold Carcass Fat	0.17
Cow Live weight	0.27
Weanling Quality	0.34
350-450 Day Weight	0.36
450-550 Day Weight	0.35
550-650 Day Weight	0.27
Skeletal Composite	0.17

3.7.5. Base

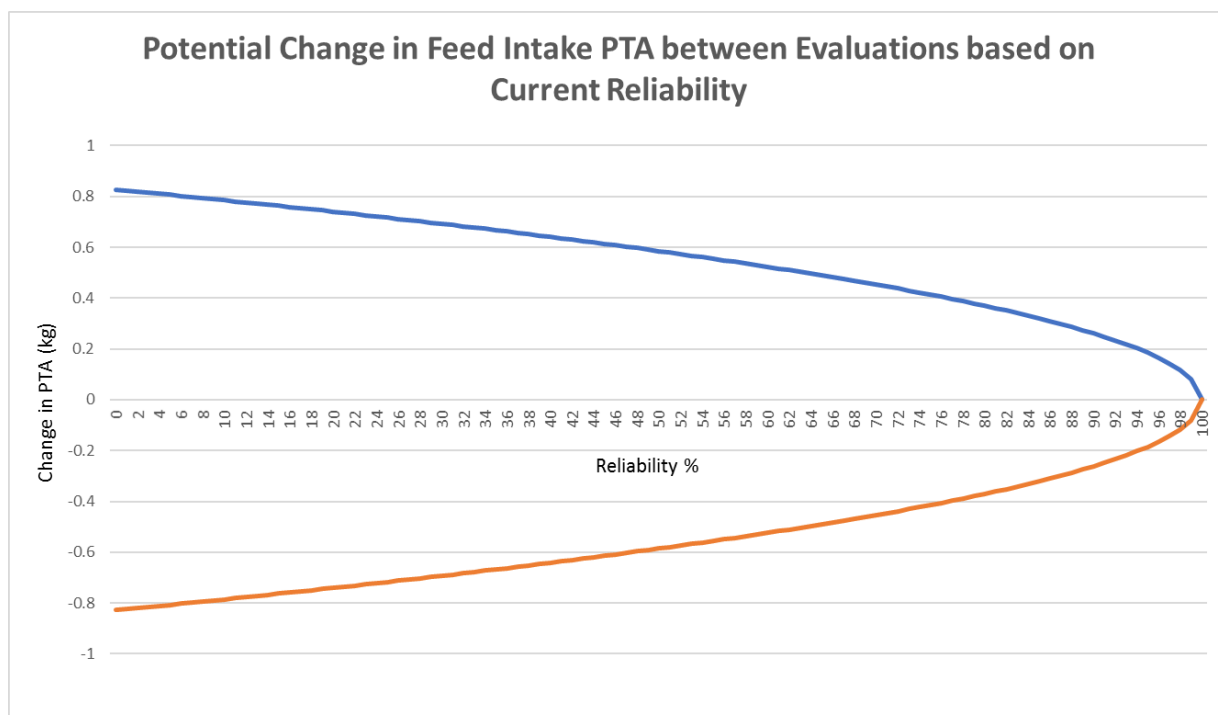
The base for Feed Intake as a trait is derived from the PTA's of the same base animals (93,711 animals in the current beef evaluation with a carcass record & born in the 2000 to 2002 period) used for the carcass traits bases. There is no reference phenotype for the trait.

3.7.6. Economic Weight & Relative Emphasis

Trait	Terminal Index		Replacement Index	
	Trait Emphasis	Economic Weight	Trait Emphasis	Economic Weight
Feed Intake	16%	-€38.63	4%	-€26.86

See section 1.16 – Economic Values

3.7.7. 95% Confidence Interval



3.7.8. Transformations of proofs based on Feed Intake Data

Assuming that the coefficient of variation and heritability of average daily feed intake at Tully are the same as for lifetime feed dry matter intake, then it can be shown that the genetic regression of lifetime feed dry matter intake (LDMI) on Tully average daily feed intake (TADFI) proofs is

$$\text{LDMIproof} = \text{TADFIproof} \times r_g \times \text{mean(LDMI)} / \text{mean(ADFI)}$$

The mean lifetime feed intake of 4600kg (i.e. mean(LDMI)) was as assumed above, and the mean Tully feed intake was 8.58 kg. Given the difference in diet between Tully and a typical industry system, and because Tully records only reflect intake for a part of the animal's life, we assume a genetic correlation (r_g) between the two feed intake definitions of 0.7. Thus,

$$\text{LDMIproof} = \text{TADFIproof} \times 375$$

3.8. Cow Live Weight

3.8.1. Definition

The weight of an adult female who has had previously had a calf.

3.8.2. Trait Explanation

Cow Live Weight is derived from live weights on cows from WHPR visits and mart weights and the cull cow carcass weights received from factories. Cull Cow Weight will always be recorded as the animals are slaughtered and is also a very good indicator of Cow Live Weight. Cow Live Weight as a trait is used to account for the higher intake of larger cows over their lifetime. Cow Live Weight is used to account for heifer and cow intake. The larger the cow, the higher her feed intake, increasing feed costs and ultimately, a negative impact on the profitability of the farm system. There is an important point in the construction of the Replacement Index which takes into account the fact that intake traits of a cow (grouped under Cow Live Weight) are expressed each lactation a cow is alive.

3.8.3. Heritability

The heritability of Cow Live Weight is 32%, meaning it is a trait where we can actively breed for improvement, and make significant, cumulative gains. Cows with a high Live Weight are likely to breed daughters with high Cow Live Weight. There is a huge amount of genetic variation in Cow Live Weight, with PTAs of AI bulls over 60% reliability ranging from -50kg to 121kg.

3.8.4. Correlations

As not many Cow live weights are recorded outside of mart weights and WHPR recording herds, there are many traits which provide a good indication of Cow Live Weight.

<i>Trait</i>	<i>Genetic Correlation</i>
Cull Cow Carcass Weight	0.74
Cold Carcass Weight	0.50
350-450 Day Weight	0.30
450-550 Day Weight	0.35
550-650 Day Weight	0.40
Skeletal Composite	0.20

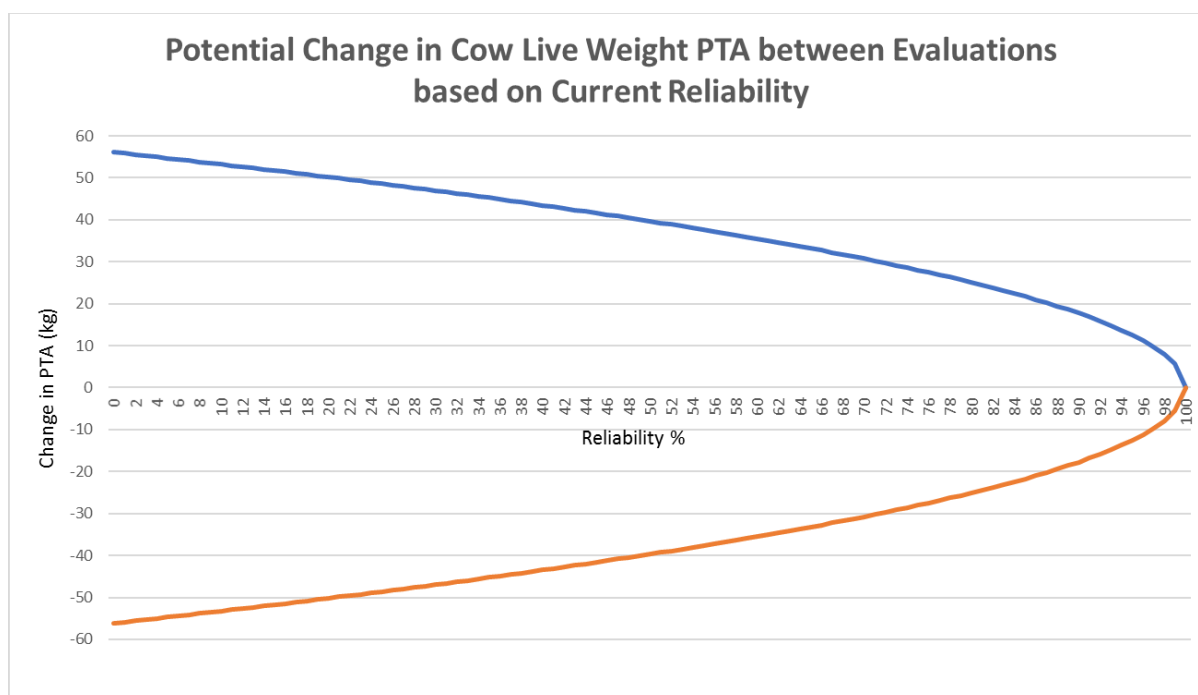
3.8.5. Base

The base for Cow Live Weight as a trait is derived from the PTA's of the same base animals (93,711 animals in the current beef evaluation with a carcass record & born in the 2000 to 2002 period) used for the Carcass traits bases. There is no reference phenotype for the trait.

3.8.6. Economic Weight & Relative Emphasis

Trait	Replacement Index	
	Trait Emphasis	Economic Weight
Cow Live Weight	14%	-€1.31
See section 1.16 – Economic Values		

3.8.7. 95% Confidence Interval



3.9. Cull Cow Weight

3.9.1. Definition

Cull Cow Carcass Weight is defined as the weight of both half carcasses of a cull cow after being bled, eviscerated and after removal of skin, removal of external genitalia, the limbs at the carpus and tarsus, head, tail, kidneys and kidney fats and the udder.

3.9.2. Trait Explanation

Conversely to Cow Live Weight, Cull Cow Weight has a positive effect on the overall index because it is used to account for the extra revenue accruing from larger cows when they are slaughtered. There is an important point in the construction of the Replacement Index which accounts for the fact that Cull Cow Weight is only expressed once in a cow's lifetime. Cull Cow Weight data is collected from factory slaughter records.

3.9.3. Heritability

The heritability of Cull Cow Weight is 29%, meaning it is a trait where we can actively breed for improvement, and make significant, cumulative gains. There is a huge amount of genetic variation in Cull Cow Weight, with PTAs of AI bulls over 60% reliability ranging from -20kg to 85kg.

3.9.4. Correlations

As Cull Cow Weight can only be obtained once a cow has been slaughtered, there are a number of traits with strong correlations to Cull Cow Weight which are good indicators.

<i>Trait</i>	<i>Genetic Correlation</i>
Cow Live weight	0.74
Carcass Weight	0.60
550-650 Day Weight	0.40
450-550 Day Weight	0.38
350-450 Day Weight	0.35
250-350 Day Weight	0.30
150-250 Day Weight	0.27
Skeletal Composite	0.30

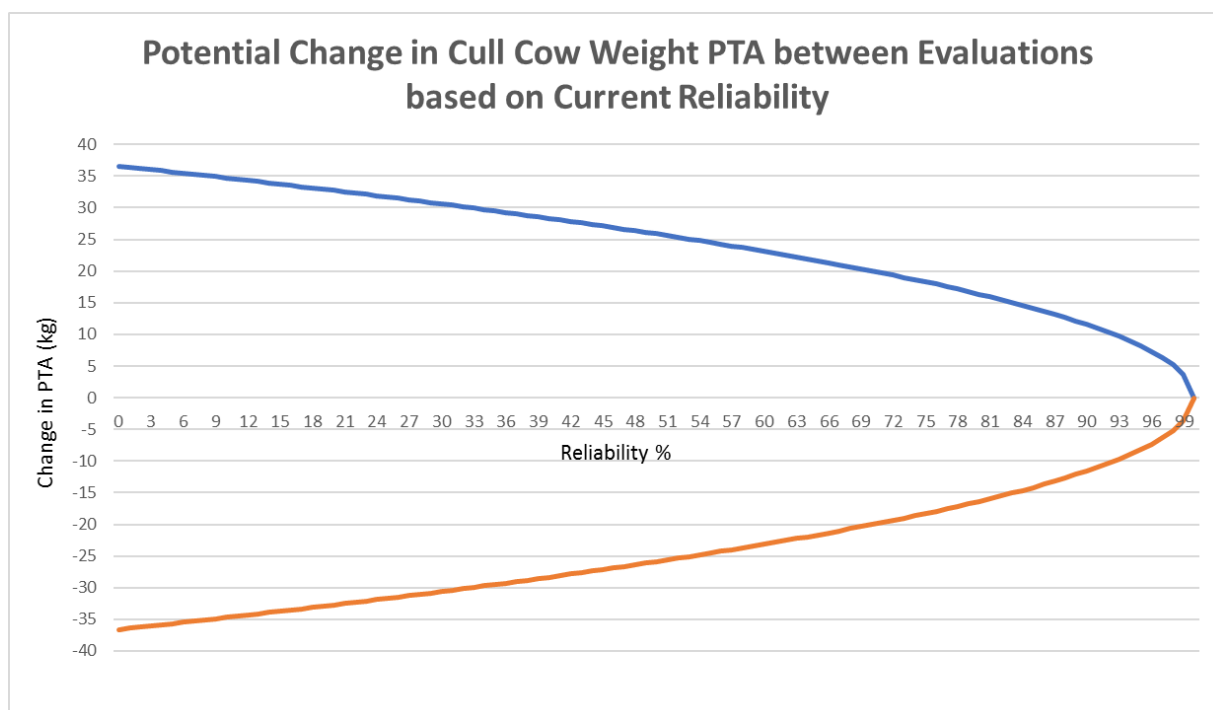
3.9.5. Base

The base for Cull Cow Weight as a trait is derived from the PTA's of the same base animals (93,711 animals in the current beef evaluation with a carcass record & born in the 2000 to 2002 period) used for the carcass traits bases. There is no reference phenotype for the trait.

3.9.6. Economic Weight & Relative Emphasis

Trait	Replacement Index	
	Trait Emphasis	Economic Weight
Cull Cow Weight	7%	€0.91
See section 1.16 – Economic Values		

3.9.7. 95% Confidence Interval



4.0. Milk Traits

4.1. Traits in Model

The traits included in the Milk multi-trait evaluation are: 50-150 day weight, 150-250 day weight, 250-350 day weight, Carcass Weight, Cow Milk Scores, Foreign Weaning Weight EBV (if applicable) and Foreign Maternal Weaning Weight EBV (if applicable).

4.2. Contemporary Groups

For Cow Milk Scores, contemporary groups are formed on a calving month basis. Animals in groups of less than 5 animals are included for each trait. Maximum contemporary group size is 30 animals. Pedigree females are separated from commercial females. Embryo Transfer (ET) calves are excluded. Contemporary groups are random, which helps account for environmental variation and helps estimate breeding values for smaller breeds.

4.3. Edits

There are a number of edits to the data for the Milk evaluation. If there is no variation in Cow Milk Scores within a herd they are excluded from the evaluation. If animals were linear scored and weighed, then 75% of eligible animals need to be scored to have weights included in the evaluation. The number of eligible animals is calculated as follows:

$$\frac{\text{Number of Animals Scored} + \text{Number of Sick Animals} + \text{Number Previously Scored}}{\text{Total Number of Animals Eligible to be Scored}}$$

Only mart weights of single animals are used for the evaluation. Weight restrictions also apply and weights are excluded if they fall outside the parameters below:

Weight Type	Less than	Greater than	ADG less than	ADG greater than
50-150 day weight	55	350	0.4	2.0
150-250 day weight	105	600	0.4	2.0
250-350 day weight	145	870	0.4	2.0

4.4. Milk

4.4.1. Definition

Milk is reflective of the ability a cow has to provide adequate nutrition for a calf prior to weaning, reflected in the weaning weight of the calf.

4.4.2. Trait Explanation

Milk as a trait is derived from live weights and Cow Milk Scores (recorded from BDP, BGP and BDGP schemes). Cow Milk Scores have been recorded since 2012, originally voluntarily, but became a requirement under a number of Department of Agriculture schemes. To date (March 2018) over

three million Cow Milk Scores have been recorded (Cow Milk Score is recorded for each lactation separately). Cow Milk scores are recorded by herd owners, and cows are scored on a 5-point scale (Very Poor, Poor, Average, Good, Very Good) relative to herd mates.

4.4.3. Heritability

Analysis has shown Cow Milk Score to have a heritability of 0.2 and repeatability of 0.14. Maternal Weaning Weight has a heritability of 0.25. These traits have moderate heritability and good rates of genetic gain can be made through selective breeding. Genetic variation for Milk PTA in AI sires with over 60% reliability ranges from -16.4kg to 19.1kg.

4.4.4. Correlations

There is a correlation of 0.8 between Maternal Weaning Weight and Cow Milk Score. This means that Cow Milk Score is a very good predictor of Maternal Weaning Weight and vice versa.

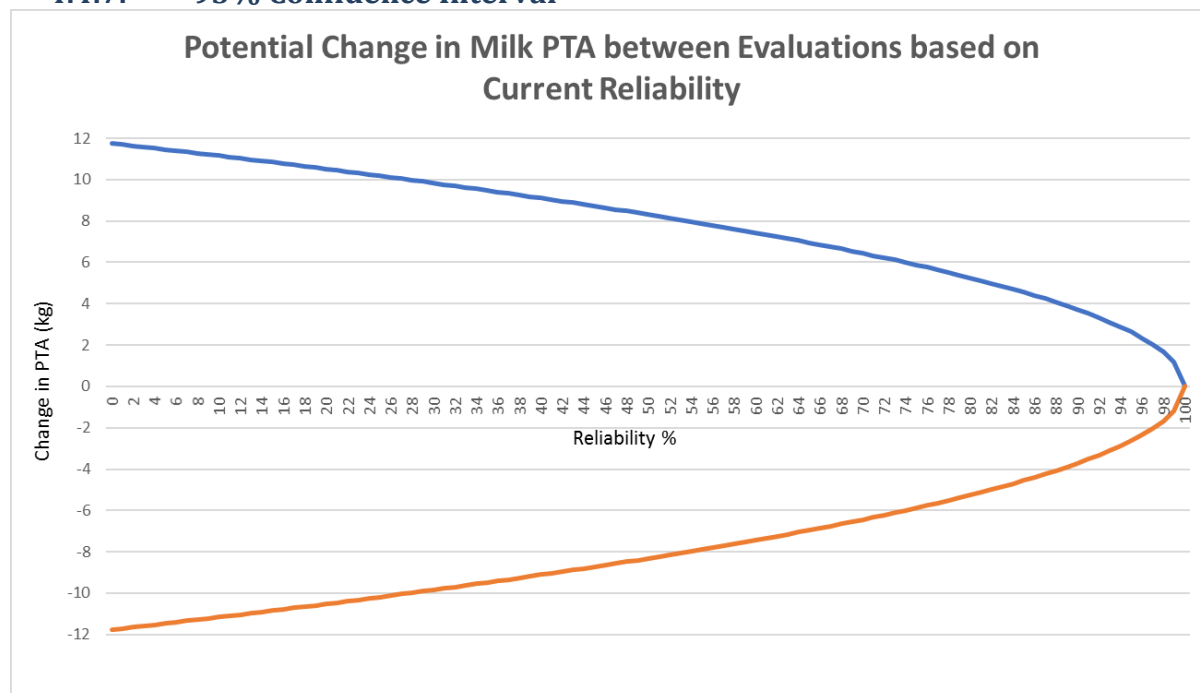
4.4.5. Base

The base animals for Milk evaluations are the progeny of 110 high reliability AI sires. The grand-progeny average Weaning Weight for those 110 AI sires is 299 kg at 207 days of age.

4.4.6. Economic Weight & Relative Emphasis

Trait	Replacement Index	
	Trait Emphasis	Economic Weight
Milk	18%	€5.58
See section 1.16 – Economic Values		

4.4.7. 95% Confidence Interval



5.0. Calving Traits

5.1. Traits in Model

The traits that feed into the Calving evaluation are: Calving Difficulty, Mortality, Gestation, 0-10 day weight, 150-250 day weight, 250-350 day weight, Carcass Weight, Foreign Calving Difficulty EBV (if applicable), and Foreign Maternal Calving Difficulty EBV (if applicable).

5.2. Contemporary Groups

First calved heifers are included in contemporary groups of their own, instead of being compared with older cows. Animals in groups of less than 5 animals are included for each trait. Maximum contemporary group size is 30 animals. Pedigree females are separated from commercial females. Embryo Transfer (ET) calves are excluded. Contemporary groups are random, which helps account for environmental variation and helps estimate breeding values for smaller breeds.

5.3. Edits

Only animals with parities 1 to 10 are included. Twin births are excluded. Known abortions are excluded. There is no editing on Calving Ease scoring patterns in herds. Births of Embryo Transfer (ET) calves are excluded. Dams are excluded if they are under 500 days of age, or over 12,000 days. Gestation is calculated in the database prior to evaluations. Gestations of less than 270 days and over 300 days are excluded from evaluations.

5.4. Calving Difficulty

5.4.1. Definition

(Dystocia) Abnormal or difficult labour, causing difficulty in delivering the foetus and/or placenta.

5.4.2. Trait Explanation

Calving Difficulty as a trait is derived from recorded calving ease score at birth of progeny of an animal, birth weights, birth measurements, early life weights, and carcass weights. Calving Ease Score is a numerical score quantifying calving ease, ranging from an easy, unassisted calving through to an abnormal presentation/requiring intervention as follows:

1: Normal Calving 2: Some Assistance 3: Considerable Difficulty 4: Vet Assistance

Direct Calving Difficulty is the level of difficulty because of the characteristics of the calf (body shape and size, etc.). Calving Ease is recorded at registration of an animal either through the Department of Agriculture AIM System, online at agfood.ie or through Animal Event sheets. Animals registered

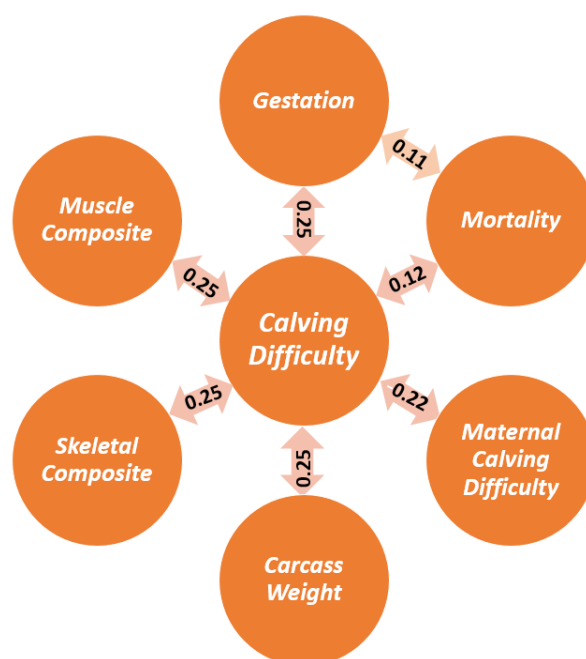
without a Calving Ease Score can be subsequently recorded on the ICBF website (BDGP Requirement).

5.4.3. Heritability

Calving Difficulty has a heritability of 9%. Essentially 91% of the variance comes from factors outside of direct genetic control. There is a large amount of genetic variation in Calving Difficulty, with AI bulls over 60% reliability ranging from 0.5% to 22.4%.

5.4.4. Correlations

Calving Difficulty is correlated with many traits which are summarised in the graphic below.



5.4.5. Base

The base figures for Calving Difficulty are derived from the progeny average of 823 highly reliable AI sires. This is obtained from the phenotypic calving records of 1,163,179 progeny from the 823 AI sires. As shown in the table, 95% of calving easings recorded are considered normal or slight assistance. 5% of births are considered difficult or requiring veterinary intervention.

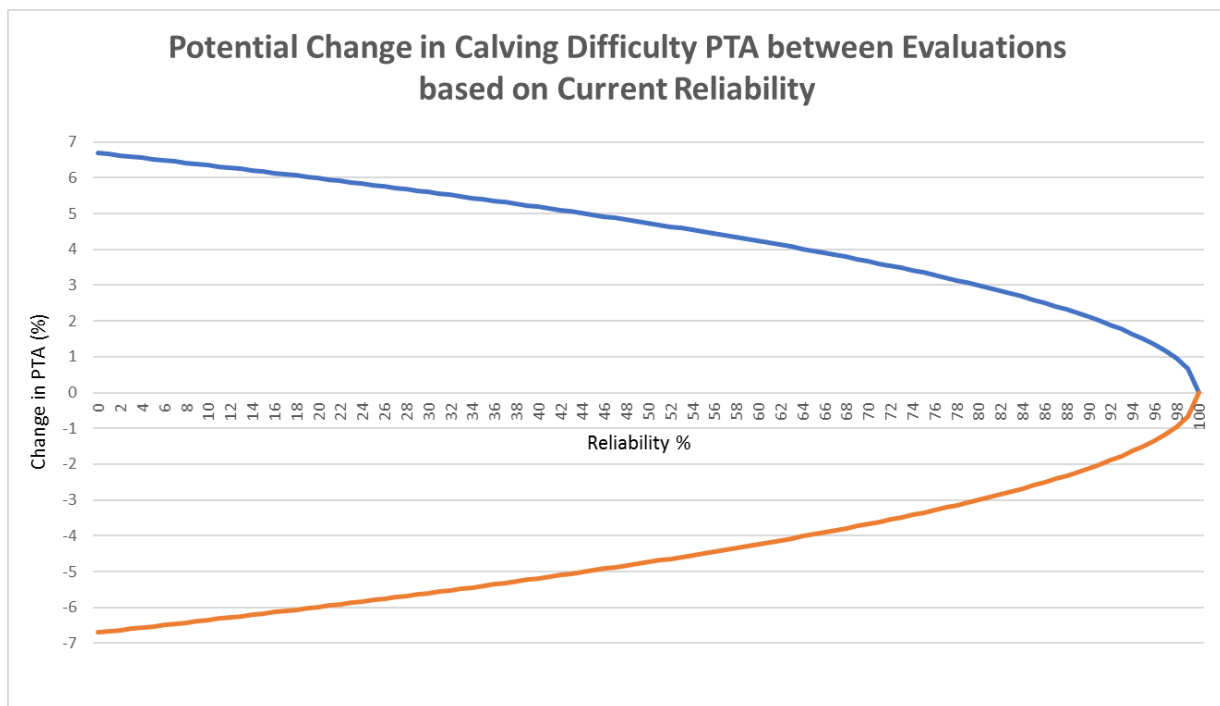
Calving score	Count	%
1	892,968	77%
2	214,150	18%
3	36,159	3%
4	19,902	2%
Total	1,163,179	100%

5.4.6. Economic Weight & Relative Emphasis

Trait	Terminal Index		Replacement Index	
	Trait Emphasis	Economic Weight	Trait Emphasis	Economic Weight
Calving Difficulty	18%	-€4.65	1%	-€5.12

See section 1.16 – Economic Values

5.4.7. 95% Confidence Interval



5.5. Maternal Calving Difficulty

5.5.1. Definition

Abnormal or difficult labour, causing difficulty in delivering the foetus and/or placenta attributable to the dam.

5.5.2. Trait Explanation

Maternal Calving Difficulty is the level of difficulty experienced in an animal's female progeny due to the characteristics of the cow giving birth (pelvic size, calving ability, etc.). Maternal Calving Difficulty is the maternal effect of Calving Difficulty (See section: 1.14. Maternal Effects). It is measured using Calving Ease Score. Calving Ease Score is a numerical score quantifying calving ease, ranging from an easy, unassisted calving through to an abnormal presentation/requiring intervention as follows:

1: Normal Calving 2: Some Assistance 3: Considerable Difficulty 4: Vet Assistance

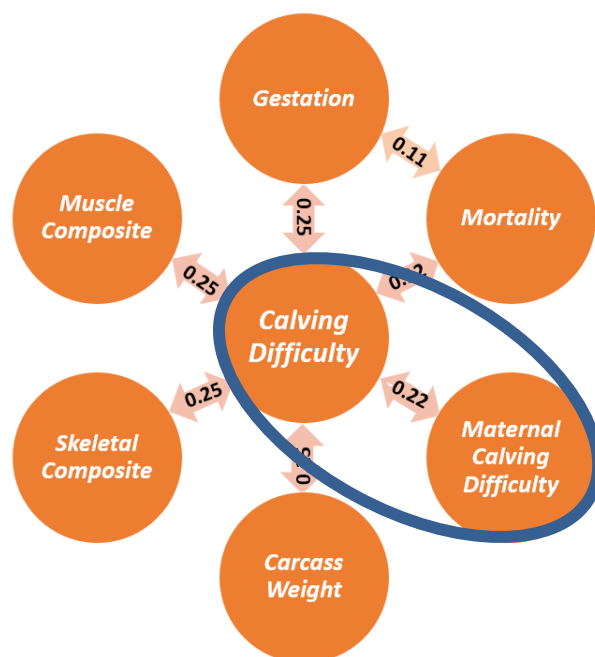
Calving Ease is recorded at registration of an animal either through the Department of Agriculture AIM System, online at agfood.ie or through Animal Event sheets. Animals registered without a Calving Ease Score can be subsequently recorded on the ICBF website.

5.5.3. Heritability

Maternal Calving Difficulty has heritability of 4%, so breeding for improved Maternal Calving Ease can be a slow process, in comparison to breeding for improvements in the Carcass traits. However, progress can be made due to the large amount of genetic variation in the trait. There is a huge amount of genetic variation in Maternal Calving Difficulty, with PTAs of AI bulls over 60% reliability ranging from 1.0% to 32.99%.

5.5.4. Correlations

Maternal Calving Difficulty is negatively correlated with Calving Difficulty. As the correlation is -0.22, it means that many animals may have a low calving difficulty PTA, and have a higher maternal calving difficulty PTA. Because the correlation is -0.22, and not close to 2, it means many animals can have a low PTA for both.



5.5.5. Base

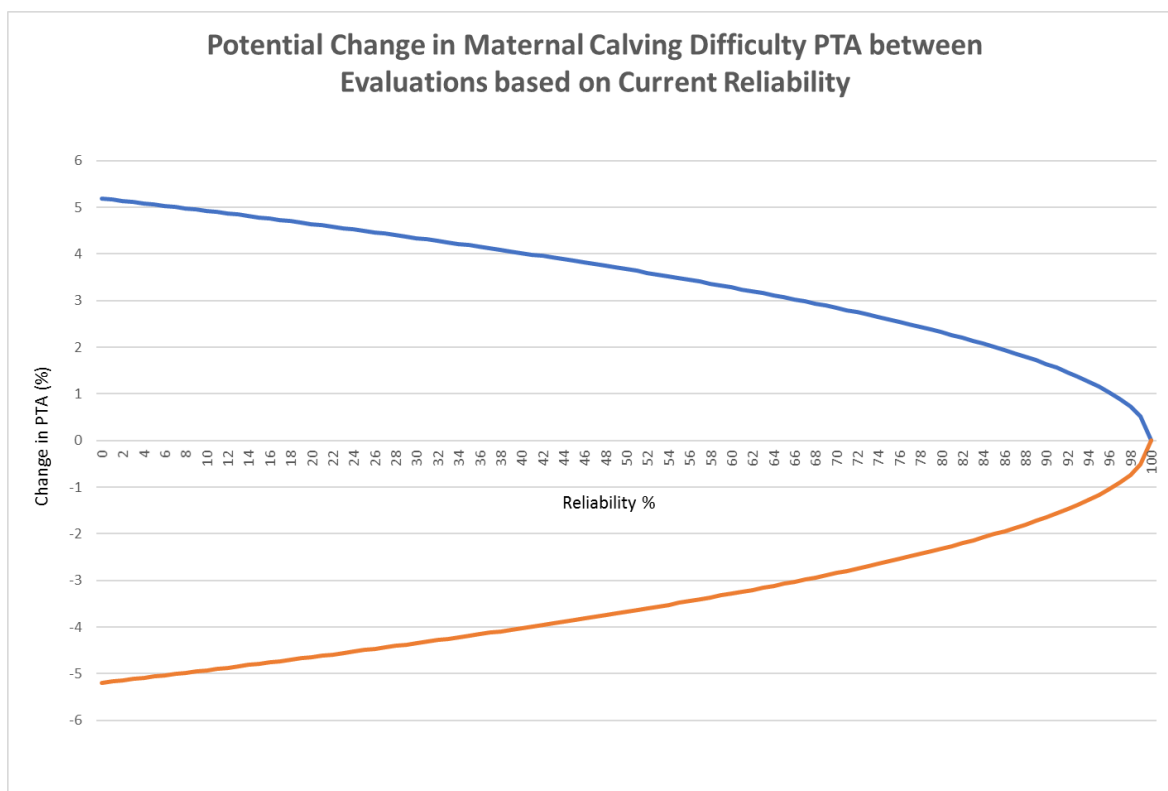
The base figures for Maternal Calving Difficulty are derived from the progeny average of 823 highly reliable AI sires. This is obtained from the phenotypic calving records of 1,163,179 progeny from the 823 AI sires. As shown in the table, 95% of calving eases recorded are considered normal or slight assistance. 5% of births are considered difficult or requiring veterinary intervention.

Calving score	Count	%
1	892,968	77%
2	214,150	18%
3	36,159	3%
4	19,902	2%
Total	1,163,179	100%

5.5.6. Economic Weight & Relative Emphasis

Trait	Replacement Index	
	Trait Emphasis	Economic Weight
Maternal Calving Difficulty	6%	-€4.98
See section 1.16 – Economic Values		

5.5.7. 95% Confidence Interval



5.6. Gestation

5.6.1. Definition

The number of days between a known conception date and a subsequent calving date.

5.6.2. Trait Explanation

Gestation Length as a trait is derived from the number of days between the recorded serve date and the recorded birth date. Gestation length is therefore driven by the recording of serve dates by AI Technicians on handheld devices or on the ICBF website and by the birth records recorded on AIM and Animal Event Sheets. To record serves from natural service or DIY AIs on the ICBF website, just log into *Online Services*, click on *Record Events* and then click *Heat & AI/Serve*.

5.6.3. Heritability

Gestation is a highly heritable trait at 35%. Bulls with long gestations will often sire animals who will also have long gestations. Gestation length as a trait is under a lot of genetic control. There is a huge amount of genetic variation in Gestation, with PTAs of AI bulls over 60% reliability ranging from -4.62 days to 6.65 days.

5.6.4. Correlations

As can be seen from the graphic included under Calving Difficulty (See section 3.4.4), Gestation has a 0.25 correlation with Calving Difficulty. Gestation and Mortality also have a correlation of 0.11.

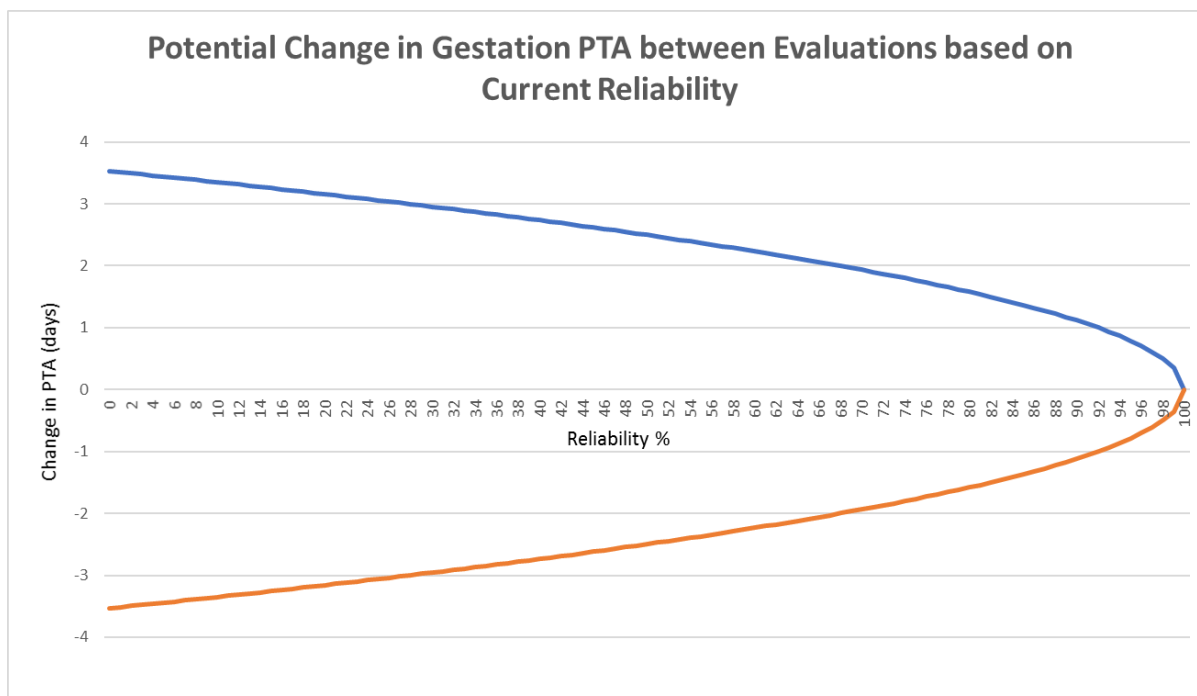
5.6.5. Base

The base figure for Gestation length is calculated from the progeny of 823 high reliability AI sires (605,672) and is 283.9 days.

5.6.6. Economic Weight & Relative Emphasis

Trait	Terminal Index		Replacement Index	
	Trait Emphasis	Economic Weight	Trait Emphasis	Economic Weight
Gestation	4%	-€2.25	2%	-€2.48
See section 1.16 – Economic Values				

5.6.7. 95% Confidence Interval



5.7. Mortality

5.7.1. Definition

Mortality rate is a measure of the number of deaths (in general, or due to a specific cause, *i.e.* associated with calving, within 5 days of birth).

5.7.2. Trait Explanation

Mortality as a trait is derived from the number of dead progeny sired by a bull, where the progeny has been stillborn or died within 5 days of birth. This is recorded through the Department of Agriculture AIM system where animals have been marked as stillborn or where animals have died within five days of birth and have a movement to a Fallen Animal Collection service.

5.7.3. Heritability

Mortality has heritability of 4%, so breeding for reduced Mortality can be a slow process, in comparison to breeding for improvements in the Carcass traits. Because Mortality is multi-factorial trait under a lot of environmental influence, it is difficult to accurately estimate the heritability of the trait. There is a huge amount of genetic variation in Mortality, with PTAs of AI bulls over 60% reliability ranging from -1.26% to 3.49%.

5.7.4. Correlations

There is a positive genetic correlation between Calving Difficulty and Mortality, as increased calving difficulty will see an increase in calf mortality. The genetic correlation between Mortality and Calving Difficulty is 12%.

5.7.5. Base

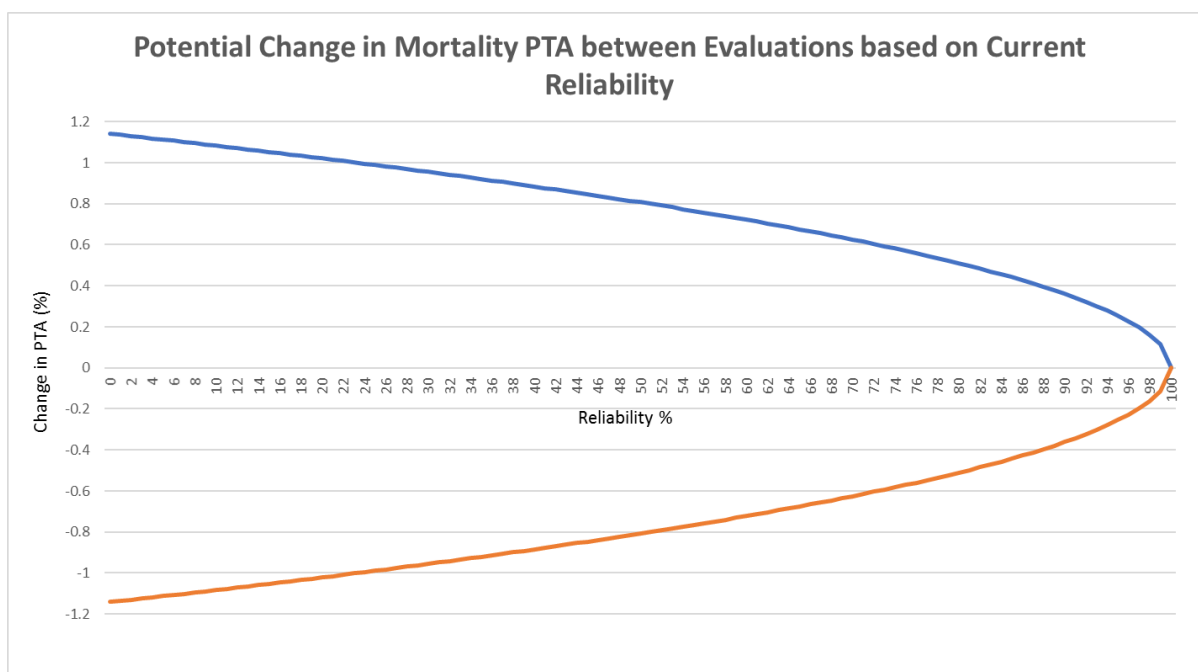
The base for Mortality comes from the records of 1,837,249 animals. The mortality rate for these animals is 2%.

<i>Calf Mortality</i>	<i>Count</i>	<i>%</i>
Alive	1,796,531	98%
Dead	40,718	2%
Total	1,837,249	100%

5.7.6. Economic Weight & Relative Emphasis

Trait	Terminal Index		Replacement Index	
	Trait Emphasis	Economic Weight	Trait Emphasis	Economic Weight
Mortality	3%	-€5.34	7%	-€5.87
See section 1.16 – Economic Values				

5.7.7. 95% Confidence Interval



6.0. Fertility Traits

6.1. Traits in Model

The animal traits that feed into the Fertility traits evaluation are: Age at First Calving, Calving Interval, Survival, Calving Difficulty, Carcass Weight and Carcass Fat. The Carcass traits are included as predictor traits.

6.2. Contemporary Groups

Show cattle form their own separate contemporary groups. Pedigree females are separated from commercial females. Embryo Transfer (ET) calves are excluded. Animals in groups of less than 5 animals are included for each trait. Maximum contemporary group size is 30 animals. Contemporary groups are random, which helps account for environmental variation and helps estimate breeding values for smaller breeds.

6.3. Edits

Animals with flushing events recorded with ICBF will have all calving interval data from 365 days prior to the flushing event excluded from the evaluation. Flushing events must be recorded with ICBF for this edit. Technicians are encouraged to record the flushing event on the screens available. Calving intervals of less than 300 days and greater than 1000 days are excluded from the evaluation as it is assumed there has been a recording error. Calving interval records after the 14th parity are not included in the evaluation. Records where the Age at First Calving is less than 660 days or greater than 1278 days are not included. Survival records beyond parity 10 are not included in the evaluation.

6.4. Age at First Calving

6.4.1. Definition

Age at First Calving is the age (in days) at which a female gives birth for the first time.

6.4.2. Trait Explanation

Age at First Calving is recorded automatically recorded as the date of birth of the first offspring is recorded with the Department of Agriculture. When the record is received in ICBF, the offspring date of birth is subtracted from the date of birth of the dam, to give the number of days between the two dates. The number of days is the age of the dam at first calving. As Age at First Calving can be heavily influenced by management systems, herd effects play a large role in the evaluation of this trait.

6.4.3. Heritability

Age at First Calving has heritability of 31%, which is high unlike many of the other fertility traits. Females who calve at the 22-24 month target, are quite likely to have daughters that meet the same target. There is a lot of genetic variation for the trait Age at First Calving, meaning there is a lot of genetic progress that can be made. The range of PTA in AI bulls over 60% reliability is from -60.9 days to 47.5 days.

6.4.4. Correlations

Age at First Calving is correlated to many traits, listed below.

<i>Trait</i>	<i>Genetic Correlation</i>
Calving Interval	0.18
Survival	0.15
Calving Difficulty	0.24
Carcass Weight	-0.07
Carcass Fat	0.08

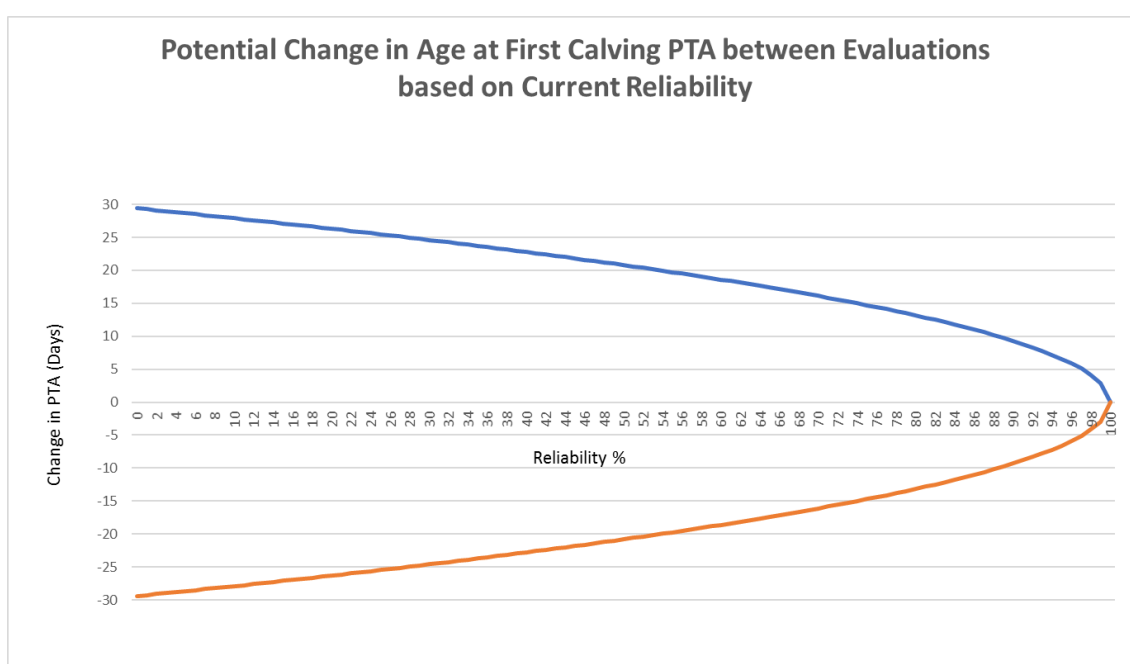
6.4.5. Base

The base animals for the fertility evaluations are 67 high reliability AI sires. The progeny average Age at First Calving of those AI sires is 940 days (based on 115,785 animals).

6.4.6. Economic Weight & Relative Emphasis

Trait	Replacement Index	
	Trait Emphasis	Economic Weight
Age at First Calving	6%	-€0.99
See section 1.16 – Economic Values		

6.4.7. 95% Confidence Interval



6.5. Calving Interval

6.5.1. Definition

Calving Interval is the number of days elapsed between successive calving events.

6.5.2. Trait Explanation

The aim with Calving Interval is to have it as close to 365 days as possible. It is recorded by the database calculating the number of days between successive calvings. For this reason, it is essential to record abortions/pregnancies that do not make it to full term.

6.5.3. Heritability

Calving Interval has a heritability of just 2.4%. This means genetic gain for this trait is not as rapid as traits like feed intake (43% heritability) but because there is a lot of genetic variation in Calving Interval, genetic progress can still be made. The range of PTA in AI bulls over 60% reliability is from -12.06 days to 13.76 days.

6.5.4. Correlations

Calving Interval is strongly (negatively) correlated to Survival, and to Carcass Fat as a predictor trait. Correlations with the other traits in the model are in the table below.

<i>Trait</i>	<i>Genetic Correlation</i>
Age at First Calving	0.18
Survival	-0.35
Calving Difficulty	0.22
Carcass Weight	0.23
Carcass Fat	-0.41

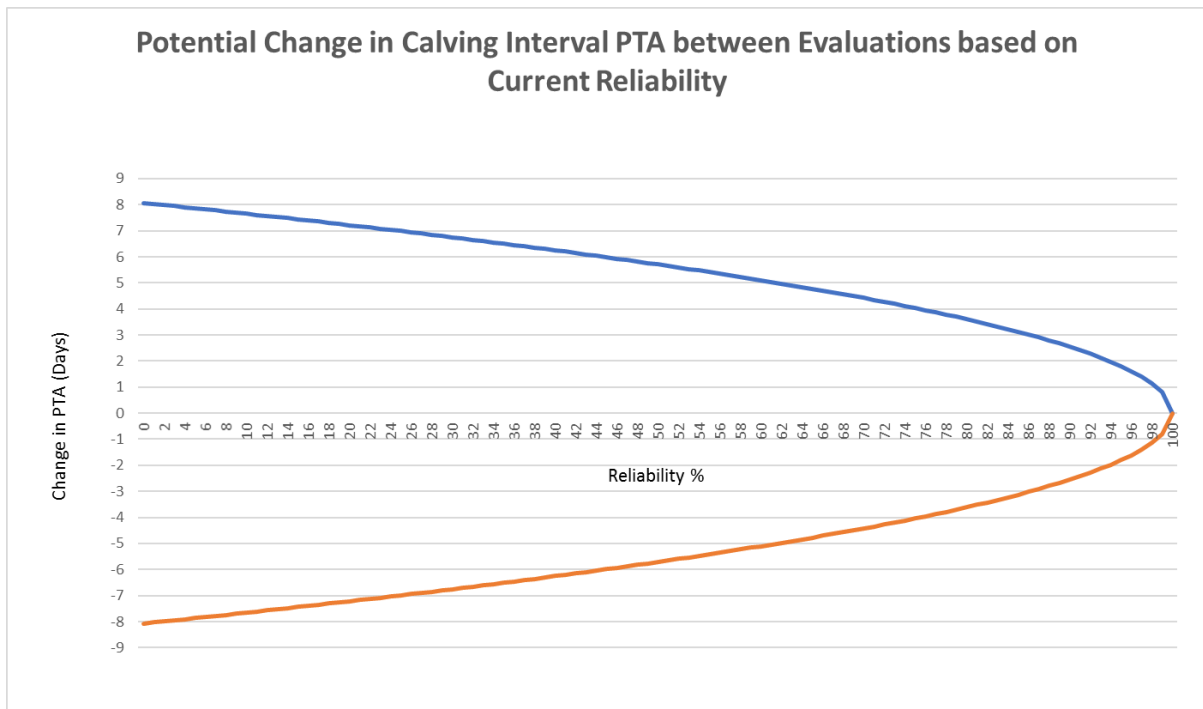
6.5.5. Base

The base animals for the fertility evaluations are 67 high reliability AI sires. The progeny average Calving Interval of these AI sires is 402 days (based on 593,483 calving intervals).

6.5.6. Economic Weight & Relative Emphasis

<i>Trait</i>	<i>Replacement Index</i>	
	<i>Trait Emphasis</i>	<i>Economic Weight</i>
Calving Interval	9%	-€5.07
See section 1.16 – Economic Values		

6.5.7. 95% Confidence Interval



6.6. Survival

6.6.1. Definition

Survival is the persistence of a cow from one parity to the next.

6.6.2. Trait Explanation

Survival as a trait is derived from the number of female progeny that persist through parities 1 to 10, as it is a repeatability model.

6.6.3. Heritability

Survival has a heritability of 1.7%. Again, there are many issues which impact on a cow's survival in a herd, which affects how much variation can be attributed to genetics. However, genetic gain is cumulative and lasting; there is a lot of genetic variation for Survival, in AI bulls over 60% reliability the PTAs range from -5.93% to 5.51%.

6.6.4. Correlations

Survival is correlated to many traits, but strongest correlations are with the other fertility traits and Carcass Weight.

<i>Trait</i>	<i>Genetic Correlation</i>
Age at First Calving	0.15
Calving Interval	-0.35
Calving Difficulty	-0.07
Carcass Weight	0.31
Carcass Fat	0.09

6.6.5. Base

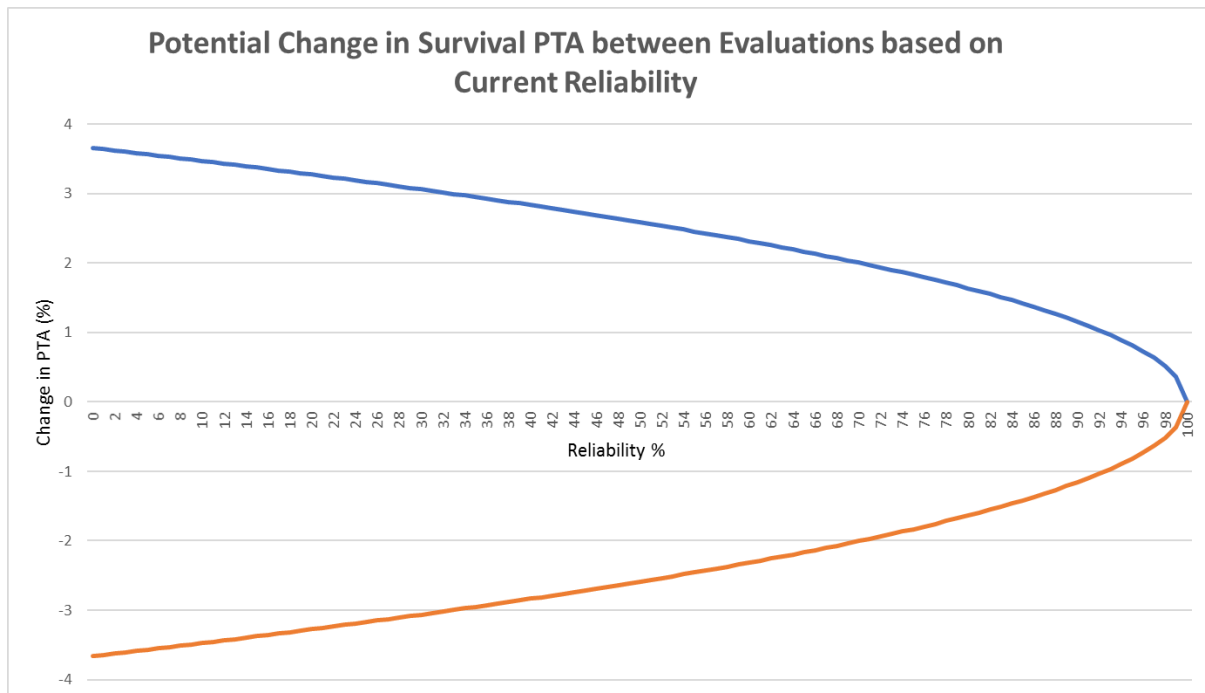
The base animals for Survival comes from the progeny records of 67 high reliability AI sires. The average progeny Survival for those AI sires is in the table to the right:

<i>Survival</i>	<i>Count</i>	<i>%</i>
Survived	600,686	84%
Culled	115,279	16%
Total	715,965	100%

6.6.6. Economic Weight & Relative Emphasis

<i>Trait</i>	<i>Replacement Index</i>	
	<i>Trait Emphasis</i>	<i>Economic Weight</i>
Survival	8%	€8.86
See section 1.16 – Economic Values		

6.6.7. 95% Confidence Interval



7.0. Docility Traits

7.1. Traits in Model

Three traits make up the Docility Model: Farmer Docility Score, Linear Docility Score and Cow Docility Score.

7.2. Contemporary Groups

Herds need to have variation in contemporary group (at least three scores). Contemporary groups need at least three different sires for Farm Docility Scores and a minimum of two different sires for Linear Docility Scores. Only animals Farm Docility Scored with contemporary groups of 10 or more are included, but only animals Linear Docility Scored with contemporary groups of 5 or more are included. Maximum contemporary group size is 30. Show animals and ET calves are in their own separate contemporary groups. Pedigree and commercial animals are grouped separately.

7.3. Edits

There are a number of edits in calculating the breeding values for Docility. Farmer Docility scores must be recorded prior to the sale of the animal. Animals must be scored between 150-300 days for both traits, Farm Docility Score and Linear Docility Score. If animals are linear scored, and less than 75% of eligible calves are scored on the same day, the docility score will be excluded. The number of eligible animals is calculated as follows:

$$\frac{\text{Number of Animals Scored} + \text{Number of Sick Animals} + \text{Number Previously Scored}}{\text{Total Number of Animals Eligible to be Scored}}$$

7.4. Docility

7.4.1. Definition

Docility describes the way in which an animal behaves, with regard to humans, other animals and during specific activities such as calving or feeding.

7.4.2. Trait Explanation

Docility is derived from docility linear scores and farmer recorded calf and cow docility scores. Technicians use a 1- 10 scale to measure docility, and farmer records are on a 5-point scale (Very Good / Very Quiet, Good / Quiet, Average, Poor / Difficult, Very Poor / Very Difficult). Docility of animals is very important to reduce farm accidents, and subsequent costs such as lost work days. Cow Docility published is essentially the same trait as the weanling Docility. However, the economic value is different for weanling versus cow.

7.4.3. Heritability

The heritability of docility is 35%, making it one of the more heritable traits along with the Carcass traits. There is a huge amount of genetic variation in Docility, with PTAs of AI bulls over 60% reliability ranging from -0.35 to 0.45.

7.4.4. Base

The base animals for the docility evaluation are 158 high reliability AI sires. The average progeny Docility for those AI sires is in the table to the right:

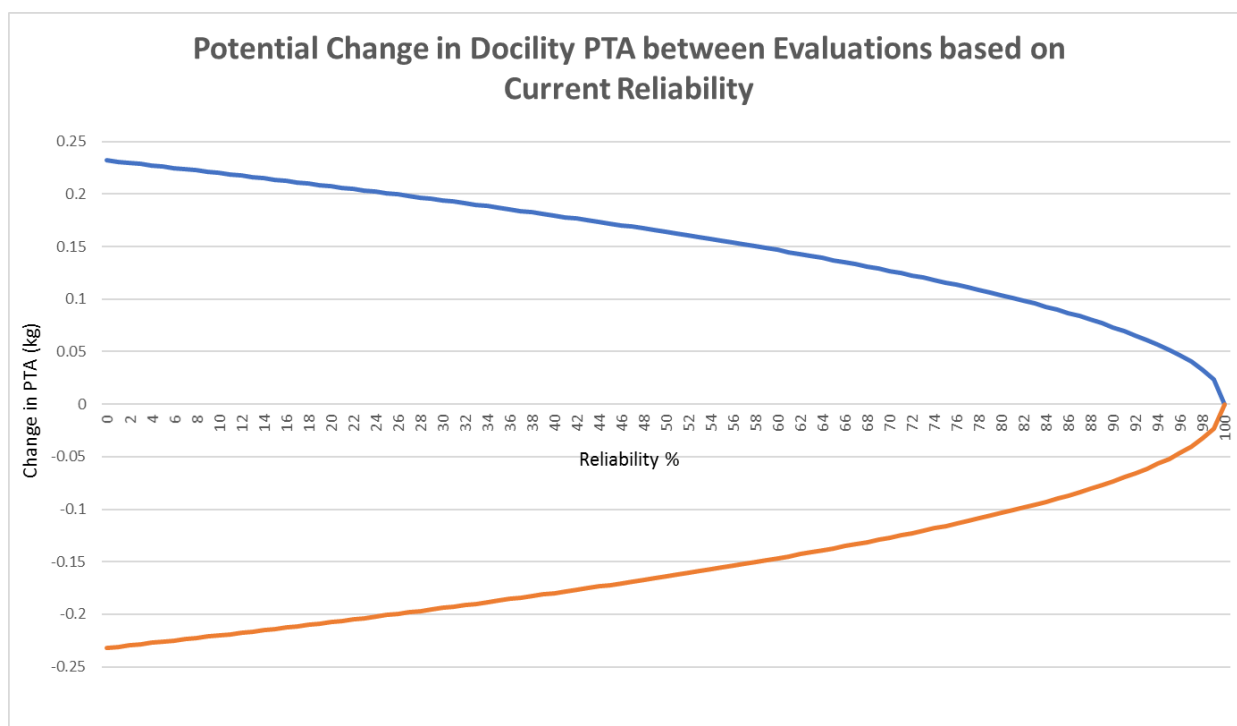
Docility score	Count	%
VG	24919	17%
G	64773	44%
A	52669	36%
P	5220	3.5%
VP	349	0.2%
Total	147930	

7.4.5. Economic Weight & Relative Emphasis

Trait	Terminal Index		Replacement Index	
	Relative Emphasis	Economic Weight	Relative Emphasis	Economic Weight
Docility	2%	€17.02	1%	€14.72
Cow Docility	-	-	4%	€77.27

See section 1.16 – Economic Values

7.4.6. 95% Confidence Interval



8.0. Dairy Beef Index



8.1. What is the Dairy Beef Index?

The Dairy Beef Index (**DBI**) is a breeding goal for Irish dairy and beef farmers to promote high quality beef cattle bred from the dairy herd that are more saleable as calves and profitable at slaughter yet, they have minimal consequences on the calving difficulty or gestation length of the dairy cow. The DBI was developed by ICBF and Teagasc and launched during Spring 2019.

8.2. Why we need a Dairy Beef Index?

The dairy herd is expanding, and it is benefitting from improvements in cow fertility, due predominantly to genetic gain arising from the Economic Breeding Index (**EBI**). Such changes have resulted in an increased number of dairy male calves and the increased usage of beef bulls in the dairy herd. Dairy farmers predominantly select beef bulls that have a short gestation length and are easy calving, without considering the beef carcass merit of the resulting calves; therefore, the quality and viability of Irish beef production is at risk of deterioration. A recent analysis of beef cattle slaughtered in Irish factories (Figure 1 and Table 1) revealed that many cattle bred from dairy dams did not meet the minimum carcass weight or carcass conformation specifications (Table 1). Improving the quality of beef cattle from the dairy herd will generate economic benefits for all involved in the beef supply chain.

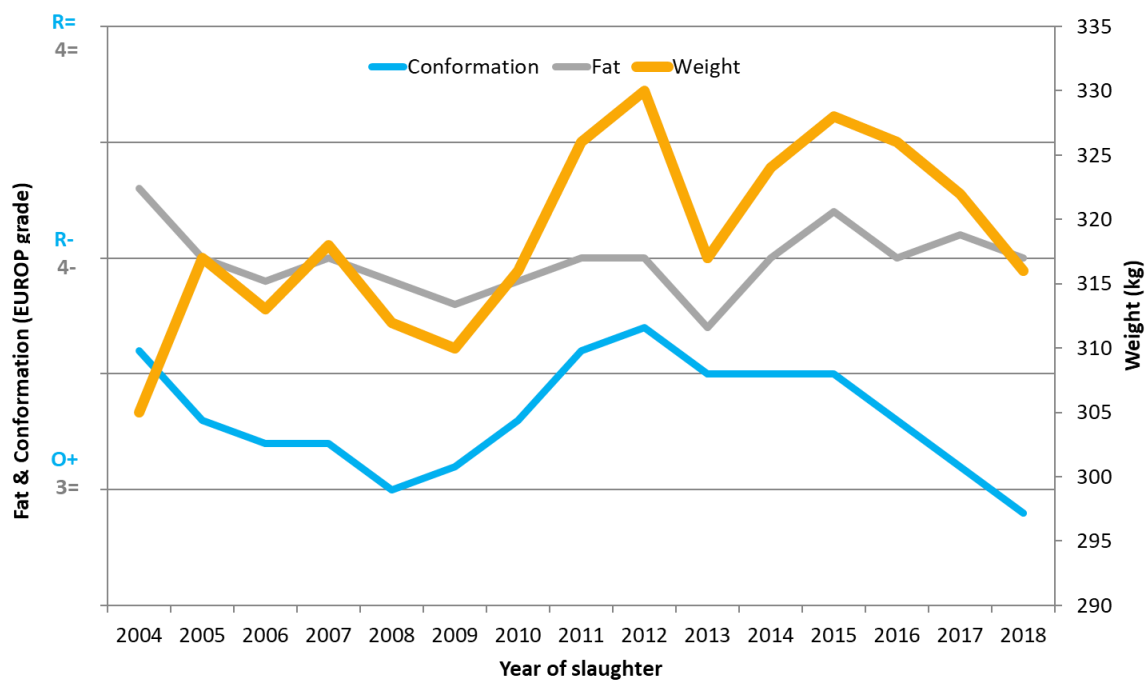


Figure 1. Average performance of beef cattle bred from to dairy dams that were slaughtered between 2004 and 2018

Table 1. Breakdown, by sire breed, of the percentage of cattle born to dairy dams that were slaughtered in 2017 which did not meet the minimum carcass weight specification or the minimum carcass conformation specification

Sire breed	Number of sires	Number of progeny	Progeny not meeting carcass weight spec (280 kg)	Progeny not meeting carcass conformation spec (O=)
Aberdeen Angus	35	2,309	32%	12%
Belgian Blue	29	2,405	8%	2%
Hereford	31	1,251	27%	17%
Limousin	25	4,834	10%	1%
Friesian	117	2,066	26%	51%
Holstein	509	957	31%	74%
Jersey	50	244	66%	84%
Norwegian Red	10	168	29%	62%

8.3. Understanding the Dairy Beef Index

The Dairy Beef Index (DBI) ranks beef bulls, for use in the dairy herd, according to their genetic merit for a range of calving performance and carcass performance traits. The overall DBI is expressed in euros (€). Each €1 increase in DBI can be interpreted as a €1 expected increase in profit for that bull’s progeny compared to progeny born to the average Holstein-Friesian bull. For example, a beef bull with a DBI of €100 is expected to produce progeny born to dairy cows that will generate €100 more profit compared to progeny sired by the average Holstein-Friesian bull. Therefore, higher DBI bulls generate more profitable progeny.

The DBI can be segregated into two main sub-indexes, 1) the value of calving sub-index which makes up 64% of the index, and 2) the value of beef sub-index which makes up the remaining 36% of the index (Figure 2). A total of 12 traits are included in the DBI; these include: gestation length, calving difficulty, calf mortality, feed intake, docility, carcass weight, carcass conformation, carcass fat, and two ‘out of spec’ traits. Where applicable, a polled and a carcass bonus trait (specific to the breed) are also included in the DBI (Figure 2). An explanation of each of the traits included in the DBI is in Table 2. A breakdown of the DBI percentiles for pedigree beef cattle born between 2013 and 2018 is in Table 3.

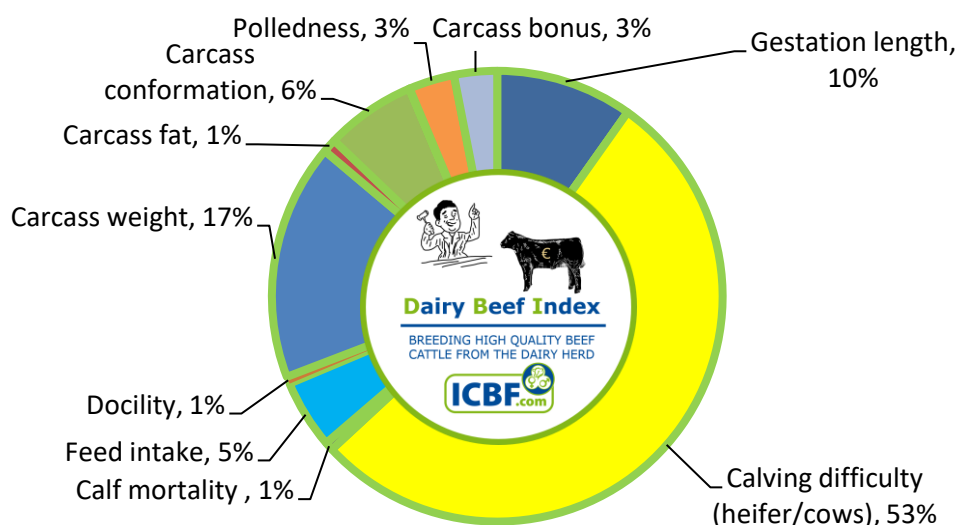


Figure 2. Relative emphasis of the traits included in the Dairy Beef Index (Spring 2019)

Table 2. Explanation of the traits included in the Dairy Beef Index together with their economic value (Spring 2019) and the desirable direction of selection

Trait	Explanation	Economic value	Desirable trait direction
Gestation length	Number of days the cow is expected to carry the foetus in-utero	-€7.47	Lower values are better
Calving difficulty	Percentage of progeny expected to require considerable assistance at calving, either with or without veterinary assistance	-€6.44	Lower values are better
Calf mortality	Percentage of progeny expected to die at or soon after birth	-€1.73	Lower values are better
Feed intake	Kilograms of feed consumed by progeny (measured as dry matter intake)	-€35.27	Lower values are better
Docility	The expected quietness of progeny	-€11.74	Lower values are better
Carcass weight	Expected weight (kg) of progeny post-slaughter	+€2.37	Higher values are better
Carcass fat	Expected carcass fat score of progeny on the EUROP classification grid	-€5.12	Lower values are better
Carcass conformation	Expected carcass conformation score of progeny on the EUROP classification grid	+€10.92	Higher values are better
Out of spec: weight	Percentage of progeny not expected to meet the minimum carcass conformation specification required (O=)	-€0.43	Lower values are better
Out of spec: conformation	Percentage of progeny not expected to meet the minimum carcass weight required (280 kg)	-€0.25	Lower values are better
Polledness	Whether all, half, or none of the progeny are expected to have horns	+€5.33	Higher values are better
Carcass bonus	Additional carcass premium paid for Aberdeen Angus and Hereford progeny	+€2.80	Higher values are better

8.4. Revamped genetic evaluation for calving difficulty in the Dairy Beef Index

The Dairy Beef Index (DBI) includes a revamped genetic evaluation for calving difficulty which has four major improvements compared to the genetic evaluation for calving difficulty (which will continue to be presented in the Euro-star indexes and the EBI for 2019). These are:

- 1) It provides a better indication of how suitable a beef bull is for use on dairy heifers and on dairy cows, by separating the heifer trait from the cow trait
- 2) More sources of data are being used (i.e., calf birth size and calf birth weight) with the farmer scored calving difficulty records which have always been used
- 3) Additional strict editing criteria are applied to the data to remove herds that have low levels of data recording
- 4) It takes into consideration that the economic value for calving difficulty is linear up to a point (i.e., a genetic merit of 2.5% for calving difficulty), after which the cost of calving difficulty increases in a non-linear fashion. This updated non-linear economic value reflects the view of dairy farmers which will only choose to use more difficult calving beef bulls where a higher price is paid for the resulting calf compared to easier calving beef bulls.

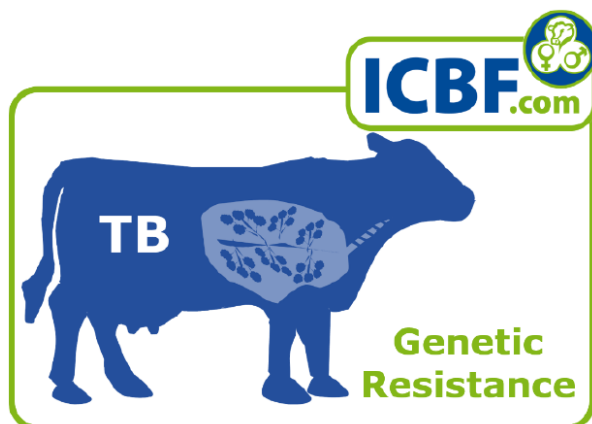
The net effect of these improvements has resulted in an increase of the average genetic merit of all animals for calving difficulty. For example, of the 70 bulls on the DBI Spring 2019 Active bull list, their genetic merit for calving difficulty has increased on average by 7.4 percentage units on the new dairy heifer scale, or by 1 percentage unit on the new dairy cow scale.

8.5. Differences between the EBI, €uro-star Indexes, and the Dairy Beef Index

	EBI	€uro-star Indexes	Dairy Beef Index
Animals that have the index	Dairy animals	Beef animals	Beef AI bulls (Spring 2019); over time both beef AI bulls and beef stock bulls will have the index
Herds that should use the index	Dairy herds	Beef herds	Dairy herds
Why use the index	To breed more profitable dairy males and females for the dairy herd	To breed more profitable beef males and females for the beef herd	To breed more profitable beef cattle from the dairy herd which are easy calving, have a short gestation, have a high calf price, and a high carcass merit
Genetic evaluation for calving difficulty	Old genetic evaluation for calving difficulty is in use for Spring 2019. Each animal's genetic merit for calving difficulty is expressed as one figure which is applicable to dairy heifers and dairy cows.	Old genetic evaluation for calving difficulty is in use for Spring 2019. Each animal's genetic merit for calving difficulty is expressed as one figure which is applicable to dairy heifers, dairy cows, beef heifers, and beef cows	Revamped genetic evaluation is used with stricter editing criteria resulting in an increase in the average genetic merit of all animals for calving difficulty. Each bull has two genetic merit figures for calving difficulty: 1) for selecting bulls for use on dairy heifers, 2) for selecting bulls for use on dairy cows

9.0. Genetic Evaluations for Health Traits

9.1. Tuberculosis (TB) Resistance Evaluations



9.1.1. What is bovine Tuberculosis and why does it need to be eradicated?

Bovine TB is an infectious disease of cattle that can elicit disease in other animals and humans. Clinical signs of TB in cattle are rarely observed in Ireland due to the rigorous surveillance and culling protocols associated with the TB eradication program. Nevertheless, the annual operational costs (€84 million in 2017) as well as

other costs to the farmer (e.g., labour) associated with the TB eradication program in Ireland are extensive. Nonetheless, Ireland needs to eradicate bovine TB to attain a high health status in humans and cattle as well as to maintain access to export markets.

9.1.2. Alternative strategies are required to hasten the eradication of bovine TB

Even though the bovine TB eradication program has been operational in Ireland for nearly 70 years TB remains prominent in Ireland; 4.89% of cattle herds were infected with TB in 2017 and 17,266 reactor cattle were removed. Therefore, it is timely that an alternative strategy be explored to complement the existing TB eradication program and hasten the eradication of bovine TB. Genetic selection is one such complementary strategy. Recent research by Teagasc and ICBF, in conjunction with the DAFM and UCD, have identified that certain family lines of cattle tend to have a higher prevalence of TB reactors than other cattle. For example, among beef and dairy AI bulls that sired many progeny across multiple TB infected herds (i.e., ≥ 50 progeny in ≥ 10 TB infected herds) there was much variation in the prevalence of TB reactors in their progeny. Bulls were used in areas considered to be TB blackspots as well as areas with a lower TB prevalence. For some bulls that had many progeny in TB infected herds, none of their progeny became TB reactors while other bulls produced progeny (that were also in the same TB infected herds) where 4 out of every 10 progeny were diagnosed as TB reactors (Figure 9.1.1.).

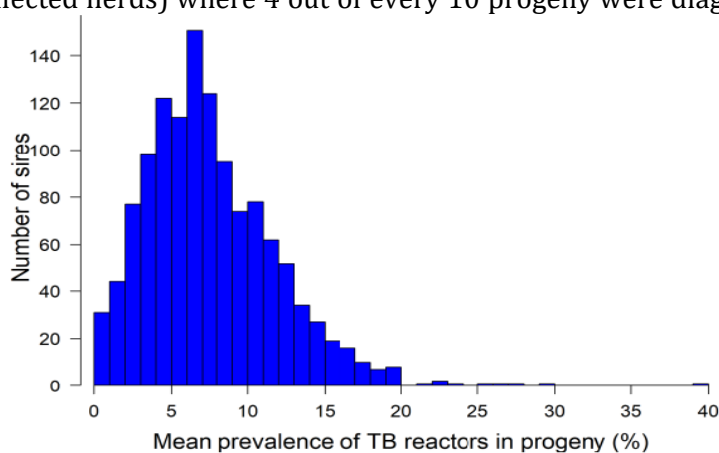


Figure 9.1.1. Average prevalence of TB reactors among the progeny of sires that had at least 50 progeny in 10 infected herds

9.1.3. Quantifying the contribution of genetics to bovine TB prevalence

It is well acknowledged that both environmental (including wildlife interactions) and herd management factors influence whether cattle become TB reactors and subsequently, whether a herd has a TB-breakdown. Until now it has not been considered that genetic differences among cattle may influence their ability to fight off TB infection. Nonetheless, innovative Irish research has revealed that 12% of the variability in TB infection is controlled by the animal's genetic ability to fight off TB infection (i.e., resistance). The benefit of using animal breeding to complement the existing eradication program for TB is that breeding is permanent and cumulative.

9.1.4. Strict criteria ensure only cattle exposed to bovine TB inform genetic evaluations

For the genetic evaluation of resistance to TB, strict criteria are used to maximise the likelihood that only cattle exposed to the bovine TB causing bacterium are used to inform the genetic evaluation. Only bovine TB results (i.e., whole-herd results and post-mortem results) from cattle that resided with herd-mates diagnosed with TB infection are included in the genetic evaluation. Like all other traits, the genetic ability of cattle to resist TB infection is compared to their herd-mates, thus ensuring comparisons are made between cattle with a similar likelihood of exposure to the bovine TB causing bacterium as well as management protocols (e.g., grazing group, age).

For example, among a herd of 100 dairy cows where 2 cows become TB reactors, the genetic evaluation compares the 2 TB reactors with the other 98 non-infected cows; the genetic evaluation also accounts for differences in the age of cows. Test results from other management groups in the herd (e.g., calves, weanlings) are not used to inform the genetic evaluation if no animal in that management group was infected with bovine TB. That said, breeding values are predicted for all cattle in that herd (e.g., the calves and weanlings that were deemed not exposed to the bovine TB causing bacterium) and cattle in other herds as an indicator of their level of resistance to bovine TB should those cattle ever become exposed to the bovine TB causing bacterium in the future. It is because of the genetic relationships among cattle in TB infected management groups with other cattle that breeding values can be generated for all cattle, irrespective of whether they have been exposed to the bovine TB causing bacterium.

9.1.5. Understanding breeding values for resistance to TB

Each animal's breeding value for resistance to TB is expressed as the predicted prevalence of TB in that animal's progeny. Therefore, lower breeding values, which mean that fewer progeny are expected to be diagnosed with TB, are more desirable. For example, a bull with a breeding value of 10% for resistance to TB is predicted to produce progeny where, on average, 1 in every 10 of his progeny will be diagnosed as a TB reactor, either during a whole-herd test or at slaughter.

9.1.6. Breeding for resistance to TB can prevent your herd from a TB-breakdown

Cattle with lower breeding values for resistance to TB are less likely to be diagnosed with TB during their lifetime compared to their herd-mates which have higher breeding values for resistance to TB. Using only TB information from their ancestors, breeding values for cattle in herds undergoing a TB-breakdown were predicted at birth (i.e., TB results of these cattle was not used in the genetic evaluation). When the TB test results of these cattle were confirmed, the number of TB reactors was

26% higher in cattle with the worst breeding values for TB resistance compared to cattle in the same herds with the best breeding values for TB resistance. The implications of preventing just one TB infection could avert a subsequent 1.5 to 4.9 secondary TB infections which arise from cattle-to-cattle transmission of TB. Therefore, breeding strategies can play a fundamental role in the acceleration of the eradication of TB without having any major negative ramifications on other traits.

9.1.7. Achieving the most profitable and healthy herd

To achieve the most profitable herd that is also more resistant to TB select cows and bulls for breeding that have the highest overall index (i.e., EBI, Replacement Index, or Terminal Index) with the lowest breeding value (i.e., lowest predicted prevalence) for resistance to TB.

9.1.8. What animals have breeding values for resistance to TB and where can I find it?

For 2019, only AI bulls will have a breeding value for resistance to TB which will initially be published on www.icbf.com in the format of a Microsoft Excel file. Breeding value for resistance to TB will eventually be incorporated into the EBI, Euro-star Indexes, animal profiles, reports etc.

9.1.9. Scientific peer-reviewed publications:

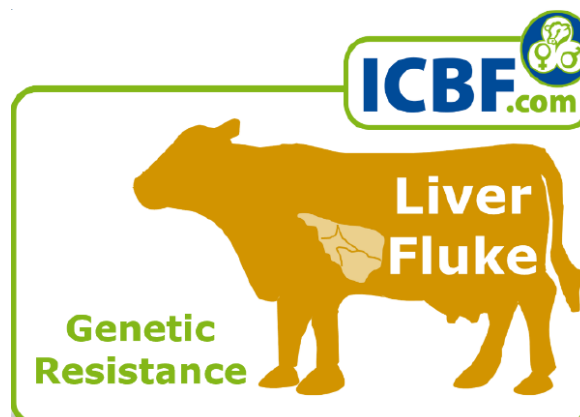
Richardson, I. W., D. G. Bradley, I. M. Higgins, S. J. More, J. McClure, and D. P. Berry. 2014. Variance components for susceptibility to *Mycobacterium bovis* infection in dairy and beef cattle. *Genetics Selection Evolution*. 46:77. <https://doi.org/10.1186/s12711-014-0077-1>

Ring, S. C., D. C. Purfield, M. Good, P. Breslin, E. Ryan, A. Blom, R. D. Evans, M. L. Doherty, D. G. Bradley, and D. P. Berry. 2019 Variance components for Bovine Tuberculosis Infection and Multi-Breed Genome Wide Association Analysis Using Imputed Whole Genome Sequence Data. *PLoS ONE*. Under Review.

9.2. Liver Fluke Resistance Evaluations

9.2.1. Importance of liver fluke

Liver fluke is a widespread problem. One in every 5 cattle slaughtered in Ireland are diagnosed with liver fluke infection. Almost all dairy and beef herds are at risk of liver fluke infection. If properly used, anthelmintic treatments can control liver fluke, but they do have limitations in dairy herds because of the associated milk withdrawal. In addition, anthelmintic treatments are often incorrectly used thus, their usage can contribute to anthelmintic resistance.



9.2.2. Breeding is complementary to traditional control strategies

It is often believed that environment and management determine whether cattle become infected with liver fluke. However, like many other traits the genetic makeup of cattle also determines their ability to fight off liver fluke infection. Ground breaking Irish research has revealed large variability in the prevalence of liver fluke infection (ranging from 0 to 75%) among the progeny of sires in liver fluke infected herds (Figure 9.2.1.). Furthermore, 1% of the inter-animal variability in liver fluke infection is controlled by the genetic ability of cattle to resist (i.e., fight off) liver fluke infection. Although the transmissible genetic variability for liver fluke infection is relatively small, it is similar to fertility which has improved through breeding. Up to half of the performance gains that have been achieved in fertility traits over the past 20 years have been due to genetic improvement, despite the low heritability of fertility traits. The benefit of breeding is that it is permanent and cumulative. Therefore, animal breeding is a sustainable way to reduce the prevalence of liver fluke in herds which will compliment traditional control strategies.

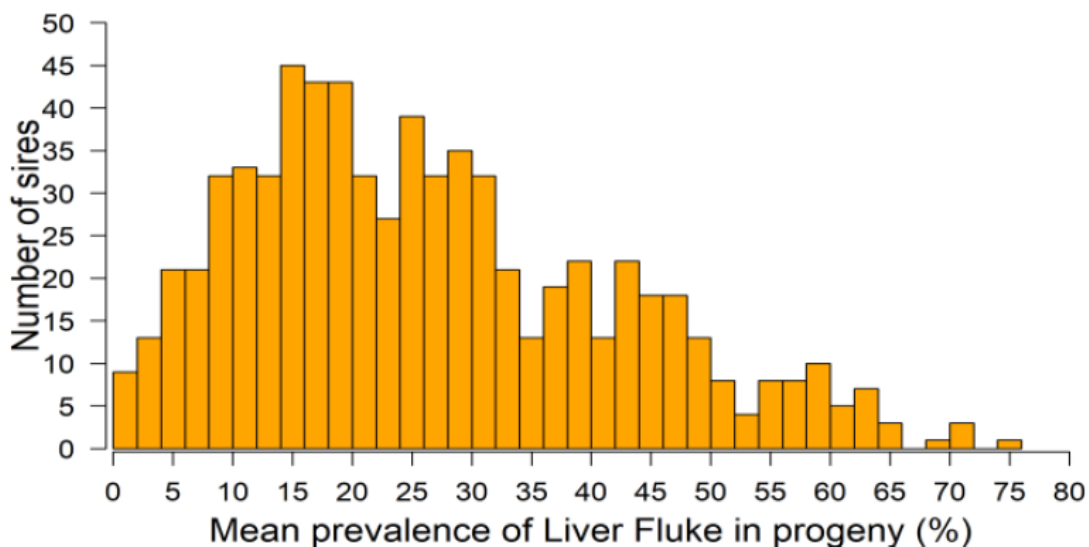


Figure 9.2.1. Average prevalence of liver fluke infection among the progeny of sires that had at least 50 progeny in 10 infected herds

9.2.3. Disentangling genetics from environment

One of the main challenges and components of genetic evaluations for any trait, especially disease traits, is disentangling genetics from environmental effects. For the genetic evaluation of liver fluke, strict criteria are used to maximise the likelihood that only animals exposed to the parasite are considered in the genetic evaluation. In brief, only liver fluke results from cattle that resided with herd-mates that were diagnosed with liver fluke infection are included in the genetic evaluation for liver fluke. Like all other traits, the genetic ability of cattle to resist liver fluke infection is compared to their herd-mates, ensuring comparisons are made between cattle with a similar likelihood of exposure to the parasite as well as management protocols (e.g., grazing group, age).

9.2.4. Understanding breeding values for resistance to liver fluke

Each animal's breeding value for resistance to liver fluke is expressed as the predicted prevalence of liver fluke in that animal's progeny. Therefore, lower breeding values, which mean fewer progeny are expected to be diagnosed with liver fluke, are more desirable. For example, a bull with a breeding value of 10% for resistance to liver fluke is predicted to produce progeny where, on average, 1 in every 10 of his progeny will be diagnosed with liver fluke infection.

9.2.5. Does breeding for resistance to liver fluke really work?

Yes. Cattle with lower breeding values for resistance to liver fluke have are likely to be diagnosed with liver fluke infection at slaughter compared to their herd-mates which have higher breeding values for resistance to liver fluke. Using only liver fluke information from their ancestors, breeding values for cattle were predicted prior to slaughter (i.e., the liver fluke result of these cattle was not used in the genetic evaluation). When these cattle were slaughtered, 36% of cows predicted to be in the highest risk group for infection were diagnosed with liver fluke. In comparison, 30% of cows predicted to be in the lowest risk group for infection were diagnosed with liver fluke.

9.2.6. What animals have breeding values for resistance to liver fluke and where can I find it?

For 2019, only AI bulls will have a breeding value for resistance to liver fluke which will initially be published on www.icbf.com in the format of a Microsoft Excel file. Breeding value for resistance to liver fluke will eventually be incorporated into the EBI, Euro-star Indexes, animal profiles, reports etc.

9.2.7. Scientific peer-reviewed publications:

Twomey, A. J., R. G. Sayers, R. I. Carroll, N. Byrne, E. O. Brien, M. L. Doherty, J. C. McClure, D. A. Graham, and D. P. Berry. 2016. Genetic parameters for both a liver damage phenotype caused by *Fasciola hepatica* and antibody response to *Fasciola hepatica* phenotype in dairy and beef cattle. *Journal of Animal Science*. 94(10): 4109-4119. <https://doi.org/10.2527/jas.2016-0621>

Twomey, A. J., R.I. Carroll, M. L. Doherty, N. Byrne, D. A. Graham, R. G. Sayers, A. Blom, and D. P. Berry. 2018. Genetic correlations between endo-parasite phenotypes and economically important traits in dairy and beef cattle. *Journal of Animal Science*. 96(2):407-421. <https://doi.org/10.1093/jas/sky008>

Twomey, A. J., D. A. Graham, M. L. Doherty, A. Blom, and D. P. Berry. 2018. Little genetic variability in resilience among cattle exists for a range of performance traits across herds in Ireland differing in *Fasciola hepatica* prevalence. *Journal of Animal Science*. 96(6): 2099-2112. <https://doi.org/10.1093/jas/sky108>