Nordic Cattle Genetic Evaluation

# NAV official genetic evaluation of Dairy Cattle

## – data and genetic models

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# 1. Introduction

Breeding values for dairy cattle breeds in Denmark, Sweden and Finland are calculated jointly by NAV (Nordic Cattle Genetic Evaluation), which has Landbrug & Fødevarer, Växa and FABA Co-op as member organizations.

This cooperation and joint evaluation make it possible to compare animals across our countries and thus make efficient use of economic resources. The genetic evaluation is performed for a wide variety of important traits. Furthermore, all economically important traits are included in a Nordic total merit index known as NTM.

The genetic evaluation system in NAV complies with international rules for registration, documentation, calculations, etc. Genetic models are validated according to Interbull standards before being applied in the routine evaluations.

Interest in breeding stock from the Nordic countries is increasing. The genetic level is high for all breeds and the Nordic countries can run genetic evaluation for economically valuable traits that are not recorded in many other countries.

In this publication, we wish to describe the methods and models used in the Nordic countries. We also want to highlight the credibility of the EBVs for Nordic dairy cattle.

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## 2. NTM - Nordic Total Merit

All traits are combined into the Nordic Total Merit index (NTM). NTM describes the total economic potential determined by genetics. Cows with high NTM bring greater economic profit to the farmer, and the use of sires with high NTM will produce offspring of higher economic value.

### Traits included in NTM

The traits included in NTM are:

- Yield
- Growth
- Fertility
- Birth
- Calving
- Udder health
- General health
- Claw health
- Feet and legs
- Udder
- Milkability
- Temperament
- Longevity
- Youngstock survival
- Saved feed

The traits are weighted in NTM based on their economic values. The economic values quantify the value of a marginal change in the trait. The weights are breed specific.

### Economic value of sub-indices

The current economic values are mainly based on the economic situation ultimo 2017. However, they are adjusted according to predictions of the economic situation for the dairy sector when the breeding goal is realized 8-10 year into the future.

The calculated economic values are marginal economic values i.e., the value of one unit improvement of the trait whilst the remaining traits are held constant. Thus, the value of, for example, protein yield is calculated as the economic profit from improving protein yield with one kg whilst all other traits remain unchanged.

Some important considerations related to the calculation of economic weights for the different traits are explained below.

#### Yield

Milk production at herd level is estimated from yield per lactation and the herd structure, including distribution of lactations, and the number of days in milking for culled cows. Further information regarding the sales price of milk and marginal feed costs is used to estimate the marginal revenue obtained by producing more milk, fat or protein.

## Growth

The economic value is evaluated for bull calves only, but it is important to keep in mind that in practice improvements in gain and EUROP score also have an impact on the slaughter value of female animals (heifers and cows).

## Fertility

The economic value of fertility is mostly due to changes in calving interval since this affects annual production per cow. The economic value is also affected by the cost of AI and the work it involves, including work related to heat detection.

## Calving traits

The cost of stillbirth consists mostly of lost income from slaughter animals i.e., decreased stillbirth rate results in more animals for slaughter. It is also associated with extra work and the cost for destruction of the dead calf. The expenses related to calving difficulty come from extra work and veterinary fees. It does not however, reflect subsequent complications since these are considered in the General Health index.

Generally, for all countries and breeds, it is assumed that a stillborn calf will require extra work of 15 minutes. In Finland, additional 30 minutes are added because it is common practice to bury stillborn calves. 75 % of the stillborn calves are assumed to be buried in Finland.

When the proportion of difficult calvings is changed, a proportional change in the percentage of difficult calvings with and without veterinary assistance is assumed. It is assumed that 20% of the difficult calvings with veterinary assistance require a caesarean or dissections (at higher cost). The same figure is used across countries and breeds. A “normal” difficult calving requires 90 minutes extra work. Caesareans and dissections require an extra 3.0 hours of work. Besides this, it is assumed that an *easy calving with help* requires 12 minutes extra compared with an *easy calving without help*.

## Udder health

The cost of poor udder health (mastitis) comes from veterinary treatments, extra work for herd personnel, and the amount of milk that is discarded following treatment with antibiotics. In the economic evaluation of udder health, the important factor is the total number of cases, not the occurrence measured as a binary trait which is used in the genetic evaluation of udder health.

## General health

Calculations within the sub-traits in the general health index follow the same principles as described for mastitis above.

## Claw health

Costs associated with extra time used for trimming and additional visits by the claw trimmer caused by disorders are included. Also, work for herd personnel and costs for medication and bandages are included.

## Conformation and workability traits

The setup for this trait group is slightly different compared with the other NTM trait groups. The traits analyzed here – Frame, Feet & Legs and Udder – are composite phenotypes. The basic economic assumptions are based on a (subjective) assessment of the extra workload when conformation is not optimal in an average herd. This was done by subjective assessment in a herd with 70 milking cows.

- Frame: There was no change in workload when all the traits included in Frame were linearly scored 1 point away from optima.
- Udder: When all the traits included in Udder were linearly scored 1 point away from optima, the extra workload was assessed to be15 minutes per day in a herd with 70 cows (91 hours per year).
- Feet & Legs: When all traits included in Feet & Legs were linearly scored 1 point away from the optima, the extra workload was assessed as being 10 minutes per day in a herd with 70 cows (61 hours per year).

With the two farmer-recorded traits, Milkability and Temperament, things are less complicated, because the recorded score can be evaluated directly. It was assumed that when the Milkability of all cows was one unit lower, the extra workload would be 10 minutes per day in a herd with 70 cows; and when the Temperament of all cows was 1 unit lower, the extra workload would be 5 minutes per day in a herd with 70 cows.

### Longevity

The value of longevity is determined by changes in the following traits: % culled in 1st lactation, % culled in 2nd lactation, and % culled in 3rd and later lactations. Changed culling rates will change the distribution of younger and older cows in the herd and change the number of calvings per year. The breeding value for longevity is heavily influenced by fertility, udder health and general health, and to some degree by the conformation of the udder and feet and legs. Therefore, a proportion of the economic value of longevity is transferred to the other traits in NTM. This transfer is based on analyses of the relationship between longevity and the other traits.

### Youngstock Survival

The direct economic effect of improving youngstock survival is increased income caused by more animals available for slaughter. Improved youngstock survival is related to extra costs for the destruction of dead calves, feeding of the calves and extra work.

### Saved feed

The economic effect of improving Saved feed is due to a reduction in feed consumption. It is expressed in kg dry matter. Saved feed is comprised of two sub traits, which are: need of energy for maintenance and efficiency in use of energy for different processes (production, maintenance, growth etc.). For maintenance the main components are need in rearing period, need in production period and income from slaughter.

## Economic weights in NTM

The economic values displayed in Table 2.1 represent the basis for forming an economically optimal breeding goal based on the used assumptions. From these the economic value of one index unit for each NTM sub-index is calculated. These are again weighted relative to the economic value of the yield index. Subsequently, the weighting of the traits in NTM may be modified slightly for example to account for factors which may not have an economic value but are important in the breeding goal for reasons such as animal welfare, ethical views, climate and environment.

Table 2.1. NAV economic values for Holstein, RDC and Jersey.

| **Trait** | | **Unit** | **EURO per unit** | | |
|---|---|---|---|---|---|
| | | | **Holstein** | **RDC** | **Jersey** |
| **MILK PRODUCTION** | | | | | |
| Milk | | Kg | -0.048 | -0.047 | -0.050 |
| Fat | | Kg | 1.30 | 1.29 | 1.72 |
| Protein | | Kg | 4.40 | 4.34 | 3.95 |
| Standard milk | | Kg | 0.156 | 0.154 | 0.157 |
| **BEEF PRODUCTION** | | | | | |
| Net daily gain | | Kg/day | 212.5 | 230.4 | 191.8 |
| EUROP form score | | Score | 23.8 | 24.4 | 13.8 |
| **CALVING TRAITS** | | | | | |
| %stillborn, 1st | | %-units | 1.6 | 1.65 | 0.86 |
| Easy calving, 1st | | 4 point scale | 5.6 | 5.789 | 10.73 |
| %stillborn, later | | %-units | 3.9 | 3.93 | 3.14 |
| Easy calving, later | | 4 point scale | 26.5 | 24.93 | 120.57 |
| **FEMALE FERTILITY** | | | | | |
| Heifer – first to last | | Day | 0.81 | 0.93 | 1.26 |
| Cow – calv. To first | | Day | 0.48 | 0.59 | 0.11 |
| Cow – first to last | | Day | 4.18 | 3.41 | 2.49 |
| Heifer - no. of ins. | | AIS | 19.62 | 22.07 | 28.66 |
| Cow – no. of ins. | | AIS | 60.03 | 55.03 | 45.99 |
| **MASTITIS*** | | | | | |
| Mastitis, 1st, 1st period | | %-units | 0.83 | 0.83 | 0.75 |
| Mastitis, 1st, 2nd period | | %-units | 0.89 | 0.87 | 0.85 |
| Mastitis, 2nd | | %-units | 1.23 | 1.051.17 | 1.20 |
| Mastitis, 3rd+ | | %-units | 2.11 | 2.07 | 2.27 |
| **GENERAL HEALTH**** | | | | | |
| Metabolic | | %-units | 3.12 | 3.12 | 3.05 |
| Ketosis | | %-units | 1.45 | 1.49 | 1.56 |
| Feet and legs | | %-units | 1.57 | 1.58 | 1.75 |
| Early reproductive | | %-units | 2.04 | 2.04 | 1.98 |
| Late reproductive | | %-units | 1.78 | 1.73 | 1.63 |
| **YOUNGSTOCK SURVIVAL** | | | | | |
| Survival heifers 1-30 days | | %-units | 3.44 | 3.35 | 1.56 |
| Survival heifers 31-458 days | | %-units | 3.69 | 3.68 | 2.06 |
| Survival bulls 1-30 days | | %-units | 1.72 | 1.92 | 0.75 |
| Survival bulls 31-184 days | | %-units | 2.29 | 2.10 | 0.75 |

| | | | | | |
|---|---|---|---|---|---|
| **CLAW HEALTH** | | | | | |
| Sole ulcer | | %-units | 0.586 | 0.595 | 0.795 |
| Sole Hemorrhage | | %-units | 0.096 | 0.097 | 0.114 |
| Heel Horn Erosion | | %-units | 0.148 | 0.154 | 0.168 |
| Digital Dermatitis | | %-units | 0.148 | 0.154 | 0.168 |
| Int. Dig. Hyperplasia | | %-units | 0.295 | 0.296 | 0.336 |
| White Line disease | | %-units | 0.096 | 0.109 | 0.114 |
| Cork Screw claws | | %-units | 0.077 | 0.089 | 0.091 |
| **LONGEVITY** | | | | | |
| Average herdlife | | Day | 0.27 | 0.25 | 0.32 |
| **CONFORMATION** | | | | | |
| Frame | | Point | 0.0 | 0.0 | 0.0 |
| Udder | | Point | 29.07 | 29.07 | 33.02 |
| Feet and legs | | Point | 19.38 | 19.38 | 22.01 |
| Milkability | | Point | 19.38 | 19.38 | 22.01 |
| Temperament | | Point | 9.69 | 9.69 | 11.01 |
| **Saved feed** | | | | | |
| Dry matter | | kg | 0.173 | 0.173 | 0.173 |

* The economic value is the value of a 1 %-point change in frequency (e.g., from 15% mastitis to 16% mastitis) corrected for the number of animals in the different groups

** The economic value is the value of a 1 %-point change in frequency

## Calculation of NTM

NTM is calculated by weighting the EBVs for each NTM sub-index (explained above). The breeding goal is the same for cows and bulls, but different weight factors for yield are used for cows without genomic test to achieve this goal. The EBVs for yield, fertility and health traits are calculated using within-trait group models. This means that any genetic correlations between the trait groups are not considered. This has no significance for bulls with many offspring or cows with a genomic test because their EBVs have high reliabilities for all traits. Cows without a genomic test have EBVs for fertility and health with low reliabilities. Therefore, the weight factor for yield is reduced because cows with high genetic merit for yield often have a genetic merit for fertility that is lower than reflected by their EBVs.

NTM is calculated as shown in the formulas below. The weights used for each standardized sub-trait are shown in Table 2.2.

Sires and cows:

$$NTM = 0 + \sum_{i=1}^{n} (breeding\ value(i) - 100) \times weight\ factor(i)$$

where

- Breeding value$_i$ = Breeding value of the $i^{th}$ trait
- Weight factor$_i$ = The weight factor for the $i^{th}$ trait

NTM is standardized to have an average of zero and a standard deviation of 10. The standardization of the indices in NTM is described in the chapter “Standardization of EBVs and NTM”.

Heifers:

$$NTM = (NTMsire + NTMdam)/2$$

Table 2.2. NTM weight factors for NAV dairy breeds.

| | Holstein | RDC | Jersey |
|---|---|---|---|
| Yield index[1] | 0.90/0.81 | 1.02/0.93 | 0.83/0.75 |
| Growth | 0.08 | 0.10 | - |
| Fertility | 0.36 | 0.36 | 0.26 |
| Birth | 0.14 | 0.11 | 0.04 |
| Calving | 0.14 | 0.10 | 0.07 |
| Udder health | 0.30 | 0.26 | 0.44 |
| General health | 0.14 | 0.11 | 0.14 |
| Claw health | 0.10 | 0.07 | 0.09 |
| Frame | - | - | - |
| Feet and legs | 0.05 | 0.06 | 0.07 |
| Udder | 0.18 | 0.26 | 0.15 |
| Milkability | 0.09 | 0.11 | 0.09 |
| Temperament | 0.04 | 0.03 | 0.03 |
| Longevity | 0.06 | 0.06 | 0.09 |
| Youngstock survival | 0.13 | 0.19 | 0.10 |
| Saved feed | 0.08 | 0.13 | 0.18 |

[1] Weight factor for bulls and genomic tested cows/weight factor for cows with no genomic test and own yield record

## Correlation between NTM and sub-indices

The expected genetic response for each sub-index when NTM is selected for, is expressed as a percentage of the maximum progress for that index and is shown in Table 2.3. Maximum progress is obtained if selection is based solely on the trait in question.

Table 2.3. Expected genetic response for each NTM sub-trait represented by the correlation between NTM and each sub-index. Bulls born in 2021-2022

| | Holstein | RDC | Jersey |
|---|---|---|---|
| Yield | 0.74 | 0.66 | 0.67 |
| Growth | 0.12 | 0.06 | 0.09 |
| Fertility | 0.25 | 0.29 | 0.22 |
| Birth | 0.17 | 0.17 | 0,05 |
| Calving | 0.16 | 0.24 | 0.23 |
| Udder health | 0.28 | 0.29 | 0.48 |
| General health | 0.29 | 0.30 | 0.42 |
| Frame | -0.03 | -0.11 | -0.06 |
| Feet & legs | 0.07 | 0.19 | 0.18 |
| Udder | 0.17 | 0.34 | 0.16 |
| Milkability | 0.05 | 0.18 | 0.07 |
| Temperament | 0.09 | 0.05 | 0.05 |
| Longevity | 0.30 | 0.48 | 0.41 |
| Claw health | 0.17 | 0.19 | 0.13 |
| Youngstock survival | 0.11 | 0.26 | 0.33[1] |
| Saved feed | 0.07 | 0.12 | 0.15 |

[1] Based on progeny tested Nordic Jersey bulls born 2009-2010

## References

https://www.nordicebv.info/wp-content/uploads/2018/11/2018.11.06-NTM-2018-report-Full.pdf.

https://www.nordicebv.info/wp-content/uploads/2020/06/2019-12-27-korrelation-med-indregning-af-NTM-til-workshop-wff_gap_-clean_TV.pdf

https://www.nordicebv.info/wp-content/uploads/2020/06/2020-01-29-follow-up-analyses-from-NAV-workshop-16-1-2020_final.pdf

https://www.nordicebv.info/wp-content/uploads/2020/06/2019-12-10-Note_Maintenance_in_NTM_gap.pdf

# 3. Genomic Prediction

Genomic evaluation is performed monthly for females and young AI bulls. A single step model is used for: Metabolic efficiency, Confirmation traits, General health, Claw health and Growth. The remaining trait groups are evaluated by a two-step model.

A single step model uses simultaneously information from pedigree, phenotypes and genotypes to estimate GEBVs, in a two-step model EBVs are in the 1st step estimated from a traditional genetic model evaluation using pedigree and phenotypes, and deregressed EBVs are together with genotyped used simultaneously in the 2nd step to estimate GEBVs.

## Evaluated traits

Genomic breeding values (GEBV) are calculated for yield, conformation, udder health, general health, young stock survival (not Jersey), longevity, calving, birth, fertility, claw health, growth, persistency, milkability, temperament and feed efficiency.

## Reference population

Reference populations (Table 3.1) for all three breeds consist of proven bulls and females, except for young stock survival, where only bulls are included in the reference population.

Females are Danish, Swedish and Finnish cows with phenotypic records.

Proven bulls are bulls that are genotyped and have reliability above a certain threshold based on the number of Danish, Swedish and Finnish daughters. Additionally, the reference groups also include foreign bulls that have Interbull proofs and where genotypes are exchanged with NAV. This includes bulls from Eurogenomics (Germany, Netherlands, France, Spain, and Poland) for Holstein, Norway for RDC and US for Jersey.

Table 3.1. Number of males and females in reference population (May 2024).

| | Bulls | Cows |
|---|---|---|
| Holstein | 41,858 | 216,140 |
| RDC | 9,314 | 120,538 |
| Jersey | 2,888 | 65,585 |

Animals with genotypes that are inconsistent with their recorded parents are excluded from the genomic evaluation.

## SNP-chips and imputation

An Illumina 50K is used as a standard. Lower density chips are imputed to this standard using the software program F-impute.

## Genetic evaluation

For genetic evaluation phenotypic information from the Nordic countries is updated four times per year. Interbull proofs on the Nordic scale are used as “phenotypic” information for foreign bulls without official Nordic EBVs and they are updated three times per year.

In the first step of the two-step model traditional EBVs are calculated by a traditional  evaluation model where phenotypic and pedigree information are included. In the second step EBVs combined across lactations from the traditional Nordic genetic evaluation are deregressed and used to calculated GEBVs for genomic tested animals.

The single step method includes the phenotypic, genomic and pedigree information simultaneously in the estimation of breeding values of all animals, both genomic tested animals and animals without an available genotype. In the single step model GEBVs are estimated for 1., 2., and 3. lactation and afterwards weighted together.

In the genomic prediction models  a  polygenic effect is included. In table 3.2 the calculation method and the size of the polygenic effect can be seen for the different trait groups in NTM. Saved feed is split in Maintenance and Metabolic since the calculation method is different.

Table 3.2. Calculation method and polygenic effect for the traits in NTM except saved feed that is split in Maintenance and Metabolic.

| Trait | Calculation method | Polygenic effect |
|---|---|---|
| Yield index | Two Step | 10% |
| Growth | Single Step | 30% |
| Fertility | Two Step | 10% |
| Birth | Two Step | 10% |
| Calving | Two Step | 10% |
| Udder health | Two Step | 10% |
| General health | Single Step | 30% |
| Claw health | Single Step | 30% |
| Frame | Single Step | 30% |
| Feet and legs | Single Step | 30% |
| Udder | Single Step | 30% |
| Milkability | Single Step | 10% |
| Temperament | Two Step | 10% |
| Longevity | Two Step | 10% |
| Youngstock survival | Two Step | 10% |
| Saved feed - Maintenance | Two Step | 10% |
| Saved feed - Metabolic | Single Step | 10% |

The standard deviations of the GEBVs are scaled to ensure that the genetic SD for the EBV and GEBV are the same.

## Reliability

Reliabilities are calculated as described in Strandén and Christensen (2011) for the two-step method and as Gao et al (2023) for the single step method.

## Publication

GEBVs are published for all genotyped females, and for AI-bulls older than 10 months.

## References

Lund, M. S., A. P. W. de Roos, A. G. de Vries, T. Druet, V. Ducrocq, S. Fritz, F. Guillaume, B. Guldbrandtsen, Z. Li, R. Reents, C. Schrooten, F. Seefried, G. Su. 2011. A common reference population from four European Holstein populations increases reliability of genomic predictions. Gen. Sel. Evol. 43:43. https://doi.org/10.1186/1297-9686-43-43.

Strandén, I and O. F. Christensen. 2011. Allele coding in genomic evaluation. Gen. Sel. Evol. 43:25. https://doi.org/10.1186/1297-9686-43-25.

M. Taskinen, E. Mäntysaari, M. Lidauer, T. Knürr, J. Pösö, G. Su. 2013. Comparison of model reliabilities from single-step and bivariate blending methods. Interbull Bull. 47:246-251, Nantes, France. https://pure.au.dk/portal/files/68214154/1331_2230_1_PB.pdf.

M. Taskinen, E. A. Mäntysaari, G. P. Aamand, I. Stranden. 2014. Comparison of breeding values form single-step and bivariate blending methods. World Congress on Genetics Applied to Livestock Production, August 1-6 2014, Vancouver, Canada. http://www.nordicebv.info/wp-content/uploads/2015/04/Comparison-of-Breeding-Values-from-Single-Step-and-Bivariate-Blending-Methods.pdf.

H. Gao, A. A. Kudinov, M.Taskinen, T.J. Pitkänen, M. H. Lidauer, E. A. Mäntysaari & I. Strandén.2023. A computationally efficient method for approximating reliabilities in large-scale single-step genomic prediction. Genetics Selection Evolution volume 55, Article number: 1 (2023)

# 4. Yield

The index for yield describes the genetic potential for milk, protein and fat production. It also describes the genetic level of protein and fat content in milk and the persistence of the lactation curve.

## Data

The breeding values for milk, fat and protein yield are based on phenotypic records of milk yield, fat and protein content collected through herd testing. Breeding values for persistency are based on estimated genetic lactation curves or milk, fat and protein yield.

## Basic editing rules

The included data are test-day records from 8 to 365 days in milk:

- lactation 1-3 from 1995 and onward (SE)
- lactation 1-10 from 1988 and onward (FI)
- lactation 1-3 from 1990 and onward (DK)

## Foreign information

Foreign information is included in the genetic evaluation for Holstein and Jersey using a modified version of a method described by Bonaiti and Boichard (1995). The latest EBVs calculated by Interbull are used for bulls. Regarding the cows, the foreign EBVs are transformed to the Nordic scale using scaling factors recommended by Interbull.

## Genetic evaluation

Separate evaluations are performed for the three breed groups:

- Holstein: Danish, Swedish and Finnish Holstein
- Red Dairy Cattle: Red Danish Cattle (RDM), Swedish Red and White (SRB), Finnish Ayrshire (FAY) and Finncattle
- Jersey: Danish and Swedish Jersey

There are many small herds in Finland which could lead to systematic group effect with very few animals. Finnish Ayrshire and Finncattle are therefore included in the Holstein evaluation.

## Model

A random regression test-day model is used including the following features:

- Multi-lactation, multi-trait model for milk, protein and fat traits
- From Finland, lactations 4-10 are considered as repeated measurements of third lactation records
- Common genetic parameters for all three countries
- Differences in environmental variances and co-variances between countries are allowed.
- Effect of milking system (AMS vs. VMS) is considered

In general, the systematic environmental part of the evaluation model is similar across countries. However, some differences between countries and breed groups remain due to differences in data and breed structure. The RDC breed group includes many sub-breeds (e.g., American Brown Swiss, Norwegian Red, and Canadian Ayrshire). Therefore, the modelling of heterosis and age effects is more complicated in the RDC breed group than in the Holstein and the Jersey group.

| | |
|---|---|
| Herd test-day | Random |
| Herd × production year | Fixed |
| Lactation curve year × season × 3 age groups (1st lactation) | Fixed |
| Lactation curve year × season (later lactations) | Fixed |
| Lactation curve correction per herd in 5-year periods | Fixed |
| Calving age per 5-year period | Fixed |
| Days pregnant | Fixed |
| Days dry in preceding lactation (2nd and later lactations) | Fixed |
| Heterosis and recombination | Fixed/random |
| Genetic groups (phantom parent groups) | Random |
| Animal | Random |

### Herd test-day

One of the most important advantages of the test-day model over models based on 305-day records is that it is possible to take factors into consideration that affect production for each test-day (e.g., change in feeding, weather, herd personnel). In the Nordic test-day model the effect of herd test-day is estimated separately for 1st and for later lactations.

### Lactation curves

To make test-day records comparable within lactation it is necessary to account for the shape of the lactation curve. Such curves differ depending on the year, season and for first parity cows also age. For each trait, lactation curves are estimated for:

- 1st lactation: Year × season (4 seasons per year) × 3 age groups
- 2nd and later lactations: Year × season (4 seasons per year)

### Calving age

In general, the fixed effect calving age is modelled by monthly age classes within lactation. However, in the RDC breed group the effect of calving age on yield depends on the breed composition. The age-dependent development in yield is more pronounced in American Brown Swiss than it is in Ayrshire and Swedish Red and White. Therefore, an interaction of age and breed combination was introduced. The age effects are nested with 5-year periods.

### Days pregnant

A specific correction for the effect of pregnancy is included in the test-day model by including effect of days pregnant. Ten day classes in the period 120 – 240 days of pregnancy are used. Additionally, one group class for less than 120 days and one for more than 240 days pregnancy was created.

### Days dry

The effect of days dry prior to lactation is included for 2nd and 3rd lactations. For days dry below 70 days 7-day classes are used. Days dry is calculated by two methods:

- Exact drying-off date recorded
- Midpoint between last test-day with yield and next test date or calving.

The effect of days dry is estimated separately for the two groups.

### Production year × month

The general monthly fluctuation in yield is described by the effect of production year and month. For

Finland, there are separate classes for lactations 1-4 and lactations 5-10 are grouped together.

Herd × production year
Yearly differences within the herd are considered by means of a fixed effect of herd x production year.

## Heterosis and recombination loss

In the Jersey and Holstein group, heterosis is estimated within countries for the following breed combinations:

Holstein
- Original Danish Black & White × Holstein Friesian
- Original Danish Red & White × Holstein Friesian
- Holstein × FAY (only the Finnish part of data)
- With FAY-heterosis (only the Finnish part of data)

Jersey
- Original Danish Jersey × US Jersey
- Original Danish Jersey × New Zealand Jersey

In the RDC breed group effects of heterosis and recombination loss are included. Both effects are modelled by the effect of total heterosis and recombination loss within a country, and by random deviations for the following breed combinations:

Finnish data
- Finnish Ayrshire × Swedish Red and White
- Finnish Ayrshire × Canadian Ayrshire
- Finnish Ayrshire × Holstein (all sub-breeds)

Swedish data
- Swedish Red and White × Red Danish
- Swedish Red and White × American Brown Swiss
- Swedish Red and White × Canadian Ayrshire
- Swedish Red and White × Finnish Ayrshire
- Swedish Red and White × Norwegian Red
- Finnish Ayrshire × Norwegian Red

Danish data
- Red Danish Cattle × American Brown Swiss
- Red Danish Cattle × Holstein (all sub-breeds)
- Red Danish Cattle × (Swedish Red and White + Finnish Ayrshire + Norwegian Red)
- American Brown Swiss × Holstein (all sub-breeds)
- American Brown Swiss × (Swedish Red and White + Finnish Ayrshire + Norwegian Red)

## Genetic groups (phantom parent groups)

The effect of the origin, or source, of genetic constitution with respect to year and country of birth is accounted for by using the concept of phantom parent grouping. The estimates of genetic group effects are more stable when they were assumed to be random.

### Heterogenic variance (HV) correction

In the estimation of EBVs for milk production traits it is very important to account for increasing variance of EBVs through time. Especially for selection of cows, it is important to consider the possibility that variation differs between herds. The increasing variance is associated with increasing production levels.

Differences in variation between herds and over time are corrected by a simultaneous procedure. This is an iterative process involving the following steps:

- Estimation of breeding values without HV-correction
- Residual variation is calculated – and data are adjusted accordingly
- New estimation of breeding values
- New HV-adjustment
- The iteration continues until the HV-adjustment become negligible

For the HV-adjustment the following assumptions are made:

- Definition of base: All variances are adjusted to variance of the base animals which cows born 01.01.2001-20.6.2003.
- Base variances: These values retain the relationship among country-wise environmental variances. This is necessary because environmental parameters differ between countries.

#### Permanent environmental effects within lactations

Two types of permanent environmental effects are included in the yield evaluation: (1) within lactation to describe the overall environment in a single lactation, and (2) across lactations (1 to 3). For Finland yield data from all lactation are included in the evaluation; thus, the environmental effects across 3rd and later lactations are also estimated.

### Residual effect per test-day

The residual effect per test-day is assumed to be constant over lactation.

## Forming 305-day breeding values

As a result of the genetic evaluation genetic lactation curves for milk, protein and fat yield were constructed for each animal. These lactation curves simply consist of the animals' daily breeding values for each trait. To obtain 305-day breeding values the daily breeding values between 8-312 days in milk are summed.

The breeding value for protein content within lactation is calculated from the ratio of protein to milk yield in the following way:

$$EBV_{\text{protein\%}} = ((EBV_{\text{protein yield}}+\text{phenotypic mean}_{\text{protein yield}})/(EBV_{\text{milk yield}}+\text{phenotypic mean}_{\text{milk yield}}))*100$$

EBV for fat yield is calculated in similar manner.

Genetic parameters are shown in Table 4.1 – 4.3.

Table 4.1. Genetic parameters for Red Dairy Cattle (RDC) used in the Nordic test-day model summarized for 305 days and based on 10 test-days. Heritabilities on the diagonal and genetic correlations above the diagonal, phenotypic correlations below the diagonal.

| | 1st lactation | | | 2nd lactation | | | 3rd lactation | | |
|---|---|---|---|---|---|---|---|---|---|
| | M | P | F | M | P | F | M | P | F |
| M1 | **0.39** | 0.86 | 0.71 | 0.86 | 0.71 | 0.55 | 0.84 | 0.65 | 0.51 |
| P1 | 0.93 | **0.33** | 0.78 | 0.72 | 0.83 | 0.62 | 0.71 | 0.81 | 0.61 |
| F1 | 0.80 | 0.82 | **0.34** | 0.56 | 0.64 | 0.84 | 0.50 | 0.56 | 0.80 |
| M2 | 0.58 | 0.53 | 0.43 | **0.29** | 0.87 | 0.70 | 0.98 | 0.81 | 0.67 |
| P2 | 0.54 | 0.58 | 0.48 | 0.94 | **0.27** | 0.81 | 0.85 | 0.97 | 0.80 |
| F2 | 0.43 | 0.46 | 0.53 | 0.82 | 0.86 | **0.26** | 0.63 | 0.73 | 0.97 |
| M3 | 0.48 | 0.43 | 0.35 | 0.60 | 0.58 | 0.49 | **0.26** | 0.85 | 0.65 |
| P3 | 0.42 | 0.46 | 0.38 | 0.56 | 0.63 | 0.53 | 0.94 | **0.25** | 0.78 |
| F3 | 0.34 | 0.37 | 0.45 | 0.47 | 0.52 | 0.58 | 0.83 | 0.86 | **0.21** |

Table 4.2. Genetic parameters for Holstein in Nordic test-day model summarized for 305 days and based on 10 test-days. Heritability's on the diagonal and genetic correlations above the diagonal, phenotypic correlations below the diagonal.

| | 1st lactation | | | 2nd lactation | | | 3rd lactation | | |
|---|---|---|---|---|---|---|---|---|---|
| | M | P | F | M | P | F | M | P | F |
| M1 | **0.43** | 0.86 | 0.46 | 0.85 | 0.71 | 0.23 | 0.81 | 0.63 | 0.10 |
| P1 | 0.92 | **0.35** | 0.67 | 0.75 | 0.84 | 0.46 | 0.72 | 0.81 | 0.33 |
| F1 | 0.75 | 0.85 | **0.36** | 0.42 | 0.68 | 0.85 | 0.43 | 0.70 | 0.78 |
| M2 | 0.52 | 0.48 | 0.37 | **0.29** | 0.84 | 0.42 | 0.99 | 0.78 | 0.32 |
| P2 | 0.46 | 0.50 | 0.45 | 0.94 | **0.25** | 0.72 | 0.84 | 0.99 | 0.62 |
| F2 | 0.31 | 0.39 | 0.51 | 0.79 | 0.88 | **0.29** | 0.47 | 0.76 | 0.98 |
| M3 | 0.47 | 0.43 | 0.34 | 0.49 | 0.44 | 0.34 | **0.27** | 0.79 | 0.37 |
| P3 | 0.41 | 0.46 | 0.42 | 0.42 | 0.47 | 0.41 | 0.92 | **0.25** | 0.69 |
| F3 | 0.22 | 0.31 | 0.45 | 0.30 | 0.39 | 0.49 | 0.79 | 0.86 | **0.29** |

Table 4.3. Genetic parameters for Jerseys in Nordic test-day model summarized for 305 days and based on 10 test-days. Heritability's on the diagonal and genetic correlations above the diagonal, phenotypic correlations below the diagonal.

| | 1st lactation | | | 2nd lactation | | | 3rd lactation | | |
|---|---|---|---|---|---|---|---|---|---|
| | M | P | F | M | P | F | M | P | F |
| M1 | **0.44** | 0.91 | 0.74 | 0.88 | 0.84 | 0.49 | 0.90 | 0.84 | 0.49 |
| P1 | 0.95 | **0.38** | 0.86 | 0.78 | 0.90 | 0.65 | 0.81 | 0.91 | 0.66 |
| F1 | 0.87 | 0.92 | **0.35** | 0.65 | 0.83 | 0.86 | 0.67 | 0.83 | 0.86 |
| M2 | 0.56 | 0.52 | 0.46 | **0.27** | 0.86 | 0.57 | 0.99 | 0.86 | 0.53 |
| P2 | 0.53 | 0.54 | 0.51 | 0.95 | **0.23** | 0.80 | 0.88 | 0.99 | 0.78 |
| F2 | 0.41 | 0.46 | 0.51 | 0.87 | 0.93 | **0.22** | 0.58 | 0.79 | 0.99 |
| M3 | 0.50 | 0.46 | 0.40 | 0.55 | 0.51 | 0.43 | **0.27** | 0.88 | 0.55 |
| P3 | 0.46 | 0.48 | 0.44 | 0.51 | 0.54 | 0.48 | 0.95 | **0.23** | 0.77 |
| F3 | 0.34 | 0.39 | 0.44 | 0.41 | 0.47 | 0.51 | 0.86 | 0.92 | **0.23** |

## Index

The index for yield is based on the sub-indices for milk, fat and protein. The standardization of the breeding values is described in the chapter "Standardization of EBVs and NTM".

The EBVs from different lactations are combined. Standardized milk, fat and protein indices are combined in the total yield index using weight factors based on economic calculations (Table 4.4).

Table 4.4. Calculation of yield index. Subscript of EBV refers to lactation.

| Breed | Index | Combined index |
|---|---|---|
| All | Milk | $0.30\times EBV_{milk1}+0.25\times EBV_{milk2}+0.45\times EBV_{milk3}$ |
| All | Fat | $0.30\times EBV_{fat1}+0.25\times EBV_{fat2}+0.45\times EBV_{fat3}$ |
| All | Protein | $0.30\times EBV_{protein1}+0.25\times EBV_{protein2}+0.45\times EBV_{protein3}$ |
| RDC | Yield | -0.25×milk index+0.55×fat index+0.70×protein index |
| HOL | Yield | -0.25×milk index+0.55×fat index+0.70×protein index |
| JER | Yield | -0.30×milk index+0.65×fat index+0.65×protein index |

The following relative indices for milk production are published for cows and sires:

- Breeding value for milk yield
- Breeding value for protein yield
- Breeding value for fat yield
- Yield index: Total breeding value, based on breed specific breeding goals for yield

Further EBVs on a fixed base are published and used for export purposes – see Appendix 1

## Correlation between yield index and underlying traits

The expected progress of each trait expressed as a percentage of maximum progress for that trait is shown in Table 4.5. Maximum progress is obtained if selection is based solely on the trait in question.

Table 4.5. Correlations between yield index and indices for milk, fat and protein for Nordic genotyped bulls born 2021-2022.

| Index | RDC | HOL | JER |
|---|---|---|---|
| Milk | 0.18 | 0.11 | 0.26 |
| Fat | 0.88 | 0.90 | 0.96 |
| Protein | 0.73 | 0.73 | 0.77 |

## Expected effect of breeding values

Phenotypic breed averages and values for one EBV unit for single traits can be found per breed:

https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/RDC
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/HOL
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/JER

From these, the effect of using a specific bull can be calculated. For yield traits, it is EBVs for milk, fat and protein yield that are presented as kg milk, fat and protein.

## Breeding value for persistency

The EBV for persistency is expressed as the amount of milk lost or gained due to the shape of an animal's lactation curve from day 100 to 300 days in milk. The loss (or gain) in milk is calculated by taking the animal's EBV for day 100 and then multiplying it by 200. This gives the theoretical 200-day yield if a constant curve is assumed. This is then deducted from the yield measured by true genetic lactation curve between days 100-299. The bigger the derived value is, the more persistent the lactation curve of the animal is.

Breeding values are calculated as:

$EBV_{percistency} = EBV_{day101} \times 200 - EBV_{d101\text{-}d300}$, where

- $EBV_{day101}$ is the breeding value for milk on day 101
- $EBV_{d101\text{-}d300}$ is the sum of breeding values for milk in the period 101 - 300 days

The EBVs for persistency across traits and lactations are standardized in the same way as 305-day yield. Breeding values for each trait across lactations are calculated using the lactation weights 0.3, 0.25 and 0.45 for 1st, 2nd and 3rd+lactation, respectively.

## Breeding values for protein and fat percentage

Breeding values for protein and fat percentages are calculated from 305-day EBVs using the procedure employed for persistency:

- EBVs for each trait and lactation
- EBVs for each trait and lactation are found by standardization to a common base and standard deviation.

- Across lactation EBVs are calculated using lactation weights 0.30, 0.25 and 0.45 for 1st, 2nd and 3rd+ lactation, respectively.

Calculation of breeding values in kg is described in Appendix 1.

## References

Bonaiti, B., D. Boichard. Accounting for foreign information in genetic evaluation. Interbull Bulletin no. 11, Proceedings of the Interbull annual meeting, Prague, Czech Republic, September 7th – 8th, 1995. https://journal.interbull.org/index.php/ib/article/view/221/221.

Lidauer, M., J. Pedersen, J. Pösö, E. A. Mäntysaari, I. Strandén, P. Madsen, U.S. Nielsen, J.-Å. Eriksson, K. Johansson, G.P. Aamand: Joint Nordic Test Day Model: Evaluation Model. Interbull Open Meeting, Kuopio, Finland, June 4th – 6th, 2006. https://journal.interbull.org/index.php/ib/article/view/956/947.

Mäntysaari, E.A., M. Lidauer, J. Pösö, I. Strandén, P. Madsen, J. Pedersen, U.S. Nielsen, K. Johansson, J.-Å. Eriksson, G.P. Aamand: Joint Nordic Test Day Model: Variance Components. Interbull Open Meeting, Kuopio, Finland, June 4th – 6th, 2006. https://journal.interbull.org/index.php/ib/article/view/955/946.

Pösö, J., J. Pedersen, M. Lidauer, E. A. Mäntysaari, I. Strandén, P. Madsen, U.S. Nielsen, J.-Å. Eriksson, K. Johansson, G.P. Aamand: Joint Nordic Test Day Model: Experiences with the New Model. Interbull Open Meeting, Kuopio, Finland, June 4th – 6th, 2006. https://journal.interbull.org/index.php/ib/article/view/957/948.

# 5. Growth

The index for growth describes the genetic growth ability of male offspring in terms of daily carcass gain and carcass conformation score.

## Data

### Trait definitions

Daily carcass gain is divided into two traits depending on the production system. Male calves are raised with either a short intensive or a long extensive fattening period. Herds are divided into two groups, one with a short (less than 550 days) fattening period (CGS), and one with a long (more than 550 days) fattening period (CGL). The division is based on yearly herd means for age at slaughter. Trait abbreviations are shown in Table 5.1.

Carcass conformation score (CS) is recorded following the EUROP system in 15 ordered classes. All three countries use the same scale.

Carcass fat score (FS) is classified in 15 classes in Sweden and Finland and 5 classes in Denmark. The Swedish and Finnish fat scores are divided by 3 to enable comparison with the Danish data.

Table 5.1. Abbreviations and definitions of traits included in evaluation of growth.

| Abbreviation | Definition |
|---|---|
| CGS | Short fattening period, up to 550 days (DK, FI, SE) |
| CGL | Long fattening period, more than 550 days (FI, SE) |
| CS | Carcass conformation score (15 classes) |
| FS | Carcass fat score; indicator trait (FI and SE 15 classes, DK 5 classes) |

### Basic editing rules

The data used in the genetic evaluation:
- Denmark from year 1990
- Finland from year 2005
- Sweden from year 1996

Records are included if:
- Carcass Weight > 100 kg
- Carcass weight/age in days < 1 kg/day
- Calves have been in the herd more than 90 days before slaughter (only Denmark)
- Slaughter age is within 200-550 days (Jersey)
- Slaughter age within 200-900 days (other breeds)

### Pre-corrections

All traits were pre-corrected for heterogeneous variance due to year of birth and country.

## Genetic evaluation

Separate genetic evaluations are made for Holstein, RDC and Jersey.

## Model

The model for estimation of breeding values is a single step multi-trait animal model:

| | |
|---|---|
| Herd × year | Random |
| Herd × period | Fixed |
| Dam age × country | Fixed |
| Year × month of birth × country | Fixed |
| Heterosis | Regression |
| Genetic groups | Fixed |
| Animal | Random |

A polygenic effect on 0.30 is used and a genotype cut on birthday 01.01.2009.

### Heterosis

Heterosis is accounted for by using the regression on expected total heterosis.

For Jersey, there are few records of CGL. Therefore, this trait is not evaluated for Jersey. The Jersey evaluation contains information from Denmark and Sweden and only for CGS, CS and FS

## Genetic parameters

The genetic parameters used for the 4 traits in the evaluation are displayed in Table 5.2.

Table 5.2. Genetic parameter for Holstein, RDC and Jersey for the genetic evaluation of growth. Heritabilities on the diagonal and genetic correlations below the diagonal.

| | CGS | CGL | CS | FS |
|---|---|---|---|---|
| | | *Holstein* | | |
| CGS | **0.28** | | | |
| CGL | 0.98 | **0.32** | | |
| CS | 0.41 | 0.36 | **0.29** | |
| FS | 0.17 | 0.17 | 0.35 | **0.18** |
| | | *RDC* | | |
| CGS | **0.36** | | | |
| CGL | 0.97 | **0.29** | | |
| CS | 0.34 | 0.32 | **0.29** | |
| FS | - 0.14 | -0.12 | 0.15 | **0.23** |
| | | *Jersey* | | |
| CGS | **0.22** | | | |
| CS | 0.43 | | **0.16** | |
| FS | 0.09 | | 0.34 | **0.11** |

## Index

The index for growth is based on the sub-indices for daily gain and classification score. The standardization of the breeding values is described in the chapter “Standardization of EBVs and NTM”.

The EBVs on the original scale for growth and classification are combined by weighting them with their respective economic values (Table 5.3).

Table 5.3. Calculation of growth index

| | |
|---|---|
| Holstein | 100.65×CGS+100.65×CGL+13.8×CS |
| RDC | 111.4×CGS+111.4×CGL+13.6×CS |
| Jersey | 45.6×CGS+10.1×CS |

The growth index is published for both sires and dams.

## Correlation between the growth index and the underlying traits

The expected progress of each trait, when the index for growth is selected for, expressed as a percentage of maximum progress for that trait, is shown in Table 5.4. The maximum progress is obtained if selection is solely based on the trait in question.

Table 5.4. Correlation between the growth index and indices for weight gain and classification score for Nordic genotyped bulls born 2021-2022

| Index | RDC | HOL | JER |
|---|---|---|---|
| Weight gain | 0.87 | 0.81 | 0.54 |
| Classification | 0.75 | 0.84 | 0.96 |

## Expected effect of the breeding values

Phenotypic breed averages and values for one EBV unit for single traits can be found for each breed:

https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/RDC
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/HOL
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/JER

From these, the effect of using a specific bull can be calculated. For growth traits, it is breeding values for the short- and long fattening period and carcass conformation (EUROP).

## References

Johansson, K., Nielsen, U.S., Pösö, J., Eriksson, J-Å. and Pedersen Aamand, G. 2009. Joint Nordic genetic evaluation of growth and carcass traits in dairy breeds. Interbull Open meeting, Barcelona, Spain, August 21-24, 2009. https://journal.interbull.org/index.php/ib/article/view/1084/1075.

# 6. Fertility

The index for fertility describes the genetic ability of the bulls' daughters to start or resume breeding after calving, to show heat and to become pregnant after insemination.

## Data

## Trait definition

In the evaluation for fertility the following fertility traits (Table 6.1) are considered for heifers and cows in the first three lactations.

Table 6.1. Abbreviations and definitions of traits included in evaluation of fertility.

| Abbreviation | Definition |
|---|---|
| AIS | Number of inseminations (0=heifers, 1-3=cows) |
| ICF | Interval (number of days) from calving to first insemination (cows) |
| IFL | Interval (number of days) from first to last insemination (0=heifers, 1-3=cows) |
| NRR | Non-return rate (0=heifers, 1-3=cows) at 56 days after first inseminations |
| HST | Heat strength (0=heifers, 1-3=cows) (data only from Sweden) |
| CR | Conception rate (0=heifers, 1-3=cows) |

These fertility traits are clustered into three groups:

| | |
|---|---|
| Group 1 | NRR0, IFL0, NRR1-3, ICF1-3, and IFL1-3 |
| Group 2 | AIS0, HST0, AIS1-3, HST1-3, ICF1-3 |
| Group 3 | CR0, CR1-3 |

## Basic editing rules

The data included are from 1983 in Sweden, 1986 in Denmark, and 1993 in Finland for HOL. For RDC collection of data started in 1982 in Sweden, 1985 in Denmark, and 1992 in Finland. Jersey data from Denmark has been collected since 1985, from Sweden since 1986, and from Finland since 2003.

Fertility data is included if:

- Heifers, age at 1st insemination: 270-900 days
- Age at 1st calving: 550-1100 days, maximum in Jersey 975 days
- Heifers and cows, IFL: 0-365 days
- Heifers and cows, AIS: 1-8 inseminations, inseminations from 6 to 8 are set to 5
- Cows, ICF: 20 - 230 days
- Cows, ICF + IFL: 20 - 365 days
- Gestation length 260 - 302 days
- Heifers or cows sired by AI bull
- Heifers and cows are not moved to other herd in the insemination period
- Heifers and cows are not donor or recipient
- Cows are in 1st-3rd lactations

Editing rules for conception rate are in Appendix 2.

### Pre-corrections

All traits are pre-corrected for heterogeneous variance due to country, year of first calving and parity. AIS and IFL are pre-corrected for the effect of use of sexed semen. An average effect of use of sexed semen is 11% for all breeds and parities. A pre-corrected AIS = original AIS – nsex * 0.11. Scaled on an average cycle, coefficients for use of sexed semen in IFL are 3.8 days in heifers and 4.6 days in cows. Therefore, a pre-corrected IFL = original IFL – nsex * coefficient. Nsex refers to a number of inseminations carried out with a sexed semen.

## Genetic evaluation

Separate genetic evaluations are made for Holstein, RDC and Jersey (including Danish, Swedish and Finnish populations).

## Model

The model for estimating breeding values is a multi-trait animal model. The heifer traits are separate traits from the cow traits. Also, cow traits in lactations 1, 2 and 3 are considered as separate traits in a multi-trait multi-lactation analysis.

Model for IFL and NRR for heifer:

| | |
|---|---|
| Herd x year of birth | Fixed |
| First insemination year x month x country | Fixed |
| Age at first insemination x country | Fixed |
| Inbreeding coefficient | Regression |
| Heterosis | Regression |
| Animal | Random |

Model for CR for heifers:

| | |
|---|---|
| Herd × birth year | Fixed |
| Insemination year × month × country | Fixed |
| Age at first insemination in heifers × country | Fixed |
| Semen type × time-period × country | Fixed |
| Insemination number | Fixed |
| Insemination bull breed x time period | Fixed |
| Inbreeding coefficient | Regression |
| Heterosis | Regression |
| Permanent environment | Random |
| Animal | Random |

Model for IFL, AIS, and HST for cows:

| | |
|---|---|
| Herd × first calving year | Fixed |
| First insemination year × month × country | Fixed |
| Age at first insemination in heifers × country | Fixed |
| Inbreeding coefficient | Regression |
| Heterosis | Regression |
| Animal | Random |

Model for NRR for cows:

| | |
|---|---|
| Herd × first calving year | Fixed |
| First insemination year × month × country | Fixed |
| Age at first insemination in heifers × country | Fixed |
| Semen type of first ins. × time-period × country | Fixed |
| Inbreeding coefficient | Regression |
| Heterosis | Regression |
| Animal | Random |

Model for ICF for cows:

| | |
|---|---|
| Herd × first calving year | Fixed |
| Calving year × month × country | Fixed |
| Age at first insemination in heifers × country | Fixed |
| Inbreeding coefficient | Regression |
| Heterosis | Regression |
| Animal | Random |

Model for CR for cows:

| | |
|---|---|
| Herd × first calving year | Fixed |
| Insemination year × month × country | Fixed |
| Age at first insemination in heifers × country | Fixed |
| Semen type × time-period × country | Fixed |
| Insemination number | Fixed |
| Insemination bull breed x time period | Fixed |
| Inbreeding coefficient | Regression |
| Heterosis | Regression |
| Permanent environment | Random |
| Animal | Random |

For Finland, the fixed effects (other than HY) are nested within breeds since Finland also has RDC data in HOL evaluation and HOL data in RDC evaluation to increase the contemporary group size.

### Herd-period

For heifer traits herd*birth year is used; for cow traits herd*year of first calving is used.

### Heterosis

The proportion of total heterozygosity is included in the HOL, RDC and JER evaluations.

### Inbreeding coefficient

Precomputed inbreeding coefficients were used to construct $\boldsymbol{A}^{-1}$ using standard rules. Further to account for negative effect of inbreeding, the mixed models were modified by inclusion of a linear regression of cow's phenotype on inbreeding coefficient.

### Semen type

Includes effect of sexed and unsexed semen

### Insemination bull breed

Breed of the service sire of the dairy cow and heifer is considered. Within breed they are grouped based on decade of insemination. Breeds with less than 1,000 observations were combined to the same joint group. The major service breeds are Holstein, RDC, Jersey, Finncattle, Limousine, Belgian Blue, Blonde D'Aquitaine, Simmental, Aberdeen Angus, and Charolais

### Genetic groups (phantom parent groups)

Genetic groups for animals with unknown parents are included for all breeds in the pedigree file. The genetic groups are constituted by breed, country, and birth year periods.

## Genetic parameters

The genetic parameters used for the fertility traits in the evaluation are shown in Table 6.2 – 6.7.

Table 6.2. Heritabilities (the diagonal), genetic (upper triangle) and residual (lower triangle) correlations for Holstein in trait group 1.

| | NRR0 | IFL0 | NRR1 | ICF1 | IFL1 | NRR2 | ICF2 | IFL2 | NRR3 | ICF3 | IFL3 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| NRR0 | **0.01** | -0.85 | 0.45 | 0.15 | -0.40 | 0.25 | 0.10 | -0.20 | 0.15 | 0.08 | -0.10 |
| IFL0 | -0.45 | **0.02** | -0.25 | 0.10 | 0.40 | -0.15 | 0.05 | 0.25 | -0.10 | 0.03 | 0.20 |
| NRR1 | 0.01 | -0.01 | **0.02** | 0.25 | -0.70 | 0.65 | 0.20 | -0.60 | 0.60 | 0.15 | -0.50 |
| ICF1 | 0.01 | 0.01 | 0.02 | **0.05** | 0.36 | 0.15 | 0.86 | 0.30 | 0.10 | 0.79 | 0.25 |
| IFL1 | -0.02 | 0.03 | -0.30 | -0.04 | **0.03** | -0.55 | 0.40 | 0.85 | -0.45 | 0.35 | 0.74 |
| NRR2 | 0.01 | 0.00 | 0.02 | 0.01 | -0.01 | **0.02** | 0.15 | -0.74 | 0.73 | 0.10 | -0.65 |
| ICF2 | 0.00 | 0.01 | 0.02 | 0.09 | 0.06 | 0.04 | **0.05** | 0.38 | 0.05 | 0.85 | 0.35 |
| IFL2 | 0.00 | 0.03 | -0.02 | 0.02 | 0.04 | -0.29 | -0.05 | **0.03** | -0.61 | 0.31 | 0.88 |
| NRR3 | 0.01 | 0.00 | 0.02 | 0.01 | -0.01 | 0.03 | 0.02 | 0.00 | **0.02** | 0.09 | -0.70 |
| ICF3 | 0.00 | 0.02 | 0.01 | 0.08 | 0.03 | 0.02 | 0.12 | 0.09 | 0.05 | **0.05** | 0.38 |
| IFL3 | 0.00 | 0.02 | -0.01 | 0.01 | 0.03 | -0.03 | 0.02 | 0.04 | -0.30 | -0.05 | **0.03** |

Table 6.3. Heritabilities (the diagonal), genetic (upper triangle) and residual (lower triangle) correlations for RDC and Jersey in trait group 1.

| | NRR0 | IFL0 | NRR1 | ICF1 | IFL1 | NRR2 | ICF2 | IFL2 | NRR3 | ICF3 | IFL3 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| NRR0 | **0.015** | -0.85 | 0.45 | 0.15 | -0.40 | 0.25 | 0.10 | -0.20 | 0.15 | 0.08 | -0.10 |
| IFL0 | -0.47 | **0.015** | -0.25 | 0.10 | 0.40 | -0.15 | 0.05 | 0.25 | -0.10 | 0.03 | 0.20 |
| NRR1 | 0.01 | -0.01 | **0.015** | 0.25 | -0.70 | 0.65 | 0.20 | -0.60 | 0.60 | 0.15 | -0.50 |
| ICF1 | 0.02 | -0.01 | 0.03 | **0.04** | 0.36 | 0.15 | 0.86 | 0.30 | 0.10 | 0.79 | 0.25 |
| IFL1 | -0.02 | 0.03 | -0.34 | -0.03 | **0.03** | -0.55 | 0.40 | 0.85 | -0.45 | 0.35 | 0.74 |
| NRR2 | 0.02 | -0.02 | 0.03 | 0.01 | -0.01 | **0.015** | 0.15 | -0.74 | 0.73 | 0.10 | -0.65 |
| ICF2 | 0.01 | 0.00 | 0.03 | 0.09 | 0.04 | 0.06 | **0.04** | 0.38 | 0.05 | 0.85 | 0.35 |
| IFL2 | -0.02 | 0.02 | -0.03 | 0.03 | 0.06 | -0.35 | -0.04 | **0.03** | -0.61 | 0.31 | 0.88 |
| NRR3 | 0.00 | -0.01 | 0.03 | 0.00 | -0.03 | 0.04 | 0.03 | -0.02 | **0.015** | 0.09 | -0.7 |
| ICF3 | 0.01 | 0.00 | 0.02 | 0.06 | 0.03 | 0.03 | 0.1 | 0.05 | 0.07 | **0.04** | 0.38 |
| IFL3 | -0.02 | 0.03 | -0.01 | 0.01 | 0.05 | -0.03 | 0.03 | 0.09 | -0.33 | -0.05 | **0.03** |

Table 6.4. Heritabilities (the diagonal), genetic (upper triangle) and residual (lower triangle) correlations for Holstein in trait group 2.

| | AIS0 | HST0 | AIS1 | HST1 | ICF1 | AIS2 | HST2 | ICF2 | AIS3 | HST3 | ICF3 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| AIS0 | **0.025** | 0.15 | 0.55 | 0.08 | 0.12 | 0.50 | 0.05 | 0.08 | 0.45 | 0.03 | 0.06 |
| HST0 | 0.07 | **0.02** | 0.08 | 0.55 | 0.45 | 0.05 | 0.45 | 0.35 | 0.03 | 0.40 | 0.30 |
| AIS1 | 0.04 | -0.01 | **0.03** | 0.20 | 0.20 | 0.75 | 0.15 | 0.17 | 0.60 | 0.10 | 0.15 |
| HST1 | 0.01 | 0.01 | 0.06 | **0.02** | 0.50 | 0.15 | 0.60 | 0.40 | 0.10 | 0.40 | 0.35 |
| ICF1 | -0.01 | 0.00 | -0.06 | 0.06 | **0.05** | 0.15 | 0.40 | 0.85 | 0.10 | 0.30 | 0.74 |
| AIS2 | 0.02 | 0.00 | 0.03 | -0.01 | 0.00 | **0.03** | 0.20 | 0.20 | 0.80 | 0.15 | 0.17 |
| HST2 | -0.01 | 0.01 | 0.01 | 0.03 | 0.01 | 0.05 | **0.02** | 0.50 | 0.15 | 0.60 | 0.40 |
| ICF2 | 0.00 | 0.01 | 0.01 | 0.01 | 0.08 | -0.09 | 0.05 | **0.05** | 0.15 | 0.40 | 0.88 |
| AIS3 | 0.02 | 0.00 | 0.02 | 0.00 | 0.00 | 0.03 | -0.01 | -0.02 | **0.03** | 0.20 | 0.20 |
| HST3 | 0.02 | 0.01 | -0.01 | 0.01 | 0.02 | 0.01 | 0.05 | 0.02 | 0.05 | **0.02** | 0.50 |
| ICF3 | 0.02 | 0.00 | -0.01 | 0.01 | 0.05 | 0.02 | 0.01 | 0.08 | -0.10 | 0.05 | **0.05** |

Table 6.5. Heritabilities (the diagonal), genetic (upper triangle) and residual (lower triangle) correlations for RDC and Jersey in trait group 2.

| | AIS0 | HST0 | AIS1 | HST1 | ICF1 | AIS2 | HST2 | ICF2 | AIS3 | HST3 | ICF3 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| AIS0 | **0.025** | 0.15 | 0.55 | 0.08 | 0.12 | 0.50 | 0.05 | 0.08 | 0.45 | 0.03 | 0.06 |
| HST0 | 0.07 | **0.02** | 0.08 | 0.55 | 0.45 | 0.05 | 0.45 | 0.35 | 0.03 | 0.40 | 0.30 |
| AIS1 | 0.03 | 0.00 | **0.03** | 0.20 | 0.20 | 0.75 | 0.15 | 0.17 | 0.60 | 0.10 | 0.15 |
| HST1 | 0.01 | 0.01 | 0.07 | **0.02** | 0.50 | 0.15 | 0.60 | 0.40 | 0.10 | 0.40 | 0.35 |
| ICF1 | -0.02 | 0.00 | -0.07 | 0.05 | **0.04** | 0.15 | 0.40 | 0.85 | 0.10 | 0.30 | 0.74 |
| AIS2 | 0.04 | 0.01 | 0.05 | 0.00 | 0.00 | **0.03** | 0.20 | 0.20 | 0.80 | 0.15 | 0.17 |
| HST2 | 0.00 | 0.01 | 0.00 | 0.03 | 0.02 | 0.07 | **0.02** | 0.50 | 0.15 | 0.60 | 0.40 |
| ICF2 | -0.01 | 0.00 | -0.01 | 0.01 | 0.08 | -0.10 | 0.04 | **0.04** | 0.15 | 0.40 | 0.88 |
| AIS3 | 0.02 | 0.01 | 0.04 | 0.01 | -0.01 | 0.06 | 0.01 | -0.01 | **0.03** | 0.20 | 0.20 |
| HST3 | 0.02 | 0.01 | -0.01 | 0.02 | 0.00 | 0.01 | 0.04 | 0.03 | 0.05 | **0.02** | 0.50 |
| ICF3 | 0.00 | 0.00 | -0.02 | 0.02 | 0.05 | -0.01 | 0.01 | 0.10 | -0.11 | 0.03 | **0.04** |

Table 6.6. Heritabilities (the diagonal), genetic (upper triangle) and permanent environment (lower triangle) correlations for Holstein in trait group 3. Residual correlations are zero.

| | CR0 | CR1 | CR2 | CR3 |
|---|---|---|---|---|
| CR0 | **0.01** | 0.72 | 0.55 | 0.53 |
| CR1 | 0.07 | **0.025** | 0.93 | 0.92 |
| CR2 | 0.06 | 0.09 | **0.03** | 0.96 |
| CR3 | 0.055 | 0.076 | 0.10 | **0.03** |

Table 6.7. Heritabilities (the diagonal), genetic (upper triangle) and permanent environment (lower triangle) correlations for RDC and Jersey in trait group 3. Residual correlations are zero.

| | CR0 | CR1 | CR2 | CR3 |
|---|---|---|---|---|
| CR0 | **0.01** | 0.65 | 0.57 | 0.47 |
| CR1 | 0.05 | **0.02** | 0.93 | 0.84 |
| CR2 | 0.03 | 0.09 | **0.023** | 0.95 |
| CR3 | 0.02 | 0.07 | 0.10 | **0.025** |

## Index

The index for fertility is based on the sub-indices for AIS, ICF and IFL. The standardization of the relative breeding values is described in the chapter “Standardization of EBVs and NTM”.

The EBVs for each trait in the fertility index, IFL, ICF and AIS, are combined by weighting them with their respective economic values (Table 6.8).

Table 6.8. Calculation of the fertility index.

| | |
|---|---|
| HOL | $0.73\times IFL_0+0.62\times ICF_{1\text{-}3}+2.35\times IFL_{1\text{-}3}+10.17\times AIS_0+35.55\times AIS_{1\text{-}3}$ |
| RDC | $0.61\times IFL_0+0.56\times ICF_{1\text{-}3}+1.78\times IFL_{1\text{-}3}+10.14\times AIS_0+27.24\times AIS_{1\text{-}3}$ |
| JER | $0.93\times IFL_0+0.28\times ICF_{1\text{-}3}+1.61\times IFL_{1\text{-}3}+9.27\times AIS_0+27.14\times AIS_{1\text{-}3}$ |

The fertility index is published for sires and cows.

## Correlation between the fertility index and the underlying traits

The expected progress of each trait when the fertility index is selected for, expressed as a percentage of maximum progress for that trait, is shown in Table 6.9. Maximum progress is obtained if selection is solely based on the trait in question.

Table 6.9. Correlation between the fertility index and indices for $ICF_{1\text{-}3}$, $IFL_0$, $IFL_{1\text{-}3}$, $AIS_0$ and $AIS_{1\text{-}3}$

| Index | RDC | HOL | JER |
|---|---|---|---|
| $ICF_{1\text{-}3}$ | 0.53 | 0.53 | 0.57 |
| $IFL_0$ | 0.50 | 0.60 | 0.70 |
| $IFL_{1\text{-}3}$ | 0.98 | 0.99 | 0.96 |
| $AIS_0$ | 0.53 | 0.59 | 0.76 |
| $AIS_{1\text{-}3}$ | 0.89 | 0.89 | 0.87 |

## Effect of 10 index units

Phenotypic breed averages and values for one breeding value unit for single traits can be found for each breed:

https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/RDC
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/HOL
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/JER

From these, the effect of using a specific bull can be calculated for interval from calving to first insemination, interval from first to last insemination and number of inseminations.

## References

K. Muuttoranta, A.-M. Tyrisevä, E.A. Mäntysaari, J. Pösö, G.P. Aamand, J.-Å. Eriksson, U.S. Nielsen, M.H. Lidauer. 2015. Genetic parameters for female fertility in Nordic dairy cattle. Interbull Bulletin, 49 (2015), pp. 32–35 https://journal.interbull.org/index.php/ib/article/view/1372/1439

K. Muuttoranta, A.-M. Tyrisevä, E.A. Mäntysaari, J. Pösö, G.P. Aamand, J.-Å. Eriksson, U.S. Nielsen, M.H. Lidauer. Genetic parameters for a multiple-trait linear model conception rate evaluation. 2016. Proceedings of the 67th Annual Meeting of the European Association for Animal Production, Belfast, UK, 29 Aug - 1 Sept 2016. Page 628. DOI: http://dx.doi.org/10.3920/978-90-8686-830-8

# 7. Calving and Birth

The index for calving (calving$^{\text{maternal}}$) and birth (calving$^{\text{direct}}$) describes the genetic ability of calving ease and stillbirth. It is expressed by the daughters/offspring of a bull.

## Data

### Trait definitions

Records from the first to fifth calving are included and are referred to as first versus later calvings, respectively. Direct and maternal effects are estimated for all traits.

The traits (Table 7.1) are survival within the first 24 hours (stillbirth), calving ease and calf size. Stillbirth is registered as 0 or 1, calving ease is measured in 4 categories (2 categories in SWE up to 2012), and calf size is measured in 4 classes (only DNK data). Afterwards due to the "European Golden Standards" the traits are converted to Snell Score to approximate the categorical data to a normal distribution when using a linear model.

Table 7.1. Abbreviations and definitions of traits included in evaluation of calving traits.

| Abbreviation | Definition |
|---|---|
| SB 1st calving, SB ≥ 2nd calving | stillbirth in the first 24 hours after birth |
| CE 1st calving, CE ≥ 2nd calving | calving ease |
| CS 1st calving, CS ≥ 2nd calving | calf size |

### Basic editing rules

The time period for inclusion of data varies between traits and countries as it can be seen in table 7.2.

Table 7.2 Year for inclusion of data.

| | **Denmark** | **Finland** | **Sweden** |
|---|---|---|---|
| Stillbirth | 1985- | 1992- | 1985- |
| Calving ease | 1985- | 2004- | 1985- |
| Calf size | 1985- | No | No |

Birth records are included if:

- Single births
- Calf is not the result of ET
- Sex is known for the calf
- Calving date is known
- Sire or grandsire is a known sire
- Sire or grandsire is either Holstein, RDC or Jersey
- Excluding Danish Jersey bull calves born after 1.1.2022

### Pre-corrections

All traits were pre-corrected for heterogeneous variance by snell score by using the following stratums: country, 5-year periods and sex of calf.

## Genetic evaluation

Separate genetic evaluations were made for Holstein, RDC and Jersey.

## Model

The following multi-trait animal model with direct and maternal effects is used for Holstein, Jersey and RDC:

| | |
|---|---|
| Age at calving in months (heifers) or lactation number (cows) | Fixed |
| Year of calving × month of calving × country | Fixed |
| Sex of calf × year of calving × country | Fixed |
| Herd × 5-year period | Fixed |
| Inbreeding coefficient of the calf | Fixed |
| Inbreeding coefficient of the cow | Fixed |

| | |
|---|---|
| HerdxYear within 5-year-period | Random |
| Permanent environmental effect of the cow (later calvings) | Random |
| Genetic effect of calf (defined by A-matrix with inbreeding included) | Random |
| Genetic effect of cow (defined by A-matrix with inbreeding included) | Random |
| Genetic groups | Random |
| Direct effect of animal | Random |
| Maternal effect of animal | Random |

## Genetic groups (phantom parent groups)

Genetic groups for animals with unknown parents were included. The phantom parent groups were defined according to year of birth and country of origin.

## Inbreeding

Inbreeding is included in the A-matrix of the genetic model and furthermore, inbreeding depression is included as fixed regression effects of the model both for calf and cow.

## Genetic parameters

The parameters used in the genetic evaluation are shown in Table 7.3 and 7.4. The genetic correlations between maternal and direct traits were assumed to be non-existent and set to zero.

Table 7.3. Heritabilities and genetic correlations for traits used in the index for calving, heritabilities on the diagonal, genetic correlations above the diagonal.

| | | Calving traits (maternal) | | | | | |
|---|---|---|---|---|---|---|---|
| | | 1. calving | | | Later calvings | | |
| | Breed | Stillbirth (SB) | Calving ease (CE) | Calf size (CS) | Stillbirth (SB) | Calving ease (CE) | Calf size (CS) |
| SB1.clv | RDC | **0.038** | 0.400 | 0.000 | 0.600 | 0.337 | 0.000 |
| | HOL | **0.036** | 0.591 | 0.000 | 0.599 | 0.329 | 0.000 |
| | JER | **0.023** | 0.479 | 0.000 | 0.479 | 0.163 | 0.000 |
| CE 1.clv | RDC | | **0.065** | 0.000 | 0.350 | 0.600 | 0.000 |
| | HOL | | **0.090** | 0.000 | 0.623 | 0.716 | 0.000 |
| | JER | | **0.043** | 0.000 | 0.238 | 0.512 | 0.000 |
| CS 1.clv | RDC | | | **0.060** | 0.000 | 0.000 | 0.600 |
| | HOL | | | **0.059** | 0.000 | 0.000 | 0.600 |
| | JER | | | **0.040** | 0.000 | 0.000 | 0.500 |
| SB 2.clv | RDC | | | | **0.019** | 0.401 | 0.000 |
| | HOL | | | | **0.011** | 0.582 | 0.000 |
| | JER | | | | **0.016** | 0.481 | 0.000 |
| CE 2.clv | RDC | | | | | **0.035** | 0.000 |
| | HOL | | | | | **0.047** | 0.000 |
| | JER | | | | | **0.026** | 0.000 |
| CS 2.clv | RDC | | | | | | **0.058** |
| | HOL | | | | | | **0.057** |
| | JER | | | | | | **0.040** |

Table 7.4. Heritabilities and genetic correlations for traits used in the index for birth, heritability's on the diagonal, genetic correlations above the diagonal.

| | | Calving traits (direct) | | | | | |
|---|---|---|---|---|---|---|---|
| | | 1. calving | | | Later calvings | | |
| | Breed | Stillbirth (SB) | Calving ease (CE) | Calf size (CS) | Stillbirth (SB) | Calving ease (CE) | Calf size (CS) |
| SB1.clv | RDC | **0.058** | 0.650 | -0.550 | 0.729 | 0.485 | -0.540 |
| | HOL | **0.040** | 0.709 | -0.523 | 0.617 | 0.532 | -0.513 |
| | JER | **0.034** | 0.441 | 0.000 | 0.786 | 0.335 | 0.000 |
| CE 1.clv | RDC | | **0.077** | -0.500 | 0.435 | 0.500 | -0.451 |
| | HOL | | **0.117** | -0.546 | 0.584 | 0.608 | -0.534 |
| | JER | | **0.022** | 0.000 | 0.389 | 0.803 | 0.000 |
| CS 1.clv | RDC | | | **0.247** | -0.406 | -0.576 | 0.500 |
| | HOL | | | **0.223** | -0.418 | -0.464 | 0.600 |
| | JER | | | **0.150** | 0.000 | 0.000 | 0.600 |
| SB 2.clv | RDC | | | | **0.021** | 0.600 | -0.450 |
| | HOL | | | | **0.011** | 0.631 | -0.485 |
| | JER | | | | **0.016** | 0.443 | 0.000 |
| CE 2.clv | RDC | | | | | **0.035** | -0.400 |
| | HOL | | | | | **0.077** | -0.518 |
| | JER | | | | | **0.026** | 0.000 |
| CS 2.clv | RDC | | | | | | **0.234** |
| | HOL | | | | | | **0.206** |
| | JER | | | | | | **0.150** |

Table 7.5. Direct and maternal genetic variances.

| | Direct | | | Maternal | | |
|---|---|---|---|---|---|---|
| Trait | HOL | RDC | JER | HOL | RDC | JER |
| SB1 | 0.0108 | 0.0091 | 0.0074 | 0.0097 | 0.0058 | 0.0050 |
| CE1 | 0.0538 | 0.0326 | 0.0042 | 0.0402 | 0.0270 | 0.0083 |
| CS1 | 0.1365 | 0.1583 | 0.0937 | 0.0298 | 0.0306 | 0.0221 |
| SB2 | 0.0017 | 0.0022 | 0.0017 | 0.0017 | 0.0020 | 0.0017 |
| CE2 | 0.0252 | 0.0110 | 0.0026 | 0.0150 | 0.0108 | 0.0026 |
| CS2 | 0.1197 | 0.1477 | 0.0957 | 0.0282 | 0.0297 | 0.0226 |

Table 7.6. Residual variance and Herd year variance (within 5-year period).

| | Residual variance | | | H x Y variance | | |
|---|---|---|---|---|---|---|
| Trait | HOL | RDC | JER | HOL | RDC | JER |
| SB1 | 0.2573 | 0.1483 | 0.2111 | 0.0012 | 0.0014 | 0.0013 |
| CE1 | 0.4077 | 0.3897 | 0.1850 | 0.0482 | 0.0213 | 0.0034 |
| CS1 | 0.4764 | 0.4829 | 0.5312 | 0.0306 | 0.0173 | 0.0586 |
| SB2 | 0.1530 | 0.1045 | 0.1055 | 0.0005 | 0.0012 | 0.0006 |
| CE2 | 0.3035 | 0.3021 | 0.0958 | 0.0011 | 0.0093 | 0.0011 |
| CS2 | 0.4616 | 0.4829 | 0.5425 | 0.0277 | 0.0143 | 0.0287 |

Table 7.7 Permanent cow variances.

| | Permanent cow variance | | |
|---|---|---|---|
| Trait | HOL | RDC | JER |
| SB2 | 0.0030 | 0.0017 | 0.0017 |
| CE2 | 0.0115 | 0.0108 | 0.0022 |
| CS2 | 0.0098 | 0.0266 | 0.0094 |

## Index

The index for birth and calving is based on the sub-indices for stillbirth and calving ease. The standardization of the relative breeding values is described in the chapter “Standardization of EBVs and NTM”.

The EBVs on the original scale for stillbirth and calving ease are combined by weighting them with their respective economic values that are based on economic calculations (Table 7.8).

Table 7.8. Calculation of index for calving and birth. The same economic values are used. Subscripts of BV on the original scale refer to lactation.

| | | |
|---|---|---|
| Holstein | | $205\times SB_1+10.90\times CE_1+330\times SB_{\geq 2}+14.80\times CE_{\geq 2}$ |
| RDC | | $201\times SB_1+11.35\times CE_1+337\times SB_{\geq 2}+15.62\times CE_{\geq 2}$ |
| Jersey | | $79\times SB_1+15.70\times CE_1+146\times SB_{\geq 2}+33.70\times CE_{\geq 2}$ |

The indexes for calving and birth are published for sires and cows.

## Correlation between the calving index and underlying traits

The expected progress for each trait, when maternal calving and direct calving are selected for, expressed as the proportion of maximum progress for that trait (Table 7.9 and 7.10). The maximum progress is obtained if selection is solely based on the trait in question. The results are based on Nordic AI bulls born after 2015.

Table 7.9. Correlations between index for calving and maternal indices for stillbirth and calving ease.

| Index | HOL | RDC | JER |
|---|---|---|---|
| $SB_1$ | 0.96 | 0.93 | 0.90 |
| $CE_1$ | 0.69 | 0.66 | 0.71 |
| $SB_{\geq 2}$ | 0.81 | 0.86 | 0.84 |
| $CE_{\geq 2}$ | 0.46 | 0.66 | 0.42 |

Table 7.10. Correlations between index for birth and direct indices for stillbirth and calving ease.

| Index | HOL | RDC | JER |
|---|---|---|---|
| $SB_1$ | 0.96 | 0.95 | 0.95 |
| $CE_1$ | 0.73 | 0.71 | 0.72 |
| $SB_{\geq 2}$ | 0.82 | 0.90 | 0.93 |
| $CE_{\geq 2}$ | 0.63 | 0.75 | 0.67 |

## Expected effect of breeding values

Phenotypic breed averages and values for one breeding value unit for single traits can be found for each breed:

https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/RDC
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/HOL
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/JER

From these, the effect of using a specific bull can be calculated. The average for still birth is percent claves born alive. The average for calving ease is percent calvings without assistant.

## References

# 8. Udder health

The index for udder health describes the genetic ability of the cow to resist mastitis. The breeding goal is to reduce the frequency of clinical mastitis.

## Data

### Trait definition

Records on clinical mastitis (CM) and somatic cell count (SCC) from 1st to 3rd lactation and fore udder attachment (UA) and udder depth (UD) from 1st lactation are used in the genetic evaluation of udder health. The traits included in the genetic evaluation are given in Table 8.1, together with the trait definitions. Data on SCC and udder conformation is only used as indicator traits.

Table 8.1. Abbreviations and definitions of traits included in the udder health genetic evaluation.

| | Definition | DIM[1] | Lact. |
|---|---|---|---|
| CM11 | Clinical mastitis (1) or not (0) | -15-50 | 1 |
| CM12 | -“- | 51-305 | 1 |
| CM2 | -“- | -15-150 | 2 |
| CM3 | -“- | -15-150 | 3 |
| | | | |
| SCC1 | Log somatic cell count | 5-305 | 1 |
| SCC2 | -“- | -“- | 2 |
| SCC3 | -“- | -“- | 3 |
| | | | |
| UA | Fore udder attachment | | 1 |
| UD | Udder depth | | 1 |

[1] Days in milk

### Basic editing rules

Denmark: CM, SCC and udder conformation data from 1990.
Finland: CM, SCC and udder conformation data from 1984, 1988 and 1992, respectively.
Sweden: CM, SCC and udder conformation data from 1984, 1995 and 1992, respectively.

Sweden, Finland and Denmark include records from herds that participate actively in health recording. Active herds are defined as herds in which a certain percentage of the cows are treated for mastitis. Traits are recorded as 0 = no disease or 1 = disease occurred.

### Pre-corrections

All traits are pre-corrected for heterogeneous variance within breed, country and year of calving.

### Genetic evaluation

Separate genetic evaluations are made for Holstein, Red dairy cattle (RDC) (including Finncattle) and Jersey (data only from Denmark).

### Model

The model for estimation of breeding values is a multi-trait random regression test-day animal model.

Model:

| | |
|---|---|
| Herd × year of calving | Random |
| Herd × period | Fixed |
| Calving age × country | Fixed |
| Calving year × calving month × country | Fixed |
| Heterosis | Regression |
| Animal | Random |

## Heterosis

Heterosis is accounted for by applying the regression to the expected total heterosis of all included populations.

## Genetic parameters

The genetic parameters for clinical mastitis and udder conformation traits used in the evaluation for Holstein, Red dairy cattle and Jersey are presented in Table 8.2. The genetic correlations are the same for all three breeds.

Table 8.2. Heritabilities (the diagonal) and genetic correlations (below) for clinical mastitis (CM) and udder conformation traits for Holstein, RDC and Jersey.

| | | CM11 | CM12 | CM2 | CM3 | UA | UD |
|---|---|---|---|---|---|---|---|
| CM11 | Holstein<br>RDC<br>Jersey | **0.05**<br>**0.04**<br>**0.04** | | | | | |
| CM12 | Holstein<br>RDC<br>Jersey | 0.66 | **0.03**<br>**0.02**<br>**0.02** | | | | |
| CM2 | Holstein<br>RDC<br>Jersey | 0.67 | 0.97 | **0.06**<br>**0.05**<br>**0.04** | | | |
| CM3 | Holstein<br>RDC<br>Jersey | 0.68 | 0.81 | 0.93 | **0.07**<br>**0.04**<br>**0.06** | | |
| UA | Holstein<br>RDC<br>Jersey | -0.37 | -0.22 | -0.15 | -0.13 | **0.27**<br>**0.30**<br>**0.24** | |
| UD | Holstein<br>RDC<br>Jersey | -0.56 | -0.38 | -0.28 | -0.25 | 0.80 | **0.41**<br>**0.39**<br>**0.32** |

The heritability of test-day somatic cell count during the first three lactations ranged from 0.08 to 0.15 for Holstein, RDC and Jersey.

The genetic correlations between SCC and CM ranged from 0.45 to 0.70 depending on parity and stage of lactation for all three breeds. Genetic correlations between SCC and udder conformation traits ranged from -0.20 to -0.40 for all three breeds.

Genetic correlations between SCC recorded in the first three lactations in different stages of lactations were high, ranging from 0.56 – 1.00.

## Index

The index for udder health is based on the sub-indices for clinical mastitis in 1st to 3rd lactation.

The standardization of the relative breeding values is described in the chapter “Standardization of EBVs and NTM”.

In Table 8.3 the weighting of the EBVs on the original scale for the four mastitis traits is presented.

Table 8.3. Calculation of index for udder health for Holstein, Red dairy cattle and Jersey.

| | |
|---|---|
| Udder Health | 0.15×CM11+0.15×CM12+0.25×CM2+0.45×CM3 |

## Correlations between index for udder health and underlying traits

The expected progress of each trait when the udder health index is selected for, expressed as a percentage of the maximum progress for that trait, is shown in Table 8.4. The maximum progress is obtained if selection is solely based on the trait in question.

Table 8.4. Correlation between the index for udder health and indices for clinical mastitis in 1st to 3rd lactation.

| Index | RDC | HOL | JER |
|---|---|---|---|
| CM11 | 0.79 | 0.84 | 0.85 |
| CM12 | 0.97 | 0.97 | 0.96 |
| CM2 | 0.98 | 0.98 | 0.97 |
| CM3 | 0.97 | 0.97 | 0.96 |

## Expected effect of breeding values

Phenotypic breed averages and values for one breeding value unit for single traits can be found for each breed:

https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/RDC
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/HOL
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/JER

From these, the effect of using a specific bull can be calculated for the number of mastitis treatments.

## References

Negussie, E., M. Lidauer, E. A. Mäntysaari, I. Strandén, J. Pösö, U. S. Nielsen, K. Johansson, J.-Å. Eriksson, G. P. Aamand. 2010. Combining test day SCS with clinical mastitis and udder type traits: A Random regression model for joint genetic evaluation of udder health in Denmark, Finland and Sweden. 37th ICAR Session and Interbull Open Meeting, Riga, Latvia, 31st May – 4th June 2010. https://journal.interbull.org/index.php/ib/article/view/1153/1144.

# 9. General health

The index for general health describes the genetic resistance of bulls' daughters to reproductive, digestive and feet and leg problems.

## Data

### Trait definition

Records from 1st to 3rd lactation on early reproductive disorders (ERP), late reproductive disorders (LRP), ketosis (KET), other metabolic diseases (OMB), and feet and legs problems (FL) are used in the genetic evaluation for general health. Indicator traits in the evaluation are β-hydroxybutyrate (BHB) and acetone (ACE) records from milk recording in 1st to 3rd lactation. Table 9.1 gives the disease groups, originally defined by Österås et al. (2002) but modified during the 2017 revision of the GH evaluation (General Health Final Report), used in each of the traits.

Table 9.1. Disease groups in the genetic evaluation.

| ERP | LRP | KET | OMB | FL |
|---|---|---|---|---|
| • Retained placenta<br>• Hormonal reproductive disorders<br>• Infective reproductive disorders<br>• Other reproductive disorders | • Hormonal reproductive disorders<br>• Infective reproductive disorders<br>• Other reproductive disorders | • Ketosis | • Milk fever<br>• Other metabolic diseases<br>• Other feed related disorders<br>• Other diseases | • Feet and leg problems |

The traits included in the genetic evaluation are given in Table 9.2 together with the trait definitions.

Table 9.2. Abbreviations and definitions of traits included in the evaluation.

| **Abbreviation and lactation** | **Definition** |
|---|---|
| ERP1-ERP3 | Early reproductive disorders (1) or not (0), 0 to 40 DIM |
| LRP1-LRP3 | Late reproductive disorders (1) or not (0), 41 to 305 DIM |
| OMB1-OMB3 | Other metabolic diseases (1) or not (0), -15 to 305 DIM |
| KET1-KET3 | Ketosis (1) or not (0), -15 to 305 DIM |
| FL1-FL3 | Feet and legs problems (1) or not (0), -15 to 305 DIM |
| BHB1-BHB3 | β-hydroxybutyrate mmol/L, 10 to 60 DIM |
| ACE1-ACE3 | Acetone, mmol/L, 10 to 60 DIM |

### Basic editing rules

Data records included from 1990 for all three countries and include data from all active disease-recording herds. Active herds are defined as herds in which a certain percentage of cows are diagnosed with mastitis. Disease traits are recorded as 0 = no disease or 1 = disease occurred. Beta-hydroxybutyrate and acetone, are recorded in mmol/L.

## Heterogeneous variance adjustment

Disease frequencies vary across countries. Phenotypes of all traits are pre-adjusted for heterogeneous variance due to country, year of calving and breed (all Finnish breeds are in both the Holstein and the RDC evaluation, additionally, FIC is pooled together with RDC, to avoid small contemporary groups).

For the veterinary treatment traits, differences in disease frequencies and heritabilities are taken into account by scaling the observations with varying factors and weights over time so that adjusted observations have the same genetic variance on the observed scale (and different heritability on the observed scale).

To handle differences in phenotypic standard deviation of BHB and acetone records between Finland and Denmark and across years of sampling, the variation in phenotypic records were adjusted according to country, calving year and breed. The impact of HV adjustment for acetone and BHB has a marginal effect on the EBVs for bulls and cows.

## Genetic evaluation

Separate genetic evaluations are prepared for Holsteins (incl. Red Holstein), Red dairy cattle (including Finncattle) and Jerseys.

## Model

The model for estimation of breeding values is a single step multi-trait, multi-lactation animal model:

| | |
|---|---|
| Country * Herd-year | Fixed |
| Country * Calving age | Fixed |
| Country * Year-month of calving | Fixed |
| Lactation stage (only BHB/ACE) | Fixed |
| Genetic groups | Random |
| Cow PE (only BHB/ACE) | Random |
| Animal | Random |

A polygenic effect on 0.30 is used and a genotype cut on birthday 01.01.2009.

## Genetic parameters

The genetic parameters used for the 21 traits in the evaluation are shown in tables 9.3, 9.4 and 9.5. The parameter estimates were either (re)-estimated in the first part (2017) or the second part (2019) of the revision of the GH evaluation (General Health Final Report). For computational reasons, residual correlations between lactations were set to zero.

Table 9.3. Genetic correlations (above), residual correlations (under) and heritability's on the diagonal in 1st, 2nd and 3rd lactation, Holstein.

| **Trait** | **ERP1** | **LRP1** | **MB1** | **KET1** | **FL1** | **ERP2** | **LRP2** | **OMB2** | **KET2** | **FL2** | **ERP3** | **LRP3** | **OMB3** | **KET3** | **FL3** | **BHB1** | **ACE1** | **BHB2** | **ACE2** | **BHB3** | **ACE3** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **ERP1** | **0.034** | 0.37 | 0.40 | 0.31 | 0.15 | 0.72 | 0.32 | 0.29 | 0.33 | 0.08 | 0.64 | 0.18 | 0.30 | 0.20 | 0.16 | 0.05 | 0.03 | -0.03 | -0.01 | -0.02 | 0.05 |
| **LRP1** | 0.02 | **0.004** | 0.27 | 0.22 | 0.14 | 0.34 | 0.93 | 0.17 | 0.04 | 0.11 | 0.33 | 0.90 | 0.19 | 0.09 | 0.19 | 0.02 | 0.05 | -0.01 | -0.06 | 0.01 | -0.03 |
| **MB1** | 0.04 | 0.01 | **0.006** | 0.74 | 0.37 | 0.24 | 0.13 | 0.79 | 0.60 | 0.32 | 0.16 | 0.15 | 0.48 | 0.53 | 0.35 | 0.47 | 0.65 | 0.22 | 0.37 | 0.22 | 0.33 |
| **KET1** | 0.05 | 0.01 | 0.08 | **0.010** | 0.18 | 0.24 | 0.07 | 0.67 | 0.70 | 0.12 | 0.16 | 0.03 | 0.52 | 0.67 | 0.09 | 0.64 | 0.75 | 0.39 | 0.44 | 0.46 | 0.52 |
| **FL1** | 0.01 | 0.00 | 0.01 | 0.01 | **0.013** | 0.10 | 0.09 | 0.32 | 0.17 | 0.96 | 0.01 | 0.02 | 0.20 | 0.10 | 0.91 | 0.02 | 0.04 | -0.01 | -0.03 | -0.01 | 0.01 |
| **ERP2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.030** | 0.30 | 0.26 | 0.26 | 0.03 | 0.98 | 0.27 | 0.23 | 0.20 | 0.09 | 0.00 | -0.01 | -0.01 | -0.02 | 0.00 | -0.01 |
| **LRP2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.04 | **0.005** | 0.13 | 0.06 | 0.11 | 0.35 | 0.94 | 0.15 | 0.10 | 0.22 | -0.02 | -0.03 | 0.01 | 0.01 | 0.00 | 0.01 |
| **MB2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.06 | 0.01 | **0.008** | 0.60 | 0.32 | 0.25 | 0.11 | 0.83 | 0.61 | 0.39 | 0.47 | 0.54 | 0.32 | 0.50 | 0.37 | 0.51 |
| **KET2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.05 | 0.01 | 0.08 | **0.010** | 0.20 | 0.24 | 0.01 | 0.44 | 0.97 | 0.17 | 0.45 | 0.48 | 0.55 | 0.72 | 0.60 | 0.77 |
| **FL2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 | 0.02 | 0.02 | **0.011** | -0.04 | 0.00 | 0.16 | 0.15 | 0.97 | -0.01 | -0.01 | 0.01 | 0.01 | 0.01 | 0.02 |
| **ERP3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.034** | 0.34 | 0.22 | 0.19 | 0.04 | 0.00 | -0.02 | 0.01 | 0.04 | 0.00 | 0.01 |
| **LRP3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.05 | **0.005** | 0.12 | 0.08 | 0.09 | -0.01 | 0.00 | 0.00 | 0.03 | 0.00 | 0.01 |
| **OMB3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.07 | 0.01 | **0.020** | 0.49 | 0.22 | 0.40 | 0.33 | 0.38 | 0.45 | 0.50 | 0.58 |
| **KET3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.05 | 0.01 | 0.09 | **0.015** | 0.12 | 0.39 | 0.42 | 0.55 | 0.71 | 0.63 | 0.79 |
| **FL3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 | 0.02 | 0.02 | **0.012** | 0.00 | 0.00 | 0.00 | 0.01 | -0.03 | -0.02 |
| **BHB1** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.15** | 0.88 | 0.81 | 0.69 | 0.75 | 0.52 |
| **ACE1** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.49 | **0.053** | 0.62 | 0.69 | 0.60 | 0.56 |
| **BHB2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.115** | 0.88 | 0.96 | 0.75 |
| **ACE2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.49 | **0.032** | 0.88 | 0.91 |
| **BHB3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.077** | 0.85 |
| **ACE3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.50 | **0.030** |

Table 9.4. Genetic correlations (above), residual correlations (under) and heritability’s on the diagonal in 1st, 2nd and 3rd lactation, RDC.

| **Trait** | **ERP1** | **LRP1** | **MB1** | **KET1** | **FL1** | **ERP2** | **LRP2** | **OMB2** | **KET2** | **FL2** | **ERP3** | **LRP3** | **OMB3** | **KET3** | **FL3** | **BHB1** | **ACE1** | **BHB2** | **ACE2** | **BHB3** | **ACE3** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **ERP1** | **0.007** | 0.20 | 0.29 | 0.28 | 0.01 | 0.74 | 0.05 | 0.28 | 0.14 | 0.14 | 0.78 | 0.22 | 0.27 | 0.26 | 0.07 | 0.04 | 0.04 | -0.04 | -0.06 | 0.02 | 0.01 |
| **LRP1** | 0.01 | **0.008** | 0.18 | -0.08 | 0.17 | 0.36 | 0.83 | 0.03 | 0.07 | 0.11 | 0.28 | 0.75 | 0.12 | 0.22 | 0.09 | -0.01 | -0.06 | 0.00 | 0.03 | 0.04 | 0.03 |
| **MB1** | 0.01 | 0.00 | **0.003** | 0.63 | 0.43 | 0.09 | -0.02 | 0.81 | 0.60 | 0.05 | 0.23 | -0.16 | 0.52 | 0.62 | 0.18 | 0.46 | 0.62 | 0.22 | 0.38 | 0.24 | 0.35 |
| **KET1** | 0.01 | 0.00 | 0.05 | **0.010** | -0.05 | 0.03 | -0.21 | 0.43 | 0.81 | -0.09 | 0.09 | -0.17 | 0.29 | 0.71 | -0.16 | 0.63 | 0.73 | 0.40 | 0.46 | 0.45 | 0.52 |
| **FL1** | 0.01 | -0.01 | 0.02 | 0.00 | **0.005** | 0.14 | 0.09 | 0.21 | 0.05 | 0.80 | 0.12 | 0.02 | -0.01 | 0.05 | 0.84 | 0.02 | 0.11 | -0.02 | 0.01 | -0.06 | -0.04 |
| **ERP2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.008** | 0.28 | 0.13 | -0.09 | 0.20 | 0.96 | 0.37 | 0.11 | 0.10 | 0.09 | -0.01 | 0.00 | 0.00 | -0.04 | 0.01 | -0.03 |
| **LRP2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.03 | **0.006** | -0.08 | -0.14 | 0.07 | 0.23 | 0.92 | -0.06 | -0.02 | 0.10 | 0.01 | 0.00 | -0.01 | 0.01 | -0.03 | -0.05 |
| **MB2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.02 | 0.00 | **0.008** | 0.46 | -0.03 | 0.27 | -0.17 | 0.87 | 0.51 | 0.15 | 0.47 | 0.54 | 0.32 | 0.49 | 0.36 | 0.50 |
| **KET2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.06 | **0.009** | -0.03 | 0.00 | -0.08 | 0.37 | 0.95 | -0.01 | 0.46 | 0.52 | 0.53 | 0.70 | 0.60 | 0.77 |
| **FL2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | -0.01 | 0.01 | 0.00 | **0.010** | 0.09 | 0.21 | -0.06 | -0.10 | 0.93 | 0.01 | -0.02 | 0.01 | -0.03 | 0.00 | -0.01 |
| **ERP3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.013** | 0.29 | 0.16 | 0.21 | 0.07 | -0.01 | 0.04 | 0.01 | 0.02 | 0.00 | 0.01 |
| **LRP3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.03 | **0.007** | -0.07 | 0.01 | 0.15 | -0.03 | -0.07 | 0.02 | 0.05 | 0.03 | 0.04 |
| **OMB3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.02 | -0.01 | **0.025** | 0.45 | 0.06 | 0.40 | 0.33 | 0.37 | 0.46 | 0.49 | 0.57 |
| **KET3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 | 0.06 | **0.013** | -0.04 | 0.39 | 0.43 | 0.55 | 0.69 | 0.62 | 0.76 |
| **FL3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | -0.02 | 0.00 | 0.00 | **0.009** | -0.02 | -0.03 | 0.02 | 0.02 | 0.00 | 0.01 |
| **BHB1** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.149** | 0.88 | 0.80 | 0.68 | 0.75 | 0.51 |
| **ACE1** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.49 | **0.053** | 0.61 | 0.68 | 0.59 | 0.55 |
| **BHB2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.115** | 0.88 | 0.96 | 0.75 |
| **ACE2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.49 | **0.032** | 0.88 | 0.91 |
| **BHB3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.077** | 0.85 |
| **ACE3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.50 | **0.030** |

Table 9.5. Genetic correlations (above), residual correlations (under) and heritability's on the diagonal in 1st, 2nd and 3rd lactation, Jersey.

| **Trait** | **ERP1** | **LRP1** | **MB1** | **KET1** | **FL1** | **ERP2** | **LRP2** | **OMB2** | **KET2** | **FL2** | **ERP3** | **LRP3** | **OMB3** | **KET3** | **FL3** | **BHB1** | **ACE1** | **BHB2** | **ACE2** | **BHB3** | **ACE3** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **ERP1** | **0.009** | 0.32 | 0.47 | 0.39 | 0.28 | 0.83 | 0.53 | 0.45 | 0.29 | 0.24 | 0.76 | 0.38 | 0.26 | 0.38 | 0.14 | 0.04 | 0.05 | -0.01 | 0.00 | 0.00 | 0.01 |
| **LRP1** | 0.02 | **0.004** | -0.05 | 0.10 | 0.04 | 0.33 | 0.81 | 0.17 | 0.26 | 0.23 | 0.35 | 0.81 | 0.05 | 0.48 | 0.01 | 0.00 | -0.04 | 0.03 | -0.05 | -0.02 | -0.01 |
| **MB1** | 0.02 | 0.00 | **0.004** | 0.55 | 0.22 | 0.43 | 0.37 | 0.63 | 0.36 | 0.23 | 0.18 | 0.18 | 0.51 | 0.38 | 0.10 | 0.33 | 0.40 | 0.29 | 0.32 | 0.27 | 0.27 |
| **KET1** | 0.03 | 0.00 | 0.02 | **0.013** | 0.34 | 0.10 | 0.40 | 0.47 | 0.45 | 0.19 | 0.13 | 0.16 | 0.07 | 0.49 | 0.12 | 0.60 | 0.72 | 0.29 | 0.37 | 0.26 | 0.33 |
| **FL1** | 0.00 | 0.00 | 0.01 | 0.01 | **0.013** | 0.16 | 0.11 | 0.01 | 0.31 | 0.81 | 0.40 | -0.10 | -0.04 | 0.39 | 0.85 | 0.08 | 0.04 | 0.05 | -0.04 | 0.02 | 0.06 |
| **ERP2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.010** | 0.47 | 0.38 | 0.37 | 0.18 | 0.88 | 0.45 | 0.27 | 0.27 | 0.23 | -0.06 | -0.05 | -0.01 | 0.01 | 0.00 | -0.01 |
| **LRP2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.06 | **0.003** | 0.53 | 0.47 | 0.44 | 0.34 | 0.75 | 0.20 | 0.46 | 0.07 | 0.07 | 0.13 | -0.02 | 0.06 | 0.01 | 0.04 |
| **MB2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.04 | 0.01 | **0.005** | 0.40 | 0.14 | 0.29 | 0.27 | 0.82 | 0.42 | 0.10 | 0.31 | 0.47 | 0.18 | 0.37 | 0.26 | 0.24 |
| **KET2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.02 | 0.00 | 0.02 | **0.005** | 0.32 | 0.32 | 0.58 | 0.17 | 0.70 | 0.26 | 0.23 | 0.26 | 0.15 | 0.10 | 0.24 | 0.31 |
| **FL2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 | 0.02 | 0.00 | **0.008** | 0.26 | 0.09 | -0.02 | 0.21 | 0.76 | -0.07 | -0.07 | -0.04 | -0.03 | -0.02 | -0.03 |
| **ERP3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.014** | 0.29 | 0.19 | 0.34 | 0.48 | 0.00 | 0.00 | 0.00 | -0.01 | -0.01 | -0.01 |
| **LRP3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.05 | **0.002** | 0.15 | 0.53 | -0.10 | 0.01 | -0.01 | 0.02 | -0.04 | 0.02 | 0.04 |
| **OMB3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.04 | 0.01 | **0.010** | 0.39 | 0.08 | 0.21 | 0.26 | 0.28 | 0.30 | 0.33 | 0.23 |
| **KET3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.03 | 0.01 | 0.02 | **0.005** | 0.13 | 0.41 | 0.32 | 0.38 | 0.09 | 0.34 | 0.35 |
| **FL3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | -0.01 | 0.00 | 0.01 | 0.01 | **0.006** | -0.01 | 0.02 | -0.01 | 0.05 | 0.01 | -0.01 |
| **BHB1** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.052** | 0.91 | 0.79 | 0.46 | 0.60 | 0.22 |
| **ACE1** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.53 | **0.017** | 0.71 | 0.71 | 0.53 | 0.33 |
| **BHB2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.053** | 0.64 | 0.87 | 0.52 |
| **ACE2** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.49 | **0.013** | 0.50 | 0.56 |
| **BHB3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.042** | 0.73 |
| **ACE3** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.48 | **0.010** |

## Index

The sub-index for general health is calculated based on breeding values for reproductive disorders, metabolic diseases, ketosis and feet and leg problems. The standardization of the breeding values (BV) is described in the chapter “Standardization of EBVs and NTM”.

The EBV on the original scale for early reproduction, late reproduction disorders, other metabolic diseases, ketosis and feet and leg problems are combined over lactations. Across lactation EBV on the original scale are combined by means of economic values based on economic calculations (Table 9.6).

Table 9.6. Calculation of the index traits across lactations (ERP, LRP, OMB, KET and FL) and the general health index for Holstein, RDC and Jersey. Subscript refers to lactation.

| | |
|---|---|
| ERP | $0.3 * ERP_1 + 0.25 * ERP_2 + 0.45 * ERP_3$ |
| LRP | $0.3 * LRP_1 + 0.25 * LRP_2 + 0.45 * LRP_3$ |
| OMB | $0.3 * OMB_1 + 0.25 * OMB_2 + 0.45 * OMB_3$ |
| KET | $0.3 * KET_1 + 0.25 * KET_2 + 0.45 * KET_3$ |
| FL | $0.3 * FL_1 + 0.25 * FL_2 + 0.45 * FL_3$ |
| | |
| General health (HOL) | GH = 2.04*ERP + 1.78*LRP + 3.12* OMB + 1.45* KET + 1.57*FLP |
| General health (RDC) | GH = 2.04*ERP + 1.73*LRP + 3.12* OMB + 1.49* KET + 1.58*FLP |
| General health (JER) | GH = 2.04*ERP + 1.63*LRP + 3.05* OMB + 1.56* KET + 1.75*FLP |

## Correlation between General Health index and underlying traits

The expected progress of each trait, expressed as a percentage of maximum progress for that trait, when the index for general health is selected for is shown in Table 9.7. Maximum progress is obtained if selection is based solely on the trait in question.

Table 9.7. EBV correlations between the General Health index and the five sub-index traits for Nordic genotyped bulls born in 2021 - 2022

| | HOL | RDC | JER |
|---|---|---|---|
| ERP[a] | 0.80 | 0.75 | 0.64 |
| LRP[b] | 0.60 | 0.64 | 0.39 |
| OMB[c] | 0.82 | 0.73 | 0.86 |
| KET[d] | 0.67 | 0.52 | 0.78 |
| FLP[e] | 0.55 | 0.50 | 0.62 |

[a]Early Reproductive Disorders (ERP), [b]Late Reproductive Disorders (LRP), [c]Other Metabolic Disorders (OMB), [d]Ketosis (KET), [e]Feet & Legs (FLP).

## Expected effect of breeding values

Phenotypic breed averages and values per one breeding value unit for single traits can be found per breed:

https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/RDC
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/HOL
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/JER

From these effects specific bull’s effects can be calculated.

## References

Østerås, O., Valde, J. P., Lindberg, A., Lawson, L., Saloniemi, H. and Agger, J., F., 2002. Disease incidence in dairy cows in Nordic countries. Comparison of national disease reporting systems. Final report from NKJ project 1.276. Norwegian Dairy Association, Ås, Norway.

Joint Genetic Evaluation of General health Traits in Denmark, Finland and Sweden. K. Johansson, J. Pösö, U. Sander Nielsen, J-Å. Eriksson and G. P. Aamand. BULLETIN NO. 38, 2008. Pp 107-112.

# 10. Claw health

The index for claw health describes the genetic resistance of a bulls’ daughters to claw disorders.

## Data

### Trait definition

The index for claw health is based on registrations done by claw trimmers. Breeding values (EBVs) are calculated for seven claw disorders or groups of claw disorders (Table 10.1).

Table 10.1. Claw disorders included in claw health index and abbreviations.

| Abbreviation | Claw disorder |
|---|---|
| SU | Sole Ulcer |
| SH | Sole Hemorrhage |
| HH | Heel Horn Erosion |
| DE | Digital Dermatitis |
| DE | Interdigital dermatitis |
| SP | Verrucose dermatitis |
| SP | Interdigital Hyperplasia |
| WLS | Double sole |
| WLS | White line separation |
| CSC | Cork screw claw |

For some disease’s incidences are recorded as: no disease, mild or severe disease (sole ulcer, sole hemorrhage, heel horn erosion, digital dermatitis/interdigital dermatitis). Other diseases are recorded as: no disease or disease (verrucose dermatitis+interdigital hyperplasia, cork screw claw, double sole/white line separation).

### Basic editing rules

The data used in genetic evaluation:

- Denmark from year 2010
- Finland from year 2003
- Sweden from year 2003

Records are used if they are registered in the period from calving to calving or up to 430 days after calving. In each lactation one to three trimmings are included. The distance between the consecutive trimmings must be at least twelve weeks.

Data from herds that have no recorded claw disorders/group of claw disorders within calendar year are not included in the evaluation. This validation is made for each of the seven claw diseases/groups of claw diseases.

## Genetic evaluation

Separate genetic evaluations are made for Holstein, RDC (including Finncattle) and Jersey (data only from Denmark).

**Model**

The model for estimation of breeding values is a single step multiple-trait multiple-lactation animal model:

| | |
|---|---|
| Herd × 5-year period | Fixed |
| Year × month of trimming × Country | Fixed |
| Lactation stage × Country | Fixed |
| Calving age × Country | Fixed |
| Herd × year × season | Random |
| Permanent environment | Random |
| Animal | Random |

A polygenic effect on 0.30 is used and a genotype cut on birthday 01.01.2009.

## Genetic parameters

The heritabilities and standard deviations used for the 21 traits in the evaluation are displayed in Table 10.2, 10.3 and 10.4.

Table 10.2. Heritabilities and genetic standard deviations for Holstein.

| Trait | Lactation | Phenotypic SD | $h^2$ | Genetic SD | Permanent SD |
|---|---|---|---|---|---|
| DE | 1 | 0.417 | 0.053 | 0.096 | 0.166 |
| HH | 1 | 0.393 | 0.032 | 0.071 | 0.118 |
| SH | 1 | 0.500 | 0.022 | 0.074 | 0.124 |
| SU | 1 | 0.318 | 0.036 | 0.061 | 0.111 |
| CSC | 1 | 0.116 | 0.006 | 0.009 | 0.049 |
| SP | 1 | 0.151 | 0.046 | 0.033 | 0.081 |
| WLS | 1 | 0.152 | 0.009 | 0.014 | 0.042 |
| DE | 2 | 0.423 | 0.052 | 0.096 | 0.182 |
| HH | 2 | 0.440 | 0.043 | 0.091 | 0.157 |
| SH | 2 | 0.469 | 0.024 | 0.072 | 0.146 |
| SU | 2 | 0.336 | 0.048 | 0.074 | 0.131 |
| CSC | 2 | 0.127 | 0.005 | 0.009 | 0.063 |
| SP | 2 | 0.208 | 0.070 | 0.055 | 0.128 |
| WLS | 2 | 0.195 | 0.020 | 0.028 | 0.059 |
| DE | 3 | 0.409 | 0.038 | 0.080 | 0.177 |
| HH | 3 | 0.471 | 0.040 | 0.094 | 0.160 |
| SH | 3 | 0.513 | 0.022 | 0.076 | 0.168 |
| SU | 3 | 0.404 | 0.048 | 0.089 | 0.157 |
| CSC | 3 | 0.131 | 0.004 | 0.008 | 0.059 |
| SP | 3 | 0.228 | 0.084 | 0.066 | 0.145 |
| WLS | 3 | 0.240 | 0.020 | 0.034 | 0.080 |

Table 10.3. Heritabilities and genetic standard deviations for RDC.

| Trait | Lactation | Phenotypic SD | $h^2$ | Genetic SD | Permanent SD |
|---|---|---|---|---|---|
| DE | 1 | 0.373 | 0.03 | 0.064 | 0.168 |
| HH | 1 | 0.415 | 0.04 | 0.083 | 0.125 |
| SH | 1 | 0.522 | 0.04 | 0.108 | 0.123 |
| SU | 1 | 0.266 | 0.02 | 0.041 | 0.091 |
| CSC | 1 | 0.138 | 0.02 | 0.021 | 0.068 |
| SP | 1 | 0.136 | 0.02 | 0.021 | 0.068 |
| WLS | 1 | 0.157 | 0.00 | 0.011 | 0.037 |
| DE | 2 | 0.376 | 0.03 | 0.065 | 0.184 |
| HH | 2 | 0.452 | 0.06 | 0.107 | 0.153 |
| SH | 2 | 0.450 | 0.04 | 0.087 | 0.168 |
| SU | 2 | 0.240 | 0.02 | 0.033 | 0.101 |
| CSC | 2 | 0.155 | 0.03 | 0.029 | 0.090 |
| SP | 2 | 0.188 | 0.04 | 0.039 | 0.116 |
| WLS | 2 | 0.180 | 0.02 | 0.022 | 0.057 |
| DE | 3 | 0.368 | 0.03 | 0.066 | 0.176 |
| HH | 3 | 0.484 | 0.07 | 0.128 | 0.162 |
| SH | 3 | 0.484 | 0.04 | 0.095 | 0.194 |
| SU | 3 | 0.291 | 0.03 | 0.047 | 0.124 |
| CSC | 3 | 0.155 | 0.04 | 0.031 | 0.088 |
| SP | 3 | 0.205 | 0.06 | 0.048 | 0.131 |
| WLS | 3 | 0.218 | 0.02 | 0.033 | 0.078 |

Table 10.4. Heritabilities and genetic standard deviations for Jersey.

| Trait | Lactation | Phenotypic SD | $h^2$ | Genetic SD | Permanent SD |
|---|---|---|---|---|---|
| DE | 1 | 0.418 | 0.071 | 0.111 | 0.156 |
| HH | 1 | 0.394 | 0.006 | 0.033 | 0.094 |
| SH | 1 | 0.525 | 0.011 | 0.055 | 0.095 |
| SU | 1 | 0.312 | 0.019 | 0.043 | 0.121 |
| CSC | 1 | 0.120 | 0.003 | 0.007 | 0.043 |
| SP | 1 | 0.156 | 0.004 | 0.010 | 0.060 |
| WLS | 1 | 0.155 | 0.001 | 0.004 | 0.038 |
| DE | 2 | 0.425 | 0.071 | 0.113 | 0.162 |
| HH | 2 | 0.453 | 0.015 | 0.056 | 0.087 |
| SH | 2 | 0.485 | 0.005 | 0.033 | 0.118 |
| SU | 2 | 0.331 | 0.012 | 0.036 | 0.160 |
| CSC | 2 | 0.129 | 0.003 | 0.007 | 0.064 |
| SP | 2 | 0.216 | 0.010 | 0.022 | 0.094 |
| WLS | 2 | 0.199 | 0.000 | 0.003 | 0.057 |
| DE | 3 | 0.412 | 0.037 | 0.080 | 0.173 |
| HH | 3 | 0.464 | 0.021 | 0.068 | 0.068 |
| SH | 3 | 0.542 | 0.004 | 0.033 | 0.158 |
| SU | 3 | 0.403 | 0.023 | 0.061 | 0.189 |
| CSC | 3 | 0.133 | 0.007 | 0.011 | 0.061 |
| SP | 3 | 0.237 | 0.016 | 0.030 | 0.106 |
| WLS | 3 | 0.247 | 0.001 | 0.006 | 0.086 |

The genetic correlations used in the evaluation are in Table 10.5 to 10.10 for Holstein and RDC. Because correlations for Jersey, had large standard errors, it was decided to use the Holstein correlations for Jersey as well.

Table 10.5. Genetic correlations in lactation 1. Holstein and Jersey.

| | | Lactation 1 | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | DE | HH | SH | SU | CSC | SP | WLS |
| | | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
| Lactation 1 | 1 | **1.00** | 0.62 | 0.11 | 0.21 | 0.00 | 0.60 | 0.07 |
| | 2 | 0.00 | **1.00** | 0.23 | 0.25 | 0.41 | 0.55 | 0.15 |
| | 3 | 0.00 | 0.00 | **1.00** | 0.54 | 0.54 | 0.11 | 0.41 |
| | 4 | 0.00 | 0.00 | 0.00 | **1.00** | 0.37 | 0.10 | 0.54 |
| | 5 | 0.00 | 0.00 | 0.00 | 0.00 | **1.00** | 0.02 | 0.38 |
| | 6 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **1.00** | -0.07 |

Table 10.6. Genetic correlations in lactation 2 and between lactation 1 and 2. Holstein and Jersey

| | | Lactation 2 | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | DE | HH | SH | SU | CSC | SP | WLS |
| | | 8 | 9 | 10 | 11 | 12 | 13 | 14 |
| Lactation 1 | 1 | **0.94** | 0.52 | 0.18 | 0.21 | -0.21 | 0.58 | 0.15 |
| | 2 | 0.51 | **0.93** | 0.21 | 0.32 | 0.25 | 0.50 | 0.15 |
| | 3 | 0.03 | 0.30 | **0.94** | 0.56 | 0.57 | 0.18 | 0.44 |
| | 4 | 0.22 | 0.30 | 0.65 | **0.90** | 0.30 | 0.14 | 0.54 |
| | 5 | 0.07 | 0.46 | 0.57 | 0.43 | **0.90** | 0.04 | 0.34 |
| | 6 | 0.49 | 0.48 | 0.06 | 0.15 | -0.20 | **0.97** | -0.04 |
| | 7 | 0.06 | 0.11 | 0.64 | 0.57 | 0.47 | -0.11 | **0.91** |
| Lactation 2 | 8 | **1.00** | 0.47 | 0.11 | 0.15 | -0.14 | 0.48 | 0.07 |
| | 9 | 0.00 | **1.00** | 0.24 | 0.30 | 0.38 | 0.46 | 0.04 |
| | 10 | 0.00 | 0.00 | **1.00** | 0.70 | 0.57 | 0.10 | 0.66 |
| | 11 | 0.00 | 0.00 | 0.00 | **1.00** | 0.30 | 0.20 | 0.67 |
| | 12 | 0.00 | 0.00 | 0.00 | 0.00 | **1.00** | -0.16 | 0.36 |
| | 13 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **1.00** | -0.01 |

Table 10.7. Genetic correlations in lactation 3 and to lactation 1, 2 and 3. Holstein and Jersey.

| | | Lactation 3 | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | DE | HH | SH | SU | CSC | SP | WLS |
| | | 15 | 16 | 17 | 18 | 19 | 20 | 21 |
| Lactation 1 | 1 | **0.89** | 0.54 | 0.07 | 0.10 | -0.21 | 0.61 | 0.19 |
| | 2 | 0.47 | **0.93** | 0.11 | 0.10 | 0.18 | 0.50 | 0.23 |
| | 3 | 0.07 | 0.16 | **0.89** | 0.48 | 0.63 | 0.10 | 0.47 |
| | 4 | 0.12 | 0.13 | 0.63 | **0.86** | 0.16 | 0.20 | 0.53 |
| | 5 | -0.07 | 0.31 | 0.62 | 0.26 | **0.85** | 0.00 | 0.33 |
| | 6 | 0.50 | 0.49 | 0.01 | 0.08 | -0.20 | **0.96** | 0.16 |
| | 7 | -0.06 | -0.11 | 0.65 | 0.40 | 0.31 | -0.11 | **0.85** |
| Lactation 2 | 8 | **0.93** | 0.41 | 0.05 | 0.01 | -0.16 | 0.54 | 0.06 |
| | 9 | 0.39 | **0.90** | 0.23 | 0.09 | 0.25 | 0.47 | 0.04 |
| | 10 | 0.06 | 0.06 | **0.94** | 0.59 | 0.58 | 0.03 | 0.68 |
| | 11 | 0.06 | 0.21 | 0.66 | **0.89** | 0.28 | 0.16 | 0.68 |
| | 12 | -0.24 | 0.18 | 0.67 | 0.15 | **0.88** | -0.19 | 0.26 |
| | 13 | 0.52 | 0.50 | 0.10 | 0.14 | -0.13 | **0.96** | 0.13 |
| | 14 | -0.02 | -0.02 | 0.66 | 0.57 | 0.29 | -0.08 | **0.92** |
| Lactation 3 | 15 | **1.00** | 0.40 | -0.04 | -0.13 | -0.14 | 0.55 | 0.00 |
| | 16 | 0.00 | **1.00** | 0.02 | 0.08 | 0.13 | 0.47 | 0.00 |
| | 17 | 0.00 | 0.00 | **1.00** | 0.58 | 0.63 | 0.02 | 0.60 |
| | 18 | 0.00 | 0.00 | 0.00 | **1.00** | 0.00 | 0.13 | 0.58 |
| | 19 | 0.00 | 0.00 | 0.00 | 0.00 | **1.00** | -0.25 | 0.25 |
| | 20 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **1.00** | 0.06 |

Table 10.8. Genetic correlations in lactation 1. RDC.

| | | Lactation 1 | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | DE | HH | SH | SU | CSC | SP | WLS |
| | | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
| Lactation 1 | 1 | **1.00** | 0.52 | 0.24 | 0.12 | -0.15 | 0.62 | 0.10 |
| | 2 | 0.00 | **1.00** | 0.19 | 0.25 | 0.01 | 0.43 | 0.07 |
| | 3 | 0.00 | 0.00 | **1.00** | 0.53 | 0.24 | 0.07 | 0.44 |
| | 4 | 0.00 | 0.00 | 0.00 | **1.00** | 0.26 | 0.05 | 0.51 |
| | 5 | 0.00 | 0.00 | 0.00 | 0.00 | **1.00** | 0.01 | 0.15 |
| | 6 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **1.00** | -0.09 |

Table 10.9. Genetic correlations in lactation 2 and between lactation 1 and 2. RDC.

| | Lactation 2 | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | DE | HH | SH | SU | CSC | SP | WLS |
| | | 8 | 9 | 10 | 11 | 12 | 13 | 14 |
| Lactation 1 | 1 | **0.98** | 0.55 | 0.18 | 0.06 | -0.15 | 0.60 | 0.12 |
| | 2 | 0.58 | **0.98** | 0.26 | 0.14 | 0.05 | 0.42 | 0.09 |
| | 3 | 0.16 | 0.14 | **0.97** | 0.47 | 0.29 | 0.09 | 0.42 |
| | 4 | 0.03 | 0.25 | 0.57 | **0.87** | 0.39 | 0.10 | 0.49 |
| | 5 | -0.19 | 0.07 | 0.36 | 0.22 | **0.89** | 0.02 | 0.26 |
| | 6 | 0.71 | 0.46 | 0.07 | 0.11 | -0.02 | **0.93** | 0.03 |
| | 7 | 0.01 | 0.09 | 0.49 | 0.51 | 0.12 | 0.09 | **0.76** |
| Lactation 2 | 8 | **1.00** | 0.62 | 0.11 | 0.02 | -0.20 | 0.67 | 0.02 |
| | 9 | 0.00 | **1.00** | 0.25 | 0.20 | 0.13 | 0.43 | 0.13 |
| | 10 | 0.00 | 0.00 | **1.00** | 0.56 | 0.42 | 0.07 | 0.51 |
| | 11 | 0.00 | 0.00 | 0.00 | **1.00** | 0.35 | 0.09 | 0.51 |
| | 12 | 0.00 | 0.00 | 0.00 | 0.00 | **1.00** | -0.06 | 0.26 |
| | 13 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **1.00** | 0.13 |

Table 10.10. Genetic correlations in lactation 3 and to lactation 1, 2 and 3. RDC.

| | | Lactation 3 | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | DE | HH | SH | SU | CSC | SP | WLS |
| | | 15 | 16 | 17 | 18 | 19 | 20 | 21 |
| Lactation 1 | 1 | **0.91** | 0.49 | 0.22 | 0.08 | -0.21 | 0.65 | 0.05 |
| | 2 | 0.52 | **0.97** | 0.18 | 0.14 | -0.09 | 0.37 | 0.08 |
| | 3 | 0.20 | 0.12 | **0.95** | 0.46 | 0.25 | 0.08 | 0.31 |
| | 4 | 0.00 | 0.26 | 0.63 | **0.82** | 0.36 | 0.13 | 0.44 |
| | 5 | -0.01 | 0.09 | 0.37 | 0.25 | **0.74** | -0.04 | 0.20 |
| | 6 | 0.62 | 0.45 | 0.15 | 0.04 | -0.15 | **0.91** | 0.03 |
| | 7 | 0.02 | 0.09 | 0.51 | 0.49 | 0.07 | 0.06 | **0.81** |
| Lactation 2 | 8 | **0.94** | 0.57 | 0.15 | 0.05 | -0.29 | 0.71 | -0.03 |
| | 9 | 0.60 | **0.99** | 0.19 | 0.23 | -0.02 | 0.39 | 0.13 |
| | 10 | 0.20 | 0.24 | **0.98** | 0.56 | 0.34 | 0.04 | 0.42 |
| | 11 | 0.10 | 0.24 | 0.67 | **0.91** | 0.23 | 0.08 | 0.54 |
| | 12 | -0.01 | 0.13 | 0.43 | 0.39 | **0.91** | -0.10 | 0.21 |
| | 13 | 0.53 | 0.41 | 0.16 | 0.07 | -0.18 | **0.98** | 0.10 |
| | 14 | 0.08 | 0.14 | 0.53 | 0.45 | 0.19 | 0.10 | **0.96** |
| Lactation 3 | 15 | **1.00** | 0.57 | 0.25 | 0.14 | -0.15 | 0.54 | 0.05 |
| | 16 | 0.00 | **1.00** | 0.19 | 0.24 | -0.06 | 0.35 | 0.15 |
| | 17 | 0.00 | 0.00 | **1.00** | 0.65 | 0.33 | 0.13 | 0.45 |
| | 18 | 0.00 | 0.00 | 0.00 | **1.00** | 0.38 | 0.10 | 0.47 |
| | 19 | 0.00 | 0.00 | 0.00 | 0.00 | **1.00** | -0.14 | 0.14 |
| | 20 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **1.00** | 0.07 |

## Index

The index for claw health is based on seven sub-indices. The standardization of the breeding values is described in the chapter "Standardization of EBVs and NTM". Table 10.11 gives the economic importance of claw diseases used in the calculation of economic weights.

Table 10.11. Economic importance of claw diseases in EURO.

| | RDC, HOL, JER | |
|---|---|---|
| | Mild disease | Severe disease |
| Digital Dermatitis/Interdigital dermatitis | 100 | 200 |
| Heel Horn Erosion | 100 | 200 |
| Verrucose dermatitis/Interdigital Hyperplasia | Only one class | 200 |
| Sole Hemorrhage | 60 | 120 |
| Sole Ulcer | 120 | 1310 |
| Cork screw claw | Only one class | 48 |
| Double sole/White line separation | Only one class | 60 |

For the individual traits, EBVs on the original scale for first, second and third lactation are weighted by 0.30, 0.25 and 0.45. The EBVs on the original scale across lactation for the seven traits are combined by weighting with the economic values that are based on economic calculations (Table 10.12).

Table 10.12. Calculation of claw index.

| | |
|---|---|
| Holstein | 0.0418×SU+0.0591×SH+0.0564×HH+ 0.0521×DE+0.0231×SP+0.0129×WLS+ 0.009×CSC |
| RDC | 0.0525×SU+0.0679×SH+0.0697×HH+ 0.0473×DE+0.0183×SP+0.0091×WLS+ 0.0146×CSC |
| Jersey | 0.0247×SU+0.0401×SH+0.0504×HH+ 0.0428×DE+0.0169×SP+0.0082×WLS+ 0.0059×CSC |

The index for claw health index is published for both bulls and cows.

## Correlation between the index for claw health and underlying traits

The expected progress of each trait when the claw health index is selected for, expressed as a percentage of the maximum progress for that trait, is shown in Table 10.13. The maximum progress is obtained if selection is solely based on the trait in question.

Table 10.13. Correlation between the index for claw health and sub-indices for Nordic genotyped bulls born in 2021 - 2022.

| Index | HOL | RDC | JER |
|---|---|---|---|
| Digital Dermatitis/Interdigital dermatitis | 0.60 | 0.59 | 0.54 |
| Heel Horn Erosion | 0.62 | 0.64 | 0.59 |
| Verrucose dermatitis/Interdigital Hyperplasia | 0.60 | 0.56 | 0.47 |
| Sole Hemorrhage | 0.69 | 0.73 | 0.76 |
| Sole Ulcer | 0.80 | 0.83 | 0.90 |
| Cork screw claw | 0.26 | 0.43 | 0.38 |
| Double sole/ White line separation | 0.57 | 0.60 | 0.76 |

## Expected effect of breeding values

Phenotypic breed averages and values for one breeding value unit for single traits can be found for each breed:

https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/RDC
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/HOL
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/JER

From these effects, the effect of using a specific bull can be calculated for number of treatments for each claw disorder: sole ulcer, sole hemorrhage, digital dermatitis+interdigital dermatitis, verrucose dermatitis+interdigital hyperplasia, double sole+white line separation and cork screw claw.

When interpreting the effects of the index for claw heath it is important to remember that dermatitis, heel horn erosion, sole ulcer and sole haemorrhage are scored in three classes: 0 (no disease), 1 (mild disease) and 2 (severe disease) and the unit is in points. Skin proliferation, white line separation and cork screw claws are scored in two classes: 0 (no disease) and 1 (disease) and the unit is in points. With a scale from 0-1, values can be multiplied with 100 to get it in frequency (%).

## References

Johansson, K., J.-Å. Eriksson, U. S. Nielsen, J. Pösö, G. P. Aamand. 2011. Genetic evaluation of claw health in Denmark, Finland and Sweden. Interbull Bulletin No. 44, Pp 225-228. https://journal.interbull.org/index.php/ib/article/view/1223/1346.

# 11. Conformation, milkability and temperament

The indices for linear conformation traits describe different aspects of the conformation of a cow. The linear traits are combined into groups of traits describing the frame, the feet and legs, and the udder. Indices for milkability and temperament describe how rapidly the cow can be milked and her general temperament.

## Data

### Trait definitions

The traits for the genetic evaluation are either classified by a classifier (frame, feet-legs and udder) or registered by the farmer (milkability and temperament) and are shown in Table 11.1. Traits that are measured from Automatic Milking Systems (AMS) and go into the genetic evaluation are shown in Table 11.2. Classification is undertaken by official classifiers employed by agricultural advisory services in the individual countries. A scale from 1-9 is used.

Data from TruTest milk meters, automatic measures of milking speed from AMS and conventional milking parlours are used in the genetic evaluation for milkability. Milkability is defined as the average flow of solids (fat and protein content measured in kilograms per minute), Data from 1-7 test-days in first lactation are included in the genetic evaluation. In the genetic evaluation for milkability, data from the three sources mentioned above are used as same trait. It has been shown that genetically they reflect the same biological trait. However, if the cow has both an automatic measure of milking speed and a farmer evaluation, only the automatic measurement is used in the genetic evaluation.

Data on udder coordinates from AMS are used in the genetic evaluation for linear measures of front and rear teat placement, udder depth and udder balance.

The milking robots measure the distance of specific points of the udder for each milking from a fixed set of points. These observations are expressed on a fictional scale, i.e., without an actual unit. The average of the given trait over a period from 30 to 60 days after last calving is used in the analysis instead of single observations as for the linear udder assessments.

Table 11.1. Traits classified in the Nordic countries.

| Group of traits | Traits |
|---|---|
| Frame | stature, body depth, chest width, rib structure, top line, rump width, rump angle |
| Feet and legs | rear legs (side view), rear legs (rear view), hock quality, bone quality, foot angle |
| Udder | fore udder attachment, rear udder height, rear udder width, udder cleft/support, udder depth, teat length, teat thickness, teat placement (front), teat placement (back), udder balance |
| Workability | Milkability, temperament |

Table 11.2. Traits recorded in Automatic Milking Systems.

| Group of traits | Traits |
|---|---|
| Udder | Teat placement front, teat placement back, udder depth, udder balance |
| Workability | Milkability |

The definition of conformation traits accords with ICAR standards. A description of the traits can be found at: www.landbrugsinfo.dk/Kvaeg/Avl/Kaaring-og-eksterioertal/Filer/tegninger_lin_reg_malkeng.pdf

## Basic editing rules

In Denmark classification for almost all the traits shown in table 1 began in 1990. However, a few classifications were introduced later: classification of rear udder height and rear teat placement started in 2000 and udder balance in 2003.

In Sweden classification for most of the traits in table 1 began in 1993, classification of teat thickness and rear teat placement was added in 2003.

In Finland, some traits have been classified since 1994, stature, rear legs (side view), foot angle, fore udder attachment, rear udder height, udder cleft/support, udder depth, teat length, udder balance. More traits were added in 2000 (body depth, chest width, rib structure, rump width, rump angle, rear legs rear view, rear udder width, teat placement front, teat placement back). Classification of top line started in 2003. The last traits (hock quality, bone quality, teat thickness) were added in 2006.

For conformation traits only genotypes from animals born after 1. January 2009 are used.

## Pre-corrections

Linear conformation traits and temperament are adjusted for heterogeneous variance within country-classifier-year. When the number of records within classifier-year group is smaller than 50 the group is country-year.

Milkability (flow and classification) is adjusted for heterogeneous variance within country-year-registration type.

Udder coordinates from AMS are adjusted for heterogeneous variance within country, type of robot (currently only one type), breed and visit year.

## Genetic evaluation

Separate genetic evaluations are made for Holstein, RDC (including Finncattle) and Jersey. From all countries, data from 1 to 3 parities are used. However, if a Finnish cow has classifications in later parities - up to 10 the latest classification replaces the classification in 3rd lactation. For milkability and temperament, only records from 1st lactation are used. AMS measurements of udder coordinates from 1-3 lactations are used in the genetic evaluation as correlated trait to linear measurements of teat placement front, teat placement back, udder depth and udder balance.

## Model

The model for conformation traits is a single step multi-trait multi-lactation animal model where teat coordinates from AMS are used as correlated trait for teat placement front, teat placement back, udder depth and udder balance.
The model for estimation of breeding values for milkability is a single step animal model and for temperament (linear traits) it is a single-trait animal model.

| | |
|---|---|
| Herd × five year period[1] | Fixed |
| Classifier × year[1] | Fixed |
| Year × month of calving x country | Fixed |
| Calving age × year × country × breed | Fixed |
| Lactation stage × year × country[2] | Fixed |
| Time of visit × country[1] | Fixed |
| Herd × year (SWE, FIN)/Herd × half year (DNK) | Fixed |
| Milkings per day[3] | Fixed |
| Animal | Random |
| Residual | Random |

[1] Only linear traits
[2] Defined differently for linear traits and teat coordinates
[3] Only teat coordinates

For conformation and milkability a polygenic effect on 0.30 is used and a genotype cut on birthday 01.01.2009.

## Genetic groups (phantom parent groups)

Genetic groups are created for unknown parents according to birth year, country of origin and breed.

## Genetic parameters

The genetic parameters used for the 24 traits in the evaluation are shown in Table 11.3-11.7.

Table 11.3. Heritabilities ($h^2$) and genetic correlations used in the genetic evaluation for Holstein.

| | Heritability | | | Correlations between lact. | | |
|---|---|---|---|---|---|---|
| Trait | 1. lact. | 2. lact. | 3.lact | 1.-2. | 1.-3. | 2.-3. |
| 1. Stature | 0.60 | 0.60 | 0.60 | 0.94 | 0.94 | 0.94 |
| 2. Body depth | 0.25 | 0.28 | 0.27 | 0.94 | 0.93 | 0.93 |
| 3. Chest width | 0.17 | 0.21 | 0.21 | 0.91 | 0.91 | 0.91 |
| 4. Rib structure | 0.27 | 0.23 | 0.20 | 0.94 | 0.94 | 0.94 |
| 5. Top line | 0.17 | 0.19 | 0.21 | 0.94 | 0.88 | 0.88 |
| 6. Rump width | 0.28 | 0.34 | 0.34 | 0.94 | 0.94 | 0.94 |
| 7. Rump angle | 0.32 | 0.38 | 0.38 | 0.94 | 0.94 | 0.94 |
| 8. Rear legs, side view | 0.20 | 0.22 | 0.25 | 0.97 | 0.95 | 0.99 |
| 9. Rear legs, back rear view | 0.11 | 0.16 | 0.18 | 0.98 | 0.98 | 0.99 |
| 10. Hock quality | 0.17 | 0.20 | 0.20 | 0.98 | 0.96 | 0.99 |
| 11. Bone quality | 0.21 | 0.29 | 0.30 | 0.97 | 0.97 | 0.99 |
| 12. Foot angle | 0.12 | 0.15 | 0.16 | 0.97 | 0.95 | 0.99 |
| 13. Fore udder attachment | 0.21 | 0.24 | 0.26 | 0.92 | 0.88 | 0.94 |
| 14. Rear udder height | 0.19 | 0.22 | 0.21 | 0.93 | 0.90 | 0.95 |
| 15. Rear udder width | 0.21 | 0.23 | 0.27 | 0.89 | 0.86 | 0.96 |
| 16. Udder cleft/support | 0.20 | 0.21 | 0.23 | 0.94 | 0.93 | 0.94 |
| 17. Udder depth | 0.39 | 0.50 | 0.48 | 0.94 | 0.91 | 0.96 |
| 18. Teat length | 0.35 | 0.37 | 0.40 | 0.94 | 0.95 | 0.94 |
| 19. Teat thickness | 0.29 | 0.32 | 0.33 | 0.93 | 0.90 | 0.94 |
| 20. Teat placement (front) | 0.32 | 0.31 | 0.30 | 0.93 | 0.89 | 0.94 |
| 21. Teat placement (back) | 0.28 | 0.34 | 0.31 | 0.93 | 0.91 | 0.94 |
| 22. Udder balance | 0.16 | 0.22 | 0.19 | 0.93 | 0.91 | 0.96 |
| 24. Temperament | 0.11 | - | - | - | - | - |

Table 11.4. Heritabilities ($h^2$) and genetic correlations used in the genetic evaluation for RDC.

| | Heritability | | | Correlations between lact. | | |
|---|---|---|---|---|---|---|
| Trait | 1. lact. | 2. lact. | 3.lact | 1.-2. | 1.-3. | 2.-3. |
| 1. Stature | 0.77 | 0.63 | 0.63 | 0.94 | 0.94 | 0.94 |
| 2. Body depth | 0.29 | 0.33 | 0.31 | 0.94 | 0.94 | 0.94 |
| 3. Chest width | 0.12 | 0.17 | 0.16 | 0.94 | 0.92 | 0.94 |
| 4. Rib structure | 0.15 | 0.16 | 0.17 | 0.94 | 0.94 | 0.94 |
| 5. Top line | 0.19 | 0.25 | 0.26 | 0.94 | 0.90 | 0.90 |
| 6. Rump width | 0.40 | 0.36 | 0.36 | 0.94 | 0.94 | 0.94 |
| 7. Rump angle | 0.27 | 0.40 | 0.37 | 0.94 | 0.94 | 0.94 |
| 8. Rear legs, side view | 0.19 | 0.25 | 0.25 | 0.99 | 0.98 | 0.99 |
| 9. Rear legs, back rear view | 0.11 | 0.19 | 0.17 | 0.99 | 0.95 | 0.99 |
| 10. Hock quality | 0.30 | 0.32 | 0.29 | 0.98 | 0.98 | 0.99 |
| 11. Bone quality | 0.47 | 0.42 | 0.42 | 0.99 | 0.99 | 0.99 |
| 12. Foot angle | 0.10 | 0.12 | 0.11 | 0.98 | 0.94 | 0.96 |
| 13. Fore udder attachment | 0.22 | 0.28 | 0.25 | 0.93 | 0.88 | 0.94 |
| 14. Rear udder height | 0.23 | 0.27 | 0.31 | 0.94 | 0.93 | 0.94 |
| 15. Rear udder width | 0.25 | 0.26 | 0.26 | 0.94 | 0.94 | 0.94 |
| 16. Udder cleft/support | 0.17 | 0.22 | 0.39 | 0.93 | 0.89 | 0.94 |
| 17. Udder depth | 0.34 | 0.36 | 0.26 | 0.93 | 0.92 | 0.94 |
| 18. Teat length | 0.44 | 0.42 | 0.44 | 0.94 | 0.94 | 0.94 |
| 19. Teat thickness | 0.27 | 0.31 | 0.28 | 0.94 | 0.92 | 0.94 |
| 20. Teat placement (front) | 0.27 | 0.24 | 0.29 | 0.94 | 0.94 | 0.94 |
| 21. Teat placement (back) | 0.26 | 0.26 | 0.28 | 0.93 | 0.94 | 0.94 |
| 22. Udder balance | 0.16 | 0.24 | 0.20 | 0.94 | 0.92 | 0.94 |
| 24. Temperament | 0.14 | - | - | - | - | - |

Table 11.5. Heritabilities ($h^2$) and genetic correlations used in the genetic evaluation for Jersey.

| | Heritability | | | Correlations between lact. | | |
|---|---|---|---|---|---|---|
| Trait | 1. lact. | 2. lact. | 3.lact | 1.-2. | 1.-3. | 2.-3. |
| 1. Stature | 0.41 | 0.58 | 0.55 | 0.94 | 0.90 | 0.94 |
| 2. Body depth | 0.24 | 0.26 | 0.24 | 0.94 | 0.94 | 0.94 |
| 3. Chest width | 0.16 | 0.20 | 0.17 | 0.94 | 1.00 | 0.93 |
| 4. Rib structure | 0.22 | 0.27 | 0.24 | 0.93 | 0.92 | 0.92 |
| 5. Top line | 0.18 | 0.23 | 0.18 | 0.93 | 0.94 | 0.94 |
| 6. Rump width | 0.27 | 0.39 | 0.33 | 0.94 | 0.93 | 0.93 |
| 7. Rump angle | 0.29 | 0.37 | 0.38 | 0.94 | 0.93 | 0.93 |
| 8. Rear legs, side view | 0.14 | 0.16 | 0.14 | 0.99 | 0.95 | 0.96 |
| 9. Rear legs, back rear view | 0.06 | 0.09 | 0.08 | 0.96 | 0.94 | 0.90 |
| 10. Hock quality | 0.12 | 0.15 | 0.12 | 0.99 | 0.99 | 0.99 |
| 11. Bone quality | 0.14 | 0.20 | 0.14 | 0.96 | 0.98 | 0.98 |
| 12. Foot angle | 0.13 | 0.11 | 0.11 | 0.99 | 0.97 | 0.99 |
| 13. Fore udder attachment | 0.22 | 0.23 | 0.27 | 0.92 | 0.87 | 0.93 |
| 14. Rear udder height | 0.23 | 0.21 | 0.19 | 0.93 | 0.82 | 0.89 |
| 15. Rear udder width | 0.25 | 0.24 | 0.26 | 0.92 | 0.86 | 0.96 |
| 16. Udder cleft/support | 0.17 | 0.21 | 0.41 | 0.92 | 0.90 | 0.94 |
| 17. Udder depth | 0.34 | 0.44 | 0.37 | 0.92 | 0.92 | 0.96 |
| 18. Teat length | 0.44 | 0.39 | 0.35 | 0.94 | 0.94 | 0.94 |
| 19. Teat thickness | 0.27 | 0.33 | 0.34 | 0.94 | 0.92 | 0.94 |
| 20. Teat placement (front) | 0.27 | 0.32 | 0.28 | 0.93 | 0.78 | 0.93 |
| 21. Teat placement (back) | 0.26 | 0.31 | 0.29 | 0.94 | 0.89 | 0.94 |
| 22. Udder balance | 0.16 | 0.24 | 0.19 | 0.92 | 0.84 | 0.92 |
| 24. Temperament | 0.11 | - | - | - | - | - |

Table 11.6. Heritabilities ($h^2$) depending on information source in genetic evaluation for milkability.

| | Heritability | | | | |
|---|---|---|---|---|---|
| Data source | Farmer | Flow – average over testdays (TD) | | | |
| | 1-9 | 1 TD | 2 TD | 3 TD | 4-7 TD |
| RDC & Holstein | 0.22 | 0.34 | 0.39 | 0.41 | 0.43 |
| Jersey | 0.16 | 0.32 | 0.40 | 0.43 | 0.47 |

Table 11.7. Heritabilities ($h^2$) for conformation traits measured by AMS and genetic correlation to classified traits in ( ) used in the genetic evaluation of Holstein, RDC and Jersey.

| | Heritability (genetic correlations between AMS and linear traits) |
|---|---|
| Udder depth, | 0.66 (0.93) |
| Teat placement (front) | 0.57 (-0.91) |
| Teat placement (rear) | 0.45 (-0.91) |
| Udder balance | 0.47 (0.94) |

## Index

### Linear traits

The standardization of the breeding values for the linear traits is described in the chapter “Standardization of EBVs and NTM”.

### Composite traits

In the composite indices for frame, feet and legs and udder, the linear traits are combined according to optimum and weight. The contribution to the index is calculated as the deviation of future daughters from the breed’s optimum for the linear trait in question multiplied by the relative weight factor. As the bulls with the lowest average deviation from the optimum for the breed are to obtain the highest contribution to the index, the value is multiplied by -1 before the figure 100 is added. The standardization of the breeding values for frame, feet and legs, and udder, is described in the chapter “Standardization of EBVs and NTM”.

$$\text{Index} = 100 + s \times \sum_{i=1}^{n} ki \times (\text{PD\_LIN}i \div \text{OPTIMUM}i)$$

where

- $\text{PD\_LIN}_i$ = predicted value of future daughters for the $i^{th}$ trait included in the index
- $\text{OPTIMUM}_i$ = optimum for the $i^{th}$ trait
- s = standardizing factor
- $k_i$ = weight factor

Optimum and weighting factors for the breeds are shown in Table 11.8 and 11.9.

Table 11.8. Optima for Holstein, RDC and Jersey.

| | Holstein | RDC | Jersey |
|---|---|---|---|
| 1. Stature | * | * | 129 |
| 2. Body depth | 9 | 9 | 6 |
| 3. Chest width | 9 | 9 | 5 |
| 4. Rib structure | 9 | 9 | 6 |
| 5. Top line | 7 | 7 | 7 |
| 6. Rump width | 9 | 9 | 6 |
| 7. Rump angle | 5 | 5 | 5 |
| 8. Rear legs, side view | 5 | 5 | 5 |
| 9. Rear legs, back rear view | 8 | 8 | 9 |
| 10. Hock quality | 9 | 9 | 9 |
| 11. Bone quality | 8 | 7.5 | 9 |
| 12. Foot angle | 6.5 | 7 | 6.5 |
| 14. Fore udder attachment | 9 | 9 | 9 |
| 15. Rear udder height | 9 | 9 | 9 |
| 16. Rear udder width | 9 | 9 | 9 |
| 17.Udder cleft/support | 8 | 9 | 9 |
| 18. Udder depth | 9 | 9 | 9 |
| 19. Teat length | 5.5 | 5.5 | 5.5 |
| 20. Teat thickness | 5 | 6 | 6 |
| 21. Teat placement (front) | 8 | 8 | 7.5 |
| 22. Teat placement (back) | 5 | 5 | 5 |
| 23. Udder balance | 5 | 5 | 5 |

* As high as possible

Table 11.9. Weight factors for Holstein, RDC and Jersey.

| | Holstein | RDC | Jersey |
|---|---|---|---|
| 1. Stature | 5 | 15 | 6 |
| 2. Body depth | 25 | 25 | 14 |
| 3. Chest width | 30 | 30 | 13 |
| 4. Rib structure | 20 | 10 | 10 |
| 5. Top line | - | - | 25 |
| 6. Rump width | 20 | 20 | 11 |
| 7. Rump angle | - | - | 11 |
| Codes for body | | | 10 |
| 8. Rear legs, side view | 10 | 15 | 20 |
| 9. Rear legs, back rear view | 30 | 25 | 20 |
| 10. Hock quality | 18 | 25 | 20 |
| 11. Bone quality | 17 | 15 | 15 |
| 12. Foot angle | 25 | 20 | 25 |
| 14. Fore udder attachment | 20 | 20 | 20 |
| 15. Rear udder height | 10 | 8 | 10 |
| 16. Rear udder width | - | 5 | - |
| 17.Udder cleft/support | 20 | 12 | 10 |
| 18. Udder depth | 25 | 20 | 25 |
| 19. Teat length | - | 10 | - |
| 20. Teat thickness | - | 10 | 10 |
| 21. Teat placement (front) | - | 10 | - |
| 22. Teat placement (back) | -15 | 5 | -10 |
| 23. Udder balance | -10 | - | - |

Weight factors are indicating desired direction in grey

## Correlation between indices for type traits and underlying traits

The expected progress of each trait, expressed as a percentage of maximum progress for that trait, is shown in Table 11.10. The maximum progress is obtained if selection is solely based on the trait in question.

Table 11.10. Correlation between GEBVs for composite type indices (frame, feet and legs, udder) and underlying traits for Nordic genotyped bulls born in 2021 – 2022.

| | Holstein | RDC | Jersey |
|---|---|---|---|
| | | Index for frame | |
| Stature | 0.79 | 0.71 | 0.84 |
| Body depth | 0.74 | 0.82 | 0.55 |
| Chest width | 0.56 | 0.76 | 0.36 |
| Rib structure | 0.54 | 0.25 | 0.48 |
| Top line | 0.12 | -0.12 | 0.55 |
| Rump width | 0.71 | 0.72 | 0.62 |
| Rump angle | 0.11 | -0.01 | 0.11 |
| | | Index for feet and legs | |
| Rear legs, side view | -0.09 | -0.31 | -0.52 |
| Rear legs, rear view | 0.66 | 0.43 | 0.59 |
| Hock quality | 0.62 | 0.87 | 0.44 |
| Bone quality | 0.64 | 0.87 | 0.41 |
| Foot angle | 0.06 | -0.16 | 0.51 |
| | | Index for mammary system | |
| Fore udder attachment | 0.74 | 0.63 | 0.78 |
| Rear udder height | 0.52 | 0.42 | 0.60 |
| Rear udder width | 0.27 | 0.33 | 0.28 |
| Udder cleft | 0.12 | 0.24 | 0.19 |
| Udder depth | 0.86 | 0.72 | 0.87 |
| Teat length | 0.00 | 0.40 | 0.27 |
| Teat thickness | -0.10 | 0.33 | 0.22 |
| Teat placement (front) | 0.04 | 0.30 | -0.03 |
| Teat placement (back) | 0.07 | 0.20 | -0.01 |
| Udder balance | 0.04 | 0.35 | 0.38 |

## Expected effect of breeding values

Phenotypic breed averages and values for one breeding value unit for single traits can be found for each breed:
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/RDC
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/HOL
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/JER

From these, the effect of using a specific bull can be calculated for temperament and milkability, frame, feet and legs and udder.

## References

# 12. Longevity

The index for longevity describes the genetic ability of the bulls' daughters to survive. Bulls with high EBV for longevity produce daughters with a longer productive life.

## Data

### Trait definition

In the evaluation of longevity, the following five traits are considered:

| Abbreviation | Definition |
|---|---|
| DAY11 | Days from 1st calving to end of 1st lactation – including maximum 365 days in 1st lactation |
| DAY12 | Days from 1st calving to end of 2nd lactation – including maximum 365 days per lactation |
| DAY13 | Days from 1st calving to end of 3rd lactation – including maximum 365 days per lactation |
| DAY14 | Days from 1st calving to end of 4th lactation – including maximum 365 days per lactation |
| DAY15 | Days from 1st calving to end of 5th lactation – including maximum 365 days per lactation |

Only information from the first 5 lactations is used. If a cow is culled after 5th lactation, this information is not used.

For each trait, a cow should have had the opportunity to obtain the record before the record is included. For example, for a DAY15 record to be included the cow should be at least 5 years from 1st calving.

### Basic editing rules

Data from year 1985 in Sweden, 1985 for Denmark, and 1988 in Finland is included. Moreover, information is included if:

- Age at 1st calving is between 450 and 1280 days
- Only a lactation that is completed in the herd of 1st calving is included. If a cow is moved to another herd during its lifetime, data from current and future lactations is excluded

### Genetic evaluation

Separate genetic evaluations are made for Holstein, RDC (including Finncattle) and Jersey.

## Model

The model for estimation of breeding values is a multi-trait animal model:

| | |
|---|---|
| Age at 1st calving | Fixed |
| Year × month of 1st calving | Fixed |
| Herd × 5-year period | Fixed |
| Heterosis | Regression |
| Genetic groups (as phantom parent groups) | Random |
| Herd × year of 1st calving | Random |
| Animal | Random |

## Heterosis

Proportion of heterozygosity is considered as follows:

RDC:

- Original Red Danish Cattle (RDM) × American Brown Swiss (ABS)
- Original Red Danish Cattle × American Red Holstein (RED)
- American Brown Swiss × American Red Holstein
- Swedish Red and White (SRB) × Norwegian Red (NRF)
- Swedish Red and White × Finnish Ayrshire (FAY)
- Original Red Danish Cattle × Nordic Red (NRF+SRB+FAY)
- American Brown Swiss × Nordic Red
- Canadian Ayrshire (CAY) × Nordic Red
- American Red Holstein × Nordic Red
- Finnish Ayrshire × Finncattle (FIC)
- Total Holstein in the Finnish Holstein evaluation

HOL:

- Original Danish Black & White × Holstein Friesian
- Original Danish Red & White × Holstein Friesian
- Holstein × Red Dairy cattle

JER:

- Original Danish Jersey × US Jersey

## Genetic groups (phantom parent groups)

Genetic groups are modelled by phantom parent grouping.

## Genetic parameters

The genetic parameters used for the longevity traits in the evaluation appear in Table 12.1 - 12.3.

Table 12.1. Genetic parameters for longevity in RDC. Heritability is on the diagonal, genetic correlations above the diagonal, and environmental correlations below the diagonal.

| | DAY11 | DAY12 | DAY13 | DAY14 | DAY15 |
|---|---|---|---|---|---|
| DAY11 | **0.029** | 0.946 | 0.902 | 0.869 | 0.843 |
| DAY12 | 0.839 | **0.044** | 0.978 | 0.957 | 0.938 |
| DAY13 | 0.711 | 0.924 | **0.057** | 0.984 | 0.975 |
| DAY14 | 0.632 | 0.847 | 0.958 | **0.066** | 0.988 |
| DAY15 | 0.585 | 0.794 | 0.915 | 0.974 | **0.072** |

Table 12.2. Genetic parameters for longevity in Holstein Heritability is on the diagonal, genetic correlations above the diagonal, and environmental correlations below the diagonal.

| | DAY11 | DAY12 | DAY13 | DAY14 | DAY15 |
|---|---|---|---|---|---|
| DAY11 | **0.035** | 0.944 | 0.891 | 0.858 | 0.836 |
| DAY12 | 0.777 | **0.052** | 0.987 | 0.969 | 0.955 |
| DAY13 | 0.640 | 0.929 | **0.062** | 0.996 | 0.989 |
| DAY14 | 0.566 | 0.853 | 0.969 | **0.069** | 0.998 |
| DAY15 | 0.525 | 0.803 | 0.930 | 0.986 | **0.072** |

Table 12.3. Genetic parameters for longevity in Jersey. Heritability is on the diagonal, genetic correlations above the diagonal, and environmental correlations below the diagonal.

| | DAY11 | DAY12 | DAY13 | DAY14 | DAY15 |
|---|---|---|---|---|---|
| DAY11 | **0.035** | 0.967 | 0.937 | 0.916 | 0.902 |
| DAY12 | 0.783 | **0.051** | 0.993 | 0.981 | 0.971 |
| DAY13 | 0.646 | 0.935 | **0.060** | 0.997 | 0.991 |
| DAY14 | 0.569 | 0.861 | 0.971 | **0.063** | 0.998 |
| DAY15 | 0.524 | 0.807 | 0.930 | 0.985 | **0.064** |

## Index

The index for longevity is based on DAY13. The standardization of the relative breeding values is described in the chapter “Standardization of EBVs and NTM.”

The longevity index is published for sires and cows.

## Effect of 10 index units

Phenotypic breed averages and values for one breeding value unit for single traits can be found for each breed:

https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/RDC
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/HOL
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/JER

From these effects of specific bulls can be calculated as days in production.

# 13. Youngstock survival

The index for youngstock survival describes the genetic ability of the bulls' offspring to survive from birth to maturity. Bulls with high indices for youngstock survival produce offspring with a lower mortality in the rearing period.

## Data

### Trait definition

In the evaluation of youngstock survival, the following four traits are considered:

| Abbreviation | Definition |
|---|---|
| Heifer period 1 (HP1) | Heifer calf survival in the period: 1 to 30 days |
| Heifer period 2 (HP2) | Heifer calf survival day in the period: 31 to 458 days |
| Bull period 1 (BP1) | Bull calf survival day in the period 1 to 30 days |
| Bull period 2 (BP2) | Bull calf survival day in the period 31 to 183 days |

Heifer period 1 (HP1): 1-30 days

- HP1 is defined as missing in the following cases:
    - If the heifer is killed during day 1-7
    - If the heifer is slaughtered, exported or otherwise lost during day 1-30
    - If the heifer is less than 30 days old at the date of data extraction
    - If the heifer dies day 30 or before, then the HP1 variable is defined 0, otherwise it is 1

Heifer period 2 (HP2): 31-458 days

- HP2 is defined as missing in the following cases:
    - If HP1 = 0 or HP1 is missing
    - If the heifer is slaughtered, exported or otherwise lost during day 31-458
    - If the heifer is less than 458 days old at date of data extraction
    - If the heifer dies in the period, then the HP2 variable is defined 0, otherwise it is 1

Bull period 1 (BP1): 1-30 days

- BP1 is defined as missing in the following cases:
    - If the bull is killed during day 1-7
    - If the bull is slaughtered, exported or otherwise lost during day 1-30
    - If the bull is less than 30 days old at the date of data extraction
    - If the bull dies day 30 or before, then the HP1 variable is defined 0, otherwise it is 1

Bull period 2 (BP2): 31-184 days

- BP2 is defined as missing in the following cases:
    - If HP1 = 0
    - If the bull is slaughtered, exported or otherwise lost during day 31-184
    - If the bull is less than 184 days old at the date of data extraction
    - If the bull dies in the period, then the HP2 variable is defined 0, otherwise it is 1

## Basic editing rules

Start year of data collection was 1999 in Sweden (2009 for bull calves), 1998 for Denmark, and 2004 for Finland.

Moreover, information is deleted, if:

- Calf is stillborn
- Calves euthanized right after birth (euthanized up to day 7 after birth)
- Multiple birth (twins, triplets)
- Abortions and defect calves
- ET-calves, unknown sex, castrates
- Missing vitality, herd, birth date or invalid parity
- Calves with unknown dam
- Breed not RDC, HOL, JER or FIC (crossbred calves are excluded)

## Pre-corrections

Pre-corrections for heterogeneous variance between countries are made.

## Genetic evaluation

Separate genetic evaluations are made for Holstein, Red dairy cattle (including Finn cattle) and Jersey.

## Model

The model for estimation of breeding values is a multi-trait animal model:

| | |
|---|---|
| Herd × 5-year | Fixed |
| Country × year × birth month | Fixed |
| Country × transfer (0/1) × calendar month of transfer (only HP2 and BP2) | Fixed |
| Heterosis (described below) | Fixed |
| Herd × year | Random |
| Phantom parent groups | Random |
| Herd × year of birth | Random |
| Animal | Random |

For Jersey country effects are not included

## Heterosis

Proportion of heterozygosity is considered as follows:

RDC:

- ABS = RDM × ABS + ABS × HF + ABS × (SRB+FAY+NRF)
- NOR = Nordic heterosis + CAY × NOR + FAY × FIC
- RDC×HF = RDM × HF + HF × (SRB+FAY+NRF)
- RDM×Nordic breeds = RDM × (SRB+FAY+NRF)

HOL:

- BW × HF + RW × HF
- HOL × RDC (only Finland)

JER:

- DJ × USJ

### Effect of relocation

The effect of transfer on survival in period 1 (HP1 and BP1) is problematic because a transfer is not possible if the calf is dead. Therefore, calves transferred late in the period will have a high survival rate.

## Genetic groups (phantom parent groups)

In general, the phantom parent groups are defined using the same procedure as for yield records. However, some year-groups have been merged to obtain larger phantom parent groups.

## Genetic parameters

The genetic parameters used for the traits in youngstock survival are shown in Table 13.1 – 13.3.

Table 13.1. Holstein. Genetic and residual variances, heritabilities (the diagonal), genetic correlations (above the diagonal) and residual correlations (below the diagonal). Standard errors in parenthesis.

| | Gen. var. | Res. var. | HP1 | BP1 | HP2 | BP2 |
|---|---|---|---|---|---|---|
| **HP1** | 0.0003 | 0.0294 | **0.009 (0.001)** | 0.90 (0.13) | 0.51 (0.13) | 0.40 (0.15) |
| **BP1** | 0.0002 | 0.0347 | 0.00 | **0.007 (0.001)** | 0.42 (0.21) | 0.44 (0.13) |
| **HP2** | 0.0004 | 0.0337 | 0.01 (0.004) | 0.00 | **0.011 (0.002)** | 0.95 (0.04) |
| **BP2** | 0.0011 | 0.0382 | 0.00 | -0.03 (0.004) | 0.00 | **0.027 (0.003)** |

Table 13.2. RDC: Genetic and residual variances, heritabilities (the diagonal), genetic correlations (above the diagonal) and residual correlations (below the diagonal). Standard errors in parenthesis.

| | Gen. var. | Res. var. | HP1 | BP1 | HP2 | BP2 |
|---|---|---|---|---|---|---|
| **HP1** | 0.0002 | 0.0293 | **0.007 (0.001)** | 0.95 (0.10) | 0.75 (0.08) | 0.61 (0.14) |
| **BP1** | 0.0002 | 0.0404 | 0.00 | **0.007 (0.001)** | 0.78 (0.12) | 0.58 (0.08) |
| **HP2** | 0.0010 | 0.0331 | -0.03 (0.003) | 0.00 | **0.023 (0.003)** | 0.89 (0.05) |
| **BP2** | 0.0019 | 0.0543 | 0.00 | -0.03 (0.003) | 0.00 | **0.034 (0.004)** |

Table 13.3. Jersey. Genetic and residual variances, heritabilities (the diagonal), genetic correlations (above the diagonal) and residual correlations (below the diagonal). Standard errors in parenthesis.

| | Gen. var. | Res. var. | HP1 | BP1 | HP2 | BP2 |
|---|---|---|---|---|---|---|
| **HP1** | 0.0011 | 0.0605 | **0.018 (0.002)** | 0.95 (0.05) | 0.42 (0.12) | 0.34 (0.18) |
| **BP1** | 0.0012 | 0.0820 | 0.00 | **0.015 (0.003)** | 0.39 (0.18) | 0.39 (0.17) |
| **HP2** | 0.0007 | 0.0582 | -0.08 (0.004) | 0.00 | **0.012 (0.002)** | 0.99 (0.06) |
| **BP2** | 0.0008 | 0.0771 | 0.00 | -0.11 (0.005) | 0.00 | **0.010 (0.003)** |

## Index

The index for youngstock survival is based on sub-indices for HP1, HP2, BP1 and BP2. The standardization of the relative breeding values is described in the chapter “Standardization of EBVs and NTM”.

The EBVs for HP1, HP2, BP1 and BP2 are combined by weighting with the economic values that are based on economic calculations (Table 13.4).

Table 13.4. Calculation of index for youngstock survival.

| | |
|---|---|
| Holstein | 3.58 × HP1 + 4.29 × HP2 + 1.78 × BP1 + 2.79 ×BP2 |
| RDC | 3.40 × HP1 + 4.06 × HP2 + 1.89 × BP1 + 2.96 × BP2 |
| Jersey | 1.92 × HP1 + 2.38 × HP2 + 0.19 × BP1 + 0.73 × BP2 |

The index for young stock survival is published for sires.

## Correlation between index for youngstock survival and underlying traits

The expected progress of each trait when selecting for youngstock survival expressed as percentage proportion of the maximum progress for that trait is shown in table 13.5. The maximum progress is obtained if selection is solely based on the trait in question.

Table 13.5. Correlations between the index for youngstock survival and indices for HP1, HP2, BP1 and BP2.

| Index | RDC | HOL | JER |
|---|---|---|---|
| HP1 | 0.86 | 0.77 | 0.83 |
| HP2 | 0.98 | 0.94 | 0.89 |
| BP1 | 0.87 | 0.76 | 0.81 |
| BP2 | 0.94 | 0.91 | 0.86 |

## Effect of 10 index units

Phenotypic breed averages and values for one breeding value unit for single traits can be found for each breed:

https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/RDC
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/HOL
https://nordic.mloy.fi/NAVBull/Phenotypes/ENG/JER

From these, the effect of using a specific bull can be calculated for survival in the early and late period for heifers and bull calves.

## References

https://www.nordicebv.info/wp-content/uploads/2015/04/CalfSurvivalFinalReport.pdf.

# 14. Saved feed

The index for Saved feed describes the genetic ability of the bulls' daughters to save feed related to lower maintenance costs and higher metabolic efficiency.

## Data

### Trait definition

In the evaluation for Saved feed the following traits (Table 14.1) are considered for cows in the first three to six lactations

Table 14.1. Abbreviations and definitions of traits included in the evaluation of Saved feed.

| Abbreviation | Definition |
|---|---|
| MBW | Metabolic Body Weight ($BW^{0.75}$), measured in 1st to 3rd parity, by scale and tape |
| STA | Stature height in 1st parity, used from the conformation evaluation |
| BD | Body depth in 1st parity, used from the conformation evaluation |
| CW | Chest width in 1st parity, used from the conformation evaluation |
| RFI | Residual feed intake (metabolic efficiency), measured from 1st to 6th parity in research herds and by the CFIT system from VikingGenetics |

### Basic editing rules - Maintenance

The body weight (BW) data are from 1990 in Finland (primarily tape) and 2007 in Denmark (only scale) for all breeds. For conformation traits - see basic editing rules above.

Body weight measured by scale is included if:

- Body weight in the range 300-1,100 kg for HOL and RDC, 100-900 kg for JER
- Age at 1st calving 20-36 months
- Measured 5-305 days in milk
- More than 10 cows need to be measured per month within herd, with a minimum of 200 observations
- Scales with stable measurements over time
- Cows are in 1st-3rd lactation

Body weight measured by tape is included if:

- Body weight in the range 282-1,000 kg for HOL and RDC
- Age at 1st calving 20-38 months
- Measured 5-365 days in milk

### Basic editing rules - RFI

There are 3 data sources of individually measured feed intake data in this evaluation, (1) the Efficient Dairy Genome Project (**EDGP**) on Holstein cows, (2) Luke on Red cows and (3) the Cattle Feed Intake (**CFIT**) by VikingGenetics with data from Holstein, Red cows and Jersey cows.

EDGP data

The EDGP dataset is a joint consortium of research farm data, where the consortium provide access to each other's feed intake data with the purpose of promoting a genetic evaluation for feed efficiency.

In this project there is used data from following research farms:
- Elora – Canada
- DRTC – Canada
- Foulum – Denmark
- Beltsville – USA
- Ellinbank – Australia

Data is not used from Strickhof and Posieux in Switzerland due to few cows and the data from Langhill in United Kingdom due to very heterogenous data.

## Luke data

The dataset from Luke contains feed intake on daily level for 1st parity cows at the research farms Rehtijarvi, Minkio, Viikki and Maaninka in Finland. Data from research farms in Finland are edited according to research criteria and therefore these data was not edited before RFI calculation/precorrection.

## CFIT data

CFIT data is provided by VikingGenetics on all three breeds, using 3D technology to identify the individual cows´ daily feed intake and body weight. CFIT data is merged with the test day data from the Danish cattle database.

Data for RFI calculation are included if:
- Days in milk are less than 330 days
- Calving age at 1st calving in the range 20-34 month for HOL and 18-35 for JER
- Cows are not moved to another herd with lactation
- More than two test days and six feed intake days - only CFIT data
- Daily dry matter intake in the range 2-50 kg dry matter – only EDGP data
- Daily feed intake not in the range 10-100 kg – only CFIT
- BW not in the range 300-1,100 kg for HOL+RDC and 100-900 kg for JER
- Daily milk production not in the range 5-100 kg
- Daily fat production not in the range 0.05-5.0 kg – only EDGP
- Fat content not in the range 2.5-10.0% for JER and 2.5-8.0% for HOL+RDC – only CFIT
- Daily protein production not in the range 0.05-4.0 kg - only EDGP
- Protein content not in the range 2.0-8.0% for JER and 2.0-6.0% for HOL+RDC – only CFIT
- Change in BW ($\Delta$BW) on daily level in the interval -15 to 15 for EDGP data and -7.5 to 7.5 kg for CFIT data

Afterwards outliers were defined as greater than the range mean±4xSD for the single phenotypes. Outliers was set missing. Production, feed intake and BW data are interpolated by animal and parity to maximize the number of records. This is especially important for production data in CFIT data, since production data here only is measured once a month and feed intake is measured on weekly basis.

## Pre-corrections – Maintenance

Single MBW observations that comes from scales are pre-corrected for the scale × season and stage of lactation effects based on a linear model fitted to the raw MBW data. The pre-corrected MBW observations are used to form MBW averages that are used as the observations for the evaluation.

In a second step, weights ($w_{ij}$) are calculated for each MBW observations to account for the type of measurement and the number of observations behind the MBW observation (Lidauer et al., 2019):

$$w_{ij} = 1 \Big/ \left( r_{jk} + \frac{1 - r_{jk}}{n_{ij}} \right) - s_k \ ,$$

where $r_{jk}$ is the repeatability of observations in parity *j* under measurement method *k* (tape, scale), $n_{ij}$ is the number of observations for animal *i* in parity *j*, and $s_k$ accounts for the difference in accuracy of one single MBW observation made either by tape or by scale (Lidauer et al., 2019):

## Pre-correction - RFI

The use of RFI as selections criteria for feed efficiency was firstly described by Koch et al. (1963), using the phenotypic covariance matrix. Kennedy et al. (1993) developed the theory of using genetic RFI, using the genetic covariance matrix. However, limiting literature describes how to use genetic RFI – therefor calculation of RFI is performed using phenotypic RFI.

Li et al. (2017) demonstrated that the assumptions on having 1 regression for ECM and ΔBW might be wrong, because they fluctuate during lactation in her results. This assumption will be adapted in the model construction of RFI in this project.

The first step is to calculate the phenotype for RFI. The model used to calculate the phenotype is for all breeds:

$$\boldsymbol{DMI_{lpP} = CA_p + CA_p^2 + LACP_P + HYS + YS_{LACP} + ECM_{lP} + MBW_P + \Delta BW_{lP} + e_{iw}}$$

where

DMI is the average daily dry matter intake,

*CA*$_p$ is the linear regression for age at calving nested within *p* parity (*p*=1, 2, ..,6),

CA$^2_p$ is the quadratic terms for age at calving nested within *p* parity (*p*=1, 2, ..,6),

*LACP* is the fixed effect lactation period nested within *P* (1st or later lactations)

*HYS* is the fixed effect of Herd x Year x Season (quarters for date of observation)

*YS*$_{LACP}$ is the fixed effect of Year x Season x Lactation period

ECM is the regression on energy corrected milk nested within *l* lactation period (*l*=2,3,…,11) and *P* (1st or later lactations)

MBW is the regression of metabolic body weight nested within *P* (1st or later lactations)

$\Delta BW$ is the regression of change in body weight nested within *l* lactation period (*l*=2,3,…,11) and *P* (1st or later lactations)

e is the residual of the model that is used for genetic evaluation.

This model creates a residual/phenotype for each test day across lactation and parities. Therefor it is crucial to correct for heterogeneous variance to avoid that the effect of lactation stage and parity goes into the breeding values.

## Heterogeneous variance correction for RFI

For each breed there is calculated an average standard deviation for RFI across parities, lactation stages and year x season. The next step is to standardize all residuals to the average variance by:

$$\hat{y} = \mu_{PlY} + ((y_i - \mu_{PlY}) \times (\hat{\sigma}/\sigma_{PlY}))$$

Where

$\hat{y}$ is the standardized phenotype,

$\mu_{PlY}$ is the mean RFI level in P (1st or later lactations), l lactation period and Y year x season,
$y_i$ is the residual for the *i* observation of a cow
$\hat{\sigma}$ is the standard deviation that is standardized for,
$\sigma_{PlY}$ is the standard deviation level in P (1st or later lactations), l lactation period and Y year x season.

After the standardization the fixed effects of HYS and $YS_{LACP}$ from the RFI model, is added to the heterogeneous corrected phenotype. The reason for doing that is to avoid that additive variance is lost in herd and seasonal effects. The effect of HYS and $YS_{LACP}$ will be included in the genetic model.

## Genetic evaluation

## Model for maintenance

Genetic evaluations are done combined for Holstein and RDC (including Danish, Swedish and Finnish populations). For Jersey only scale measurements from Denmark are used.

The model for estimating breeding values is a multi-trait animal model of 6 traits, MBW in 1st, 2nd, and 3rd parity and the three conformation traits (STA, BD, CW) used as correlated information.

MBW model:

| | |
|---|---|
| Year x Month | Fixed |
| Herd × 5-year period | Fixed |
| Age at 1st calving | Regression |
| Herd × year of calving | Random |
| Animal | Random |

The model for conformation traits is identical to model used in the conformation genetic evaluation.

Genetic groups (phantom parent groups)
Genetic groups for animals with unknown parents are included for all breeds in the pedigree file. The genetic groups are treated as random and are constituted by sex, breed, country and birth year periods.

## Model for RFI

The model for estimating breeding values is single step single trait animal model assuming RFI from different lactations are repeated measurement of the same trait. For Holstein the model is multi trait single step animal model assuming RFI from different lactations are repeated measurement of the same trait and RFI from non-Nordic research herds measure a different.

RFI model:

| | |
|---|---|
| Herd x Year x Season | Fixed |
| Year x Season x Lactation period | Fixed |
| Permanent environment | Random |
| Animal | Random |
| Residual | Random |

Genetic groups (phantom parent groups)
Genetic groups for animals with unknown parents are included for all breeds in the pedigree file. The genetic groups are treated as random and are constituted by breed, country and birth year periods.

A polygenic effect on 0.10 is used and a genotype cut on birthday 01.01.2009.

## Genetic parameters

The genetic parameters used for the Saved feed traits in the evaluation are shown in Table 14.2 – 14.4.

Table 14.2. Heritability's (the diagonal), genetic (upper triangle) and residual (lower triangle) correlations for Holstein and RDC.

| | MBW1 | MBW2 | MBW3 | STA | BD | CW |
|---|---|---|---|---|---|---|
| MBW1 | **0.46** | 0.98 | 0.96 | 0.65 | 0.51 | 0.58 |
| MBW2 | 0.34 | **0.51** | 0.99 | 0.68 | 0.49 | 0.55 |
| MBW3 | 0.26 | 0.40 | **0.56** | 0.68 | 0.48 | 0.53 |
| STA | 0.22 | 0.21 | 0.20 | **0.60** | 0.21 | 0.17 |
| BD | 0.14 | 0.09 | 0.07 | 0.05 | **0.18** | 0.55 |
| CW | 0.13 | 0.10 | 0.05 | 0.08 | 0.24 | **0.26** |

Table 14.3. Heritability's (the diagonal), genetic (upper triangle) and residual (lower triangle) correlations for JER.

| | MBW1 | MBW2 | MBW3 | STA | BD | CW |
|---|---|---|---|---|---|---|
| MBW1 | **0.46** | 0.98 | 0.96 | 0.65 | 0.51 | 0.58 |
| MBW2 | 0.34 | **0.51** | 0.99 | 0.68 | 0.49 | 0.55 |
| MBW3 | 0.26 | 0.40 | **0.56** | 0.68 | 0.48 | 0.53 |
| STA | 0.22 | 0.21 | 0.20 | **0.41** | 0.21 | 0.17 |
| BD | 0.14 | 0.10 | 0.07 | 0.05 | **0.16** | 0.55 |
| CW | 0.13 | 0.10 | 0.05 | 0.08 | 0.24 | **0.24** |

Table 14.4. Heritability's (the diagonal), genetic (upper triangle) and residual (lower triangle) correlations for HOL, RDC & JER.

| | RFI |
|---|---|
| RFI | **0.15** |

## Index

A combined maintenance index is calculated, based on the EBVs from the first three parities (Table 14.5), and the lactation weights from the NAV report 2018.

Table 14.5. Calculation of the MBW index.

| | |
|---|---|
| MBW123 | 0.30×MBW1 + 0.25 × MBW2 + 0.45×MBW3 |

The maintenance index is published for sires and cows.

The Metabolic efficiency index (RFI) is in the precorrection adjusted for parity and only 1 breeding value is published. Metabolic efficiency indices are published for bulls and cows.

## References

M.H. Lidauer, A.-M. Leino, R.S. Stephansen, J. Pösö, U.S. Nielsen, W.F. Fikse, G.P. Aamand. 2019. Genetic evaluation for Maintenance – Towards breeding values for Saved feed in Nordic dairy cattle. Interbull Bulletin, 55 (2019), pp. 21–25 https://journal.interbull.org/index.php/ib/article/view/1477

Kennedy, B., J. Van der Werf, and T. Meuwissen. 1993. Genetic and statistical properties of residual feed intake. Journal of Animal Science 71(12):3239-3250.

Koch, R. M., L. A. Swiger, D. Chambers, and K. E. Gregory. 1963. Efficiency of Feed Use in Beef Cattle 1. Journal of Animal Science 22(2):486-494.

Li, B., B. Berglund, W. Fikse, J. Lassen, M. H. Lidauer, P. Mäntysaari, and P. Løvendahl. 2017. Neglect of lactation stage leads to naive assessment of residual feed intake in dairy cattle. Journal of Dairy Science 100(11):9076-9084.

Lidauer, M. H., A. M. Leino, R. S. Stephansen, J. Pösö, U. N. Nielsen, F. W. Fikse, and G. P. Aamand. 2019. Genetic Evaluation for Maintenance – Towards Genomic Breeding Values for Saved Feed in Nordic Dairy Cattle.

# 15. Standardization of EBVs and NTM

## Estimated breeding values

EBVs for the yield traits, growth, fertility, birth, calving, udder health, general health, claw health, frame, feet and legs, udder, milkability, temperament, longevity and young stock survival are standardized in the same way. The formula for adjusting the mean and standard deviation of EBV is:

$$\text{EBV} = (\text{EBV}_{\text{animal}} - \text{Mean}) \times \text{Standardization factor}$$

Standardization of the mean and standard deviation is done within breed groups.

## Mean

EBVs of all animals are adjusted in such a way that animals in the base population have an average index of 100.

### Genetic base

EBVs for RDC, Holstein and Jersey bulls and females are expressed on a cow base except for growth where the EBV are expressed on bull calf base. The genetic base is for the genetic evaluation included cows from Denmark, Sweden and Finland that are 3-5 years of age at the date of publication. EBVs for growth are instead expressed on a genetic base of 3-5 year old bull calves. For Finn Cattle the EBVs are expressed on a base of 3-7 year old cows. GEBVs for crossbred animals are expressed on a genetic base of 1-7 year old crossbred cows.

## Standard deviation

Standard deviations of EBVs for all animals are standardized so that sires in the base population have a standard deviation of 10. The base population consists of AI sires from Denmark, Sweden and Finland born in 1997 and 1998.

## NTM

NTM is calculated by multiplying each standardized sub-index by a weighting factor. Weighting factors are standardized to give a standard deviation of 10 in NTM for AI sires from Denmark, Sweden and Finland born in 1997 and 1998.

The mean NTM in the base population is not adjusted, because it is based on adjusted EBVs for all sub-indices.

# 16. Genetic evaluation of Dairy x Dairy crossbred

GEBVs for main trait groups are calculated for female crosses between Holstein, RDC and Jersey. Breeding values for main trait groups are combined in a total merit index based on economic values. The breeding goal is economic performance.

## Traits

Genomic breeding values are calculated on main trait level, while breed differences are estimated on sub traits level. Therefore, for combines main traits the sub trait which explains most of the variation is chosen to reflect the total sum of sub traits in the main traits. Table 16.1 shows traits that are evaluated.

Table 16.1. Traits in genetic evaluation for DxD crossbreds.

| **Main trait group** | **Chosen sub-trait** |
|---|---|
| Yield | Milk, fat, and protein |
| Growth | Carcass classification score |
| Fertility | 1st to last insemination, cows |
| Birth | Calf survival, 1st calving |
| Calving | Calf survival, 1st calving |
| Udder health | Clinical mastitis 2nd lactation |
| General Health | Other Metabolic Disorders |
| Claw health | Sole ulcers |
| Youngstock survival | Heifer period 2 (31-458 days) |
| Milkability | |
| Temperament | |
| Longevity | |
| Saved feed | Maintenance |

## Procedure for calculation

Genomic predictions are performed doing three major steps:

- Imputation and phasing of genotypes
- Assignment to breed of origin
- Summing SNP effects based on solutions from pure breeds

GEBV for animal i is calculated as:

$$GEBV_{BOM,i} = \sum_{b=1}^{N_b} (\boldsymbol{v}'_{\boldsymbol{b}}(\boldsymbol{w}_{\boldsymbol{i},\mathbf{1}} \circ \boldsymbol{s}_{\mathbf{1},\boldsymbol{i},\boldsymbol{b}}) + \boldsymbol{v}'_{\boldsymbol{b}}(\boldsymbol{w}_{\boldsymbol{i},\mathbf{2}} \circ \boldsymbol{s}_{\mathbf{2},\boldsymbol{i},\boldsymbol{b}})) + \mu_b \frac{\sum \boldsymbol{s}_{\mathbf{1},\boldsymbol{i},\boldsymbol{b}} + \sum \boldsymbol{s}_{\mathbf{2},\boldsymbol{i},\boldsymbol{b}}}{2m} + a_i$$

Where:

- $\boldsymbol{w}_{\boldsymbol{i},\boldsymbol{j}}$contains haplotype j coded as 0 and 1 for the alternative alleles
- $\boldsymbol{v}_{\boldsymbol{b}}$ is a vector of marker effects for breed b
- $\circ$ is element vise multiplication

- $\boldsymbol{s}_{j,i,\boldsymbol{b}}$ is a vector of breed of origin indication for allele $j$ of animal $i$ to breed b, with 1 for alleles assigned to breed b and 0 for alleles assigned to other breeds and proportional values for alleles that could not be assigned
- $\mu_b$ is the intercept, accounting for difference in breed averages for breed b
- $m$ is the number of markers
- $a_i$ is a residual polygenic effect

## Haplotypes and assignment of breed of origin

The pedigree is traced back for 5 generations for the genotyped crossbred cows. The crossbred animals are included if sire and maternal grandsire is either Holstein, Jersey or RDC and dam is either Holstein, Jersey, RDC or crossbred. Genotypes are extracted on these crossbred cows and their genotyped purebred ancestors. The imputation is conducted using F-Impute 3, following a two-step process. Initially, imputation is separately executed for the purebred animals, with an additional 20k animals per breed within each purebred group to improve the imputation accuracy of the purebred ancestors. Subsequently, the crossbred animals are imputed and phased by using the imputed purebred genotypes as reference. Assignment to breed of origin is done by the Allor program. Animals where >0.1% of the alleles could not be assigned are excluded from the calculation of GEBVs.

## Marker effects

SNP solutions for main trait groups from the pure breed genomic prediction of RDC, Holstein and Jersey are used for all traits, except fertility and Saved feed where respectively interval from 1. to last insemination and maintenance is used. The SNP solutions from official genomic evaluation for Holstein, RDC and Jersey are on breed specific index scales. The sum of SNP solutions is adjusted to the scale of the chosen sub-trait and then converted to original phenotypic scale to make them comparable across breeds. The sum of the SNP solutions for Holstein, Jersey and RDC are multiplied by the phenotypic values of +1 index unit in each of the breeds. In the cases where no SNP solution was available for a particular marker in a breed, the effect of the marker was set to zero.

## Polygenic effect

Polygenic effect ($a_i$) is calculated from genotyped purebred ancestors. If polygenic effect is available for a parent or parents, it is multiplied by 0.5 and included. If it is not available for one or more parents, then the grandparents are considered and the effect multiplied by 0.25, and great-great-grandparents in the same manner. Polygenic effects are also multiplied by the phenotypic values of +1 index unit to make them comparable across breeds.

## Breed differences

The intercept terms, $\mu_b$ is taking the genetic difference between the breeds into account. For chosen sub-traits that are part of combined main trait groups the actual breed differences is modified by the level of the other traits in the main trait group. In table 16.2 the breed differences used in the genomic prediction of crossbred animals is shown.

Table 16.2. Calculated breed level differences compared to Holstein level.

| Trait | Unit | Breed difference compared to Holstein | |
|---|---|---|---|
| | | RDC | Jersey |
| 305-day milk yield | Kg | -1371 | -3922 |
| 305-day fat yield | Kg | -25,3 | -6,0 |
| 305-day protein yield | Kg | -32,0 | -73,0 |
| Carcass classification score | EUROP score | 0,60 | -2,85 |
| 1st to last insemination, cows | Days | -3,3 | -12.5 |
| Calf survival, 1st calving (direct) | 0/1 | 0,55 | 1,07 |
| Calf survival, 1st calving (maternal) | 0/1 | 0,61 | 1,07 |
| Clinical mastitis 2nd lactation | 0/1 | -1,00 | 0,90 |
| Other Metabolic Disorders | 0/1 | -3,36 | 0,14 |
| Sole ulcers | 0/1 | -0,06 | -0,45 |
| Heifer period 2 (31-458 days) | 0/1 | | |
| Milkability | L/minute | -14 | 19 |
| Temperament | Points | 0,1 | 0 |
| Longevity | Days | -10 | 113 |
| Maintenance | Kg feed | 2,8 | 26,8 |
| Stature | Centimeter | -7,8 | -19,8 |
| Body depth | Points | -0,4 | -0,1 |
| Chest width | Points | -0,2 | -0,1 |
| Rib structure | Points | -0,6 | -0,2 |
| Top line | Points | -0,1 | -0,6 |
| Rump width | Points | -0,5 | -2,5 |
| Rump angle | Points | 0,4 | 0,1 |
| Rear legs side view | Points | 0,3 | 0,2 |
| Rear legs rear view | Points | -0,3 | 0,1 |
| Hock quality | Points | 0,1 | -0,2 |
| Bone quality | Points | -0,1 | 0,2 |
| Foot angle | Points | -0,1 | -0,5 |
| Fore udder attachment | Points | -0,3 | -0,1 |
| Rear udder width | Points | -0,7 | -0,5 |
| Rear udder height | Points | -0,9 | -0,3 |
| Udder cleft | Points | -0,6 | -0,8 |
| Udder depth | Points | -1,1 | -1,1 |
| Udder balance | Points | -0,7 | -0,6 |
| Teat length | Points | -0,7 | 0,2 |
| Teat thickness | Points | -0,1 | 0,0 |
| Teat placement front | Points | -0,6 | -0,5 |
| Teat placement back | Points | -0,5 | -0,7 |

## Calculation of combined conformation traits

In the composite indices for frame, feet & legs and udder, the linear traits are combined according to optimum and weight. The contribution to the index is calculated as the deviation of future offspring from the breed's optimum for the linear trait in question multiplied by the relative weight factor. As the cows with the lowest average deviation from the optimum for the breed are to obtain the highest contribution to the index, the value is multiplied by -1 before the figure 100 is added.

$$\text{Index} = 100 + s \times \sum_{i=1}^{n} ki \times (\text{PD\_LINi} \div \text{OPTIMUMi})$$

Where:

- $\text{PD\_LIN}_i$ = predicted value of future offspring for the $i^{th}$ trait included in the index
- $\text{OPTIMUM}_i$ = optimum for the $i^{th}$ trait
- s = standardizing factor
- $k_i$ = weight factor

Optimum and weighting factors used for the cross breeds are shown in Table 16.3.

Table 16.3. Optimum and weight factors for cross bred cows.

| | Optimum | Weight factors |
|---|---|---|
| 1. Stature | 155 | 5 |
| 2. Body depth | 9 | 25 |
| 3. Chest width | 9 | 30 |
| 4. Rib structure | 9 | 20 |
| 5. Top line | 7 | - |
| 6. Rump width | 9 | 20 |
| 7. Rump angle | 5 | - |
| 8. Rear legs, side view | 5 | 10 |
| 9. Rear legs, back rear view | 8 | 30 |
| 10. Hock quality | 9 | 18 |
| 11. Bone quality | 8 | 17 |
| 12. Foot angle | 6.5 | 25 |
| 14. Fore udder attachment | 9 | 20 |
| 15. Rear udder height | 9 | 10 |
| 16. Rear udder width | 9 | - |
| 17.Udder cleft/support | 8 | 20 |
| 18. Udder depth | 9 | 25 |
| 19. Teat length | 5.5 | - |
| 20. Teat thickness | 5 | - |
| 21. Teat placement (front) | 8 | - |
| 22. Teat placement (back) | 5 | -15 |
| 23. Udder balance | 5 | -10 |

## Calculation of NTM – Nordic total merit index

NTM is calculated by weighting the GEBVs. NTM is calculated as shown in the formulas below. The weights used for each standardized sub-trait are shown in Table 16.4.

$$NTM = 0 + \sum_{i=1}^{n} (breeding\ value(i) - 100) \times weight\ factor(i)$$

Where:

- Breeding value$_i$ = Breeding value of the i$^{th}$ trait
- Weight factor$_i$ = The weight factor for the i$^{th}$ trait

NTM is standardized to have an average of zero and a standard deviation of 10.

Table 16.4. NTM weight factors for genomic tested crossbred cows.

| | |
|---|---|
| Yield index | 0.90 |
| Growth | 0.08 |
| Fertility | 0.36 |
| Birth | 0.14 |
| Calving | 0.14 |
| Udder health | 0.30 |
| General health | 0.14 |
| Claw health | 0.10 |
| Frame | - |
| Feet and legs | 0.05 |
| Udder | 0.18 |
| Milkability | 0.09 |
| Temperament | 0.04 |
| Longevity | 0.06 |
| Youngstock survival | 0.13 |
| Saved feed | 0.08 |

## Standardization of EBVs and NTM

For all traits, a rolling base population consisting of 1–7 years old crossbred females at date of publication is applied. The average These cows are used to calculated mean GEBV. The GEBV of a female for each trait is therefore calculated as

$$(GEBV - Mean) \times \text{Standardization factor of Holstein} + 100$$

## References

Eiríksson, J.H., Karaman, E., Su, G. et al. Breed of origin of alleles and genomic predictions for crossbred dairy cows. Genet Sel Evol 53, 84 (2021). https://doi.org/10.1186/s12711-021-00678-3.

Fogh, A. et al. Nordic genomic prediction for crossbred dairy females. Proceedings of the 2022 Interbull Meeting (2022). https://journal.interbull.org/index.php/ib/article/view/1835

# Appendix 1
# Breeding values expressed in kilograms on a 2005-base

The breeding values (EBV) in kilograms are based on the solutions from the animal BLUP-model. The units used the evaluation model is kilograms. Normally, breeding values are expressed on a rolling base. However, the solutions from the evaluation model can also be expressed on different fixed bases. Currently the 2005 base is used. The 2005-base is comprised of cows born in 2005 that have at least one observation included in the yield evaluation.

The calculation is based on the solution per trait and lactation.
EBV kg milk 1st lact. = milk solution 1st lact – mean of base animals milk solution 1st lact.
EBV kg milk 2nd lact. = milk solution 2nd lact – mean of base animals milk solution 2nd lact.
EBV kg milk 3rd lact. = milk solution 3rd lact – mean of base animals milk solution 3rd lact.

EBV kg protein 1st lact. = protein solution 1st lact – mean of base animals protein solution 1st lact.
EBV kg protein 2nd lact. = protein solution 2nd lact – mean of base animals protein solution 2nd lact.
EBV kg protein 3rd lact. = protein solution 3rd lact – mean of base animals protein solution 3rd lact.

EBV kg fat 1st lact. = fat solution 1st lact – mean of base animals fat solution 1st lact.
EBV kg fat 2nd lact. = fat solution 2nd lact – mean of base animals fat solution 2nd lact.
EBV kg fat 3rd lact. = fat solution 3rd lact – mean of base animals fat solution 3rd lact.

### The EBV of total production of milk, protein and fat are calculated by:

EBV kg milk total = 0.30 × EBV kg milk 1st lact. + 0.25 × EBV kg milk 2nd lact. + 0.45 × EBV kg milk 3rd lact.
EBV kg prot. total = 0.30 × EBV kg prot. 1st lact. + 0.25 × EBV kg prot. 2nd lact. + 0.45 × EBV kg prot. 3rd lact.
EBV kg fat total = 0.30 × EBV kg fat 1st lact. + 0.25 × EBV kg fat 2nd lact. + 0.45 × EBV kg fat 3rd lact.

Previously other fixed bases have been used. Below are differences between the current base and previously used bases.

**Base difference: 2005 base – 2000 base**

| | HOL | RDC | JER |
|---|---:|---:|---:|
| Milk 1st,(kg) | 490.1 | 436.8 | 296.6 |
| Milk 2nd, (kg) | 556.0 | 525.8 | 359.0 |
| Milk 3rd, (kg) | 504.0 | 557.6 | 353.1 |
| Protein 1st, (kg) | 18.16 | 17.03 | 13.45 |
| Protein 2nd, (kg) | 20.92 | 21.24 | 16.45 |
| Protein 3rd, (kg) | 19.65 | 22.28 | 16.60 |
| Fat 1st, (kg) | 18.31 | 16.05 | 15.24 |
| Fat 2nd, (kg) | 20.34 | 20.86 | 18.22 |
| Fat 3rd, (kg) | 18.90 | 22.09 | 15.12 |
| Pct protein 1st | 0.02 | 0.03 | 0.03 |
| Pct protein 2nd | 0.02 | 0.03 | 0.03 |
| Pct protein 3rd | 0.03 | 0.04 | 0.04 |
| Pct fat 1st | -0.03 | -0.03 | -0.05 |
| Pct fat 2nd | -0.03 | -0.02 | -0.05 |
| Pct fat 3rd | -0.02 | -0.02 | -0.09 |
| Persistency 1st | -8.4 | 0.4 | 30.3 |
| Persistency 2nd | 5.1 | 24.7 | 18.6 |
| Persistency 3rd | 21.8 | 18.7 | 24.9 |
| | | | |
| **Total milk, (kg)** | **512.6** | **487.6** | **326.6** |
| **Total protein, (kg)** | **19.29** | **19.34** | **14.98** |
| **Total fat, (kg)** | **19.04** | **18.70** | **16.11** |
| **Total pct protein** | **0.02** | **0.03** | **0.03** |
| **Total pct fat** | **-0.03** | **-0.02** | **-0.06** |
| **Total persistency** | **1.7** | **11.4** | **25.7** |

**Base difference: 2005 base – 1995 base**

| | **HOL** | **RDC** | **JER** |
|---|---:|---:|---:|
| Milk 1st,(kg) | 1188.5 | 969.7 | 830.5 |
| Milk 2nd, (kg) | 1309.2 | 1088.4 | 872.7 |
| Milk 3rd, (kg) | 1163.5 | 1131.6 | 879.2 |
| Protein 1st, (kg) | 41.54 | 37.33 | 31.09 |
| Protein 2nd, (kg) | 46.39 | 43.60 | 33.71 |
| Protein 3rd, (kg) | 42.73 | 44.84 | 34.36 |
| Fat 1st, (kg) | 37.66 | 36.32 | 36.42 |
| Fat 2nd, (kg) | 40.36 | 42.94 | 37.93 |
| Fat 3rd, (kg) | 36.33 | 44.73 | 32.32 |
| Pct protein 1st | 0.02 | 0.05 | -0.06 |
| Pct protein 2nd | 0.02 | 0.07 | -0.04 |
| Pct protein 3rd | 0.04 | 0.07 | -0.03 |
| Pct fat 1st | -0.17 | -0.07 | -0.28 |
| Pct fat 2nd | -0.17 | -0.04 | -0.26 |
| Pct fat 3rd | -0.14 | -0.04 | -0.34 |
| Persistency 1st | -4.2 | -34.0 | 34.6 |
| Persistency 2nd | 22.9 | -34.4 | 8.5 |
| Persistency 3rd | 59.4 | -43.9 | 12.4 |
| | | | |
| **Total milk, (kg)** | **1219.7** | **1037.7** | **852.9** |
| **Total protein, (kg)** | **43.23** | **40.71** | **32.53** |
| **Total fat, (kg)** | **38.20** | **39.99** | **36.05** |
| **Total pct protein** | **0.03** | **0.06** | **-0.04** |
| **Total pct fat** | **-0.16** | **-0.05** | **-0.29** |
| **Total persistency** | **16.7** | **-36.1** | **22.3** |

# Appendix 2

**Defining phenotypes for conception rate (CR):** Each new insemination is preliminarily set to successful i.e., CR=1. If it is followed by a new insemination the former CR is set to CR=0 or missing phenotype if the cow was inseminated in the same cycle (<= 5 days).

If a cow is checked for pregnancy, the last insemination is updated accordingly. If a cow faced an early abortion, i.e., inseminations started again after successful pregnancy check, the last insemination before pregnancy check is left as successful.

After calving, it is checked whether the last insemination is within the limits of acceptable pregnancy period (260-302 days). If the pregnancy period is longer, the last insemination is set to zero (possible that a farm bull was used). If the pregnancy period is shorter, it is checked iteratively whether some of the former inseminations is within acceptable limits, in which case insemination for this day is set to 1. All inseminations that are newer than this successful insemination are set to missing values. **Note**, in principle two possibilities exist if the last insemination does not fit within the acceptable limits but results in too short a pregnancy period: a cow calved too early or pregnant cow was inseminated. Based on the consultancy of a veterinarian, the latter is more common since AI technicians have skills to inseminate cows so that a possible pregnancy is not terminated. Therefore, the latter option was selected.

**Special case for defining phenotypes:** if there is only one insemination record and positive pregnancy check result after this, the last insemination is accepted as successful, even if the pregnancy period is too short, i.e., too early calving occurred.

If a non-consecutive calving was noticed or a cow started with insemination records, inseminations that were done within 365 days from the new calving are considered. This means that with an average pregnancy period of 281 days and an average cycle of 21 days, as a maximum 5 inseminations are included for the new calving. All earlier inseminations are set to missing values.

If a cow was sold during a service period, all subsequent inseminations are set to missing and those before accepted. If the service period occurred before or after the cow was sold, inseminations are accepted.

When a cow is slaughtered, the last phenotype is left successful only in the case of a positive pregnancy check; otherwise, it is set to zero.

**Open records due to the data extraction:** All data is used to define phenotypes before removing data that is too new (150-d gap, see below), therefore only a small fraction of the data belongs to the class of the open records. In this class of open records, the last CR is set to 0 if the lactation length is > 260 days and days from the data extraction to the last insemination is > 340 days. For the remaining open records, CR is set to 0.7, i.e., average NRR in heifers. The rationale behind this is that if there are no events during 150 days before the extraction of data, it is very probable that a cow is pregnant and has not calved yet.

**Limits used:** Records within 150 days from data extraction are excluded from the data set. Only the first 10 inseminations are accepted in the data. The same limits that are used for other fertility traits are used for CR data: for first insemination in heifers the lowest value (270 d) and the highest age (900 d), lowest (550 d) and highest (Jersey 975 d, others 1100 d) first calving age, heifers not older than 3.4 years without calving or culling, cows not longer than 2 years since last calving, ICF within limits of 20 - 230 days, IFL in maximum 365 days.