

Nordic Cattle Genetic Evaluation

NAV routine genetic evaluation of Dairy Cattle – data and genetic models

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Genetic evaluation within NAV

Introduction.....	6
NTM - Nordic Total Merit	7
Traits included in NTM.....	7
Economic value of sub-indexes.....	7
Economic weights in NTM	10
Calculation of NTM	11
Correlation between NTM and indexes	13
References	13
Yield	14
Data	14
Trait definition	14
Basic editing rules	14
Foreign information	14
Genetic evaluation	14
Model.....	15
Forming 305-day breeding values	19
Indexes	21
Correlation between yield index and underlying traits	22
Effect of 10 index units.....	22
Relative breeding values for persistence	22
Relative breeding values for protein and fat percentage.....	23
References	23
Growth	23
Data	23
Trait definition	23
Basic editing rules	24
Genetic evaluation	24
Model.....	24
Genetic parameters	25
Indexes	26

Correlation between growth index and underlying traits	26
Effect of 10 index units.....	26
References	27
Fertility	27
Data	27
Trait definition	27
Basic editing rules	27
Genetic evaluation	28
Model.....	28
Genetic parameters	29
Indexes	31
Correlation between fertility index and underlying traits.....	31
Effect of 10 index units.....	31
References	32
Calving ^{direct} and calving ^{maternal}	32
Data	32
Trait definition	32
Basic editing rules	32
Genetic evaluation	33
Model.....	33
Genetic parameters	33
Estimation of breeding values for each single trait	34
Indexes	35
Correlation between calving index and underlying traits	35
Effect of 10 index units.....	36
References	36
Udder health	36
Data	36
Trait definition	36
Basic editing rules	37
Pre-corrections	37
Genetic evaluation	37
Model.....	38

Genetic parameters	38
Indexes	39
Correlation between sub index and underlying traits	39
Effect of 10 index units.....	40
References	40
Other diseases.....	40
Data	40
Trait definition	40
Basic editing rules	41
Genetic evaluation	41
Model.....	41
Genetic parameters	42
Indexes	44
Correlation between sub-index and underlying traits.....	44
Effect of 10 index units.....	45
References	45
Claw health	45
Data	46
Trait definition	46
Basic editing rules	46
Genetic evaluation	46
Model.....	47
Genetic parameters	47
Indexes	49
Correlation between index for claw health and underlying traits	50
Effect of 10 index units.....	50
References	50
Longevity.....	50
Data	51
Trait definition	51
Basic editing rules.....	51
Pre-corrections	51

Genetic evaluation	51
Model.....	51
Genetic parameters	52
Indexes	53
Effect of 10 index units	53
Conformation, milking speed and temperament.....	54
Trait definition	54
Basic editing rules	54
Pre-corrections.....	55
Genetic evaluation	55
Model.....	55
Genetic parameters	56
Indexes	57
Linear traits	57
Composite traits	57
Correlation between sub-index and underlying traits.....	59
Effect of 10 index units.....	59
References	61
Standardization of EBVs and NTM	61
Estimated breeding values.....	61
Mean	61
Standard deviation	61
NTM	61

Introduction

Estimations of breeding values for dairy breeds in Denmark, Sweden and Finland are based on NAV (Nordic Cattle Genetic Evaluation), which is owned by Knowledge Centre for Agriculture, Cattle, the Swedish Dairy Association and FABA Breeding.

Estimated breeding values (EBVs) for all traits are made on a common basis. This cooperation makes it possible to compare animals across countries and thus make efficient use of economic resources. Genetic evaluation is performed for a wide variety of important traits. Further economically important traits are included in a Nordic total merit index known as the 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 runs.

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 most 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). The NTM describes the total economic potential determined by genetics. Cows with high NTM indexes bring greater economic benefits to the farmer, and the use of sires with high NTM will give offspring of higher economic value. NTM represents the additional value over the productive lifetime of an animal.

Traits included in NTM

The traits going into the NTM index are:

- Yield
- Growth
- Fertility
- Calving^{direct}
- Calving^{maternal}
- Udder health
- Other diseases
- Claw health
- Body
- Feet and legs
- Udder
- Longevity
- Milking speed
- Temperament

The traits are weighted together on the basis of economic values quantifying the value of a marginal change in the trait. The economic weights of Holsteins, Red Holsteins, Red dairy cattle (including Finncattle) and Jerseys differ.

Economic value of sub-indexes

The present economic values are based on the economic situation in the first part of 2007. By using the most recent prices and costs 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 form 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 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 "other diseases".

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 udder health (mastitis) arise from veterinarian treatment, extra work done by the herdsman, and the amount of milk that is discarded following treatment of the udder with antibiotics, hormones, etc. In the economic evaluation of udder health the importance 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.

Other diseases

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 traits

The setup for this trait group is somewhat different from that used with the other trait groups. The traits analysed here – Body, Feet and Legs and Udder – are phenotypes. The basic economic assumptions are shaped by a (subjective) assessment of the extra workload 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 of the traits included in Body were linearly scored at 1 point away from the optimum.
- Udder: When all of 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 and Legs: When all traits included in Feet and 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, Milking Speed and Temperament, things are less complicated, because the recorded score can be evaluated directly. It was assumed that when the Milking Speed 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 also change number of calvings per year. It is well known that the breeding value of longevity is heavily influenced by fertility, udder health and other diseases, 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 the TMI index. This transfer is based on analyses of the relationship between longevity and the other trait in the NTM-index.

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, 1 st	%-units	2.0	2.01	0.79
Easy calving, 1 st	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, 1 st	%-units	1.50	1.46	1.35
Mastitis, 2 nd	%-units	1.13	1.05	1.01
Mastitis, 3 rd +	%-units	1.44	1.49	1.75
Mastitis, all lact.	%-units	4.07	4.00	4.11
OTHER DISEASES**				
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
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				
Body	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
Milking speed	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 are used to achieve this goal.

The EBVs for yield and fertility are calculated using within-trait group models. This means that any genetic correlations between the trait groups – e.g. there is a negative genetic correlation between yield and fertility – are not taken into account.

This has no significance for bulls with many offspring, because their EBVs have high reliabilities for all traits. For cows, taking genetic correlations into account will have a significant effect, because their EBVs for fertility are based on pedigree information. For cows, it is not taken into account that cows with high genetic merit for yield often have genetic merit for fertility that is lower than the parent average.

Different weights in NTM for cows offer a simple way of taking into account the genetic correlations between yield - fertility (-40%).

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	Red Holstein	RDC	Jersey
Yield index ¹	0.75/0.68	0.75/0.68	0.92/0.84	0.87/0.78
Growth	0.06	0.11	-	-
Fertility	0.31	0.23	0.26	0.20
Calving ^{direct}	0.15	0.17	0.14	0.06
Calving ^{maternal}	0.17	0.17	0.12	0.06

Udder health	0.35	0.35	0.32	0.44
Other diseases	0.11	0.12	0.12	0.04
Claw health	0.08	0.10	0.05	0.05
Body	-	-	-	-
Feet and legs	0.12	0.15	0.09	0.04
Udder	0.25	0.24	0.32	0.26
Milking speed	0.08	0.08	0.10	0.10
Temperament	0.03	0.03	0.03	0.03
Longevity	0.11	0.11	0.07	0.08

¹ Weight factor for bulls/weight factor for cows with own yield record

Correlation between NTM and 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

	RDC	Holstein/ Red Holstein	Jersey
Yield index	0.65	0.59	0.62
Growth	0.01	0.09	-0.10
Fertility	0.20	0.44	0.45
Calving ^{direct}	0.21	0.31	0.14
Calving ^{maternal}	0.15	0.25	0.20
Udder health	0.40	0.49	0.47
Other diseases	0.27	0.47	0.21
Claw health	0.04	0.33	0.18
Body	0.00	-0.03	0.08
Feet and legs	0.17	0.24	0.22
Udder	0.29	0.25	0.16
Milking speed	0.18	0.03	0.02
Temperament	0.13	0.00	0.00
Longevity	0.56	0.68	0.49

References

http://www.nordicebv.info/NR/rdonlyres/BFC1E284-4DC9-4E7C-96F6-F7A6EAoCDF6B/o/NAV_TMI_Light_report.pdf

http://www.nordicebv.info/NR/rdonlyres/B618CoE5-FF6F-4D31-8F86-B3CE4A140043/o/NAV_TMI_report_lastversion_131108.pdf

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 indexes for protein and fat content are estimated from milk, protein and fat yield. The estimated genetic lactation curve is used to calculate a persistency index.

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

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

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 and Red Holstein 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 (including Red 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 are 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:

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

EBV for fat yield is calculated in similar manner.

Genetic parameters are shown in table 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

	1 st lactation			2 nd lactation			3 rd 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

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

Table 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

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

Indexes

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

The RBVs 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	$-0.25 * \text{milk index} + 0.25 * \text{fat index} + 1.0 * \text{protein index}$
HOL	Yield	$-0.20 * \text{milk index} + 0.40 * \text{fat index} + 0.8 * \text{protein index}$
JER	Yield	$-0.30 * \text{milk index} + 0.50 * \text{fat index} + 0.8 * \text{protein index}$

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

Effect of 10 index units

The effect of yield indexes expressed on the original scale is shown in table 6. It is expressed as the difference in the performance of two daughter groups, where there is a difference of 10 yield index units in the sires.

Table 6. Effect of +10 yield index units in the sire on performance of milk, fat and protein in daughter group

Trait	RDC	HOL	JER	High values mean
Milk, kg	263	191	183	More milk
Fat, kg	11.2	11.1	9.7	More fat
Protein, kg	10.3	9.2	8.0	More 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:

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

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

References

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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 (incl. Red Holstein), 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
<i>Holstein</i>				
CGS	0.28			
CGL	0.98	0.32		
CS	0.41	0.36	0.29	
FS	0.17	0.17	0.35	0.18
<i>RDC</i>				
CGS	0.36			
CGL	0.97	0.29		
CS	0.34	0.32	0.29	
FS	- 0.14	-0.12	0.15	0.23
<i>Jersey</i>				
CGS	0.22			

CS	0.43	0.16	
FS	0.09	0.34	0.11

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

Effect of 10 index units

The effect of growth indexes expressed on the original scale is shown in table 5. It is expressed as the difference in the performance of two groups of male offspring, where there is a difference of 10 growth index units in the sires.

Table 5. Effect of +10 growth index units in the sire on performance of weight gain and classification score in group of male offspring

	RDC	HOL	JER	High values mean
Weight gain, g/day	11	8	0	Higher weight gain
Classification score, Europe	0.17	0.13	0.10	Better classification

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)

These fertility traits are clustered into two groups:

Group 1 NRR0, IFLO, NRR1-3, ICF, and IFL1-3

Group 2 AIS0, HST0, AIS1-3, HST1-3, ICF

Basic editing rules

The data included are from 1982 in Sweden, 1985 in Denmark, and 1992 in Finland.

Fertility data are included if:

- Heifers, age at 1st insemination: 270-900 days
- Age at 1st calving: 500-1100 days
- Heifers and cows, IFL: 0-365 days
- Heifers and cows, AIS: 1-8 inseminations

- Cows, ICF: 20 - 230 days
- Cows, ICF + IFL: 20 - 365 days
- Gestation length greater than 260 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

Pre-corrections

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

Genetic evaluation

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

Model

The model for estimating breeding values is a multi-trait sire model. The heifer and cow traits are handled separately in a multi-trait analysis. However, the cows' different lactations are handled as repeated observations.

Month of first insemination * country (NRR, IFL, AIS, HST)	Fixed
Month of calving * country (ICF)	Fixed
Age at first insemination * parity * country	Fixed
Year (only Finland)	Fixed
Herd-period	Fixed
Breed	Regression
Heterosis	Regression
Genetic groups	Fixed
Herd-year ¹ (only Finland)	Random
Sire	Random

Herd-period

For heifer traits birth year is used; for cow traits year of first calving is used. The periods are one year for Denmark and Sweden and five years for Finland.

Herd-year (only Finland)

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

Breed

Proportion of breeds

- HF for Holstein

- Red Danish Cattle, original black and white, FAY, NRF, ABK, HF, SRB, Canadian AYS for the red breeds
- original JER, NZ and US Jersey for Jersey

Heterosis

Proportion of heterozygosity

- HF x original black and white for Holstein
- all heterozygosity for the red breeds
- all heterozygosity for Jersey

Genetic groups (phantom parent groups)

Genetic groups for animals with unknown parents are included for Holsteins. The genetic groups also made as interaction between breed, country and birth year period (clustered in periods of ten years).

Genetic parameters

The genetic parameters used for the fertility traits in the evaluation are shown in table 1 to 4.

Table 1. Heritability's on diagonal and genetic correlations above diagonal for traits in group 1. HOL without brackets, AYS and JER within brackets

		1	2	3	4	5
		NRRo	IFLo	NRR13	ICF13	IFL13
1	NRRo	0.008 (0.014)	-0.65 (-0.75)	0.40 (0.50)	0.10 (0.10)	-0.40 (-0.40)
2	IFLo		0.02 (0.015)	0.00 (-0.20)	0.35 (0.35)	0.40 (0.55)
3	NRR13			0.02 (0.015)	0.45 (0.20)	-0.51 (-0.51)
4	ICF13				0.04 (0.04)	0.41 (0.41)
5	IFL13					0.02 (0.03)

Table 2. Herd-year variance as proportion of total variance in group 1 (on the diagonal). Herd-year correlations between traits above diagonal. HOL without brackets, AYS and JER within brackets

		1	2	3	4	5
		NRRo	IFLo	NRR13	ICF13	IFL13
1	NRRo	0.025 (0.02)	0.05 (0.00)			
2	IFLo		0.03			

			(0.025)			
3	NRR13			0.025 (0.03)		
4	ICF13				0.15 (0.15)	-0.11 (0.00)
5	IFL13					0.03 (0.05)

Table 3. Heritability's on diagonal and genetic correlations above diagonal for traits in group 2. HOL without brackets, AYS and JER within brackets

		1	2	3	4	5
		AISo	HSTo	AIS13	HST13	ICF13
1	AISo	0.025 (0.025)	0.15 (0.15)	0.40 (0.65)		
2	HSTo		0.02 (0.03)		0.65 (0.65)	
3	AIS13			0.03 (0.03)	0.15 (0.15)	0.20 (0.20)
4	HST13				0.025 (0.025)	0.35 (0.35)
5	ICF13					0.04 (0.04)

Table 4. Herd-year variance as proportion of total variance in group 1 (on the diagonal). Herd-year correlations between traits above diagonal. HOL without brackets, AYS and JER within brackets

		1	2	3	4	5
		AISo	HSTo	AIS13	HST13	ICF13
1	AISo	0.03 (0.03)				
2	HSTo		0.10 (0.10)			
3	AIS13			0.03 (0.03)		-0.38 (-0.38)
4	HST13				0.10 (0.10)	
5	ICF13					0.15 (0.15)

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

The fertility index is published for sires.

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

Index	RDC	HOL	JER
ICF_{1-3}	0.60	0.65	0.63
IFL_0	0.75	0.75	0.80
IFL_{1-3}	0.97	0.97	0.96
AIS_0	0.68	0.54	0.78
AIS_{1-3}	0.91	0.85	0.87

Effect of 10 index units

The effect of fertility indexes expressed on the original scale is shown in table 7. It is expressed as the difference in the performance of two daughter groups, where there is a difference of 10 fertility index units in the sires.

Table 7. Effect of +10 fertility index units in the sire on performance of ICF, IFL and AIS in daughter group. Only results for cows are shown

Trait	RDC	HOL	JER	High values mean
ICF_{1-3}	-1.7	-2.2	-1.6	Longer interval
IFL_{1-3}	-4.9	-5.9	-4.0	Longer interval
AIS_{1-3}	-0.08	-0.03	-0.06	More inseminations

References

A joint Nordic model for fertility traits. *A. Fogh, A. Roth, O. Maagaard Pedersen, J.Å. Eriksson, J. Juga, M. Toivonen, I.M.A. Ranberg, T. Steine, U. Sander Nielsen, G. Pedersen Aamand*. INTERBULL Bulletin no. 31 2003. pp 52-56.

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 calvings 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 2 (SE) or 4 (DK and FI) categories, and size of calf is measured in 4 classes (only DK data).

Abbreviation	Definition
SU, 1 st calving/SU, ≥ 2 nd calving	survival over the first 24 hours after birth for heifers and cows separately
CE, 1 st calving /CE, ≥ 2 nd calving	calving ease for heifers and cows separately
CS, 1 st calving /CS, ≥ 2 nd 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-	1982-
Calving ease	1985-	2004-	1982-
Size of calf	1985-	No	No

Birth records are included if:

- Single births
- Calf is not the result of ET
- Father or grandfather is an AI sire
- Father or grandfather belongs to breeds RDC, HOL, JER, RED

Pre-corrections

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

Genetic evaluation

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

Model

The following multi-trait sire model with direct and maternal effects is used for both the Holstein 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
Year within 5-year-herd-country-group	Random
Breed effects for maternal and direct effect	Regression
Heterosis for maternal and direct effect	Regression
Genetic groups	Fixed
Sire (for direct effect)	Random
Maternal grandsire (for maternal effect)	Random

Total heterosis for maternal and direct effects

For Holstein, HF and total heterosis were included. For Red Dairy Cattle, neither breed nor heterosis components were included.

Genetic groups (phantom parent groups)

Genetic groups for animals with unknown parents were included for Holsteins. The genetic groups also made as interaction between breed, country and birth year period clustered in periods of 10 years.

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

	Breed	Calving traits (maternal)					
		1. calving			≥ 2. Calving		
		Survival (SU)	Calving ease (CE)	Size of calf (CS)	Survival (SU)	Calving ease (CE)	Size of calf (CS)
SU	RDC	0.02	0.70	-0.14	0.75	0.19	-0.42
1 st clv.	HOL	0.035	0.60	-0.02	0.60	0.34	0.05

CE	RDC	0.04	-0.52	0.76	0.71	-0.53
1 st clv.	HOL	0.06	-0.45	0.64	0.74	-0.26
CS	RDC		0.04	-0.43	-0.43	0.75
1 st clv.	HOL		0.04	-0.43	-0.43	0.70
SU	RDC			0.01	0.70	-0.58
≥ 2 nd clv.	HOL			0.01	0.60	-0.39
CE	RDC				0.02	-0.54
≥ 2 nd clv.	HOL				0.03	-0.39
CS	RDC					0.045
≥ 2 nd clv.	HOL					0.04

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

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 sire has six solutions for maternal effects and six solutions for direct effects. The variances and covariances of the sire effects (V_{ds} = direct sire, V_{ms} = maternal sire, $COV_{ds,ms}$ = covariance between direct and maternal sire effect) are calculated from the genetic variances and covariances (V_d = direct, V_m = maternal, $COV_{m,d}$ = covariance between direct and maternal) by:

$$V_{ds} = 0.25 \times V_d$$

$$V_{ms} = 0.25 \times V_m + 0.0625 \times V_d + 0.25 \times COV_{m,d}$$

$$COV_{ds,ms} = 0.25 \times COV_{d,m} + 0.125 \times V_d$$

Estimation of breeding values for each single trait

The estimated breeding values for calving^{direct} traits (CD) are calculated from the estimates for the sire of the calf by:

$$CD = 2 \times \text{effect of sire of calf} + \text{direct breed effects}$$

The estimated breeding values for calving^{maternal} traits (CM) are calculated from estimates of effect of sire of cow and effects of sire of calf by:

$$CM = 2 \times \text{effect of sire of cow} + \text{maternal breed effects} - 0.5 \times CD$$

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	$2.00 * SU_1 + 11.00 * CE_1 + 3.30 * SU_{\geq 2} + 14.90 * CE_{\geq 2}$
RDC	$2.01 * SU_1 + 11.35 * CE_1 + 3.37 * SU_{\geq 2} + 15.62 * CE_{\geq 2}$
Jersey	$0.79 * SU_1 + 15.70 * CE_1 + 1.46 * SU_{\geq 2} + 33.70 * CE_{\geq 2}$

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

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.

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	0.89
CE ₁	0.97	0.85	0.87
SU _{≥2}	0.92	0.93	0.85
CE _{≥2}	0.80	0.71	0.69

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

Index	RDC	HOL	JER
SU ₁	0.97	0.97	0.86

CE ₁	0.88	0.94	0.63
SU _{≥2}	0.83	0.87	0.93
CE _{≥2}	0.85	0.81	0.66

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 _{≥2}	-0.2	-0.5	-0.9	More stillborn calves
CE _{≥2}	-0.01	-0.02	-0.01	More difficult calvings

¹For 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 _{≥2}	-0.5	-0.3	-0.2	More stillborn calves
CE _{≥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

¹Days in milk

Basic editing rules

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

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

Sweden: CM, SCC and udder conformation data from 1984, 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 (including Red Holstein), 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	$0.25*CM_{11}+0.25*CM_{12}+0.30*CM_2+0.20*CM_3$
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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

Effect of 10 index units

The effect of indices for udder health described on the original scale is shown in Table 5. It is expressed as the difference in performance of two daughter groups, where there is a difference of 10 index units for udder health in the sires.

Table 5. Effects of +10 index units for udder health in the sire on performance of clinical mastitis in a daughter group

Trait	RDC	HOL	JER	High values mean
CM11	-1.7	-2.4	-2.6	More treatments
CM12	-1.1	-1.4	-1.7	More treatments
CM2	-2.4	-3.3	-2.9	More treatments
CM3	-2.5	-3.8	-3.6	More 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.

Other diseases

The index for other diseases describes the genetic resistance of bulls' daughters to reproductive, digestive and feet and legs diseases.

Data

Trait definition

Records from 1st to 3rd lactation on early reproductive disorders (ERP), late reproductive disorders (LRP), metabolic disorders (MB) and feet and legs diseases (FL), together with records, from the 1st lactation only, on clinical mastitis (CM), are used in the genetic evaluations of other diseases. Data for clinical mastitis are used solely as an information trait. Table 1 gives the disease groups, defined by Østerås et al (2002), used in each of the traits.

Table 1. Disease groups

ERP	LRP	MB	FL
<ul style="list-style-type: none">Retained placentaHormonal reproductive disorders	<ul style="list-style-type: none">Hormonal reproductive disordersInfective	<ul style="list-style-type: none">KetosisMilk feverOther metabolic diseases	<ul style="list-style-type: none">Feet and legs disorders

<ul style="list-style-type: none"> • Infective reproductive disorders • Other reproductive disorders 	<ul style="list-style-type: none"> • reproductive disorders • Other reproductive disorders 	<ul style="list-style-type: none"> • Other feed related disorders • Other diseases 	
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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 disease (1) or not (0), 0 to 40 DIM
LRP1-LP3	Late reproductive disease (1) or not (0), 41 to 305 DIM
MB1-MB3	Metabolic diseases (1) or not (0), -15 to 305 DIM
FL1-FL3	Feet and legs diseases (1) or not (0), -15 to 305 DIM
CM1	Clinical mastitis (1) or not (0), -15 to 305 DIM

Basic editing rules

Data begin in 1990 for all three countries. All Swedish cows covered by the data must have their 1st lactation present in the data. Sweden includes records from all cows. Finland and Denmark include data from all active herds. Active herds are defined as herds in which a certain percentage of cows are diagnosed with mastitis. Traits are recorded as 0 = no disease or 1 = disease occurred.

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 (data only from Denmark and old Danish model).

Model

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

Herd * year	Random
Herd * period(5 year)	Fixed
Calving age * country	Fixed
Year * month of calving * country	Fixed

Breed and heterosis
Genetic groups
Sire

Regression
Fixed
Random

Breed and heterosis

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 13 traits in the evaluation are shown in table 3 and 4. The parameter estimates were either found in Nielsen (1997) or estimated from current data. For computational reasons, residual correlations between lactations were set to zero.

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

Trait	1	2	3	4	5	6	7	8	9	10	11	12	13
ERP1	0.01	0.24	0.03	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
LRP1	0.25	0.01	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
MB1	0.30	0.21	0.01	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
FL1	0.00	-0.02	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
ERP2	0.75	0.25	0.30	0.00	0.01	0.23	0.03	0.01	0.00	0.00	0.00	0.00	0.00
LRP2	0.25	0.75	0.20	0.01	0.25	0.02	0.02	0.01	0.00	0.00	0.00	0.00	0.00
MB2	0.11	0.17	0.81	0.13	0.11	0.20	0.01	0.03	0.00	0.00	0.00	0.00	0.00
FL2	0.00	0.11	0.13	0.78	0.00	0.02	0.03	0.01	0.00	0.00	0.00	0.00	0.00
ERP3	0.87	0.28	0.35	0.00	0.87	0.29	0.13	0.01	0.01	0.02	0.01	0.01	0.00
LRP3	0.24	0.79	0.15	0.01	0.24	0.80	0.19	-0.01	0.28	0.02	0.03	0.01	0.00
MB3	0.14	0.02	0.69	0.19	0.14	0.17	0.85	0.12	0.16	0.00	0.03	0.03	0.00
FL3	0.00	0.01	0.25	0.78	0.00	0.09	0.23	0.69	0.00	0.00	0.23	0.01	0.00
CM1	0.33	0.18	0.39	0.23	0.27	0.15	0.32	0.19	0.22	0.12	0.25	0.15	0.02

Table 4. Genetic correlations (under), residual correlations (above) and heritability's on the diagonal in 1st lactation, Holstein

Trait	1	2	3	4	5	6	7	8	9	10	11	12	13
ERP1	0.02	0.16	0.03	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
LRP1	0.40	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
MB1	0.40	0.49	0.01	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
FL1	0.35	0.36	0.27	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
ERP2	0.68	0.55	0.40	0.34	0.02	0.18	0.04	0.01	0.00	0.00	0.00	0.00	0.00
LRP2	0.33	0.72	0.24	0.22	0.33	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00
MB2	0.17	0.24	0.78	0.28	0.17	0.28	0.01	0.64	0.00	0.00	0.00	0.00	0.00
FL2	0.10	0.21	0.35	0.84	0.10	0.20	0.39	0.01	0.00	0.00	0.00	0.00	0.00
ERP3	0.64	0.55	0.40	0.35	0.80	0.33	0.17	0.00	0.02	0.18	0.04	0.01	0.00
LRP3	0.36	0.64	0.19	0.24	0.36	0.85	0.18	0.17	0.36	0.02	0.01	0.00	0.00
MB3	0.17	0.19	0.65	0.21	0.17	0.23	0.78	0.27	0.17	0.31	0.03	0.02	0.00
FL3	0.19	0.28	0.32	0.86	0.19	0.25	0.32	0.88	0.20	0.24	0.20	0.01	0.00
CM1	0.18	0.15	0.45	0.31	0.15	0.12	0.37	0.26	0.12	0.10	0.29	0.20	0.02

Indexes

The index for other diseases is calculated on the basis of sub-indexes for reproductive, metabolic and feet and legs diseases. The standardization of the breeding values is described in the chapter “Standardization of EBVs and NTM”.

The BV on the original scale for early reproduction, late reproduction, metabolic diseases and feet and legs diseases are combined over lactations. Across lactation BV on the original scale are combined by means of economic values based on economic calculations (table 5).

Table 5. Calculation of the index for other diseases. Subscript refers to lactation

ERP	$0.5*ERP_1+0.3*ERP_2+0.2*ERP_3$
LRP	$0.5*LRP_1+0.3*LRP_2+0.2*LRP_3$
MB	$0.5*MB_1+0.3*MB_2+0.2*MB_3$
FL	$0.5*FL_1+0.3*FL_2+0.2*FL_3$
Other diseases (RDC)	$1.93*ERP+1.04*LRP+1.87*MB+1.7*FL$
Other diseases (HOL)	$2.00*ERP+1.05*LRP+1.88*MB+1.75*FL$
Other diseases (JER)	$1.91*ERP+0.94*LRP+1.70*MB+1.69*FL$

The index for other diseases is published for sires.

Correlation between sub-index and underlying traits

The expected progress of each trait when index for other diseases 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 the index for other diseases and indexes for early reproduction diseases, late reproduction diseases, metabolic diseases and feet and legs diseases

Index	RDC	HOL	JER
ERP ₁	0.76	0.81	
LRP ₁	0.47	0.76	
FL ₁	0.26	0.63	
MB ₁	0.81	0.8	0.47
ERP ₂	0.73	0.76	
LRP ₂	0.44	0.63	
FL ₂	0.23	0.44	
MB ₂	0.66	0.61	0.98
ERP ₃	0.74	0.76	
LRP ₃	0.44	0.64	
FL ₃	0.31	0.52	
MB ₃	0.62	0.61	0.98

Effect of 10 index units

The effect of indexes on other diseases expressed on the original scale is shown in table 5. It is expressed as the difference in performance of two daughter groups, where there is a difference of 10 index units for other diseases in the sires.

Table 5. Effect of +10 index units for other diseases in the sire on performance in reproductive diseases, metabolic diseases and feet and legs diseases in daughter groups

Index	RDC	HOL	JER	High values mean
ERP ₁	-0.6	-1		More treatments
LRP ₁	-0.3	-0.5		More treatments
FL ₁	-0.2	-0.5		More treatments
MB ₁	-0.5	-0.7	0.0	More treatments
ERP ₂	-1	-1		More treatments
LRP ₂	-0.7	-0.7		More treatments
FL ₂	0	-0.2		More treatments
MB ₂	-0.7	-0.8	-1.0	More treatments
ERP ₃	-1.2	-1.2		More treatments
LRP ₃	-1	-0.3		More treatments
FL ₃	-0.2	-0.3		More treatments
MB ₃	-1.1	-1.8	-2.2	More treatments

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 Other Disease 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 resist 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 (including Red Holstein), 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	Fixed
Lactation stage	Fixed
Calving age	Fixed
Herd * six month period	Random
Permanent environment	Random
Animal	Random

Genetic parameters

The genetic parameters used for the 21 traits in the evaluation are displayed in table 1 and 2. The parameters are estimated from the current data.

Table 1. Holstein and Jersey genetic parameters, genetic correlations above, and heritability's on, diagonal

Period / Trait	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
1. lact.																					
1 DE	0.04	0.58	0.03	0.05	-0.13	0.67	-0.01	0.99	0.58	0.18	-0.02	-0.05	0.52	0.02	0.99	0.65	0.29	0.19	0.03	0.52	0.24
2 HH		0.04	0.16	0.32	0.19	0.45	0.10	0.58	0.97	0.32	0.22	0.28	0.40	0.02	0.57	0.98	0.24	0.30	0.21	0.39	0.13
3 SP			0.02	0.63	0.51	0.10	0.64	0.06	0.26	0.82	0.80	0.42	-0.00	0.68	0.01	0.22	0.86	0.63	0.47	-0.08	0.62
4 SH				0.03	0.56	0.12	0.75	-0.01	0.40	0.69	0.91	0.52	0.09	0.81	-0.03	0.38	0.67	0.89	0.45	-0.01	0.72
5 SU					0.03	0.06	0.45	-0.13	0.15	0.55	0.52	0.98	0.08	0.35	-0.15	0.19	0.50	0.51	0.89	0.12	0.33
6 CSC						0.01	-0.13	0.69	0.48	0.19	0.14	0.14	0.95	-0.00	0.63	0.43	0.29	0.14	0.19	0.93	-0.02
7 WLS							0.01	-0.03	0.12	0.67	0.70	0.36	-0.19	0.88	-0.03	0.20	0.68	0.71	0.32	-0.27	0.80
2. lact.																					
8 DE								0.04	0.58	0.17	-0.04	-0.06	0.55	-0.02	0.99	0.64	0.31	0.13	0.00	0.56	0.21
9 HH									0.05	0.40	0.33	0.23	0.42	0.09	0.55	0.95	0.35	0.40	0.16	0.38	0.19
10 SP										0.05	0.81	0.48	0.17	0.79	0.12	0.39	0.95	0.79	0.50	0.06	0.76
11 SH											0.04	0.47	0.13	0.83	-0.10	0.28	0.78	0.91	0.42	0.02	0.72
12 SU												0.05	0.16	0.24	-0.08	0.26	0.44	0.50	0.90	0.21	0.23
13 CSC													0.02	-0.04	0.48	0.37	0.22	0.09	0.13	0.98	-0.05
14 WLS														0.01	-0.04	0.14	0.78	0.81	0.27	-0.17	0.88
3. lact.																					

15 DE	0.04 0.64 0.24 0.10 -0.01 0.50 0.20
16 HH	0.05 0.33 0.38 0.20 0.35 0.28
17 SP	0.06 0.77 0.49 0.12 0.77
18 SH	0.04 0.47 0.00 0.75
19 SU	0.05 0.15 0.15
20 CSC	0.02 -0.14
21 WLS	0.02

Table 2. RDC genetic parameters, genetic correlations above, and heritability's on, diagonal

Period / Trait	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
1. lact.																					
1 DE	0.04	0.66	-0.05	0.12	-0.05	0.70	0.03	0.94	0.73	0.08	0.11	-0.03	0.69	0.07	0.96	0.81	0.30	0.23	0.02	0.51	0.25
2 HH		0.06	0.21	0.32	0.03	0.58	0.08	0.69	0.84	0.25	0.56	0.08	0.56	0.03	0.69	0.86	0.34	0.35	0.18	0.49	0.19
3 SP			0.01	0.69	0.23	0.09	0.61	0.08	0.15	0.90	0.72	0.27	0.03	0.50	0.06	0.17	0.86	0.70	0.30	0.13	0.59
4 SH				0.05	0.25	0.05	0.69	0.15	0.29	0.60	0.79	0.26	0.04	0.65	0.12	0.31	0.69	0.91	0.42	0.14	0.79
5 SU					0.03	0.06	-0.16	-0.11	0.08	0.31	0.17	0.90	0.01	0.03	-0.07	0.05	0.33	0.30	0.66	0.17	0.31
6 CSC						0.03	-0.03	0.74	0.65	0.23	0.12	0.04	0.97	-0.01	0.75	0.69	0.21	0.21	0.01	0.88	0.00
7 WLS							0.01	0.11	0.07	0.51	0.66	-0.03	0.03	0.81	0.07	0.07	0.58	0.76	0.15	-0.05	0.71
2. lact.																					
8 DE								0.04	0.78	0.20	0.12	-0.06	0.72	0.01	0.99	0.86	0.38	0.25	0.07	0.55	0.18
9 HH									0.07	0.27	0.29	0.14	0.59	-0.03	0.78	0.98	0.38	0.34	0.20	0.49	0.14
10 SP										0.03	0.61	0.43	0.17	0.51	0.20	0.30	0.89	0.65	0.49	0.22	0.57
11 SH											0.05	0.18	0.11	0.68	0.10	0.29	0.66	0.82	0.26	0.15	0.73
12 SU												0.02	0.05	0.09	-0.01	0.12	0.39	0.28	0.87	0.16	0.28
13 CSC													0.04	-0.01	0.73	0.64	0.14	0.21	0.07	0.92	-0.03
14 WLS														0.01	-0.01	-0.01	0.60	0.72	0.17	-0.10	0.86
3. lact.																					
15 DE															0.05	0.86	0.37	0.22	0.08	0.56	0.18
16 HH																0.07	0.42	0.35	0.21	0.54	0.17

17 SP	0.05 0.75 0.45 0.16 0.74
18 SH	0.04 0.37 0.28 0.85
19 SU	0.02 0.18 0.30
20 CSC	0.03 -0.07
21 WLS	0.02

Indexes

An index for claw health is calculated on the basis of seven sub-indices. The standardization of the breeding values is described in the chapter “Standardization of EBVs and NTM”.

Table 3. Economic value 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 4).

Table 4. 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 sires.

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

Table 5. 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

Effect of 10 index units

The effect of indexes on claw health expressed on the original scale is shown in table 5. It is expressed as the difference in performance of two daughter groups, where there is a difference of 10 index units for claw health in the sires.

Table 5. Effect of +10 index units for claw health in the sire on performance in claw diseases in daughter groups

Index	RDC	HOL	JER	High values mean
Dermatitis				More treatments
Heal horn erosion				More treatments
Sole Ulcer				More treatments
Sole haemorrhage				More treatments
Skin Proliferation				More treatments
White Line separation				More treatments
Cork Screw Claws				More treatments

References

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

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

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

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

Basic editing rules

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

Moreover, information is included, if:

- Age at 1st calving is between 450 and 1280 days
- Only a lactation that is completed 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 (incl. Red Holstein), 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 1 st calving	Fixed
Year x month of 1 st calving	Fixed
Herd x 5-year period	Fixed
Heterosis	Regression
Genetic groups (as phantom parent groups)	Random
Herd x year of 1 st 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 on the basis of 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.

Effect of 10 index units

The effect of longevity indices expressed on the original scale is shown in table 4. It is expressed as the difference in performance between two daughter groups, where there is a difference of 10 index units for longevity between the sires.

Table 4. Effect of +10 longevity index units in the sire on performance of DAY13 in daughter group

Trait	RDC	HOL	JER	Positive values mean:
-------	-----	-----	-----	-----------------------

DAY13	34	36	35	Longer productive lifetime
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Conformation, milking speed 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 body, the feet and legs, and the udder. Indexes for milking speed and temperament describe how rapidly the cow can be milked and her general temperament.

Trait definition

The traits that are classified and go into genetic evaluation are shown in Table 1. Classification is undertaken by official classifiers employed by agricultural advisory services in the individual countries.

Table 1. Traits classified in the Nordic countries

Group of traits	Traits
Body	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	milking speed, temperament

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 of the traits shown in Table 1 in 1990. However, a few classifications were introduced later: classification of rear udder height started in 2000, rear teat placement in 2000 and udder balance in 2003.

Sweden started classification for almost all 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.

All available data from purebred cows are included in breeding values.

Pre-corrections

All traits were pre-corrected for heterogeneous variance due to country, classifier x month (Denmark) or classifier x year (Sweden and Finland).

Genetic evaluation

Separate genetic evaluations are made for Holsteins (including Red Holstein), Red dairy cattle (including Finncattle) and Jerseys. There are separate evaluations for sires and cows. Data from Finland and Sweden are the same in two evaluations. However, there are differences in data from Denmark. From Denmark only data from first parity obtained by official classifiers are included in the “sire evaluation”. In the “cow evaluation” Danish data from local classification committees and classifications in the 2nd and 3rd lactation are also included.

Model

The model for estimation of breeding values of linear traits is a single-trait animal model:

Calving month (DK)	Fixed
Calving year (FI)	Fixed
Age at calving or age at calving x lactation (SE, DK, FI)	Fixed
Month of classification (SE, FI)	Fixed
Lactation stage at classification (SE, DK, FI)	Fixed
Classifier x time period (DK, FI)	Fixed
Classifier x lactation (DK)	Fixed
Herd x time period/classifier x time period (SE)	Fixed
Herd x time period (DK, FI)	Fixed
Herd x time period (FI)	Random
Yield classes (FI)	Fixed
Time at visit (SE, FI)	Fixed
Stature classes (FI)	Fixed
Animal	Random
Genetic groups	Fixed
Residual	

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.

Table 2. Heritability's (h^2), repeatability coefficients and permanent environmental effect (C^2) applied in the genetic evaluation

Trait	RDC, Holstein and Finncattle			Jersey	
	h^2	repeatability	C^2	h^2	repeatability
1. Stature	0.61	0.80	0.10	0.42	0.72
2. Body depth	0.27	0.50	0.10	0.25	0.32
3. Chest width	0.18	0.36	0.08	0.17	0.29
4. Dairy form	0.31	0.37	0.07	0.27	0.29
5. Top line	0.21	0.36	-	0.19	0.37
6. Rump width	0.33	0.55	0.11	0.32	0.46
7. Rump angle	0.32	0.61	0.07	0.29	0.52
8. Rear legs, side view	0.23	0.59	0.06	0.14	0.33
9. Rear legs, back rear view	0.19	0.33	0.08	0.12	0.26
10. Hock quality	0.18	0.46	-	0.12	0.37
11. Bone quality	0.28	0.44	-	0.16	0.31
12. Foot angle	0.18	0.51	0.08	0.09	0.29
13. Fore udder attachment	0.25	0.49	0.07	0.25	0.43
14. Rear udder height	0.26	0.53	0.07	0.17	0.38
15. Rear udder width	0.22	0.42	0.10	0.25	0.38
16. Udder cleft/support	0.22	0.53	0.05	0.17	0.34
17. Udder depth	0.37	0.56	0.11	0.37	0.58
18. Teat length	0.41	0.58	0.05	0.42	0.55
19. Teat thickness	0.31	0.48	-	0.33	0.47
20. Teat placement (front)	0.20	0.37	0.04	0.41	0.58
21. Teat placement (back)	0.26	0.42	0.05	0.34	0.58
22. Udder balance	0.17	0.41	0.04	0.25	0.43
23. Milking speed	0.25	-	0.05	0.19	-
24. Temperament	0.15	-	0.05	0.05	-

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 body, 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 body, 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 3 and 4.

Table 3. Optimum for Holstein, RDC, Red Holstein, Jersey and Finncattle

	Holstein	RDC	Jersey	Red Holstein	Finncattle
1. Stature	148	142	129	146	136
2. Body depth	6	6	6	6.5	6
3. Chest width	5	5.5	5	6	5
4. Dairy form	6	5.5	7	5.5	5.5
5. Top line	7	7	7	7	7
6. Rump width	5.5	5	6	6	4.5
7. Rump angle	5	5	5	5.2	5
8. Rear legs, side view	5	5	5	5	5
9. Rear legs, back rear view	8	8	9	9	8
10. Hock quality	9	9	9	9	9
11. Bone quality	8	7.5	9	7	7.5
12. Foot angle	6.5	7	6.5	6.5	5
14. Fore udder attachment	9	9	9	9	9
15. Rear udder height	9	9	9	9	9
16. Rear udder width	9	9	9	9	9
17. Udder cleft/support	8	9	9	9	9
18. Udder depth	9	9	9	9	9
19. Teat length	5.5	5.5	5.5	4.5	5
20. Teat thickness	5	6	6	5.5	5
21. Teat placement (front)	8	8	7.5	8	6
22. Teat placement (back)	5	5	5	5	5
23. Udder balance	5	5	5	-	5

Table 4. Weight factors for Holstein, RDC, Red Holstein, Jersey and Finncattle

	Holstein	RDC	Jersey	Red Holstein	Finncattle
1. Stature	3	10	6	10	10
2. Body depth	15	15	14	20	15
3. Chest width	15	20	13	16	15
4. Dairy form	20	10	10	15	15
5. Top line	12	10	25	10	15
6. Rump width	15	15	11	11	20
7. Rump angle	20	20	11	8	10
8. Rear legs, side view	10	15	20	10	25
9. Rear legs, back rear view	30	25	20	15	25
10. Hock quality	18	25	20	25	20
11. Bone quality	17	15	15	20	15
12. Foot angle	25	20	25	30	15
13. Fore udder attachment	17	20	25	18	14
14. Rear udder height	10	8	5	10	9
15. Rear udder width		5			5
16. Udder cleft/support	10	12		10	9
17. Udder depth	24	20	35	18	12
18. Teat length	5	5	3	6	4
19. Teat thickness	5	5	12	6	4
20. Teat placement (front)	7	7	15	14	30
21. Teat placement (back)	12	8		6	4
22. Udder balance	10	10			9
23. Codes for body			10	10	
24. Codes for udder			5	12	

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

Table 5. Correlation between conformation traits and index for body, feet and legs, and mammary system

	RDC	Holstein/ Red Holstein	Jersey	Finn Cattle
	Index for body			
Stature	0.83	0.61	0.84	
Body depth	0.30	0.12	0.08	
Chest width	0.31	-0.18	0.29	
Dairy form	0.23	0.65	0.40	
Top line	0.13	0.36	0.47	
Rump width	0.68	0.26	0.69	
Rump angle	-0.20	0.32	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	

Effect of 10 index units

The effect of indexes for body, feet and legs, and udder, expressed on the original scale, is shown in Table 6. It is expressed as the difference in

performance of two daughter groups, where there is a difference of 10 index units in the sires.

Table 6. Effect of +10 index units for body, feet and legs, udder and workability traits in the sire on performance of linear traits in daughter group

	RDC	Hol/ Red	JER	Finn Cattle	High values mean:
	Index for body				
Stature	1.4	0.8	0.7		Higher
Body depth	0.1	0.0	0.0		Deeper
Chest width	0.0	0.0	0.0		Wider
Dairy form	0.1	0.1	0.1		More angular
Top line	0.0	0.1	0.1		More upwards
Rump width	0.2	0.1	0.2		Wider
Rump angle	-0.1	0.1	0.1		Lower pins
	Index for feet and legs				
Rear legs, side view	-0.1	0.0	-0.1		More sickled
Rear legs, rear view	0.1	0.1	0.1		More parallel
Hock quality	0.2	0.1	0.1		More dry
Bone quality	0.2	0.1	0.1		Finer and thinner
Foot angle	0.0	0.0	0.1		More steep
	Index for mammary system				
Fore udder attachment	0.2	0.2	0.2		Stronger
Rear udder height	0.2	0.1	0.1		Wider
Rear udder width	0.1	0.1	0.1		Higher
Udder cleft	0.1	0.0	0.1		Stronger
Udder depth	0.3	0.4	0.2		Higher
Teat length	0.1	0.1	0.0		Longer
Teat thickness	0.0	0.0	0.0		Thicker
Teat placement (front)	0.1	0.1	0.1		More close
Teat placement (back)	0.0	0.0	0.1		More close
Udder balance	0.1	0.1	0.1		Deep front
	Workability				
Milk ability (g/minute)	+10	+10	+10		Faster
Temperament					Better

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.

Standardization of EBVs and NTM

Estimated breeding values

EBVs for the yield traits growth, fertility, calving^{direct}, calving^{maternal}, udder health, other diseases, claw health, body, feet and legs, udder, milking speed, temperament and longevity are standardized in the same way. The formula for adjusting the mean and standard deviation of EBV is:

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

Standardization of 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	RED
Milk 1 st , (kg)	490.1	436.8	296.6	682.5
Milk 2 nd , (kg)	556.0	525.8	359.0	693.0
Milk 3 rd , (kg)	504.0	557.6	353.1	599.8
Protein 1 st , (kg)	18.16	17.03	13.45	20.77
Protein 2 nd , (kg)	20.92	21.24	16.45	20.89
Protein 3 rd , (kg)	19.65	22.28	16.60	18.10
Fat 1 st , (kg)	18.31	16.05	15.24	19.98
Fat 2 nd , (kg)	20.34	20.86	18.22	18.91
Fat 3 rd , (kg)	18.90	22.09	15.12	15.86
Pct protein 1 st	0.02	0.03	0.03	-0.04
Pct protein 2 nd	0.02	0.03	0.03	-0.04
Pct protein 3 rd	0.03	0.04	0.04	-0.03
Pct fat 1 st	-0.03	-0.03	-0.05	-0.15
Pct fat 2 nd	-0.03	-0.02	-0.05	-0.15
Pct fat 3 rd	-0.02	-0.02	-0.09	-0.13
Persistence 1 st	-8.4	0.4	30.3	7.1
Persistence 2 nd	5.1	24.7	18.6	-1.1
Persistence 3 rd	21.8	18.7	24.9	8.3
Total milk, (kg)	512.6	487.6	326.6	669.1
Total protein, (kg)	19.29	19.34	14.98	20.27
Total fat, (kg)	19.04	18.70	16.11	18.84
Total pct protein	0.02	0.03	0.03	-0.04
Total pct fat	-0.03	-0.02	-0.06	-0.15
Total persistency	1.7	11.4	25.7	4.9

Base difference: 2005 base – 1995 base

	HOL	RDC	JER	RED
Milk 1 st , (kg)	1188.5	969.7	830.5	1342.0
Milk 2 nd , (kg)	1309.2	1088.4	872.7	1387.6
Milk 3 rd , (kg)	1163.5	1131.6	879.2	1266.7
Protein 1 st , (kg)	41.54	37.33	31.09	42.61
Protein 2 nd , (kg)	46.39	43.60	33.71	45.29
Protein 3 rd , (kg)	42.73	44.84	34.36	42.03
Fat 1 st , (kg)	37.66	36.32	36.42	50.88
Fat 2 nd , (kg)	40.36	42.94	37.93	52.48
Fat 3 rd , (kg)	36.33	44.73	32.32	50.07
Pct protein 1 st	0.02	0.05	-0.06	-0.06
Pct protein 2 nd	0.02	0.07	-0.04	-0.04
Pct protein 3 rd	0.04	0.07	-0.03	-0.02
Pct fat 1 st	-0.17	-0.07	-0.28	-0.14
Pct fat 2 nd	-0.17	-0.04	-0.26	-0.12
Pct fat 3 rd	-0.14	-0.04	-0.34	-0.17
Persistence 1 st	-4.2	-34.0	34.6	-14.1
Persistence 2 nd	22.9	-34.4	8.5	-8.4
Persistence 3 rd	59.4	-43.9	12.4	28.9
Total milk, (kg)	1219.7	1037.7	852.9	1340.6
Total protein, (kg)	43.23	40.71	32.53	43.30
Total fat, (kg)	38.20	39.99	36.05	51.20
Total pct protein	0.03	0.06	-0.04	-0.05
Total pct fat	-0.16	-0.05	-0.29	-0.14
Total persistency	16.7	-36.1	22.3	-3.8