

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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Haifa Splittorff
CEO NAV

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 years 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., a 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 differs slightly from 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 be 15 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, 1 st		%-units	1.6	1.65	0.86
Easy calving, 1 st		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, 1 st , 1 st period		%-units	0.83	0.83	0.75
Mastitis, 1 st , 2 nd period		%-units	0.89	0.87	0.85
Mastitis, 2 nd		%-units	1.23	1.17	1.20
Mastitis, 3 rd +		%-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:

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

where

- Breeding value_i = Breeding value of the ith trait
- Weight factor_i = The weight factor for the ith 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

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

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3. Genomic Prediction

Genomic evaluation is performed monthly for females and young AI bulls. A single step model is used for most of the traits in NTM. The traits Calving, Birth, Young stock survival, Longevity, Under Health and Temperament are still evaluated by a two-step model.

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, Milkability, Temperament, Saved Feed and Methane (Only Holstein bulls).

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 (August 2025).

	Bulls	Cows
Holstein	42,923	287,849
RDC	9,055	146,493
Jersey	2,897	83,654

Animals, whose genotype is not consistent with their recorded parents, are excluded from the genomic evaluation.

SNP-chips and imputation

An Illumina BovineSNP50 BeadChip is used as a standard. Lower density chips are imputed to this standard using the software program F-impute (Sargolzaei et al (2014)).

Genetic evaluation

Phenotypic information from the Nordic countries is updated four times per year for genetic evaluation. 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 calculate 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 weighed together.

A polygenic effect is included in the genomic prediction models. In table 3.2 the calculation method and the size of the polygenic effect can be seen for the different trait groups in NTM.

Table 3.2. Calculation method and polygenic effect for the traits in NTM.

Trait	Calculation method	Polygenic effect
Yield index	Single Step	10%
Growth	Single Step	30%
Fertility	Single Step	30%
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	30%
Temperament	Single Step	30%
Longevity	Two Step	10%
Youngstock survival	Two Step	10%
Saved feed	Single Step	30%

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.

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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 data included 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 single step model is used including the following features:

- Multi-lactation, multi-trait single step 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 (1 st 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 (2 nd and later lactations)	Fixed
Heterosis and recombination	Fixed/random
Genetic groups (phantom parent groups)	Random
Animal	Random

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

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.

	1 st lactation			2 nd lactation			3 rd 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.

	1 st lactation			2 nd lactation			3 rd 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.

	1 st lactation			2 nd lactation			3 rd 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	$0.30 \times \text{EBV}_{\text{milk1}} + 0.25 \times \text{EBV}_{\text{milk2}} + 0.45 \times \text{EBV}_{\text{milk3}}$
All	Fat	$0.30 \times \text{EBV}_{\text{fat1}} + 0.25 \times \text{EBV}_{\text{fat2}} + 0.45 \times \text{EBV}_{\text{fat3}}$
All	Protein	$0.30 \times \text{EBV}_{\text{protein1}} + 0.25 \times \text{EBV}_{\text{protein2}} + 0.45 \times \text{EBV}_{\text{protein3}}$
RDC	Yield	$-0.25 \times \text{milk index} + 0.55 \times \text{fat index} + 0.70 \times \text{protein index}$
HOL	Yield	$-0.25 \times \text{milk index} + 0.55 \times \text{fat index} + 0.70 \times \text{protein index}$
JER	Yield	$-0.30 \times \text{milk index} + 0.65 \times \text{fat index} + 0.65 \times \text{protein index}$

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 2022-2023.

Index	RDC	HOL	JER
Milk	0.55	0.45	0.56
Fat	0.93	0.92	0.97
Protein	0.87	0.84	0.89

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:

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

- EBV_{day101} is the breeding value for milk on day 101
- $EBV_{\text{d101-d300}}$ 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.

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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 (Holstein, RDC)

Pre-corrections

All traits were pre-corrected for heterogeneous variance according 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 of 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
		<i>Holstein</i>		
CGS	0.28			
CGL	0.98	0.32		
CS	0.41	0.36	0.29	
FS	0.17	0.17	0.35	0.18
		<i>RDC</i>		
CGS	0.36			
CGL	0.97	0.29		
CS	0.34	0.32	0.29	
FS	- 0.14	-0.12	0.15	0.23
		<i>Jersey</i>		
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	$100.65 \times \text{CGS} + 100.65 \times \text{CGL} + 13.8 \times \text{CS}$
RDC	$111.4 \times \text{CGS} + 111.4 \times \text{CGL} + 13.6 \times \text{CS}$
Jersey	$45.6 \times \text{CGS} + 10.1 \times \text{CS}$

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

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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 (groups 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 herds during 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 according to country, year of 1st 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 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 single step 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
1 st insemination year x month x country	Fixed
Age at 1 st 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 1 st 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 × 1 st calving year	Fixed
1 st insemination year × month × country	Fixed
Age at 1 st insemination in heifers × country	Fixed
Inbreeding coefficient	Regression
Heterosis	Regression
Animal	Random

Model for NRR for cows:

Herd × 1 st calving year	Fixed
1 st insemination year × month × country	Fixed
Age at 1 st insemination in heifers × country	Fixed
Semen type of 1 st ins. × time-period × country	Fixed
Inbreeding coefficient	Regression
Heterosis	Regression
Animal	Random

Model for ICF for cows:

Herd × 1 st calving year	Fixed
Calving year × month × country	Fixed
Age at 1 st insemination in heifers × country	Fixed
Inbreeding coefficient	Regression
Heterosis	Regression
Animal	Random

Model for CR for cows:

Herd × 1 st calving year	Fixed
Insemination year × month × country	Fixed
Age at 1 st 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

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

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

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_{1-3} , IFL_0 , IFL_{1-3} , AIS_0 and AIS_{1-3}

Index	RDC	HOL	JER
ICF_{1-3}	0.56	0.63	0.55
IFL_0	0.63	0.54	0.77
IFL_{1-3}	0.98	0.99	0.97
AIS_0	0.64	0.51	0.75
AIS_{1-3}	0.90	0.89	0.91

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.

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7. Calving and Birth

The index for calving (calving^{maternal}) and birth (calving^{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 1 st calving, SB \geq 2 nd calving	stillbirth in the first 24 hours after birth
CE 1 st calving, CE \geq 2 nd calving	calving ease
CS 1 st calving, CS \geq 2 nd 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 stratum: 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
Herd×Year 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, heritabilities 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.

Trait	Direct			Maternal		
	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 x year variance (within 5-year period).

Trait	Residual variance			H x Y variance		
	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.

Trait	Permanent cow variance		
	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 _{≥2}	0.81	0.86	0.84
CE _{≥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 _{≥2}	0.82	0.90	0.93
CE _{≥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 calves 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

¹Days 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	0.05					
	RDC	0.04					
	Jersey	0.04					
CM12	Holstein		0.03				
	RDC	0.66	0.02				
	Jersey		0.02				
CM2	Holstein			0.06			
	RDC	0.67	0.97	0.05			
	Jersey			0.04			
CM3	Holstein				0.07		
	RDC	0.68	0.81	0.93	0.04		
	Jersey				0.06		
UA	Holstein					0.27	
	RDC	-0.37	-0.22	-0.15	-0.13	0.30	
	Jersey					0.24	
UD	Holstein						0.41
	RDC	-0.56	-0.38	-0.28	-0.25	0.80	0.39
	Jersey						0.32

The heritabilities of test-day SCC 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	$0.15 \times \text{CM11} + 0.15 \times \text{CM12} + 0.25 \times \text{CM2} + 0.45 \times \text{CM3}$
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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
<ul style="list-style-type: none">• Retained placenta• Hormonal reproductive disorders• Infective reproductive disorders• Other reproductive disorders	<ul style="list-style-type: none">• Hormonal reproductive disorders• Infective reproductive disorders• Other reproductive disorders	<ul style="list-style-type: none">• Ketosis	<ul style="list-style-type: none">• Milk fever• Other metabolic diseases• Other feed related disorders• Other diseases	<ul style="list-style-type: none">• 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. For Denmark and Sweden BHB and acetone, are recorded in mmol/L in milk. For Finland BHB recorded in mmol/L in blood.

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 (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 Denmark, Sweden, and Finland and across years of sampling, the variation in phenotypic records were adjusted according to country, parity 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 of 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 partially (re)-estimated during GH model revision in 2025 (General Health Update Final Report 2025). For computational reasons, residual correlations between lactations were set to zero.

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

Trait	ERP1	LRP1	OMB1	KET1	FL1	ERP2	LRP2	OMB2	KET2	FL2	ERP3	LRP3	OMB3	KET3	FL3	BHB1	ACE1	BHB2	ACE2	BHB3	ACE3
ERP1	0.03	0.37	0.40	0.31	0.15	0.72	0.32	0.29	0.33	0.08	0.64	0.18	0.31	0.20	0.16	0.05	0.04	-0.02	-0.01	-0.02	0.04
LRP1	0.03	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	0.03	0.04	-0.01	-0.05	0.00	-0.03
OMB1	0.04	0.01	0.01	0.74	0.37	0.24	0.13	0.79	0.59	0.32	0.16	0.15	0.48	0.53	0.35	0.47	0.48	0.38	0.37	0.29	0.28
KET1	0.06	0.01	0.09	0.01	0.18	0.24	0.07	0.67	0.70	0.12	0.16	0.03	0.52	0.66	0.09	0.56	0.59	0.45	0.45	0.37	0.37
FL1	0.01	0.01	0.02	0.02	0.01	0.10	0.09	0.32	0.17	0.96	0.01	0.02	0.21	0.10	0.91	0.03	0.03	-0.01	-0.02	-0.02	0.00
ERP2	0.00	0.00	0.00	0.01	0.02	0.03	0.30	0.26	0.26	0.03	0.98	0.27	0.23	0.20	0.09	0.00	-0.01	-0.01	-0.01	-0.01	-0.01
LRP2	0.00	0.00	0.00	0.00	0.00	0.04	0.01	0.13	0.06	0.12	0.35	0.94	0.15	0.10	0.22	-0.02	-0.03	0.01	0.01	0.01	0.01
MB2	0.00	0.00	0.00	0.00	0.00	0.06	0.01	0.01	0.60	0.32	0.25	0.11	0.83	0.61	0.39	0.38	0.38	0.46	0.46	0.40	0.40
KET2	0.00	0.00	0.00	0.00	0.00	0.05	0.01	0.08	0.01	0.20	0.24	0.01	0.44	0.96	0.17	0.46	0.46	0.53	0.55	0.51	0.53
FL2	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.02	0.01	-0.04	0.00	0.16	0.15	0.97	-0.01	0.00	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	0.03	0.34	0.22	0.19	0.05	0.00	-0.02	0.01	0.03	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	0.01	0.12	0.08	0.09	-0.01	0.01	0.00	0.02	0.01	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	0.02	0.49	0.22	0.28	0.28	0.38	0.38	0.45	0.45
KET3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.01	0.09	0.02	0.12	0.35	0.36	0.49	0.51	0.51	0.53
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	0.01	0.00	0.00	-0.01	0.01	-0.02	-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	0.08	0.88	0.85	0.72	0.78	0.66
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	0.05	0.73	0.79	0.67	0.70
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	0.09	0.89	0.95	0.86
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	0.60	0.05	0.87	0.94
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	0.08	0.92
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	0.62	0.04

Table 9.4. Genetic correlations (above), residual correlations (under) and heritability's (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	0.01	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	0.03	-0.03	-0.06	0.02	0.02
LRP1	0.02	0.01	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	0.02	0.04	0.03
MB1	0.02	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	0.31	0.26	0.26	0.20	0.20	0.14
KET1	0.01	0.01	0.08	0.01	-0.04	0.03	-0.21	0.43	0.81	-0.10	0.09	-0.18	0.29	0.70	-0.16	0.63	0.63	0.56	0.55	0.46	0.47
FL1	0.02	0.00	0.04	0.03	0.005	0.14	0.09	0.21	0.05	0.80	0.12	0.02	-0.01	0.05	0.84	0.01	0.08	-0.01	0.01	-0.05	-0.03
ERP2	0.01	0.01	0.01	0.02	0.03	0.01	0.28	0.14	-0.09	0.20	0.95	0.37	0.11	0.10	0.09	-0.01	0.01	-0.01	-0.04	0.01	-0.02
LRP2	0.00	0.00	0.00	0.00	0.00	0.03	0.01	-0.08	-0.14	0.07	0.23	0.92	-0.06	-0.02	0.10	-0.01	-0.03	-0.01	0.02	-0.02	-0.03
MB2	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.01	0.46	-0.03	0.27	-0.17	0.87	0.51	0.15	0.28	0.20	0.32	0.22	0.28	0.19
KET2	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.06	0.01	-0.04	0.00	-0.08	0.37	0.94	-0.01	0.54	0.54	0.65	0.66	0.60	0.61
FL2	0.00	0.00	0.00	0.00	0.00	0.01	-0.01	0.01	0.00	0.01	0.09	0.21	-0.06	-0.09	0.93	0.01	0.00	0.01	-0.02	-0.01	-0.01
ERP3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.29	0.16	0.21	0.07	-0.01	0.04	0.01	0.01	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	0.01	-0.08	0.01	0.15	-0.02	-0.05	0.02	0.05	0.02	0.03
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	0.03	0.44	0.06	0.20	0.12	0.27	0.19	0.32	0.23
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	0.01	-0.04	0.47	0.46	0.56	0.57	0.60	0.60
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	0.01	-0.02	-0.02	0.01	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	0.14	0.89	0.93	0.81	0.90	0.85
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	0.00	0.09	0.83	0.89	0.77	0.87
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	0.14	0.90	0.93	0.88
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	0.71	0.09	0.80	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	0.13	0.92
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	0.72	0.09

Table 9.5. Genetic correlations (above), residual correlations (under) and heritability's (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	0.01	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	0.00	0.01	0.00	0.02
LRP1	0.03	0.004	-0.04	0.11	0.04	0.33	0.79	0.17	0.27	0.23	0.34	0.79	0.05	0.48	0.01	-0.02	-0.05	-0.02	-0.08	-0.01	-0.02
MB1	0.03	0.01	0.004	0.55	0.22	0.43	0.37	0.63	0.36	0.22	0.18	0.17	0.51	0.38	0.10	0.46	0.47	0.37	0.36	0.32	0.30
KET1	0.03	0.00	0.06	0.01	0.33	0.10	0.40	0.47	0.46	0.19	0.13	0.16	0.08	0.49	0.12	0.64	0.67	0.49	0.50	0.39	0.39
FL1	0.01	0.01	0.02	0.01	0.01	0.16	0.12	0.02	0.31	0.81	0.40	-0.09	-0.05	0.39	0.84	0.08	0.06	0.05	0.01	0.05	0.06
ERP2	0.00	0.00	0.00	0.00	0.01	0.01	0.47	0.38	0.37	0.18	0.88	0.45	0.27	0.27	0.23	-0.04	-0.03	-0.02	0.02	-0.02	-0.02
LRP2	0.00	0.00	0.00	0.00	0.00	0.06	0.003	0.53	0.46	0.44	0.35	0.75	0.20	0.46	0.07	0.08	0.12	0.03	0.08	0.01	0.05
MB2	0.00	0.00	0.00	0.00	0.00	0.04	0.01	0.01	0.40	0.14	0.28	0.27	0.82	0.42	0.10	0.39	0.42	0.45	0.49	0.42	0.41
KET2	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.05	0.01	0.32	0.32	0.57	0.18	0.70	0.26	0.48	0.51	0.58	0.58	0.55	0.54
FL2	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.00	0.01	0.26	0.09	-0.02	0.21	0.76	-0.06	-0.05	-0.04	-0.03	-0.04	-0.03
ERP3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.29	0.19	0.33	0.48	-0.01	-0.01	0.00	0.00	0.01	0.00
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	0.02	0.01	0.04	0.01	0.03	0.05
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	0.01	0.39	0.08	0.27	0.27	0.38	0.36	0.46	0.46
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	0.05	0.01	0.14	0.42	0.42	0.53	0.51	0.58	0.66
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	0.01	0.00	0.01	0.01	0.03	-0.01	0.00
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	0.08	0.93	0.86	0.62	0.81	0.54
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	0.56	0.05	0.82	0.74	0.79	0.69
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	0.09	0.84	0.94	0.73
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	0.59	0.04	0.81	0.87
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	0.08	0.84
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	0.65	0.04

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. GEBV correlations between the General Health index and the five sub-index traits for Nordic genotyped bulls born in 2022 - 2023

	HOL	RDC	JER
ERP ^a	0.75	0.72	0.70
LRP ^b	0.54	0.73	0.47
OMB ^c	0.76	0.74	0.87
KET ^d	0.63	0.54	0.81
FLP ^e	0.48	0.57	0.61

^aEarly Reproductive Disorders (ERP), ^bLate Reproductive Disorders (LRP), ^cOther Metabolic Disorders (OMB), ^dKetosis (KET), ^eFeet & 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

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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.

Update of genetic parameters and inclusion of Swedish and Finnish β -hydroxybutyrate and acetone measurements to the Nordic General Health evaluation model. K. Johansson, J. Pösö, U. Sander Nielsen, J-Å. Eriksson and G. P. Aamand. BULLETIN NO. 61, 2025.

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 diseases, 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 of 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	Lacta- tion	Phenotypic SD	h^2	Genetic SD	Perma- nent 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	Lacta- tion	Pheno- typic 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. Due to large standard errors of correlation estimates for Jersey, 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	$0.0418 \times \text{SU} + 0.0591 \times \text{SH} + 0.0564 \times \text{HH} + 0.0521 \times \text{DE} + 0.0231 \times \text{SP} + 0.0129 \times \text{WLS} + 0.009 \times \text{CSC}$
RDC	$0.0525 \times \text{SU} + 0.0679 \times \text{SH} + 0.0697 \times \text{HH} + 0.0473 \times \text{DE} + 0.0183 \times \text{SP} + 0.0091 \times \text{WLS} + 0.0146 \times \text{CSC}$
Jersey	$0.0247 \times \text{SU} + 0.0401 \times \text{SH} + 0.0504 \times \text{HH} + 0.0428 \times \text{DE} + 0.0169 \times \text{SP} + 0.0082 \times \text{WLS} + 0.0059 \times \text{CSC}$

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 health 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, udder balance, teat length, teat thickness, teat placement (front), teat placement (back)
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 1st to 3rd 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 1st to 3rd parity 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 step, single-trait animal model.

Herd × five year period ¹	Fixed
Classifier × year ¹	Fixed
Year × month of calving × 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

¹Only linear traits

²Defined differently for linear traits and teat coordinates

³Only teat coordinates

For conformation, milkability and temperament 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.

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

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

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

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

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

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

Data source	Heritability				
	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)
Udder balance	0.47 (0.94)
Teat placement (front)	0.57 (-0.91)
Teat placement (rear)	0.45 (-0.91)

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”.

$$\text{Index} = 100 + s \times \sum_{i=1}^n k_i \times (\text{PD_LIN}_i \div \text{OPTIMUM}_i)$$

where

- PD_LIN_i = predicted value of future daughters for the i^{th} trait included in the index
- 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. Optimum for Holstein, RDC and Jersey.

	Holstein	RDC	Jersey
Stature	*	*	129
Body depth	9	9	6
Chest width	9	9	5
Rib structure	9	9	6
Top line	7	7	7
Rump width	9	9	6
Rump angle	5	5	5
Rear legs, side view	5	5	5
Rear legs, back rear view	8	8	9
Hock quality	9	9	9
Bone quality	8	7.5	9
Foot angle	6.5	7	6.5
Fore udder attachment	9	9	9
Rear udder height	9	9	9
Rear udder width	9	9	9
Udder cleft/support	8	9	9
Udder depth	9	9	9
Udder balance	5.4	5	5
Teat length	5.5	5.5	5.5
Teat thickness	5	6	6
Teat placement (front)	8	8	7.5
Teat placement (back)	6.2	5	5

* As high as possible

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

	Holstein	RDC	Jersey
Stature	5	15	6
Body depth	25	25	14
Chest width	30	30	13
Rib structure	20	10	10
Top line	-	-	25
Rump width	20	20	11
Rump angle	-	-	11
Codes for body			10
Rear legs, side view	10	15	20
Rear legs, back rear view	30	25	20
Hock quality	18	25	20
Bone quality	17	15	15
Foot angle	25	20	25
Fore udder attachment	18	20	20
Rear udder height	5	8	10
Rear udder width	5	5	-
Udder cleft/support	17	12	10
Udder depth	18	14	25
Udder balance	-15	-	-
Teat length	3	14	-
Teat thickness	4	12	10
Teat placement (front)	-	10	-
Teat placement (back)	-15	5	-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 2022 – 2023.

	Holstein	RDC	Jersey
	Index for frame		
Stature	0.79	0.97	-0.21
Body depth	0.76	0.57	0.48
Chest width	0.54	0.46	0.17
Rib structure	0.55	0.36	0.35
Top line	0.10	0.04	0.48
Rump width	0.72	0.74	0.28
Rump angle	0.13	0.08	-0.33
	Index for feet and legs		
Rear legs, side view	0.16	-0.43	-0.47
Rear legs, rear view	0.63	0.41	0.52
Hock quality	0.70	0.82	0.55
Bone quality	0.68	0.86	0.48
Foot angle	-0.05	-0.15	0.39
	Index for mammary system		
Fore udder attachment	0.71	0.55	0.76
Rear udder height	0.43	0.34	0.50
Rear udder width	0.31	0.29	0.16
Udder cleft	0.02	0.10	0.17
Udder depth	0.81	0.58	0.87
Udder balance	0.06	0.30	0.29
Teat length	0.23	0.56	0.30
Teat thickness	0.07	0.45	0.29
Teat placement (front)	-0.05	0.24	-0.09
Teat placement (back)	-0.08	0.11	-0.10

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 1 st calving to end of 1 st lactation – including maximum 365 days in 1 st lactation
DAY12	Days from 1 st calving to end of 2 nd lactation – including maximum 365 days per lactation
DAY13	Days from 1 st calving to end of 3 rd lactation – including maximum 365 days per lactation
DAY14	Days from 1 st calving to end of 4 th lactation – including maximum 365 days per lactation
DAY15	Days from 1 st calving to end of 5 th 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 1 st calving	Fixed
Year × month of 1 st calving	Fixed
Herd × 5-year period	Fixed
Heterosis	Regression
Genetic groups (as phantom parent groups)	Random
Herd × year of 1 st 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 × RDC

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:

- $ABS = RDM \times ABS + ABS \times HF + ABS \times (SRB + FAY + NRF)$
- $NOR = \text{Nordic heterosis} + CAY \times NOR + FAY \times FIC$
- $RDC \times HF = RDM \times HF + HF \times (SRB + FAY + NRF)$
- $RDM \times \text{Nordic breeds} = RDM \times (SRB + FAY + NRF)$

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	$3.58 \times \text{HP1} + 4.29 \times \text{HP2} + 1.78 \times \text{BP1} + 2.79 \times \text{BP2}$
RDC	$3.40 \times \text{HP1} + 4.06 \times \text{HP2} + 1.89 \times \text{BP1} + 2.96 \times \text{BP2}$
Jersey	$1.92 \times \text{HP1} + 2.38 \times \text{HP2} + 0.19 \times \text{BP1} + 0.73 \times \text{BP2}$

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 considering the milk production and the body weight.

Data

Trait definition

In the evaluation for Saved feed the following traits (Table 14.1) are considered for cows in the first to fifth lactations. Saved feed index is based on data from commercial dairy herds with CFIT equipment and research herds (Foulum for Holstein, and LUKE for RDC). CFIT data is provided by VikingGenetics on all three breeds, using 3D technology to identify the individual cows' daily feed intake and body weight.

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

Abbreviation	Definition
BW	Body Weight (KG), measured with CFIT camera or by scale for research herds
ECM	Energy corrected milk, calculated based on data for official yield recording of milk, fat and protein
DMI	Daily dry matter intake, measured with CFIT camera or by feeding boxes for research herds

Basic editing rules

Data is included if:

- Age at 1st calving 20-35 months for HOL and RDC, 18-35 for JER.
- Measured 14-294 days in milk
- Cows in 1st-5th lactation

Body weight is included if:

- Body weight between 300-1100 kg for HOL and RDC, 100-900 kg for JER

ECM is included if:

- Milk yield per day between 5-100 kg
- Fat percent between 2.5-10 %
- Protein percent between 2 -8 %

DMI is included if:

- DMI per day between 10-100 kg

Outliers were defined as greater than the range $\text{mean} \pm 4 \times \text{SD}$ for the single phenotypes. Outliers were set missing. Data is corrected for heterogeneous variance within breed, herd, year, CFITversion and parity (first or later).

Genetic evaluation

Genetic evaluation is run separately for each breed. The model is similar for all breeds. Parameters are estimated breed-wise, but HOL parameters are used for RDC evaluation.

Model

DMI, ECM, and BW were analyzed using breed-specific two-trait random regression models where primiparous and multiparous lactations were treated different traits:

$$y = Xb + Za + Wpe + Mp + e,$$

where y is a vector of phenotypes for DMI, ECM, or BW across the two parity groups (primiparous or multiparous) and weeks in lactation (week 0-45); b is a vector of fixed effects for age at first calving (only primiparous), parity (only multiparous), calving herd \times calving year \times calving season, the regression on lactation curve (5th order Legendre polynomial terms nested within herd); a is a vector of additive genetic random regression coefficients (Legendre polynomials: intercept, linear); pe is a vector of permanent environmental random regression coefficients (Legendre polynomials: intercept, linear, quadratic); p is a vector of random effects for animal \times parity (only multiparous); e is a vector of residuals nested within trait; and X , Z , W , and M are design matrices.

The estimated (co)variance components were used to predict lactation-wise genomic breeding values for DMI, ECM and BW using similar singlestep setup as for other singlestep traits.

For Saved feed a polygenic effect on 0.30 is used and a genotype cut on birthday 01.01.2009.

Genetic parameters

Lactation-wise (2 to 44 weeks in milk) heritabilities (Table 14.2) is moderate for DMI and ECM and high for BW

Table 14.2. Heritabilities for DMI, ECM and BW on breed level.

	ECM 1.	ECM 2+	DMI 1.	DMI 2+	BW 1.	BW 2+
HOL & RDC	0.50	0.48	0.43	0.49	0.52	0.58
JER	0.47	0.52	0.22	0.50	0.46	0.61

The genetic correlations between parity groups is high for DMI (HOL: 0.90; JER: 0.82), high for ECM (HOL: 0.89; JER: 0.94), and high for BW (HOL: 0.95; JER: 0.90).

The genomic breeding values for BW change (ΔBW) is derived from the BW model as the difference between GEBVs at day 30 in milk and day 280 in milk. We used the GEBVs of the traits to calculate breeding values for Saved Feed within each combination of parity group and breed:

$$GEBV_{\text{Saved Feed}} = 0.40 \times GEBV_{\text{ECM}} + 4.0 \times GEBV_{\Delta BW} - GEBV_{\text{DMI}}$$

Parity-specific $GEBV_{\text{Saved Feed}}$ values were weighted with 1/3 emphasis on primiparous lactation and 2/3 emphasis on multiparous lactations. The breeding values for Saved Feed is standardized to have a mean of 100 and a standard deviation (SD) of 10 for base animals, defined as three to five years old (rolling base) cows with phenotypes.

References

15. Maintenance efficiency

The index for Maintenance was earlier a part of the Saved feed index together with metabolic efficiency (phenotypic RFI). The Maintenance efficiency index is no longer included in the saved feed index and the Maintenance efficiency index is thus no longer a part of NTM. However, it is still published as an information trait. The maintenance index is not a singlestep index.

Data

Trait definition

In the evaluation for Maintenance the following traits (Table 15.1) are considered for cows in the first to third lactations.

Table 15.1. Abbreviations and definitions of traits included in the evaluation of Maintenance.

Abbreviation	Definition
MBW	Metabolic Body Weight ($BW^{0.75}$), measured in 1 st to 3 rd parity by scale or tape
STA	Stature height in 1 st parity, used from the conformation evaluation
BD	Body depth in 1 st parity, used from the conformation evaluation
CW	Chest width in 1 st parity, used from the conformation evaluation

Basic editing rules

The body weight (BW) data are from 1990 in Finland (primarily tape) and 2007 in Denmark (only scale) for all breeds. For conformation traits (STA, BD and CW) - 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

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

Pre-corrections

Single MBW observations that come 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):

$$w_{ij} = \frac{1}{\left(r_{jk} + \frac{1-r_{jk}}{n_{ij}}\right)^{-S_k}},$$

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):

Model

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 x 5-year period	Fixed
Age at 1 st calving	Regression
Herd x 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.

Genetic parameters

The genetic parameters used for the Maintenance traits in the evaluation are shown in Table 15.2 – 15.3.

Table 15.2. 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 15.3. 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

Index

A combined maintenance index is calculated, based on the EBVs from the first three parities (Table 15.4)

Table 15.4. Calculation of the MBW index.

MBW123		$0.30 \times \text{MBW1} + 0.25 \times \text{MBW2} + 0.45 \times \text{MBW3}$
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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>

16. Methane

The index for methane describes the genetic ability of the bulls' offspring to emit methane, that originates from enteric fermentation of fiber in the rumen. Bulls with high indices for methane produce offspring with a lower production of methane.

Data

Trait definition

The phenotype for methane is daily methane concentrations (MeC, in parts per million (ppm)), recorded by sniffers, i.e., non-invasive measurement devices installed in the feeding bins of automated milking systems (AMS). Daily records are obtained by averaging the MeC during a specific visit in the AMS and subsequently averaging the MeC over all visits to the same AMS on the given day. If cows are accessing different AMS on a given day, a phenotype for each accessed AMS is calculated. The measured MeC are corrected for daily variation, background MeC and head-lifting. A description of these corrections can be found in Løvendahl et al. (2024). MeC records are separated in two traits, one for cows in 1st parity (MeC1) and one for cows in 2nd to 5th parities (MeC2).

Basic editing rules

Only sniffer data from Denmark recorded after 01.01.2020 is used in the evaluation.

MeC records are included if:

- Recorded between 0 and 365 days in milk,
- Cows are not fed with methane-mitigating feed additives, such as Bovaer®
- Parity 1 to 5
- Below 10,000 ppm. Sniffers are calibrated for a measuring range between 0 and 10,000 ppm. Values above 1,000 ppm are set to 1,000 ppm due to a long tail of extreme values.

Genetic evaluation

Evaluations are carried out for Holstein AI bulls.

Model

The model for estimation of breeding values is a single-step multi-trait repeatability animal model with MeC1 and MeC2 as separate traits.

Herd-year-season of measuring day x AMS x sniffer unit	Fixed
Week in milk	Fixed
Calving year × calving month	Fixed
Age of calving	Fixed (only for MeC1)
Parity number	Fixed (only for MeC2)
Permanent environment	Random
Animal	Random

A polygenic effect of 0.30 is used and genotypes are cut on birthday 01.01.2009.

Genetic groups (phantom parent groups)

Genetic groups are created for unknown parents according to birth year.

Genetic parameters

The genetic parameters for MeC1 and MeC2 used in the evaluation for Holstein are presented in Table 16.1. The genetic correlation between MeC1 and MeC2 is 0.92.

Table 16.1. Genetic (gen.), permanent environmental (pe.) and residual (res.) variances (var.), heritabilities and repeatabilities for methane concentrations in first (MeC1) and higher parities (MeC2).

Trait	Gen. var.	Pe. Var.	Res. var.	Heritability	Repeatability
MeC1	3,004	4,205	16,614	0.13	0.41
MeC2	6,466	4,694	22,936	0.19	0.51

Index

The index for methane is based on sub-indices for MeC1 and MeC2. The standardization of the relative breeding values is described in the chapter “Standardization of EBVs and NTM”. For the ease of interpretation, breeding values are multiplied with -1, which means that higher breeding values are favorable, i.e. they indicate lower methane production.

The methane index (MeC) is calculated based on the standardized EBVs for MeC1 and MeC2:

$$\text{MeC} = (\text{MeC1} * 1 + \text{MeC2} * 2)/3$$

The methane index is published for Holstein AI-bulls born after 2008 with a genomic test in the Nordic system and paid Nordic fee or official NTM and minimum of 10 daughters with methane observations.

Difference between the 10% best and worst cows with EBV

Phenotypic differences between the best and worst 10% cows with phenotypes according to their EBV can be found in Table 16.2. The difference indicates that selecting bulls with higher breeding values results in offsprings with a lower methane production.

Table 16.2. Mean methane production (in ppm) and breeding value for the 10% best and worst cows with phenotypes.

	Mean MeC1	Mean EBV MeC1	Mean MeC2	Mean EBV MeC2
10% best	284	120	257	120
10% worst	536	70	612	81

References

Løvendahl, P., V. Milkevych, R. K. Nielsen, M. Bjerring, C. Manzanilla-Pech, K. Johansen, G. F. Difford, and T. M. Villumsen. 2024. A data-driven approach to the processing of sniffer-based gas emissions data from dairy cattle. *Comput. Electron. Agric.* 227:, 109559.

17. 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:

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

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.

18. 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 18.1 shows traits that are evaluated.

Table 18.1. Traits in genetic evaluation for DxD crossbreds.

Main trait group	Chosen sub-trait
Yield	Milk, fat, and protein
Growth	Carcass classification score
Fertility	1 st to last insemination, cows
Birth	Calf survival, 1 st calving
Calving	Calf survival, 1 st calving
Udder health	Clinical mastitis 2 nd 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:

$$GEBV_{BOM,i} = \sum_{b=1}^{N_b} (v'_b(w_{i,1} \circ s_{1,i,b}) + v'_b(w_{i,2} \circ s_{2,i,b})) + \mu_b \frac{\sum s_{1,i,b} + \sum s_{2,i,b}}{2m} + a_i$$

Where:

- $w_{i,j}$ contains haplotype j coded as 0 and 1 for the alternative alleles
- v_b is a vector of marker effects for breed b
- \circ is element wise multiplication

- $s_{j,i,b}$ 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
- μ_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 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, μ_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 18.2 the breed differences used in the genomic prediction of crossbred animals is shown.

Table 18.2. 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
1 st to last insemination, cows	Days	-3,3	-12,5
Calf survival, 1 st calving (direct)	0/1	0,55	1,07
Calf survival, 1 st calving (maternal)	0/1	0,61	1,07
Clinical mastitis 2 nd 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.

$$\text{Index} = 100 + s \times \sum_{i=1}^n k_i \times (\text{PD_LIN}_i \div \text{OPTIMUM}_i)$$

Where:

- PD_LIN_i = predicted value of future offspring for the i^{th} trait included in the index
- 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 18.3.

Table 18.3. Optimum and weight factors for cross bred cows.

	Optimum	Weight factors
Stature	155	5
Body depth	9	25
Chest width	9	30
Rib structure	9	20
Top line	7	-
Rump width	9	20
Rump angle	5	-
Rear legs, side view	5	10
Rear legs, back rear view	8	30
Hock quality	9	18
Bone quality	8	17
Foot angle	6.5	25
Fore udder attachment	9	20
Rear udder height	9	10
Rear udder width	9	-
Udder cleft/support	8	20
Udder depth	9	25
Udder balance	5	-10
Teat length	5.5	-
Teat thickness	5	-
Teat placement (front)	8	-
Teat placement (back)	5	-15

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 18.4.

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

Where:

- Breeding value_i = Breeding value of the ith trait
- Weight factor_i = The weight factor for the ith trait

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

Table 18.4. 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-baser

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 = $0.30 \times \text{EBV kg milk 1}^{\text{st}} \text{ lact.} + 0.25 \times \text{EBV kg milk 2}^{\text{nd}} \text{ lact.} + 0.45 \times \text{EBV kg milk 3}^{\text{rd}} \text{ lact.}$

EBV kg prot. total = $0.30 \times \text{EBV kg prot. 1}^{\text{st}} \text{ lact.} + 0.25 \times \text{EBV kg prot. 2}^{\text{nd}} \text{ lact.} + 0.45 \times \text{EBV kg prot. 3}^{\text{rd}} \text{ lact.}$

EBV kg fat total = $0.30 \times \text{EBV kg fat 1}^{\text{st}} \text{ lact.} + 0.25 \times \text{EBV kg fat 2}^{\text{nd}} \text{ lact.} + 0.45 \times \text{EBV kg fat 3}^{\text{rd}} \text{ lact.}$

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 1 st , (kg)	490.1	436.8	296.6
Milk 2 nd , (kg)	556.0	525.8	359.0
Milk 3 rd , (kg)	504.0	557.6	353.1
Protein 1 st , (kg)	18.16	17.03	13.45
Protein 2 nd , (kg)	20.92	21.24	16.45
Protein 3 rd , (kg)	19.65	22.28	16.60
Fat 1 st , (kg)	18.31	16.05	15.24
Fat 2 nd , (kg)	20.34	20.86	18.22
Fat 3 rd , (kg)	18.90	22.09	15.12
Pct protein 1 st	0.02	0.03	0.03
Pct protein 2 nd	0.02	0.03	0.03
Pct protein 3 rd	0.03	0.04	0.04
Pct fat 1 st	-0.03	-0.03	-0.05
Pct fat 2 nd	-0.03	-0.02	-0.05
Pct fat 3 rd	-0.02	-0.02	-0.09
Persistence 1 st	-8.4	0.4	30.3
Persistence 2 nd	5.1	24.7	18.6
Persistence 3 rd	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 1 st , (kg)	1188.5	969.7	830.5
Milk 2 nd , (kg)	1309.2	1088.4	872.7
Milk 3 rd , (kg)	1163.5	1131.6	879.2
Protein 1 st , (kg)	41.54	37.33	31.09
Protein 2 nd , (kg)	46.39	43.60	33.71
Protein 3 rd , (kg)	42.73	44.84	34.36
Fat 1 st , (kg)	37.66	36.32	36.42
Fat 2 nd , (kg)	40.36	42.94	37.93
Fat 3 rd , (kg)	36.33	44.73	32.32
Pct protein 1 st	0.02	0.05	-0.06
Pct protein 2 nd	0.02	0.07	-0.04
Pct protein 3 rd	0.04	0.07	-0.03
Pct fat 1 st	-0.17	-0.07	-0.28
Pct fat 2 nd	-0.17	-0.04	-0.26
Pct fat 3 rd	-0.14	-0.04	-0.34
Persistence 1 st	-4.2	-34.0	34.6
Persistence 2 nd	22.9	-34.4	8.5
Persistence 3 rd	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.