Nordic Cattle Genetic Evaluation

NAV routine genetic evaluation of Dairy Cattle

– data and genetic models

NAV

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5th edition

Genetic evaluation within NAV

Introduction

Breeding values for dairy cattle breeds in Denmark, Sweden and Finland are calculated jointly by NAV (Nordic Cattle Genetic Evaluation), which is owned by SEGES, Växa Sverige and FABA Co-op.

This cooperation and joint evaluation makes it possible to compare animals across our countries and thus make efficient use of economic resources. Genetic evaluation is performed for a wide variety of important traits. Further, 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 on registration, documentation, calculations, etc. Genetic models are also 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 in all breeds and the Nordic countries are able to 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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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 benefits to the farmer, and the use of sires with high NTM will give offspring of higher economic value.

Traits included in NTM

The traits going into NTM are:

- Yield
- Growth
- Fertility
- Calving$^{\text{direct}}$
- Calving$^{\text{maternal}}$
- Udder health
- General health
- Claw health
- Feet and legs
- Udder
- Milkability
- Temperament
- Longevity
- Youngstock survival

The traits are weighted together on the basis of economic values quantifying the value of a marginal change in the trait. The economic weights are breed specific.

Economic value of sub-indexes

The present economic values are based on the economic situation in the first part of 2007. This is done by using the most recent prices and costs and with prediction for the coming 10 years. It is possible to give the best prediction as to economic outcomes in the future.

The economic values calculated are marginal economic values, i.e. values of one unit improvement in the trait when the remaining traits are held constant. Thus the value of, for example, milk protein is calculated as the economic profit secured by improving the yield with one kg of milk protein with all other traits being held constant.

Some important considerations bearing on the calculation of economic weights for the different traits are explained below.

Yield

Milk production at herd level is estimated from lactation yield and the herd structure, including distribution at different lactations, and the number of days in lactation for culled cows. Further information on the sale 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 bear 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 consequences of fertility are mostly due to changes in calving interval, since this has an effect on annual production per cow. They are also affected by the cost of AI, and the work it involves, and to the cost of any work involved in heat detection.

There is an important relationship between fertility and yield. Fertility has an impact on yield through the effect of pregnancy. The basic assumptions portray the average number of dry days as longer than the recommended 45-50 days. Therefore it is assumed that a shorter calving interval will reduce the average number of dry days but not the average days in milk.

Calving traits

The cost of stillbirth is mostly lost income connected with the raising of heifers and bull calves, but it also arises from extra work and the cost of destruction. The cost of calving difficulty mostly arises from extra work and veterinary fees; it does not reflect subsequent complications, however, since these are taken into account in the group of “general health”.

Generally, for all countries and breeds, it is assumed that a stillborn calf will require extra work of 0.25 hours. In Finland an extra 0.5 hours is added because it is common practice to bury stillborn calves.

When the percentage of difficult calvings is changed, a proportional change in the percentage of difficult calvings with, and without, a veterinary assistance is assumed. It is assumed that 20% of difficult calvings with veterinary assistance require caesarean or dissections (at higher cost).

The same figure is used across countries and breeds. A “normal” difficult calving requires 90 minutes extra work by the herdsmen. Caesareans and dissections require an extra 3.0 hours’ work by the herdsmen. Besides this, it is assumed that an easy calving **with help** requires 12 minutes extra as compared with an easy calving **without help**.

Udder health

The costs of poor udder health (mastitis) arise from veterinarian treatments, extra work done by the herdsman, and the amount of milk that is discarded following treatment of the udder with antibiotics etc. In the economic evaluation of udder health the important factor is the total number of cases, not the occurrence measured as a binary trait. Therefore the relationship between these two figures must be known. The input to the calculation is the average of the traits evaluated and the corresponding total number of cases. It is assumed that a change in the evaluated trait will change the total number of cases proportionately.

General health

Calculations within groups follow the same principles as those described for mastitis above.

Claw health

Costs associated with extra time used for trimming and extra visits caused by disease are included. Further extra work by herdsman and costs for medication and bandages etc. are also included.

Conformation and workability traits

The setup for this trait group is somewhat different from that used with the other trait groups. The traits analysed here – Body, Feet&Legs and Udder – are composite phenotypes. The basic economic assumptions are shaped by a (subjective) assessment of the extra workload when conformation is not optimal in an average herd. In the original Danish setup, this was done by subjective assessment of a herd of 70 milking cows.

- Body: There was no impact on workload when all the traits included in Body were linearly scored at 1 point away from the optimum.
- Udder: When all the traits included in Udder were linearly scored at 1 point away from the optimum, the extra workload was assessed as being 15 minutes per day (91 hours per year).
- Feet&Legs: When all traits included in Feet&Legs were linearly scored at 1 point away from the optimum, the extra workload was assessed as being 10 minutes per day (61 hours per year).

With the two farmer-evaluated 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; and that when the Temperament of all cows was 1 unit lower, the extra workload would be 5 minutes per day.

Longevity

The value of longevity is measured in variation 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 number of calvings per year. It is well known that the breeding value of longevity is heavily influenced by fertility, udder health and general health, and to some degree of conformation of udder and feet and legs. Therefore, as much value as possible is transferred from longevity to the other trait in NTM. This transfer is based on analyses of the relationship between longevity and the other trait in NTM.

Youngstock Survival

The direct economic effect of increased survival of young stock is increased income due more heifers and more bull calves available for sale (export) or slaughter. Higher mortality are related to extra costs for destruction of dead calves, feeding of calves and extra work

Economic weights in NTM

The calculated economic values, displayed in table 1, represent the basis for formulating the breeding goal. However, these figures only take present economic values into account. Therefore, the economic values actually used in the Nordic countries are modified according to the farmer's expectations about evolving production circumstances, animal welfare, ethical views and environmental considerations.

Table 1. NAV-TMI economic values for the Holstein, RDC and Jersey

Trait	**Unit**	**EURO per unit**		
		Holstein	**RDC**	**Jersey**
MILK PRODUCTION				
Milk	Kg	-0.030	-0.029	-0.046
Fat	Kg	1.28	1.33	1.55
Protein	Kg	4.60	4.81	4.15
Standard milk	Kg	0.181	0.190	0.16
BEEF PRODUCTION				
Net daily gain	Kg/day	201.3	222.8	45.6
EUROP form score	Score	13.8	13.6	10.1
CALVING TRAITS				
%stillborn, 1st	%-units	2.0	2.01	0.79
Easy calving, 1st	4 point scale	11.0	11.35	15.7
%stillborn, later	%-units	3.3	3.37	1.46
Easy calving, later	4 point scale	14.9	15.62	33.7
FEMALE FERTILITY				
Heifer – first to last	Day	0.73	0.61	0.93
Cow – calv. To first	Day	0.62	0.56	0.28
Cow - first to last	Day	2.35	1.78	1.61
Heifer - no. of ins.	AIS	10.17	10.14	9.27
Cow – no. of ins.	AIS	35.55	27.24	27.14
MASTITIS**				
Mastitis, 1st	%-units	1.50	1.46	1.35
Mastitis, 2nd	%-units	1.13	1.05	1.01
Mastitis, 3rd+	%-units	1.44	1.49	1.75
Mastitis, all lact.	%-units	4.07	4.00	4.11
GENERAL HEALTH**				
Metabolic	%-units	1.88	1.87	1.70
Feet and legs	%-units	1.75	1.70	1.69
Early reproductive	%-units	2.00	1.93	1.91
Late reproductive	%-units	1.05	1.04	0.94
Youngstock survival				
Survival heifers 1-30 days	%-units	344.5	355.0	200.4
Survival heifers 31-458 days	%-units	405.0	415.1	240.6
Survival bulls 1-30 days	%-units	128.8	143.1	27.2
Survival bulls 31-184 days	%-units	179.3	202.1	79.1

Claw health				
Sole ulcer	Point	64.91	65.23	66.43
Sole Hemorrhage	Point	8.67	8.71	9.00
Heel Horn Erosion	Point	13.98	14.05	14.52
Digital Dermatitis	Point	13.98	14.05	14.52
Int. Dig. Hyperplasia	Point	25.56	25.68	24.14
White Line disease	Point	8.67	8.71	9.00
Cork Screw claws	Point	8.67	9.73	12.81
LONGEVITY				
Average, culling	Day	0.51	0.38	0.40
CONFORMATION				
Frame	Point	0.0	0.0	0.0
Udder	Point	25.6	25.5	25.6
Feet and legs	Point	17.0	17.0	17.0
Milkability	Point	17.0	17.0	17.0
Temperament	Point	8.5	8.5	8.5

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

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

Calculation of NTM

NTM is calculated on the basis of the relative breeding values for the traits in question. The modified economic weights are translated into an economic value for each unit in the breeding values for each individual trait. 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 and fertility/health are calculated using within-trait group models. This means that any genetic correlations between the trait groups are not taken into account. This has no significance for bulls with many offspring/cows with genomic test, because their EBVs have high reliabilities for all traits. Cows without a genomic test have EBV's for fertility/health with low reliability. Therefore weight factor for yield is reduced because cows with high genetic merit for yield often have genetic merit for fertility that is lower than reflected by their EBV's.

NTM is calculated as shown in the formulas below. The weights used on each standardized sub-trait are shown in table 2.

Sires and cows:

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

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. The standardization of the indexes in NTM is described in the chapter “Standardization of EBVs and NTM”.

Heifers:

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

Table 2. Weight factors for dairy breeds

	Holstein	RDC	Jersey
Yield index[1]	0.75/0.68	1.00/0.91	0.87/0.78
Growth	0.06	-	-
Fertility	0.31	0.24	0.20
Calving^{direct}	0.15	0.13	0.06
Calving^{maternal}	0.17	0.11	0.06
Udder health	0.35	0.30	0.44
General health	0.11	0.11	0.04
Claw health	0.08	0.05	0.05
Frame	-	-	-
Feet and legs	0.12	0.12	0.04
Udder	0.25	0.35	0.26
Milkability	0.08	0.09	0.10
Temperament	0.03	0.03	0.03
Longevity	0.11	0.07	0.12
Youngstock Survival	0.14	0.22	0.12

[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-indexes

The expected progress of each index when NTM is selected for, expressed as a percentage of maximum progress for that index, is shown in table 3. Maximum progress is obtained if selection is based solely on the trait in question.

Table 3. Correlation between NTM and traits in NTM

	Holstein	RDC	Jersey
Yield index	0.48	0.63	0.55
Growth	0.10	0.02	0.20
Fertility	0.43	0.22	0.32
Calving^{direct}	0.35	0.25	0.14
Calving^{maternal}	0.30	0.22	0.38
Udder health	0.42	0.27	0.56
General health	0.45	0.15	0.18
Claw health	0.36	0.05	0.10
Frame	-0.10	0.00	0.18
Feet and legs	0.19	0.33	0.12
Udder	0.14	0.26	0.30
Milkability	0.02	0.16	0.17
Temperament	0.00	0.04	0.07
Longevity	0.61	0.49	0.62
Youngstock Survival	0.27	0.26	0.36

References

http://www.nordicebv.info/wp-content/uploads/2015/05/Report-on-Economic-basis-for-a-Nordic-Total-Merit-Index_short.pdf

http://www.nordicebv.info/wp-content/uploads/2015/05/Report-on-Economic-Basis-for-a-Nordic-Total-Merit-Index.pdf

Genomic Prediction

Genomic evaluation is performed monthly for females and young AI bulls. A 2-step method is used.

Trait groups evaluated

Genomically enhanced breeding values (GEBV) are calculated for yield, conformation, udder health, general health, youngstock survival (not Jersey), longevity, calving, fertility, claw health (not Jersey), milkability and temperament.

Reference population

Reference populations for all three breeds consist of proven bulls and females for yield, conformation, udder health, milking speed and temperament (only Holstein). For the remaining traits groups only bulls are included in the reference population

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

Proven bulls are bulls that are genotyped and have reliability above a certain threshold based on Danish, Swedish and Finnish daughters. Furthermore the reference groups also include foreign bulls that have Interbull proof 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 1. Number of males and females in reference population (September 2016)

	Bulls	Cows
RDC	7.900	24.800
Holstein	21.100	32.900
Jersey	2.500	16.600

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

SNP-chips and imputation

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

Genetic evaluation

The "phenotypic" information used in the genetic evaluation is deregressed EBVs from Nordic traditional genetic evaluation. In traditional evaluation only phenotypes are included. Deregressed proofs are updated 4 times a year. Furthermore, Interbull proofs on Nordic scale are used as "phenotypic" information for foreign bulls without an official Nordic EBVs.

The SNP-model used is a linear model with 10% polygenic effect.

Standard deviation of GEBV is scaled so to ensure that genetic STD for EBV and GEBV are the same.

Reliability

Reliability is calculated as described in Strandén and Christensen (2011).

Publication

GEBV's are published for all genotyped females and AI-bulls which is older than 10 month of age.

Reference

Lund et al. Genetics Selection Evolution 2011, 43:43 A common reference population from four European Holstein populations increases reliability of genomic predictions
Strandén, I and O. F. Christensen. 2011. Allele coding in genomic evaluation. Gen. Sel. Evol. 42:25.
M. Taskinen et al. 2013. Comparison of model reliabilities from single-step and bivariate blending methods. Interbull Bull. 47:246-251, Nantes, France
M. Taskinen et al. (2014). Comparison of breeding values form single-step and bivariate blending methods. World Congress on Genetics Applied to Livestock Production, August 1-6 2014, Vancouver, Canada

Yield

Indexes for yield describe the genetic potential for milk, protein and fat production. They also describe the genetic level of protein and fat content in milk and persistence of lactation curve.

Data

Trait definition

The breeding values for milk production, protein and fat are based on production figures expressed in kilograms taken from milk records. The indices for protein and fat content are estimated from milk, protein and fat yield. The estimated genetic lactation curve is used to calculate a breeding value for persistency.

Basic editing rules

Data included are test-day records from day 8 to day 365 of lactation:

- 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 Holsteins and Jerseys using a modified version of a method described in Interbull Bulletin no. 11 (1995). The latest estimates of breeding values (EBV) calculated by Interbull are used for bulls. Where cows are concerned, the foreign national EBVs are transformed to the Nordic scale by means of a and b values recommended by Interbull.

Genetic evaluation

Separate evaluations are undertaken 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 with both Holstein and Ayrshire cows in Finland. To estimate a more accurate herd effect the Finnish Holstein animals are included in the RDC evaluations and Finnish Ayrshire and Finncattle are included in the Holstein evaluation.

Model

A random regression test-day model is used. This system has the following features:

- Multi-lactation multi-trait model for milk, protein and fat traits
- From Finland, lactations 4-10 are considered as repeated measurement 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 taken into account

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 red breed group includes a large number of sub-breeds (e.g. American Brown Swiss, Red Holstein, Norwegian Red, and Canadian Ayrshire). Therefore, the modelling of heterosis and age effects is more complicated in the red breed group than in the Holstein and the Jersey group.

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

Herd test-day

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

Lactation curves

In order to make test-day records comparable within lactation it is necessary to take into account the shape of the lactation curve. Such curves differ depending on the year, season and, for first parity cows, also age. For each trait we estimate lactations curves for:

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

These lactation curves are constant across herds. To reflect the fact that the shape of lactation curves differ from herd to herd, a modification is included. The herd dependent modification is merely a 3-parameter linear regression on days in milk (DIM) within 5-year herd periods.

Calving age

Calving age is a well-known fixed effect in evaluation for yield. In general, the effect of age is modelled by monthly age classes within. However, in the red breed group it turned out that age had a different effect on yield for the various sub-breeds. 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 introduced in the test-day model by including effect of days pregnant. Ten day classes in the period 120 – 240 days of pregnancy are used. Beyond that, own groups for less than 120 days and more than 240 days pregnancy were included.

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 are calculated by two methods:

- Exact dry 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 taken into account 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 x Holstein Friesian
- Original Danish Red & White x Holstein Friesian (mostly Red Holstein Friesian)
- Holstein x FAY (only the Finnish part of data)
- With FAY-heterosis (only the Finnish part of data)

Jersey

- Original Danish Jersey x US Jersey
- Original Danish Jersey x New Zealand Jersey

In the red 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 x Swedish Red and White

- Finnish Ayrshire x Canadian Ayrshire
- Finnish Ayrshire x Holstein (all sub-breeds)

Swedish data

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

Danish data

- Red Danish Cattle x American Brown Swiss
- Red Danish Cattle x Holstein (all sub-breeds)
- Red Danish Cattle x (Swedish Red and White + Finnish Ayrshire + Norwegian Red)
- American Brown Swiss x Holstein (all sub-breeds)
- American Brown Swiss x (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 are taken into account using the concept of phantom parent grouping. It turned out that the estimates of genetic group effects became more stable when they were assumed to be random effects.

Heterogenic variance (HV) correction

In the evaluation of breeding values for milk production traits it is very important to take into account the fact that variance has increased over time. In the selection of cows especially, it is also important to take into account the possibility that the variation is very different in different herds.

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:

- Estimates of herd x year variance
- Definition of base year. All variances are adjusted to variance of the base year. The base year is cows born 01.01.2001-20.6.2003
- "Rho"-factors that determine the relationship between variances on subsequent test-days
- Base variances. These values retain the relationship between environmental variances between countries (which is necessary because environmental parameters differ between countries).

Permanent environmental effects within lactations

There are two types of permanent environmental effect. For all countries, they are estimated within lactation to describe the overall environment in a single lactation. From Finnish data, the environmental effects across 3rd and later lactations are 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 genetic evaluation each animal is given an individual genetic lactation curve for milk, protein and fat yield. This lactation curve simply consists 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 added together.

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

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

EBV for fat yield is calculated in similar manner.

Genetic parameters are shown in table 1 - 3.

Table 1. Genetic parameters for Red Dairy Cattle in Nordic test-day model summarized for 305 days and based on 10 test-days. Heritability's on diagonal and genetic correlations above diagonal, phenotypic correlations below diagonal

	1st lactation			2nd lactation			3rd lactation		
	M	P	F	M	P	F	M	P	F
M1	**0,41**	*0,86*	*0,62*	*0,91*	*0,79*	*0,53*	*0,87*	*0,73*	*0,45*
P1	0,92	**0,35**	*0,78*	*0,76*	*0,91*	*0,69*	*0,73*	*0,86*	*0,63*
F1	0,80	0,87	**0,41**	*0,52*	*0,76*	*0,93*	*0,52*	*0,74*	*0,91*
M2	0,54	0,49	0,41	**0,24**	*0,80*	*0,51*	*0,95*	*0,75*	*0,44*
P2	0,49	0,52	0,48	0,93	**0,21**	*0,77*	*0,77*	*0,97*	*0,72*
F2	0,42	0,47	0,55	0,84	0,90	**0,28**	*0,52*	*0,75*	*0,99*
M3	0,48	0,44	0,37	0,53	0,51	0,44	**0,20**	*0,80*	*0,48*
P3	0,43	0,47	0,43	0,49	0,56	0,51	0,91	**0,19**	*0,73*
F3	0,36	0,42	0,51	0,42	0,50	0,57	0,84	0,87	**0,25**

Table 2. Genetic parameters for Holstein in Nordic test-day model summarized for 305 days and based on 10 test-days. Heritability's on diagonal and genetic correlations above diagonal, phenotypic correlations below diagonal

	1st lactation			2nd lactation			3rd lactation		
	M	P	F	M	P	F	M	P	F
M1	**0,43**	*0,86*	*0,46*	*0,85*	*0,71*	*0,23*	*0,81*	*0,63*	*0,10*
P1	0,92	**0,35**	*0,67*	*0,75*	*0,84*	*0,46*	*0,72*	*0,81*	*0,33*
F1	0,75	0,85	**0,36**	*0,42*	*0,68*	*0,85*	*0,43*	*0,70*	*0,78*
M2	0,52	0,48	0,37	**0,29**	*0,84*	*0,42*	*0,99*	*0,78*	*0,32*
P2	0,46	0,50	0,45	0,94	**0,25**	*0,72*	*0,84*	*0,99*	*0,62*
F2	0,31	0,39	0,51	0,79	0,88	**0,29**	*0,47*	*0,76*	*0,98*
M3	0,47	0,43	0,34	0,49	0,44	0,34	**0,27**	*0,79*	*0,37*
P3	0,41	0,46	0,42	0,42	0,47	0,41	0,92	**0,25**	*0,69*
F3	0,22	0,31	0,45	0,30	0,39	0,49	0,79	0,86	**0,29**

Table 3. Genetic parameters for Jerseys in Nordic test-day model summarized for 305 days and based on 10 test-days. Heritability's on diagonal and genetic correlations above diagonal, phenotypic correlations below diagonal

	1st lactation			2nd lactation			3rd lactation		
	M	P	F	M	P	F	M	P	F
M1	**0,44**	*0,91*	*0,74*	*0,88*	*0,84*	*0,49*	*0,90*	*0,84*	*0,49*
P1	0,95	**0,38**	*0,86*	*0,78*	*0,90*	*0,65*	*0,81*	*0,91*	*0,66*
F1	0,87	0,92	**0,35**	*0,65*	*0,83*	*0,86*	*0,67*	*0,83*	*0,86*
M2	0,56	0,52	0,46	**0,27**	*0,86*	*0,57*	*0,99*	*0,86*	*0,53*
P2	0,53	0,54	0,51	0,95	**0,23**	*0,80*	*0,88*	*0,99*	*0,78*
F2	0,41	0,46	0,51	0,87	0,93	**0,22**	*0,58*	*0,79*	*0,99*
M3	0,50	0,46	0,40	0,55	0,51	0,43	**0,27**	*0,88*	*0,55*
P3	0,46	0,48	0,44	0,51	0,54	0,48	0,95	**0,23**	*0,77*
F3	0,34	0,39	0,44	0,41	0,47	0,51	0,86	0,92	**0,23**

Indexes

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

The EBV's are combined over lactations. Standardized milk, fat and protein indexes are combined in the total yield index by means of weight factors based on economic calculations (table 4).

Table 4. Calculation of yield indexes. Subscript of RBV refers to lactation

Breed	Index	Combined index
All	Milk	$0.5*RBV_{milk1}+0.3*RBV_{milk2}+0.2*RBV_{milk3}$
All	Fat	$0.5*RBV_{fat1}+0.3*RBV_{fat2}+0.2*RBV_{fat3}$
All	Protein	$0.5*RBV_{protein1}+0.3*RBV_{protein2}+0.2*RBV_{protein3}$
RDC	Yield	-0.20*milk index+0.40*fat index+0.8*protein index
HOL	Yield	-0.20*milk index+0.40*fat index+0.8*protein index
JER	Yield	-0.30*milk index+0.50*fat index+0.8*protein index

The following relative indexes 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, calculated on the basis of the breeds breeding goal for yield

Further EBV's on a fixed base is 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 5. Maximum progress is obtained if selection is based solely on the trait in question.

Table 5. Correlation between yield index and indexes for milk, fat and protein

Index	RDC	HOL	JER
Milk	0.76	0.59	0.64
Fat	0.84	0.87	0.92
Protein	0.98	0.93	0.93

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 effect of specific bulls can be calculated. For yield traits it is breeding values for milk, fat and protein that are presented as kg milk, fat and protein.

Relative breeding values for persistence

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 onwards and over the next 200 days. The loss (or gain) in milk is calculated by taking the animal's breeding value for day 100 and then multiplying that 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 value derived, the more persistent is the lactation curve the animal has.

Relative breeding values are calculated as:

$EBV_{percistency} = EBV_{day101} * 200 - EBV_{d101-d300}$, where

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

The persistency EBVs for traits and lactations are then standardized by the same procedure as was used for 305-day yield. Relative breeding values per trait across lactations are calculated using the lactation weights 0.5, 0.3 and 0.2 for the 1st, 2nd and 3rd lactation, respectively.

Relative breeding values for protein and fat percentage

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

- EBVs per trait and lactation
- RBVs per trait and lactation are found by standardization to a common base and standard deviation
- Across lactation RBVs are calculated using lactation weights 0.5, 0.3 and 0.2 for 1st, 2nd and 3rd lactation, respectively.

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

References

Lidauer, M., J. Pedersen, J. Pösö, E. A. Mäntysaari, I. Strandén, P. Madsen, U.S. Nielsen, J.-Å. Eriksson, K. Johansson, G.P. Aamand: Joint Nordic Test Day Model: Evaluation Model. Interbull Open Meeting, Kuopio, Finland, June 4th – 6th, 2006.

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Pösö, J., J. Pedersen, M. Lidauer, E. A. Mäntysaari, I. Strandén, P. Madsen, U.S. Nielsen, J.-Å. Eriksson, K. Johansson, G.P. Aamand: Joint Nordic Test Day Model: Experiences with the New Model. Interbull Open Meeting, Kuopio, Finland, June 4th – 6th, 2006.

Growth

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

Data

Trait definition

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.

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 1. Abbreviations and definitions of traits included

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 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 more than 90 days in the herd before slaughter (only Denmark)
- Slaughter age is within 200-550 days (Jersey)
- Slaughter age within 200-900 days (other breeds)

Pre-corrections

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

Genetic evaluation

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

Model

The model for estimation of breeding values is a multiple 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

Heterosis

For RDC, effects of original Red Danish Cattle (RDM), Original Danish Black & White (SDM), Finnish Ayrshire (FAY), Norwegian Red (NRF), American Brown Swiss (ABK), American Holstein (HOL), Swedish Red Cattle (SRB), Canadian Ayrshire (CAY) and Finncattle (FIC), were accounted for by regressions on population proportions. For the Nordic Holstein population, the effect of Holstein versus Friesian was accounted for by regression on the population proportion. Heterosis is accounted for using the regression on expected total heterosis.

For Jerseys there are few records of CGL. Jersey evaluation contained information from Denmark and Sweden and only the CGS, CS and FS traits.

Genetic parameters

The genetic parameters used for the 4 traits in the evaluation are displayed in table 2. The parameters are estimated from the current data. Residual correlations (not shown) are somewhat higher than the genetic ones.

Table 2. Heritability's on diagonal and genetic correlations below it

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

Indexes

Index for growth is calculated on the basis of sub-indexes for weight gain and classification score. The standardization of the breeding values is described in the chapter “Standardization of EBVs and NTM”.

The BV on the original scale for growth and classification are combined by means of economic values that are based on economic calculations (table 3).

Table 3. Calculation of growth index

Holstein	100.65*CGS+100.65*CGL+13.8*CS
RDC	111.4*CGS+111.4*CGL+13.6*CS
Jersey	45.6*CGS+10.1*CS

Growth index is published both for sires and dams.

Correlation between growth index and underlying traits

The expected progress of each trait when index for growth is selected for, expressed as a percentage of maximum progress for that trait, is shown in table 4. Maximum progress is obtained if selection is based solely on the trait in question.

Table 4. Correlation between growth index and indexes for weight gain and classification score

Index	RDC	HOL	JER
Weight gain	0.86	0.67	0.67
Classification	0.86	0.95	0.95

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 of specific bulls can be calculated. For growth traits, it is breeding values for short- and long fattening period and carcass conformation (EUROP).

References

Johansson, K., Nielsen, U.S., Pösö, J., Eriksson, J-Å. and Pedersen Aamand, G. 2009. Joint Nordic genetic evaluation of growth and carcass traits in dairy breeds. Interbull Open meeting, Barcelona, Spain, August 21-24, 2009.

Fertility

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

Data

Trait definition

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

Abbreviation	Definition
AIS	Number of inseminations (0=heifers, 1-3=cows)
ICF	Interval (number of days) from calving to first insemination (cows)
IFL	Interval (number of days) from first to last insemination (0=heifers, 1-3=cows)
NRR	Non-return rate (0=heifers, 1-3=cows) at 56 days after first insemination
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 two 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 data starts at 1982 in Sweden, 1985 in Denmark, and 1992 in Finland. Jersey data from Denmark starts at 1985, from Sweden 1986, and from Finland 2003.

Fertility data are included if:

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

Editing rules for conception rate are in the Appendix 2.

Pre-corrections

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

Genetic evaluation

Separate genetic evaluations are made for Holsteins, Red dairy cattle (including Finncattle) and Jerseys (including Danish, Swedish and Finnish populations).

Model

The model for estimating breeding values is a multi-trait animal model. The heifer traits are separate traits from 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, AIS, and HST for cows:

Herd * first calving year	Fixed
First insemination year * month * country	Fixed
Age at first insemination in heifers * country	Fixed
Heterosis	Regres.
Animal	Random

Model for NRR for cows:

Herd * first calving year	Fixed
First insemination year * month * country	Fixed
Age at first insemination in heifers * country	Fixed
Semen type of first ins. * time-period * country	Fixed
Heterosis	Regres.
Animal	Random

Model for ICF for cows:

Herd * first calving year	Fixed
Calving year * month * country	Fixed
Age at first insemination in heifers * country	Fixed
Heterosis	Regression
Animal	Random

Model for CR for cows:

Herd * first calving year	Fixed
Insemination year * month * country	Fixed
Age at first insemination in heifers * country	Fixed
Semen type * time-period * country	Fixed
Insemination number	Fixed
Heterosis	Regression
Permanent environment	Random
Animal	Random

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

Herd-period

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

Heterosis

Proportion of total heterozygosity is included in HOL, RDC and JER 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 constituted by breed, country and birth year periods.

Genetic parameters

The genetic parameters used for the fertility traits in the evaluation are shown in tables 1 to 6.

Table 1. Heritabilities (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 2. Heritabilities (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 3. Heritabilities (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 4. Heritabilities (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 5. Heritabilities (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. Heritabilities (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***

Indexes

The index for fertility is calculated on the basis of sub-indexes for AIS, ICF and IFL. The standardization of the relative breeding values is described in the chapter "Standardization of EBVs and NTM".

The BV on the original scale for IFL, ICF and AIS are combined by means of economic values that are based on economic calculations (table 5).

Table 5. Calculation of fertility index

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

The fertility index is published for sires and cows.

Correlation between fertility index and underlying traits

The expected progress of each trait when index for fertility is selected for, expressed as a percentage of maximum progress for that trait, is shown in table 6. Maximum progress is obtained if selection is based solely on the trait in question.

Table 6. Correlation between fertility index and indexes for $ICF_{1\text{-}3}$, IFL_0, $IFL_{1\text{-}3}$, AIS_0 and $AIS_{1\text{-}3}$

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

Effect of 10 index units

Phenotypic breed averages and values 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 effect of specific bulls can be calculated. For fertility traits it is breeding values for interval from calving to first insemination, interval from first to last insemination and number of inseminations.

References

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

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Calving^{direct} and calving^{maternal}

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

Data

Trait definition

Records from first to fifth calving are included (these also being referred to as first versus later calvings). Direct and maternal effects are estimated for all traits.

The traits are survival, calving ease and size of calf. Survival is registered as 0 or 1, calving ease is measured in 4 categories (2 categories in SWE up to 2012), and size of calf is measured in 4 classes (only DK data).

Abbreviation	Definition
SU, 1st calving/SU, ≥ 2nd calving	survival over the first 24 hours after birth for heifers and cows separately
CE, 1st calving /CE, ≥ 2nd calving	calving ease for heifers and cows separately
CS, 1st calving /CS, ≥ 2nd calving	size of calf for heifers and cows separately

Basic editing rules

The time period for inclusion of data varies between traits and countries:

	Denmark	**Finland**	**Sweden**
Survival	1985-	1992-	1985-
Calving ease	1985-	2004-	1985-
Size of calf	1985-	No	No

Birth records are included if:
- Single births
- Calf is not the result of ET
- Sire or grandsire is a known sire
- Sire or grandsire belongs to breeds RDC, HOL, JER

Pre-corrections

All traits were pre-corrected for heterogeneous variance due to country and 5-year periods

Genetic evaluation

Separate genetic evaluations were made for Holsteins, Red dairy cattle (including Finncattle) and Jerseys (data only from Denmark).

Model

The following multi-trait animal model with direct and maternal effects is used for both the Holstein, Jersey and Red Dairy Cattle group:

Age at calving in months (heifers) or lactation number (cows)*country	Fixed
Year of calving*month of calving*country	Fixed
Sex of calf*year of calving*country	Fixed
Herd*5-year period*country	Fixed
Type of SWE CE-coding (SWE only, CE only)	Fixed
Year within 5-year-herd-country-group	Random
Heterosis for maternal and direct effect in RDC	Regression
Genetic groups	Random
Direct effect of animal	Random
Maternal effect of animal	Random

Total heterosis for maternal and direct effects

For Red Dairy Cattle, the following heterosis components were included:

- Direct: FAYxSRB, FAYxNRF, FAYxCanadian Ayrshire, SRBxNRF, SRBxCanadian Ayrshire, NRFxCanadian Ayrshire, other heterosis is pooled
- Maternal: FAYxSRB, FAYxNRF, FAYxCanadian Ayrshire, SRBxNRF, SRBxCanadian Ayrshire, NRFxCanadian Ayrshire, other heterosis is pooled

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 original

Genetic parameters

The parameters used in the genetic evaluation are shown in table 1 and 2.

Table 1. Heritability's and genetic correlations for traits used in the index for calving^{maternal}, heritability's on diagonal, genetic correlations over diagonal

		Calving traits (maternal)					
		1. calving			≥ 2. Calving		
	Breed	Survival (SU)	Calving ease (CE)	Size of calf (CS)	Survival (SU)	Calving ease (CE)	Size of calf (CS)
SU 1st clv.	RDC	0.02	0.70	-0.14	0.60	0.34	0.05
	HOL	0.035	0.60	-0.02	0.60	0.34	0.05
	JER	0.02	0.59	0.10	0.48	0.17	-0.07
CE 1st clv.	RDC		0.04	-0.52	0.64	0.74	-0.26
	HOL		0.06	-0.45	0.64	0.74	-0.26
	JER		0.02	-0.34	0.24	0.53	-0.32
CS 1st clv.	RDC			0.04	-0.43	-0.43	0.70
	HOL			0.04	-0.43	-0.43	0.70
	JER			0.03	-0.02	-0.33	0.89
SU ≥ 2nd clv.					0.01	0.70	-0.58
	JER				0.01	0.60	-0.39
					0.01	0.49	0.04
CE ≥ 2nd clv.	RDC					0.02	-0.54
	HOL					0.03	-0.39
	JER					0.01	-0.29
CS ≥ 2nd clv.	RDC						0.045
	HOL						0.04
	JER						0.03

Table 2. Heritability's and genetic correlations for traits used in the index for calving^{direct}, heritability's on diagonal, genetic correlations over diagonal

		Calving traits (direct)					
		1st calving			≥ 2nd calving		
	Breed	Survival (SU)	Calving ease (CE)	Size of calf (CS)	Survival (SU)	Calving ease(CE)	Size of calf (CS)
SU 1st clv.	RDC	0.035	0.75	-0.36	0.65	0.48	-0.38
	HOL	0.04	0.72	-0.55	0.62	0.55	-0.53
	JER	0.03	0.44	0.13	0.79	0.34	0.14
CE 1st clv.	RDC		0.06	-0.77	0.44	0.78	-0.75
	HOL		0.08	-0.75	0.60	0.63	-0.70
	JER		0.01	-0.67	0.39	0.81	-0.68
CS 1st clv.	RDC			0.23	-0.40	-0.90	0.80
	HOL			0.20	-0.53	-0.77	0.79
	JER			0.11	0.13	-0.62	0.91
SU ≥ 2nd clv.	RDC				0.01	0.65	-0.39
	HOL				0.01	0.65	-0.53
	JER				0.01	0.45	0.04
CE ≥ 2nd clv.	RDC					0.02	-0.76
	HOL					0.05	-0.75
	JER					0.01	-0.65
CS ≥ 2nd clv.	RDC						0.21
	HOL						0.18
	JER						0.11

The genetic correlations between maternal and direct traits were set to zero. The random herd variance was set to 15 % of the phenotypic variance.

Each animal has six solutions for maternal effects and six solutions for direct effects.

Indexes

The index for calving^{direct} and calving^{maternal} is calculated on the basis of sub-indexes for survival and calving ease. The standardization of the relative breeding values is described in the chapter "Standardization of EBVs and NTM".

The BV on the original scale for survival and calving ease are combined by means of economic values that are based on economic calculations (table 3).

Table 3. Calculation of index for calving^{maternal} and index for calving^{direct}. The same economic values are used. Subscripts of BV on the original scale refer to lactation

Holstein	$205*SU_1+10.90*CE_1+330*SU_{\geq 2}+14.80*CE_{\geq 2}$
RDC	$201*SU_1+11.35*CE_1+337*SU_{\geq 2}+15.62*CE_{\geq 2}$
Jersey	$79*SU_1+15.70*CE_1+146*SU_{\geq 2}+33.70*CE_{\geq 2}$

The index for calving^{maternal} and calving^{direct} is published for sires and cows.

Correlation between calving index and underlying traits

The expected progress of each trait when indexes for maternal calving and direct calving are selected for, expressed as a percentage of maximum progress for that trait, is shown in table 4 and 5. Maximum progress is obtained if selection is based solely on the trait in question. The results are based Sires born 2007-2010.

Table 4. Correlation between index for calving^{maternal} and maternal indexes for stillbirth and calving ease

Index	RDC	HOL	JER
SU_1	0.96	0.96	0.94
CE_1	0.86	0.81	0.79
$SU_{\geq 2}$	0.92	0.88	0.80
$CE_{\geq 2}$	0.81	0.61	0.73

Table 5. Correlation between index for calving^{direct} and direct indexes for stillbirth and calving ease

Index	RDC	HOL	JER
SU_1	0.90	0.97	0.94
CE_1	0.86	0.87	0.83
$SU_{\geq 2}$	0.90	0.92	0.95
$CE_{\geq 2}$	0.85	0.81	0.56

Effect of 10 index units

The effect of indexes for calving^{maternal}/calving^{direct} expressed on the original scale is shown in tables 6 and 7. It is expressed as the difference in performance of two daughter groups, where there is a difference of 10 index units for calving^{maternal}/calving^{direct} in the sires.

Table 6. Effect of +10 index units for calving^{maternal} in the sire on performance of stillbirth and calving ease in daughter groups

Index	RDC	HOL	JER	High values mean
SU_1	-0.8	-2.0	-2.4	More stillborn calves
CE_1	-0.03	-0.02/-0.12[1]	-0.03	More difficult calvings
$SU_{\geq 2}$	-0.2	-0.5	-0.9	More stillborn calves
$CE_{\geq 2}$	-0.01	-0.02	-0.01	More difficult calvings

[1] For Holstein the difference in phenotypic scale between countries gives (Sweden+Finland/Denmark)

Table 7. Effect of +10 index units for calving^{direct} in the sire on performance of stillbirth and calving ease in daughter groups

Index	RDC	HOL	JER	High values mean
SU_1	-0.9	-1.0	-1.2	More stillborn calves
CE_1	-0.02	-0.03	-0.01	More difficult calvings
$SU_{\geq 2}$	-0.5	-0.3	-0.2	More stillborn calves
$CE_{\geq 2}$	-0.02	-0.01	0.00	More difficult calvings

References

Genetic Evaluation of Calving Traits in Denmark, Finland, and Sweden. D. Boelling, U. Sander Nielsen, J. Pösö, J.Å. Eriksson and G.P. Aamand. INTERBULL Bulletin no. 37, 2007. Pp 179-185.

Udder health

The index for udder health describes the genetic ability in resistance of the cow to 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 1, together with the trait definitions. Data on SCC and udder conformation are used only as information traits.

Table 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, geometric mean	5-305	1
SCC2	-“-	-“-	2
SCC3	-“-	-“-	3
UA	Fore udder attachment		1
UD	Udder depth		1

[1]Days in milk

Basic editing rules

Denmark: CM, SCC and udder conformation data from 1990.

Finland: CM, SCC and udder conformation data from 1984, 1988 and 1992, respectively.

Sweden: CM, SCC and udder conformation data from 1984, 1982 and 1992, respectively.

Sweden includes records from all cows. 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 diagnosed by veterinary with 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 Holsteins, Red dairy cattle (RDC) (including Finncattle) and Jerseys (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 applying the regression to 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 2. The genetic correlations are the same for all three breeds.

Table 2. Heritability's (diagonal) and genetic correlations (below) for clinical mastitis and udder conformation traits for Holstein, Red dairy cattle (RDC) and Jersey.

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

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

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

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

Indexes

The index for udder health is calculated on the basis of sub-indexes for clinical mastitis from 1st to 3rd lactation.

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

In table 3 is presented the weighting of BV on the original scale for the four mastitis traits.

Table 3. Calculation of index for udder health for Holstein, Red dairy cattle and Jersey

Udder Health	0.25*CM11+0.25*CM12+0.30*CM2+0.20*CM3

Correlation between sub index and underlying traits

The expected progress of each trait when index for udder health is selected for, which is expressed as a percentage of maximum progress for that trait, is shown in table 4. Maximum progress is obtained if selection is based solely on the trait in question.

Table 4. Correlation between 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 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 effect of specific bulls can be calculated. For udder health it is breeding values for mastitis treatments.

References

Negussie, E., Lidauer, M., Mäntysaari, E. A., Strandén, I., Pösö, J., Nielsen, U. S., Johansson, K., Eriksson, J.-Å., Aamand, G. P. 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.

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 and clinical mastitis (CM) from 1st lactation. Table 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 1. Disease groups in the genetic evaluation

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

The traits included in the genetic evaluation are given in table 2 together with the trait definitions.

Table 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
CM1	Clinical mastitis (1) or not (0), -15 to 305 DIM

Basic editing rules

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

Pre-corrections

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

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 multi-trait, multi-lactation model:

Country * Herd-year	Fixed
Country * Calving age	Fixed
Country * Year-month of calving	Fixed
Breed and heterosis (only HOL)	Regression
Lactation stage (only BHB/ACE)	Fixed
Cow PE (only BHB/ACE)	Random
Animal	Random

Breed and heterosis

Currently, breed proportion and heterosis is only accounted in the Holstein evaluation. Effects of original Red Danish Cattle (RDM), Original Danish Black & white (SDM), Finnish Ayrshire (FAY), Norwegian Red (NRF), American Brown Swiss (ABK), American Holstein (HOL), Swedish Red Cattle (SRB), Canadian Ayrshire (CAY), and Finncattle (FIC), were accounted for by regressions on population proportions; heterosis was accounted for using the regression on expected total heterosis of all included populations.

Genetic parameters

The genetic parameters used for the 22 traits in the evaluation are shown in tables 3, 4 and 5. The parameter estimates were either found in Nielsen (1997) and some (re)-estimated as part of the 2017 revision of the GH evaluation (General Health Final Report). For computational reasons, residual correlations between lactations were set to zero.

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

Trait	ERP1	LRP1	MB1	KET1	FL1	ERP2	LRP2	OMB2	KET2	FL2	ERP3	LRP3	OMB3	KET3	FL3	BHB1	ACE1	BHB2	ACE2	BHB3	ACE3	CM1
ERP1	**.02**	.40	.40	.29	.35	.68	.32	.31	.33	.10	.64	.36	.29	.21	.19	.05	.03	-.03	-.01	-.03	.04	.18
LRP1	.16	**.01**	.29	.21	.36	.55	.72	.24	.06	.20	.55	.64	.19	.14	.28	-.02	.03	.00	-.05	.02	-.03	.15
MB1	.04	.01	**.01**	.74	.38	.26	.17	.80	.60	.32	.19	.21	.51	.57	.33	.48	.65	.22	.38	.23	.34	.39
KET1	.05	.00	.08	**.01**	.19	.24	.07	.67	.69	.13	.14	.02	.52	.66	.14	.65	.76	.39	.45	.47	.53	.32
FL1	.01	.01	.01	.01	**.01**	.34	.22	.36	.20	.84	.35	.24	.23	.11	.86	.01	.04	-.01	-.01	-.02	.00	.31
ERP2	.00	.00	.00	.00	.00	**.01**	.33	.28	.24	.10	.80	.36	.23	.20	.19	.00	.00	.00	-.01	.01	.00	.15
LRP2	.00	.00	.00	.00	.00	.18	**.01**	.19	.09	.20	.33	.85	.14	.14	.25	.00	-.02	.01	.02	.00	.01	.12
MB2	.00	.00	.00	.00	.00	.06	.01	**.01**	.61	.29	.25	.09	.85	.62	.39	.48	.55	.33	.51	.38	.53	.37
KET2	.00	.00	.00	.00	.00	.05	.01	.08	**.01**	.19	.22	.04	.46	.97	.18	.45	.49	.57	.73	.62	.78	.16
FL2	.00	.00	.00	.00	.00	.01	.00	.02	.02	**.01**	.00	.17	.18	.15	.87	-.01	-.01	.01	-.01	.01	.01	.25
ERP3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	**.01**	.36	.23	.15	.20	.01	-.03	.00	.03	-.01	.02	.12
LRP3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.18	**.01**	.11	.07	.24	-.01	-.01	.01	.00	.01	.00	.10
OMB3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.07	.00	**.02**	.50	.22	.41	.35	.39	.47	.51	.59	.27
KET3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.05	.01	.09	**.02**	.12	.40	.45	.56	.73	.64	.80	.11
FL3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.01	.00	.02	.02	**.01**	.03	.04	-.01	.02	-.04	.01	.20
BHB1	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	**.15**	.88	.81	.70	.76	.53	.04
ACE1	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.49	**.05**	.63	.70	.61	.57	.09
BHB2	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	**.11**	.89	.97	.76	-.02
ACE2	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.49	**.03**	.89	.92	-.05
BHB3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	**.08**	.86	-.03
ACE3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.50	**.03**	.01
CM1	.00	-.01	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	**.02**

Table 4. Genetic correlations (above), residual correlations (under) and heritability's on the diagonal in 1st, 2nd and 3rd lactation, RDC

Trait	ERP1	LRP1	MB1	KET1	FL1	ERP2	LRP2	OMB2	KET2	FL2	ERP3	LRP3	OMB3	KET3	FL3	BHB1	ACE1	BHB2	ACE2	BHB3	ACE3	CM1
ERP1	**.01**	.24	.30	.26	.00	.75	.25	.28	.11	.00	.86	.24	.26	.23	.00	.04	.04	-.02	-.07	.02	.01	.33
LRP1	.24	**.01**	.09	-.08	-.01	.24	.74	-.03	.06	.11	.28	.78	.13	.24	.01	-.02	-.09	.01	.06	.05	.05	.18
MB1	.01	.00	**.00**	.64	.39	.10	.03	.80	.63	.06	.22	-.12	.51	.63	.16	.46	.62	.22	.38	.24	.35	.41
KET1	.01	.00	.05	**.01**	-.06	.01	-.12	.43	.80	-.11	.11	-.17	.26	.69	-.20	.63	.74	.40	.47	.46	.53	.14
FL1	.01	.01	.02	.00	**.01**	.00	.01	.23	.10	.77	.00	.01	-.04	.02	.78	.01	.10	-.01	.03	-.06	-.02	.23
ERP2	.00	.00	.00	.00	.00	**.01**	.25	.09	-.10	.00	.86	.24	.09	.05	.00	-.01	.01	.01	-.03	.01	-.04	.27
LRP2	.00	.00	.00	.00	.00	.23	**.01**	-.06	-.17	.02	.29	.79	-.02	.02	.09	.02	.05	-.02	-.02	.00	-.05	.15
MB2	.00	.00	.00	.00	.00	.02	-.01	**.01**	.47	-.04	.25	-.15	.86	.49	.15	.47	.54	.32	.49	.37	.51	.15
KET2	.00	.00	.00	.00	.00	.00	.00	.06	**.01**	-.04	.02	-.06	.34	.94	.00	.47	.53	.54	.70	.59	.77	.25
FL2	.00	.00	.00	.00	.00	.01	.01	.01	.00	**.00**	.00	.00	-.08	-.15	.69	.02	-.01	.00	-.05	.00	-.03	.19
ERP3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	**.01**	.28	.18	.15	.00	.00	.05	-.02	.01	-.03	.01	.21
LRP3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.01	**.01**	-.08	.07	.00	-.04	-.09	.03	.05	.00	.01	.12
OMB3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.01	-.01	**.03**	.42	.02	.40	.34	.37	.46	.49	.57	.00
KET3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.01	.00	.06	**.01**	-.04	.39	.43	.55	.70	.62	.77	.26
FL3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.01	.01	.00	.00	**.01**	-.03	-.04	.03	.03	.00	.01	.15
BHB1	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	**.15**	.88	.81	.69	.75	.52	.00
ACE1	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.49	**.05**	.62	.69	.59	.55	.03
BHB2	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	**.11**	.88	.96	.75	.00
ACE2	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.49	**.03**	.88	.91	.01
BHB3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	**.08**	.85	-.03
ACE3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.50	**.03**	.00
CM1	.00	.00	.00	.00	.01	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	**.02**

Table 5. Genetic correlations (above), residual correlations (under) and heritability's on the diagonal in 1st, 2nd and 3rd lactation, Jersey

Trait	ERP1	LRP1	MB1	KET1	FL1	ERP2	LRP2	OMB2	KET2	FL2	ERP3	LRP3	OMB3	KET3	FL3	BHB1	ACE1	BHB2	ACE2	BHB3	ACE3	CM1
ERP1	**.01**	.32	.47	.39	.28	.83	.53	.45	.29	.24	.76	.38	.26	.38	.14	.04	.05	-.01	.00	.00	.01	.22
LRP1	.02	**.00**	-.05	.10	.04	.33	.81	.17	.26	.23	.35	.81	.05	.48	.01	.00	-.04	.03	-.05	-.02	-.01	-.21
MB1	.02	.00	**.01**	.55	.22	.43	.37	.63	.36	.23	.18	.18	.51	.38	.10	.33	.40	.29	.32	.27	.27	.39
KET1	.03	.00	.02	**.02**	.34	.10	.40	.47	.45	.19	.13	.16	.07	.49	.12	.60	.72	.29	.37	.26	.33	.06
FL1	.00	.00	.01	.01	**.01**	.16	.11	.01	.31	.81	.40	-.10	-.04	.39	.85	.08	.04	.05	-.04	.02	.06	.15
ERP2	.00	.00	.00	.00	.00	**.01**	.47	.38	.37	.18	.88	.45	.27	.27	.23	-.06	-.05	-.01	.01	.00	-.01	.31
LRP2	.00	.00	.00	.00	.00	.06	**.00**	.53	.47	.44	.34	.75	.20	.46	.07	.07	.13	-.02	.06	.01	.04	.04
MB2	.00	.00	.00	.00	.00	.04	.01	**.01**	.40	.14	.29	.27	.82	.42	.10	.31	.47	.18	.37	.26	.24	.15
KET2	.00	.00	.00	.00	.00	.02	.00	.02	**.01**	.32	.32	.58	.17	.70	.26	.23	.26	.15	.10	.24	.31	.10
FL2	.00	.00	.00	.00	.00	.01	.00	.02	.00	**.01**	.26	.09	-.02	.21	.76	-.07	-.07	-.04	-.03	-.02	-.03	.10
ERP3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	**.01**	.29	.19	.34	.48	.00	.00	.00	-.01	-.01	-.01	.24
LRP3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.05	**.00**	.15	.53	-.10	.01	-.01	.02	-.04	.02	.04	-.31
OMB3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.04	.01	**.01**	.39	.08	.21	.26	.28	.30	.33	.23	.07
KET3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.03	.01	.02	**.01**	.13	.41	.32	.38	.09	.34	.35	.15
FL3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	-.01	.00	.01	.01	**.01**	-.01	.02	-.01	.05	.01	-.01	-.03
BHB1	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	**.05**	.91	.79	.46	.60	.22	.01
ACE1	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.53	**.02**	.71	.71	.53	.33	.00
BHB2	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	**.05**	.64	.87	.52	.01
ACE2	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.49	**.01**	.50	.56	-.03
BHB3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	**.04**	.73	.00
ACE3	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.48	**.01**	.02
CM1	.00	.00	.01	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00	**.03**

Indexes

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 6).

Table 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	0.5 * ERP_1 + 0.3 * ERP_2 + 0.2 * ERP_3
LRP	0.5 * LRP_1 + 0.3 * LRP_2 + 0.2 * LRP_3
OMB	0.5 * OMB_1 + 0.3 * OMB_2 + 0.2 * OMB_3
KET	0.5 * KET_1 + 0.3 * KET_2 + 0.2 * KET_3
FL	0.5 * FL_1 + 0.3 * FL_2 + 0.2 * FL_3
General health (HOL)	2.00 * ERP + 1.05 * LRP + 1.88* (2/3* OMB) + 1.88 * (1/3 *KET) + 1.75 * FL
General health (RDC)	2.00 * ERP + 1.05 * LRP + 1.88* (2/3* OMB) + 1.88 * (1/3 *KET) + 1.75 * FL
General health (JER)	2.00 * ERP + 1.05 * LRP + 1.88* (2/3* OMB) + 1.88 * (1/3 *KET) + 1.75 * FL

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 6. Maximum progress is obtained if selection is based solely on the trait in question.

Table 6. Correlation between the index for general heath and early reproduction disorders (ERP), late reproduction disorders (LRP), other metabolic diseases (OMB), ketosis (KET) and feet and leg problems in 1st, 2nd and 3rd lactation for AI bulls born after 2007.

Index	HOL	RDC	JER
ERP_1	0.84	0.81	0.90
LRP_1	0.70	0.64	0.45
OMB_1	0.72	0.63	0.79
KET_1	0.57	0.26	0.59
FL_1	0.64	0.41	0.70
ERP_2	0.78	0.73	0.85
LRP_2	0.53	0.54	0.75
OMB_2	0.67	0.65	0.75
KET^2	0.59	0.30	0.64
FL_2	0.44	0.32	0.68
ERP_3	0.80	0.79	0.89
LRP_3	0.55	0.54	0.43
OMB_3	0.54	0.56	0.56
KET_3	0.49	0.39	0.73
FL_3	0.53	0.35	0.64

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

Nielsen, U. S., Pedersen, G. A., Pedersen, J. and Jensen J., 1997. Genetic correlations among health traits in different lactations. Interbull Bulletin No. 15 (68-75).

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

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

Claw health

The index for claw health describes the genetic resistance of bulls' daughters to diseases in the claw.

Data

Trait definition

Index for claw health is based on registrations done by claw trimmers. Breeding values (EBV's) are calculated for seven claw diseases or groups of claw diseases.

Abbreviation	Claw disease
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 incidence 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

Data are used if they are registered in the period from calving to calving or from calving to 430 days after calving, depending on what comes first. 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 registered case of a claw disease/group of claw diseases within calendar year are deleted if this is not likely. This validation is made for each of the seven claw diseases/groups of claw diseases.

Genetic evaluation

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

Model

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

Herd * five 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

Genetic parameters

The heritabilities and standard deviations used for the 21 traits in the evaluation are displayed in table 1, 2 and 3. The parameters are estimated from the current data.

Table 1. Heritability and genetic standard deviation for Holstein

Trait	Lactation	Phenotypic S.D.	h^2	Genetic S. D.	Permanent S. D.
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 2. Heritability and genetic standard deviation for Jersey

Trait	Lactation	Phenotypic S.D.	h^2	Genetic S. D.	Permanent S. D.
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

Table 3. Heritability and genetic standard deviation for RDC

Trait	Lactation	Phenotypic S.D.	h^2	Genetic S. D.	Permanent S. D.
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

Genetic correlations used in the evaluation are in tables 4 to 9 for Holstein and RDC. Because Jersey correlations had large standard errors it was decided to use the Holstein correlations for Jersey as well.

Table 4. Genetic correlations in lactation 1. Holstein & 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 5. Genetic correlations in lactation 2 and between lactation 1 and 2. Holstein & 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 6. Genetic correlations in lactation 3 and to lactation 1, 2 and 3. Holstein & 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	0,00	-0,25	0,25
	20	0,00	0,00	0,00	0,00	0,00	1,00	0,06

Table 7. 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 8. 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 9. 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

Indexes

An index for claw health is calculated based on seven sub-indices. The standardization of the breeding values is described in the chapter “Standardization of EBVs and NTM”. Table 10 gives the economic importance of claw diseases used in the calculation of economic weights.

Table 10. 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, BV on the original scale for first, second and third lactation are weighted by 0.5, 0.3 and 0.2. The BV on the original scale across lactation for the seven traits are combined by means of economic values that are based on economic calculations (table 11).

Table 11. Calculation of claw index

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

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

Correlation between index for claw health and underlying traits

The expected progress of each trait when index for claw health is selected for, expressed as a percentage of maximum progress for that trait, is shown in table 12. Maximum progress is obtained if selection is based solely on the trait in question.

Table 12. Correlation between index for claw health and sub-indices

Index	RDC	HOL	JER
Digital Dermatitis/Interdigital dermatitis	0.63	0.50	0.62
Heel Horn Erosion	0.76	0.62	0.77
Verrucose dermatitis/Interdigital Hyperplasia	0.58	0.41	0.56
Sole Hemorrhage	0.66	0.83	0.74
Sole Ulcer	0.79	0.90	0.84
Cork screw claw	0.34	0.57	0.68
Double sole/ White line separation	0.53	0.78	0.66

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 of specific bulls can be calculated. For claw traits, it is breeding values for sole ulcer, sole hemorrhage, digital dermatitis+interdigital Dermatitis, Verrucose dermatitis+Interdigital Hyperplasia, double sole+white line separation and Cork screw claw.

When interpreting effects of index for claw heath it is important to remember that Dermatitis, Heal 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

http://www.interbull.org/images/stories/KJohansson.pdf

Conformation, milk ability and temperament

The indexes 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. Indexes for milk ability and temperament describe how rapidly the cow can be milked and her general temperament.

Trait definition

The traits that are either classified by classifier (frame, feet-legs and udder) or registered by farmer (milk ability and temperament) and go into genetic evaluation are shown in Table 1. Traits that are measured from Automatic Milking Systems (AMS) and go into the genetic evaluation are shown in Table 2. Classification is undertaken by official classifiers employed by agricultural advisory services in the individual countries and a scale from 1-9 is used.

Data from TruTest Milk Meters, automatic measure of milking speed from AMS and conventional milking parlours are used in genetic evaluation for milk ability. Milk ability is defined as the average flow of solids (fat and protein content measured in kilograms per minute), Data from one up to seven test days in first lactation are included in the genetic evaluation. In the genetic evaluation for milk ability data from the three sources mentioned above are used as same trait, as 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 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 fictitious scale, thus without actual unit. The Average of the given trait over a period from 30 to 60 days after last calving are used in the analysis instead of single observations as it is for the udder linear assessments.

Table 1. Traits classified in the Nordic countries

Group of traits	Traits
Frame	stature, body depth, chest width, dairy form, top line, rump width, rump angle
Feet and legs	rear legs (side view), rear legs (rear view), hock quality, bone quality, foot angle
Udder	fore udder attachment, rear udder height, rear udder width, udder cleft/support, udder depth, teat length, teat thickness, teat placement (front), teat placement (back), udder balance
Work ability	Milk ability, temperament

Table 2. Traits recorded in Automatic Milking Systems

Group of traits	Traits
Udder	Teat placement front, teat placement back, udder depth, udder balance
Work ability	Milk ability

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

Basic editing rules

Denmark started classifying almost all the traits shown in table 1 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.

Sweden started the classification for most of the traits in table 1 in 1993, but the classification of teat thickness and rear teat placement started 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, dairy form, 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.

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.

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

Udder coordinates from AMS is 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 Holsteins, Red Dairy Cattle (including Finncattle) and Jerseys. From all countries data from 1 to 3 parities are used, however if a Finnish cow has classifications in later parities - up to 10 the latest classification replaces the classification in 3rd lactation. For milk ability and temperament only records from 1st lactation are used.

AMS measures of udder coordinates from 1-3 lactations are used in the genetic evaluation as correlated trait to linear measures of teat placement front, teat placement back, udder depth and udder balance.

Model

The model for estimation of breeding values for linear traits is a single-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.

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

[1] Only linear traits

[2] Defined differently for linear traits and teat coordinates

[3] Only teat coordinates

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 2-5.

Table 2. Heritability's (h^2) and genetic correlations applied in the genetic evaluation for Holstein

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

Table 3. Heritability’s (h^2) and genetic correlations applied in the genetic evaluation for RDC

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

Table 4. Heritability's (h²) and genetic correlations applied in the genetic evaluation for Jersey

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

Table 5. Heritability's (h²) depending on information source in genetic evaluation for milk ability

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 6. Heritability's (h^2) for conformation traits measured by AMS and genetic correlation to classified traits in parentheses used in the genetic evaluation of Holstein, RDC and Jersey

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

Indexes

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 indexes 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 Tables 7 and 8.

Table 7. Optimum for Holstein, RDC and Jersey

	Holstein	RDC	Jersey
1. Stature	155	142	129
2. Body depth	9	6	6
3. Chest width	9	5.5	5
4. Dairy form	9	5.5	6
5. Top line	7	7	7
6. Rump width	9	5	6
7. Rump angle	5	5	5
8. Rear legs, side view	5	5	5
9. Rear legs, back rear view	8	8	9
10. Hock quality	9	9	9
11. Bone quality	8	7.5	9
12. Foot angle	6.5	7	6.5
14. Fore udder attachment	9	9	9
15. Rear udder height	9	9	9
16. Rear udder width	9	9	9
17.Udder cleft/support	8	9	9
18. Udder depth	9	9	9
19. Teat length	5.5	5.5	5.5
20. Teat thickness	5	6	6
21. Teat placement (front)	8	8	7.5
22. Teat placement (back)	5	5	5
23. Udder balance	5	5	5

Table 8. Weight factors for Holstein, RDC and Jersey

	Holstein	RDC	Jersey
1. Stature	5	10	6
2. Body depth	25	15	14
3. Chest width	30	20	13
4. Dairy form	20	10	10
5. Top line		10	25
6. Rump width	20	15	11
7. Rump angle		20	11
8. Rear legs, side view	10	15	20
9. Rear legs, back rear view	30	25	20
10. Hock quality	18	25	20
11. Bone quality	17	15	15
12. Foot angle	25	20	25
13. Fore udder attachment	17	20	20
14. Rear udder height	10	8	
15. Rear udder width		5	10
16.Udder cleft/support	10	12	25
17. Udder depth	24	20	-10
18. Teat length	5	10	-10
19. Teat thickness	5	10	10
20. Teat placement (front)	7	10	
21. Teat placement (back)	12	5	
22. Udder balance	10		
23. Codes for body			
24. Codes for udder			

Correlation between sub-index and underlying traits

The expected progress of each trait, expressed as a percentage of maximum progress for that trait, is shown in table 9. Maximum progress is obtained if selection is based solely on the trait in question.

Table 9. Correlation between conformation traits and index for frame, feet and legs, and mammary system

	RDC	Holstein	Jersey
		Index for frame	
Stature	0.83	-[1]	0.84
Body depth	0.30	-[1]	0.08
Chest width	0.31	-[1]	0.29
Dairy form	0.23	-[1]	0.40
Top line	0.13	-[1]	0.47
Rump width	0.68	-[1]	0.69
Rump angle	-0.20	-[1]	0.27
		Index for feet and legs	
Rear legs, side view	-0.23	-0.14	-0.68
Rear legs, rear view	0.53	0.66	0.51
Hock quality	0.73	0.63	0.53
Bone quality	0.79	0.65	0.50
Foot angle	0.16	0.29	0.47
		Index for mammary system	
Fore udder attachment	0.75	0.6	0.79
Rear udder height	0.54	0.52	0.64
Rear udder width	0.39	0.23	0.54
Udder cleft	0.32	0.17	0.33
Udder depth	0.84	0.88	0.85
Teat length	0.16	0.15	0.15
Teat thickness	-0.07	-0.02	0.14
Teat placement (front)	0.19	0.16	0.41
Teat placement (back)	0.13	-0.01	0.40
Udder balance	0.41	0.22	0.32

[1] Frame for Holstein is not the breeding goal. Frame is used to describe the expected size of the animal

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 of specific bulls can be calculated. For conformation traits, it is breeding values for temperament and linear body, feet&leg and mammary traits.

References

A joint Nordic model for type traits, 2004. Anders Fogh, Jan-Åke Erikson, Jarmo Juga, Minna Toivonen, Jukka Pösö, Marjo Simpanen, Ulrik Sander Nielsen, Gert Pedersen Aamand. INTERBULL-meeting 2004, Sousse, Tunisia.

Longevity

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

Data

Trait definition

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

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

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

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

Basic editing rules

Data from year 1985 in Sweden, 1985 for Denmark, and 1988 in Finland, is included.

Moreover, information is included, if:

- Age at 1st calving is between 450 and 1280 days
- Only a lactation that is completed within herd of 1st calving is included. If a cow is moved during its lifetime, the record of the lactation from which it is moved and future lactations are deleted

Pre-corrections

No pre-corrections are made.

Genetic evaluation

Separate genetic evaluations are made for Holsteins, Red dairy cattle (including Finn cattle) and Jersey (data from Denmark and Sweden).

Model

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

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

Heterosis

Proportion of heterozygosity is considered as follows:

RDC:

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

HOL:

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

JER:

- Original Danish Jersey x US Jersey

Genetic groups (phantom parent groups)

Genetic groups are modelled by phantom parent grouping.

Genetic parameters

The genetic parameters used for longevity traits in the evaluation appear in Tables 1 to 3.

Table 1. Estimates of genetic parameters of longevity for Red dairy cattle. Heritability is on diagonal, genetic correlations above diagonal, and environmental correlations below 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 2. Estimates of genetic parameters of longevity for Holstein Heritability is on diagonal, genetic correlations above diagonal, and environmental correlations below 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 3. Estimates of genetic parameters of longevity for Jersey. Heritability is on diagonal, genetic correlations above diagonal, and environmental correlations below 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**

Indexes

Index for longevity is calculated 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 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 of specific bulls can be calculated. For longevity, it days in production.

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 five 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 (only heifer calves), 1998 for Denmark, and 2004 for Finland, is included.

Moreover, information is deleted, if:

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

Pre-corrections

Pre-corrections for difference in variance between countries are made.

Genetic evaluation

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

Model

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

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

For Jersey country effects are not included

Heterosis

Proportion of heterozygosity is considered as follows:

RDC:
- ABS = RDM x ABS + ABS x HF + ABS x (SRB+FAY+NRF)
- NOR = Nordic heterosis + CAY x NOR + FAY x FIC
- RDCxHF = RDM x HF + HF x (SRB+FAY+NRF)
- RDMxNordic breeds = RDM x (SRB+FAY+NRF)

HOL:
- BW x HF + RW x HF
- HOL x RDC (only Finland)

JER:
- DJ x USJ

Effect of transfer to another herd

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 by the same procedure as used for yield records. However, some year-groups have been merged in order to obtain larger phantom parent groups.

Genetic parameters

The genetic parameters used for traits in youngstock survival appear in tables 1 to 3.

Tabel 1. Holstein. Genetic and residual variances, heritabilities (diagonal), genetic correlations (above diagonal) and residual correlations (below 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)**

Tabel 2. RDC: Genetic and residual variances, heritabilities (diagonal), genetic correlations (above diagonal) and residual correlations (below 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)**

Tabel 3. Jersey. Genetic and residual variances, heritabilities (diagonal), genetic correlations (above diagonal) and residual correlations (below 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)**

Indexes

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

The BV for HP1, HP2, BP1 and BP2 are combined by means of economic values that are based on economic calculations (table 4).

Table 4. Calculation of index for young stock survival.

Holstein	0.299*HP1+0.423*HP2+0.111*BP1+0.330*BP2
RDC	0.215*HP1+0.452*HP2+0.088*BP1+0.324*BP2
Jersey	0.529*HP1+0.414*HP2+0.076*BP1+0.151*BP2

The index for youngstock survival is published for sires.

Correlation between youngstock and underlying traits

The expected progress of each trait when indexes for youngstock survival are selected for, expressed as a percentage of maximum progress for that trait, is shown in table 5. Maximum progress is obtained if selection is based solely on the trait in question.

Table 5. Correlation between index for youngstock survival and indexes 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 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 of specific bulls can be calculated. For survival traits, it is breeding values for survival in early and late period for heifers and bull calves.

References

Standardization of EBVs and NTM

Estimated breeding values

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

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

Standardization of 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.

For all traits a rolling base consisting of cows from Denmark, Sweden and Finland that are 3-5 years of age at the date of publication is applied.

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.

Mean NTM in the base population is not adjusted, because it is based on adjusted EBVs for all sub-indexes.

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

The breeding values (EBV) in kilograms are based on the solutions from the animal BLUP-model. The units used the evaluation model is kilograms. Normally breeding values are expressed on a rolling base. However, the solutions from the evaluation model can also be expressed on different fixed bases. Currently the 2005 base is used. The 2005-base is 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 = 0.5 * EBV kg milk 1st lact. + 0.3 * EBV kg milk 2nd lact. + 0.2 * EBV kg milk 3rd lact.
EBV kg prot. total = 0.5 * EBV kg prot. 1st lact. + 0.3 * EBV kg prot. 2nd lact. + 0.2 * EBV kg prot. 3rd lact.
EBV kg fat total = 0.5 * EBV kg fat 1st lact. + 0.3 * EBV kg fat 2nd lact. + 0.2 * EBV kg fat 3rd lact.

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

Base difference: 2005 base – 2000 base

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

Base difference: 2005 base – 1995 base

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

Appendix 2

Defining phenotype for CR: Each new insemination is preliminary set to successful i.e. CR=1. If it is followed with the 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 pregnancy checked, 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 and <= 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 is 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 possible pregnancy is not terminated. Therefore, the latter option was selected.

Special case for defining phenotype: 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 the non-consecutive calving was noticed or a cow started with insemination records, inseminations that have 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, 5 inseminations in maximum are included for the new calving. All earlier inseminations are set to missing values.

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

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

Open cases due to the data extraction: All data is used to define phenotypes before cutting too fresh data out (150-d gap), therefore only a small fraction of the data belongs to the class of the open cases. In this class of open cases, 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 rest of the open cases, 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 of the extraction of data, it is very probable that a cow is pregnant and not calved yet.

Limits used: Records within 150 days from data extraction are excluded from the data set. Only first 10 inseminations are accepted in the data. The same limits that are used for other fertility traits are used for CR data too: lowest (270 d) and highest age (900 d) for first insemination in heifers, 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.