

# NAV FEMALE FERTILITY EVALUATION

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A. - M. Tyrisevä\*, K. Muuttoranta\*, J. Pösö†, U. S. Nielsen‡, J.-Å. Eriksson§, G. P. Aamand#, E. A. Mäntysaari\*, and M. H. Lidauer\*

\*Natural Resources Institute Finland (Luke), Green Technology, Biometrical Genetics, 31600 Jokioinen, Finland; †Faba Co-op, 01301 Vantaa, Finland; ‡SEGES Cattle, 8200 Aarhus N, Denmark

§Växa Sverige, 75105 Uppsala, Sweden; #NAV Nordic Cattle Genetic Evaluation, 8200 Aarhus, Denmark

## Introduction

The first joint Nordic female fertility evaluation was launched in 2005 (Fogh et al., 2003). It was updated in 2014-2016 to e.g. meet the demands of genomic evaluations. The former multi-trait repeatability sire model has been now replaced by a multi-trait multi-lactation animal model with newly estimated genetic parameters. Further, NAV co-operates with EuroGenomics Consortium countries in genomic evaluations for Holstein, and there is a need to harmonize phenotypes used for fertility evaluations among countries to improve the precision of genomic evaluations. Thus, it was decided that one of the common traits would be a conception trait and it has now been included among the group of traits under fertility evaluation in Nordic countries as well. Further, use of sexed semen is becoming more and more popular in Nordic countries and must be taken into account in the evaluation models because its slightly detrimental effect on conception rate.

## Traits

Abbreviation	Definition
ICF	Interval as days from calving to first service (1-3=cows <sup>A</sup> )
NRR	Non-return rate at 56 days after first service (0=heifers, 1-3=cows)
CR	Conception rate as success, failure or probability (0=heifers, 1-3=cows)
AIS	Number of services (0=heifers, 1-3=cows)
IFL	Interval as days from first to last service (0=heifers, 1-3=cows)
HST	Heat strength (0=heifers, 1-3=cows, data only from Sweden)

<sup>A</sup>1-3 refers to combined index for cows through parities 1 to 3

### Other abbreviations used:

DNK	Denmark, Danish
FIN	Finland, Finnish
SWE	Sweden, Swedish
HOL	Holstein
RDC	Red Dairy Cattle
JER	Jersey

## Data used for evaluations

This document is based on information on August 2017 evaluation.

### Input data

Each country sends several input files including information on identity, birth date, breed, parental information, herd, calvings, inseminations, pregnancy checks, selling alive, cullings etc. For Finland and Sweden, all breeds are included in these files, whereas Denmark sends separate set of files for each breed. The data structure of the input files differs among countries, therefore editing is at first carried out separately within each country to harmonize e.g. codes for cullings. Currently, pregnancy check records are included from each country. They have been collected in the countries' data bases since the early 80's in Sweden and Denmark, and in Finland somewhat later, since 2003.

After creating phenotypes and selecting those that are within acceptable limits and creating fixed effects, breed specific data sets are created because separate genetic evaluations are carried out for Holstein (including Red Holstein), Red dairy cattle (including Finncattle) and Jersey. For Jersey, Finnish and Swedish Jersey animals are included in the Danish population because their population size is so small. Two different data sets are created within each breed, one for CR and another for the other fertility traits. This is because the CR data consists of repeated observations and its data structure and the evaluation model setting under MiX99 differs notably from those of the other fertility traits. Besides input data from countries, NAV pedigree file as well as a file comprising breed proportions is used.

After sorting input records (calvings, services, pregnancy check informations, cullings) chronologically within each cow by countries, it was noticed that records from Sweden differ somewhat from those coming from Denmark and Finland. When birth year classes until year 2011 were studied, almost 30% of the records from Sweden ended with calving record and around 65% of the records with slaughter record, whereas in Denmark and Finland the last records of the females in those birth year classes were mainly slaughter records (Denmark around 90%, Finland around 95%) and contrary to Sweden only tiny proportion were calving records. The rest of the last records in all countries consisted of services, pregnancy check results and sold alive records.

Further, the data structure in the most recent birth year classes studied (2012-2015) also differed somewhat between countries. For all countries, proportion of slaughter records decreased notably, whereas proportion of calvings, services and positive pregnancy check results increased. However, only in Sweden, also proportion of negative pregnancy check results increased, being around 10%, whereas in Denmark and Finland there was only a slight increase; their proportion remained in less than 3%. It is possible that information from negative pregnancy checks is not recorded as well as positive ones, unless the information is automatically coming to databases as may be the case with pregnancy checks from milk samples. During this project, Sweden added information on pregnancy checks from milk samples to their input data and it can explain part of this difference.

The above mentioned differences in the input data have an effect on the phenotypic records, as IFL of the records ended with calving remains in its original value, whereas records in progress and slaughter records are prolonged for IFL based on the pregnancy

control status. Therefore, it would be recommendable that all input data coming from countries would be of similar structure, although it can be very challenging, because of the very nature of the field data.

### **Data editing**

The data used for fertility evaluation is cut until the average yearly data flow is reached in each country. That is, the most historical data is excluded. The data starts in year 1982 (1983) for Sweden, in year 1985 (1986) for Denmark, and in year 1992 (1993) for Finland for RDC (HOL). Majority of the JER data comes from Denmark, starting in 1985. The year refers to the birth year of females. Heifers and cows up to third lactation are included for each breed. No restriction is set that a female's records should start from heifer records since this would, e.g., penalize herds recently joined to performance recording. However, on average 84% of females start with heifer records and less than 2% with second or third lactation records.

Females included in the fertility evaluation must be sired by a bull found in the herdbook. A breed of the female must be the same as its paternal and maternal grandsire breed is. Donors or recipients of embryo transfer are excluded. Age at first service for heifers is constrained to be from 270 to 900 d for all breeds, and age at first calving from 550 to 1100 d for RDC and HOL, and from 550 to 975 d for JER. Heifers that are older than 1240 days without calving or culling and cows having more than two years from the last calving are excluded. Double inseminations within the same cycle ( $\leq 5$  days) are excluded and the bounds of gestation length are set from 260 to 302 days. Cows changing herd during a service period are excluded for that particular parity.

Nordic countries use penalized records for ICF, IFL, AIS, and NRR for cases that were not ended with calving or for a positive pregnancy check result to take into an account an uncertainty of the final phenotype for records in progress or those ended with culling, and to decrease the effect of right hand censoring of the data. This enables utilization of all possible data and diminishes a bias inherent in the data in which the most fertile cows with calving records or verified pregnancy only are included. Penalizing means either setting some of the cow's records to missing values or prolonging the original records (IFL) by utilizing country, breed and parity specific phenotypic means. How this is carried out depends on the time between the first and/or the last insemination and culling or data extraction date as well as the pregnancy check status (positive, negative, missing). The acceptable boundaries for records to be included are 20-230 d for ICF, 0-365 d for IFL, and 1-8 services for AIS. Further, if a record reaches the above mentioned maximum, it will be reset to 180 d for ICF, 230 d for IFL, and 5 services for AIS to normalize the distributions. Detailed editing rules can be found from the separate document, see the Appendix.

For CR, all available data is used to define phenotypes of the services (success, failure). Then the last 150 days of the newest data is cut to avoid right hand censoring. Basic editing rules of the CR are the same as for the traditional phenotypes above. Defining the phenotype of each service is carried out as an iterative process. Each new insemination is preliminary set to successful, i.e., CR = 1. If it is followed with the new insemination, the former CR record is set to failure, i.e., CR = 0, or a missing phenotype, if the cow was inseminated within the same cycle ( $\leq 5$  days).

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

After calving, it is verified whether the last insemination is within the limits of acceptable pregnancy period (260-302 d). If the pregnancy period is longer, the last service is set to zero, because it is possible that, e.g., a natural service was used. If the pregnancy period is shorter, it is checked iteratively whether some of the former inseminations is within acceptable limits, in which case insemination for this day is set to 1. All inseminations that are newer than the successful one are set to missing values.

When a cow has been slaughtered, the last phenotype is left successful only in the case of a positive pregnancy check otherwise it is set to zero. For record in progress, CR is set to 0.7, i.e. average NRR in heifers. The rationale behind this is that if there are no events during 150 days before of the extraction of data, it is very probable that a cow is pregnant and not calved yet.

Only the first 10 inseminations are accepted in the data to normalize the distribution. Less than 1% of the data is outside this range.

Detailed editing rules for CR can be found in the separate document, see the Appendix.

### **Pre-corrections for heterogeneous variance**

Phenotypes of all traits are pre-corrected for heterogeneous variance due to country, year of first calving, and parity.

### **Use of sexed semen in Nordic dairy cattle and consequences for fertility models**

The use of sexed semen is becoming more and more popular in Nordic countries, especially in Jersey for which fattening of bull calves is not economical (Table 1). During the last years (2015 onwards), more than 40% of the first services in Danish JER heifers were carried out with sexed semen, for Finnish and Swedish JER heifers somewhat less, as well as for JER cows. These results are based on the raw data coming from countries and it is possible that not all services carried out with sexed semen have been marked correctly down in the databases. Therefore, its prevalence can be even higher. Use of sexed semen is the least common in RDC and countries differ in prevalence. Its use is clearly the most common in Denmark, where it has been rapidly adopted in use. For instance, around 30% of first services in Danish HOL and RDC heifers too were carried out with sexed semen during the last years, while in Finland and Sweden less than 10% (Table 1). Use of sexed semen is the most common at first service and decreases with increasing number of services. However, in JER heifers it is rather common to use sexed semen in later services also (Table 1).

For some bulls, predominantly sexed semen is marketed and used. Conception rate is somewhat lower with sexed than with conventional semen. In the Nordic data set, the diminishing effect has been around 11% units for all breeds and parities. It is therefore expected that the bulls having a lot of daughters inseminated with sexed semen have biased breeding values for fertility. Therefore, it was decided to account for the use of sexed semen

in the fertility evaluation in Nordic countries. This was done for CR, but also for NRR, IFL, and AIS. For the latter two, pre-corrected phenotypes are used because we found no proper way to model the use of sexed semen as a fixed effect. A pre-corrected AIS = original AIS – nsex × 0.11, in which nsex refers to a number of inseminations carried out with a sexed semen. Scaled on an average cycle, coefficients for use of sexed semen for IFL are 3.8 days in heifers and 4.6 days in cows. Therefore, a pre-corrected IFL = original IFL – nsex × coefficient.

**Table 1.** Prevalence of use of sexed semen in the data from 2015 onwards by breeds, parities and services from 1 to 3. The data was extracted in June 2017. For Jersey, only Danish cows are shown as the majority of the data comes from Denmark.

	Prevalence of use of sexed semen,		
	1.	2.	3.
	%		
<b>Holstein</b>			
Heifers			
DNK	30.3	17.8	7.6
FIN	7.9	5.8	3.0
SWE	8.4	5.5	2.4
Cows			
DNK	2.5	1.6	0.9
FIN	4.7	3.5	2.3
SWE	2.3	1.5	0.8
<b>RDC</b>			
Heifers			
DNK	29.1	16.4	7.2
FIN	4.6	3.0	1.7
SWE	4.3	2.7	1.2
Cows			
DNK	3.7	2.3	1.2
FIN	3.5	2.5	1.7
SWE	1.9	1.4	0.8
<b>Jersey</b>			
Heifers			
DNK	41.0	28.0	11.7
FIN	33.9	32.6	27.4
SWE	23.4	23.6	18.8
Cows			
DNK	19.3	13.8	6.1

#### Amount of data

Data used for evaluations in August 2017 consisted of 20 million HOL, 11.6 million RDC, and 2.1 million JER records both for IFL and NRR from heifers and cows in parities 1 to 3, and 13 million HOL, 7.7 million RDC, and 1.4 million JER records for ICF from cows in parities 1 to 3. The number of CR observations rose to 38 million for Holstein, 21.6 million for RDC, and 3.8 million for JER. Second parity records comprised approximately 22% of all records of heifers and cows, whereas that for third parity records was 13%. Of the cow records, 33% came from second parity cows and around 20% from third parity cows. Slight differences existed

between breeds; JER having more third parity records than HOL and RDC, and HOL having the lowest proportion of them.

### Statistical models

Separate evaluations are carried out for HOL, RDC, and JER. Despite separate evaluations for different breeds, for Finland all breeds are entered in the breed-specific data sets to increase the size of the contemporary groups. Due to this, fixed effects are nested within-breed for Finland. For simplicity this is not mentioned in the statistical models below. Fertility traits are analyzed in 3 different clusters to increase the benefits of several measures of fertility through genetic correlations under multi-trait multi-lactation setting, and to decrease on the other hand over-parameterization. For the latter reason, AIS, IFL and CR are analyzed in separate clusters since they are functions of each other. The clusters are following: 1) ICF1-3, NRR0, NRR1-3, IFLO, IFL1-3, 2) ICF1-3, AIS0, HST0, AIS1-3, HST1-3, and 3) CR0, CR1-3. Zero at the end of the trait name refers to heifers, whereas 1-3 to parities from 1 to 3.

In addition to considering heifer and cow fertility as different, but genetically correlated traits, the same applies to all parities under Nordic fertility evaluation models (Muuttoranta et al. 2015, 2018). Genetic correlations among first, second, and third parities are in general high, but not one, indicating somewhat different genetic background (Muuttoranta et al. 2015, 2018).

All traits are analyzed under linear models instead of threshold models, even if CR and NRR are binary traits following binomial distributions, and AIS and HST are score traits following Poisson distributions. However, applying threshold models for large data sets analyzed under multi-trait multi-lactation models is currently impossible due to the complexity of the setting. It is however known that linear models are rather robust against violation of assumptions. Further, several studies have implied that the use of threshold models for large data sets and having phenotypic incidence close to intermediate gives results close to those obtained from the threshold models (e.g., Boichard and Manfredi, 1994; Kadarmideen et al., 2003; Kuhn et al. 2006; Negussie et al. 2008).

### Statistical model for ICF

The following multi-lactation animal model is fitted for each breed:

$$y_{ijklmn} = hy_i + cym_j + iage_k + tothet_l + animal_m + e_{ijklmn},$$

where  $y_{ijklmn}$  is an ICF observation for cows in parities 1 to 3. The fixed effects of the model are:  $hy_i$  = herd  $\times$  first calving year,  $iy_m_j$  = calving year  $\times$  month  $\times$  country,  $iage_k$  = age of heifer at first service  $\times$  country,  $tothet_l$  = total heterosis modeled as a fixed regression effect across countries. The random effects are:  $animal_m$  = additive animal, and  $e_{ijklmn}$  = residual.

### Statistical model for NRR

The following multi-lactation animal model is fitted for each breed:

$$y_{ijklmno} = hy_i + iym_j + iage_k + stype_l + tothet_m + animal_n + e_{ijklmno},$$

where  $y_{ijklmno}$  is an NRR observation for heifers and cows in parities 1 to 3. The fixed effects of the model are:  $hy_i$  = herd  $\times$  birth year for heifers, or herd  $\times$  first calving year for cows,  $iy_mj$  = first service year  $\times$  month  $\times$  country,  $iage_k$  = age of heifer at first service  $\times$  country,  $stye_l$  = year class  $\times$  semen type of first service  $\times$  country,  $tothet_m$  = total heterosis modeled as a fixed regression effect across countries. The random effects are:  $animal_n$  = additive animal, and  $e_{ijklmno}$  = residual.

### Statistical model for IFL, AIS, and HST

The following multi-lactation animal model is fitted for each breed:

$$y_{ijklmn} = hy_i + iy_mj + iage_k + tothet_l + animal_m + e_{ijklmn},$$

where  $y_{ijklmn}$  is a pre-corrected IFL or AIS observation or an original HST observation for heifers and cows in parities 1 to 3. The fixed effects of the model are:  $hy_i$  = herd  $\times$  birth year for heifers, or herd  $\times$  first calving year for cows,  $iy_mj$  = first service year  $\times$  month  $\times$  country,  $iage_k$  = age of heifer at first service  $\times$  country,  $tothet_l$  = total heterosis modeled as a fixed regression effect across countries. The random effects are:  $animal_m$  = additive animal, and  $e_{ijklmn}$  = residual.

### Statistical model for CR

The following multi-lactation repeatability animal model is fitted for each breed:

$$y_{ijklmnopq} = hy_i + iy_mj + iage_k + service_l + stye_m + tothet_n + pe_o + animal_p + e_{ijklmnopq},$$

where  $y_{ijklmnopq}$  is a repeated CR observation for heifers and cows in parities 1 to 3. The fixed effects of the model are:  $hy_i$  = herd  $\times$  birth year for heifers, or herd  $\times$  first calving year for cows,  $iy_mj$  = insemination year  $\times$  month  $\times$  country,  $iage_k$  = age of heifer at first service  $\times$  country,  $service_l$  = service number  $\times$  country,  $stye_m$  = year class  $\times$  semen type  $\times$  country,  $tothet_n$  = total heterosis modeled as a fixed regression effect across countries. The random effects are:  $pe_o$  = permanent environment,  $animal_p$  = additive animal, and  $e_{ijklmnopq}$  = residual.

### Modeling herd $\times$ year effects

The choice of the year of calving in the herd  $\times$  year effect for cows was found to be crucial to minimize a bias caused by right-hand censoring of the data, even if the penalized phenotypes were used for traditional traits and the most recent CR data was excluded. The actual calving year would be the best choice to model the herd  $\times$  year effect for cows, because it is the closest year for observations. However, by fitting herd  $\times$  actual calving year the genetic trend in the youngest birth year classes notably improved compared to the herd  $\times$  first calving year in the model, indicating non-random distribution of daughters in the actual calving year  $\times$  season classes. The most fertile daughters calve first, belonging to the first classes and the least fertile daughters calve last, belonging to the last classes. This bias was most pronounced for interval traits. For more information, see Tyrisevä et al. (2017).

### Modeling service number effect for CR

Another crucial effect in the model fitted for CR was the service number to account for the change in expectation if a cow failed to conceive. Muuttoranta et al. (2018) showed in the simulation study that by ignoring the service number effect, the environmental trend was severely over-estimated, and genetic trends and estimates of heritability were inflated. The solutions of the service number clearly increased with the increasing number of services, capturing the change in expectation, if a cow failed to conceive at the first service (Tyrisevä et al. 2017; Muuttoranta et al. 2018).

### Genetic parameters

All variance components were re-estimated or estimated during the update of Nordic fertility evaluation models as some of the former variance components were based on values from literature or were set to zero. Further, no variance components existed for CR. More information on estimation of variance components can be found from Muuttoranta et al. (2015, 2018). The applied genetic parameters for predictions are collected in Tables 2-7.

**Table 2.** Heritabilities (diagonal), genetic (upper triangle) and residual (lower triangle) correlations for Holstein in cluster 1.

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

**Table 3.** Heritabilities (diagonal), genetic (upper triangle) and residual (lower triangle) correlations for RDC and Jersey in cluster 1.

	NRRO	IFLO	NRR1	ICF1	IFL1	NRR2	ICF2	IFL2	NRR3	ICF3	IFL3
NRRO	<b>0.015</b>	-0.85	0.45	0.15	-0.40	0.25	0.10	-0.20	0.15	0.08	-0.10
IFLO	-0.47	<b>0.015</b>	-0.25	0.10	0.40	-0.15	0.05	0.25	-0.10	0.03	0.20
NRR1	0.01	-0.01	<b>0.015</b>	0.25	-0.70	0.65	0.20	-0.60	0.60	0.15	-0.50
ICF1	0.02	-0.01	0.03	<b>0.04</b>	0.36	0.15	0.86	0.30	0.10	0.79	0.25
IFL1	-0.02	0.03	-0.34	-0.03	<b>0.03</b>	-0.55	0.40	0.85	-0.45	0.35	0.74
NRR2	0.02	-0.02	0.03	0.01	-0.01	<b>0.015</b>	0.15	-0.74	0.73	0.10	-0.65
ICF2	0.01	0.00	0.03	0.09	0.04	0.06	<b>0.04</b>	0.38	0.05	0.85	0.35
IFL2	-0.02	0.02	-0.03	0.03	0.06	-0.35	-0.04	<b>0.03</b>	-0.61	0.31	0.88
NRR3	0.00	-0.01	0.03	0.00	-0.03	0.04	0.03	-0.02	<b>0.015</b>	0.09	-0.70
ICF3	0.01	0.00	0.02	0.06	0.03	0.03	0.10	0.05	0.07	<b>0.04</b>	0.38
IFL3	-0.02	0.03	-0.01	0.01	0.05	-0.03	0.03	0.09	-0.33	-0.05	<b>0.03</b>

**Table 4.** Heritabilities (diagonal), genetic (upper triangle) and residual (lower triangle) correlations for Holstein in cluster 2.

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

**Table 5.** Heritabilities (diagonal), genetic (upper triangle) and residual (lower triangle) correlations for RDC and Jersey in cluster 2.

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

**Table 6.** Heritabilities (diagonal), genetic (upper triangle) and permanent environment (lower triangle) correlations for Holstein in cluster 3 for conception rate. Residual correlations are zero.

	CR0	CR1	CR2	CR3
CR0	<b>0.01</b>	0.72	0.55	0.53
CR1	0.07	<b>0.025</b>	0.93	0.92
CR2	0.06	0.09	<b>0.03</b>	0.96
CR3	0.055	0.076	0.10	<b>0.03</b>

**Table 7.** Heritabilities (diagonal), genetic (upper triangle) and permanent environment (lower triangle) correlations for RDC and Jersey in cluster 3 for conception rate. Residual correlations are zero.

	CR0	CR1	CR2	CR3
CR0	<b>0.01</b>	0.65	0.57	0.47
CR1	0.05	<b>0.02</b>	0.93	0.84
CR2	0.03	0.09	<b>0.023</b>	0.95
CR3	0.02	0.07	0.10	<b>0.025</b>

### **Pedigree and genetic groups**

Pedigree information used in the genetic evaluations were constructed separately for each breed group (HOL, JER, RDC) from the full NAV pedigree file comprising approximately 45 million animals from Denmark, Finland and Sweden. First, animals that were not linked to the fertility data files were pruned out. After pruning, missing and pruned parent information was replaced by genetic groups that were constructed by the breed and the birth year of the animal, and by the selection path. This resulted in pedigree files of 10.6 million HOL, 81 000 JER, and 6.1 million RDC animals, respectively. Genetic groups were treated as random effects in the breeding value predictions with a value of 0.333 added on diagonals for the genetic group equations in the inverse of the coefficient matrices. This value equals to one additional offspring in a phantom parent group.

### **Software and solving of the mixed model equations**

MiX99 software was used both for the breeding value predictions and variance component estimation (MiX99 Development Team, 2017). More information on the latter can be found from Muuttoranta et al. (2018). The prediction models were solved by iterative methods using a preconditioned conjugate gradient method with parallel computing (Strandén and Lidauer, 2001). A relative change of 1.0E-5 between solutions was set for the convergence criterion for all the applied models. Total number of equations ranged from 12.5 million (JER) to 123 million (HOL) for cluster 1, and from 8 million (JER) to 79 million (HOL) for cluster 3.

### **Indices**

The index for fertility is calculated on the basis of sub-indices for AIS, ICF and IFL. The standardization of the relative breeding values is described in the NAV documentation of routine genetic evaluations (Nordic Cattle Genetic Evaluation, 2017). Standard deviations used in standardization of animal solutions to index values are listed in Table 8.

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 9).

The fertility index is published for sires and cows.

**Table 8.** Standard deviations used in standardization of animal solutions to index values.

	<b>HOL</b>	<b>JER</b>	<b>RDC</b>
<b>ICF1</b>	5.856	4.023	4.436
<b>ICF2</b>	5.946	3.867	4.221
<b>ICF3</b>	5.696	3.678	3.968
<b>ICF1-3</b>	5.734	3.831	4.175
<b>IFLO</b>	3.604	2.894	3.467
<b>IFL1</b>	8.478	5.998	7.737
<b>IFL2</b>	8.333	5.840	8.137
<b>IFL3</b>	7.749	5.843	8.111
<b>IFL1-3</b>	6.148	5.764	7.760
<b>AISO</b>	0.0931	0.0804	0.1067
<b>AIS1</b>	0.1489	0.1241	0.1461
<b>AIS2</b>	0.1431	0.1174	0.1546
<b>AIS3</b>	0.1309	0.1184	0.1434
<b>AIS1-3</b>	0.1397	0.1168	0.1435
<b>HST0</b>	0.0199	-	0.0231
<b>HST1</b>	0.0229	-	0.0249
<b>HST2</b>	0.0232	-	0.0225
<b>HST3</b>	0.0231	-	0.0199
<b>HST1-3</b>	0.0218	-	0.0214
<b>CR0</b>	0.0347	0.0301	0.0428
<b>CR1</b>	0.0600	0.0462	0.0568
<b>CR2</b>	0.0627	0.0489	0.0625
<b>CR3</b>	0.0619	0.0517	0.0625
<b>CR1-3</b>	0.0607	0.0472	0.0590
<b>interval trait</b>	12.15	8.34	10.49
<b>fertility index</b>	27.39	19.75	26.01

**Table 9.** Calculation of fertility index.

<b>HOL</b>	$0.73 \times \text{IFLO} + 0.62 \times \text{ICF1-3} + 2.35 \times \text{IFL1-3} + 10.17 \times \text{AISO} + 35.55 \times \text{AIS1-3}$
<b>RDC</b>	$0.61 \times \text{IFLO} + 0.56 \times \text{ICF1-3} + 1.78 \times \text{IFL1-3} + 10.14 \times \text{AISO} + 27.24 \times \text{AIS1-3}$
<b>JER</b>	$0.93 \times \text{IFLO} + 0.28 \times \text{ICF1-3} + 1.61 \times \text{IFL1-3} + 9.27 \times \text{AISO} + 27.14 \times \text{AIS1-3}$

### Reliabilities

The approximated EBV reliabilities were computed by the method of Misztal and Wiggans (1988), implemented in the Apax99 software (MiX99 Development Team, 2017). For cows, an overall reliability value across parities is calculated by using weights of 0.5, 0.3, and 0.2 for the first, second, and third parity, respectively.

Even if the reliabilities are currently approximated according to Misztal and Wiggans (1988), results from the study by Tiina Lehtonen (Luke) indicate that the Tier and Meyer method (2004) would be better method for approximation and also possible to be applied in the

fertility evaluations. The whole study can be found from the separate document, see the Appendix.

### **Future improvements of the fertility evaluation models**

In the current models, total heterosis was modeled for each breed. However, recombination loss should be modeled as well. Two different models were tested with unsatisfactory results: a) recombination loss was modeled as a fixed effect across countries, and b) countries were allowed to vary around the average effect by modeling recombination loss also as a random effect within countries. The latter would possibly have worked for pure Holstein data, but in order to increase the size of the contemporary groups of Finnish animals, all breeds from Finland are included in the breed-specific data sets and RDC has a very heterogeneous breed structure. It is suggested that the modeling of heterosis and recombination loss will be changed in the future in accordance with the test-day models.

Year interaction has been included in the semen type effect since it is very probable that the skills and practices related to sexed semen are improving with the years, diminishing the deteriorating effect. This can already be seen in the solutions. However, it would be more elegant that the year interaction would be only for sexed semen and not for conventional semen. This classification is already included in the data, but not thoroughly tested. Further, AIS and IFL were pre-corrected for the sexed semen effect, but by using an overall effect that was 11% at the time of the model development. As mentioned above, the effect will be changed the most probably with the years and this should be taken into account in the pre-corrections at some point. However, it is not so straightforward task to do as the effects are based on the solutions from the MME.

Modeling age of heifers at first service has raised some debate should it be included in the model or not, as the time of puberty is partly genetically regulated. However, also management of calves and young heifers has an influence, if they are under- or overfed. However, the age of heifers has long-term influences in dairy cows, partly indirect through the effects on lactation physiology.

Effects that have probably minor effect on the evaluation models but could still be tested has been listed in Appendix.

## **Results**

### **Phenotypic level of female fertility in Nordic countries**

Breeds differed in the phenotypic level of ICF (Table 10). For all parities and countries, HOL had the longest ICF means and JER the shortest. The latter population consists mainly of Danish cows. Rather large differences in the ICF means were found among countries (Table 10). For all breeds, services started earlier in Denmark than in Finland or Sweden, and Denmark had also larger variation compared to the other two countries. The longest ICF means were found in Finland. It seems probable that differences in means between countries illustrate to some extent differences in management practices also.

Phenotypic means of heifers clearly outperformed those of cows in NRR, IFL, CR, and AIS (Table 10). The average NRR in heifers was more than 10 units higher, the average IFL more than 21 d shorter, and the average CR from 0.1 to 0.17 units higher than the means of cows. Further, AIS in heifers was less than 1.6 on average, whereas means in cows ranged from 1.81 (Jersey, parity 2) to 2.03 (DNK HOL parity 2; FIN RDC parity 1). JER heifers had somewhat poorer means than HOL and RDC heifers (FIN RDC as an exception). The most evident reason is the difference in the prevalence of use of sexed semen, which is the most common in JER heifers in the whole Nordic data (Table 1). The difference in means between parities was not so large as those between heifers and cows and the pattern differed among breeds, countries and parities (Table 10). JER cows had in general better phenotypic level of fertility than in HOL and RDC. However, countries differ and phenotypic means of fertility of Swedish RDC and HOL cows were in most cases at the same level than those in JER.

However, the Swedish IFL means were not so good as the means of NRR, CR and AIS would suggest. Given the fact that it is rather common in Sweden for farmers to do services by themselves, it is possible that countries have some differences how well all services have been recorded. Danish HOL cows had poorest fertility means in the Nordic data. Also Swedish HOL was worse than Swedish RDC, but Finland made an exception. The best female fertility means in Finland were found in HOL, both in heifers and cows. This may in part illustrate differences in management since Finnish HOL herds tend to be larger than RDC herds and the herd size is associated with the differences in management practices.

To study more the possible indications of different management practices, the frequency distributions from a subset of data from animals having next calving date were studied by countries by cross-tabulating AIS (1-5) and IFL classes (0 d, 1-50 d, 51-100 d, 101-200 d, and  $\geq 201$  d). Even if Finland tended to have more services, the distribution of the IFL within services was more skewed to the left hand side, for shorter IFL values, than those for Sweden and Denmark. This was clearly seen for Holstein. For RDC, Sweden and Finland had very similar frequency distributions. Results further imply that beside genetic differences there are also differences among countries and especially in Finland among breeds in the management.

For all breeds and countries, phenotypic trends of ICF were increasing in late 90's and early 2000's, but started to decrease after that and are again attaining or even going beyond the level of ICF seen at the early years of the data (Tables 11-13). Phenotypic trends of IFL, CR, NRR, and AIS show that in all breeds and countries and in both heifers and cows the female fertility trends have ceased to deteriorate or have started to improve at the late 2000's (Tables 11-13). Some exceptions of the improvement of the phenotypic trends can be found such as NRR trends in JER females that may still be slightly deteriorating (Table 13). For JER, use of sexed semen is recommended and its use is the most common at first service (Table 1).

**Table 10.** Phenotypic means and standard deviations of female fertility in Nordic countries by breed, country, and parity before pre-correcting traits for heterogeneous variance or for sexed semen effect. Jersey statistics is for Denmark only. Minimum (maximum) values are 20 (180) d for ICF, 0 (100) for 56-d NRR, 0 (230) d for IFL, 0 (1) for CR, and 1 (5) for AIS.

	ICF		NRR		IFL		CR		AIS	
<b>Holstein</b>	$\bar{x}$	sd	$\bar{x}$	sd	$\bar{x}$	sd	$\bar{x}$	sd	$\bar{x}$	sd
Heifers										
DNK	-	-	73.9	43.9	21.9	42.5	0.59	0.49	1.57	0.94
FIN	-	-	72.4	44.7	20.2	38.1	0.58	0.49	1.58	0.92
SWE	-	-	76.0	42.7	19.4	39.8	0.63	0.48	1.48	0.83
Parity 1										
DNK	80.0	36.6	60.5	48.9	49.3	64.4	0.43	0.50	1.99	1.20
FIN	89.5	30.3	60.4	48.9	41.1	58.1	0.45	0.50	1.92	1.16
SWE	88.3	33.6	64.3	47.9	44.8	62.3	0.47	0.50	1.83	1.09
Parity 2										
DNK	77.7	35.5	58.4	49.3	52.0	64.6	0.40	0.49	2.03	1.21
FIN	90.0	30.6	59.2	49.1	43.8	58.9	0.42	0.49	1.95	1.17
SWE	86.2	32.8	62.7	48.4	48.3	64.0	0.44	0.50	1.86	1.10
Parity 3										
DNK	79.0	35.4	58.2	49.3	52.9	64.5	0.39	0.49	2.02	1.20
FIN	91.2	30.6	59.0	49.2	44.5	58.8	0.40	0.49	1.95	1.17
SWE	86.4	32.5	62.5	48.4	48.8	63.8	0.43	0.50	1.86	1.09
<b>RDC</b>	$\bar{x}$	sd	$\bar{x}$	sd	$\bar{x}$	sd	$\bar{x}$	sd		
Heifers										
DNK	-	-	74.6	43.6	21.5	41.8	0.59	0.49	1.57	0.93
FIN	-	-	70.0	45.8	22.5	40.0	0.55	0.50	1.65	0.98
SWE	-	-	73.7	44.0	20.3	40.3	0.61	0.49	1.52	0.86
Parity 1										
DNK	76.4	34.6	61.6	48.6	45.2	60.7	0.45	0.50	1.92	1.15
FIN	88.6	29.5	56.7	49.5	45.1	59.0	0.41	0.49	2.03	1.21
SWE	85.0	30.3	61.9	48.6	42.0	58.5	0.47	0.50	1.83	1.07
Parity 2										
DNK	72.5	32.7	61.7	48.6	42.5	58.0	0.44	0.50	1.86	1.11
FIN	87.7	29.2	57.4	49.5	44.2	57.9	0.40	0.49	1.99	1.19
SWE	82.1	29.2	62.6	48.4	41.0	57.6	0.47	0.50	1.78	1.03
Parity 3										
DNK	73.8	32.7	61.2	48.7	43.0	57.8	0.43	0.49	1.86	1.11
FIN	89.0	29.4	57.5	49.4	45.1	58.3	0.38	0.49	1.98	1.18
SWE	82.3	29.2	62.4	48.4	42.4	58.4	0.46	0.50	1.78	1.03
<b>Jersey</b>	$\bar{x}$	sd	$\bar{x}$	sd	$\bar{x}$	sd	$\bar{x}$	sd		
Heifers										
DNK	-	-	71.9	45.0	23.2	43.4	0.57	0.50	1.59	0.95
Parity 1										
DNK	73.0	33.0	62.0	48.5	40.8	58.5	0.47	0.50	1.87	1.13
Parity 2										
DNK	70.2	32.0	63.0	48.3	38.2	56.2	0.47	0.50	1.81	1.10
Parity 3										
DNK	70.6	32.0	62.7	48.4	39.0	56.6	0.46	0.50	1.82	1.10

**Table 11.** Phenotypic means of Holstein females by birth years before pre-correction. For cows, observations from parities 1 to 3 are combined. The last birth years included end up earlier in cows than in heifers to obtain the average number of yearly observations.

Traits	Phenotypic means of Holstein females born in:																							
	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	
ICF cows																								
DNK	75,6	76,6	78,1	79,7	81,1	83,3	85,0	85,2	85,7	86,2	85,7	85,9	84,0	83,1	81,7	79,8	78,0	77,3	76,5	76,6	76,3			
FIN	81,4	82,0	82,4	82,7	83,5	83,8	84,9	86,5	88,6	90,2	91,9	92,6	94,4	95,6	96,4	96,4	96,1	95,1	94,3	92,1	90,0			
SWE	85,9	87,0	88,1	89,5	90,2	91,3	91,5	91,9	92,6	93,7	92,7	93,1	92,9	91,9	90,3	88,7	87,2	86,3	85,2	83,9	81,7			
NRR heifers																								
DNK	79,7	80,3	80,6	80,0	79,2	78,2	77,2	77,5	76,6	75,3	73,2	72,9	72,4	70,7	67,5	68,6	67,1	66,5	65,9	66,6	66,3	65,6	66,3	
FIN	73,3	72,8	74,0	74,6	75,4	75,9	75,5	75,0	73,4	72,8	73,7	74,2	74,4	72,8	71,7	72,0	69,9	68,9	69,2	70,7	69,8	71,4	70,2	
SWE	77,5	78,3	79,2	79,0	79,5	79,3	79,3	77,8	75,3	75,9	76,3	75,7	75,6	75,1	74,9	74,9	72,9	71,2	71,4	72,1	72,9	72,6	71,9	
NRR cows																								
DNK	61,3	61,5	61,4	61,3	61,5	61,9	62,2	61,7	61,5	60,7	60,8	60,1	60,2	58,9	57,7	55,7	54,8	54,6	54,8	54,7	54,9			
FIN	62,7	61,6	62,6	62,6	61,9	61,1	60,6	60,6	60,5	60,4	60,5	61,3	60,4	59,1	58,4	57,5	57,8	58,0	57,7	57,3	57,4			
SWE	63,7	63,8	64,7	64,3	64,0	64,0	62,9	63,2	63,7	64,0	64,1	64,6	64,7	63,6	62,7	61,8	60,8	61,4	61,9	62,1	62,0			
IFL heifers																								
DNK	16,0	16,2	16,5	17,3	18,6	19,7	21,0	21,0	21,3	22,9	24,9	25,0	25,6	26,1	27,8	25,8	27,4	26,9	27,1	25,7	25,9	26,9	25,1	
FIN	16,4	16,6	15,8	15,6	15,7	16,0	15,8	16,3	18,5	19,2	18,4	18,4	19,3	21,0	21,6	22,2	23,8	25,5	24,7	23,8	25,0	23,5	23,4	
SWE	16,2	15,5	16,6	16,4	16,7	17,4	16,7	18,6	21,6	20,9	20,7	21,8	22,5	22,7	23,4	22,7	24,6	25,6	25,5	24,4	24,5	24,8	23,3	
IFL cows																								
DNK	48,4	48,8	51,4	52,7	53,8	53,5	53,4	53,7	53,3	55,2	54,6	56,0	54,0	54,4	54,5	54,9	53,8	53,1	50,8	49,4	47,1			
FIN	31,7	32,6	32,4	33,1	34,2	35,3	36,9	38,5	39,9	41,7	43,0	43,1	46,2	49,1	51,1	51,4	50,5	48,4	48,5	47,4	45,4			
SWE	43,1	44,9	45,1	46,9	48,9	50,3	51,6	52,4	52,2	54,1	53,2	53,0	53,3	54,7	55,4	54,3	54,2	52,8	50,9	51,1	51,1			
CR heifers																								
DNK	0,66	0,66	0,66	0,65	0,63	0,62	0,61	0,61	0,60	0,59	0,57	0,57	0,56	0,55	0,53	0,55	0,54	0,54	0,54	0,55	0,55	0,54	0,55	
FIN	0,63	0,63	0,64	0,64	0,64	0,62	0,61	0,60	0,57	0,58	0,59	0,59	0,59	0,57	0,56	0,56	0,54	0,53	0,55	0,56	0,55	0,56	0,55	
SWE	0,66	0,67	0,66	0,66	0,66	0,66	0,66	0,64	0,61	0,62	0,62	0,61	0,61	0,61	0,61	0,61	0,59	0,58	0,58	0,60	0,60	0,59	0,59	
CR cows																								
DNK	0,42	0,42	0,42	0,41	0,41	0,41	0,41	0,41	0,41	0,40	0,41	0,40	0,41	0,40	0,40	0,39	0,39	0,40	0,41	0,42	0,43			
FIN	0,47	0,46	0,47	0,46	0,46	0,45	0,44	0,44	0,43	0,43	0,43	0,44	0,42	0,41	0,40	0,40	0,40	0,42	0,42	0,42	0,44			
SWE	0,47	0,46	0,46	0,45	0,45	0,44	0,43	0,43	0,44	0,43	0,43	0,44	0,44	0,43	0,42	0,42	0,42	0,44	0,45	0,46	0,46			
AIS heifers																								
DNK	1,45	1,44	1,44	1,45	1,48	1,51	1,53	1,52	1,54	1,57	1,62	1,62	1,64	1,67	1,72	1,67	1,71	1,71	1,72	1,69	1,69	1,70	1,68	
FIN	1,52	1,53	1,50	1,50	1,49	1,48	1,49	1,50	1,56	1,57	1,55	1,54	1,55	1,59	1,61	1,62	1,67	1,70	1,67	1,63	1,65	1,61	1,62	
SWE	1,43	1,41	1,40	1,41	1,40	1,40	1,40	1,46	1,53	1,51	1,50	1,52	1,53	1,54	1,55	1,54	1,59	1,63	1,62	1,58	1,56	1,55	1,56	
AIS cows																								
DNK	1,94	1,95	1,98	2,00	2,01	2,00	1,99	2,01	2,00	2,04	2,03	2,06	2,04	2,06	2,08	2,12	2,13	2,12	2,09	2,07	2,04			
FIN	1,76	1,78	1,77	1,78	1,80	1,83	1,86	1,87	1,89	1,91	1,92	1,91	1,96	2,02	2,06	2,07	2,07	2,03	2,03	2,02	1,99			
SWE	1,81	1,82	1,81	1,83	1,86	1,88	1,91	1,91	1,90	1,92	1,91	1,90	1,91	1,94	1,98	1,98	1,99	1,96	1,93	1,90	1,88			

**Table 12.** Phenotypic means of RDC females by birth years before pre-correction. For cows, observations from parities 1 to 3 are combined. The last birth years included end up earlier in cows than in heifers to obtain the average number of yearly observations.

Traits	Phenotypic means of RDC females born in:																							
	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	
ICF cows																								
DNK	73,2	74,0	73,5	74,0	74,4	76,3	77,2	78,3	79,5	80,2	80,7	80,0	79,6	78,8	76,7	75,0	74,2	73,3	73,2	74,0	75,3			
FIN	83,2	83,8	84,5	84,6	85,1	85,6	86,5	87,9	88,5	90,0	90,6	91,6	92,9	92,8	93,6	93,5	92,8	91,9	90,3	89,1	87,9			
SWE	83,6	84,1	85,2	84,9	84,9	85,4	85,3	85,4	85,8	85,9	85,8	86,1	86,6	86,0	84,8	83,7	82,3	81,5	80,6	79,7	79,3			
NRR heifers																								
DNK	76,2	77,5	77,0	77,0	78,4	78,7	78,6	77,4	77,9	78,3	76,5	77,3	75,8	73,9	72,0	72,5	70,5	67,1	69,1	69,6	69,0	67,1	68,1	
FIN	68,7	69,1	70,1	70,4	71,0	72,4	70,9	70,8	70,5	71,1	70,8	70,6	71,3	70,5	70,9	71,2	68,7	65,0	66,1	67,9	68,3	68,9	68,0	
SWE	74,2	75,0	75,5	75,2	76,2	77,9	77,7	76,2	75,4	74,8	74,4	75,3	74,6	74,3	73,9	73,3	72,7	67,0	68,5	70,5	71,0	70,3	69,1	
NRR cows																								
DNK	62,4	61,9	62,4	62,8	63,6	65,0	65,9	65,2	66,8	66,4	65,7	65,0	64,9	63,5	62,3	61,3	60,2	60,8	60,6	60,9	59,8			
FIN	57,3	58,5	58,5	57,8	58,0	57,4	56,5	57,6	57,1	57,5	57,1	57,6	57,5	57,2	57,1	56,3	54,7	54,9	55,6	56,2	56,1			
SWE	62,9	62,7	62,9	62,5	62,5	63,1	62,5	62,1	63,1	62,7	62,0	62,2	63,2	63,6	62,7	62,3	60,3	61,5	62,3	62,8	62,5			
ILF heifers																								
DNK	19,0	18,8	19,4	19,3	19,9	19,6	19,6	19,8	19,2	19,3	21,1	20,5	22,2	22,6	23,8	23,9	24,9	27,5	24,7	23,8	25,3	27,7	24,0	
FIN	20,4	20,3	19,5	19,5	19,4	19,5	20,3	20,4	21,2	21,5	21,7	22,6	22,9	24,0	23,9	23,9	26,8	30,8	29,4	27,2	27,9	27,4	27,1	
SWE	18,7	18,3	19,8	19,0	18,8	17,6	17,2	18,7	19,6	20,3	21,7	21,0	22,2	22,4	23,2	23,9	25,1	30,7	28,1	26,5	27,6	29,1	26,7	
IFL cows																								
DNK	41,9	44,2	43,3	41,8	42,0	41,4	40,1	41,8	39,5	40,5	43,5	44,1	44,8	45,8	45,3	45,9	45,8	42,6	41,2	41,4	42,5			
FIN	39,4	39,0	39,2	40,1	40,6	41,7	43,8	43,8	45,1	46,2	47,4	46,6	48,5	48,4	49,7	50,8	52,1	51,2	47,8	46,1	46,3			
SWE	40,7	42,1	42,4	42,1	41,9	41,7	42,8	44,2	43,8	44,3	45,1	45,7	45,3	45,4	45,5	46,2	48,1	45,9	43,9	44,8	47,6			
CR heifers																								
DNK	0,62	0,63	0,61	0,62	0,62	0,62	0,62	0,62	0,63	0,63	0,61	0,63	0,61	0,60	0,58	0,59	0,58	0,55	0,57	0,59	0,58	0,55	0,58	
FIN	0,57	0,57	0,59	0,59	0,59	0,57	0,55	0,55	0,54	0,55	0,55	0,54	0,55	0,54	0,54	0,54	0,51	0,48	0,50	0,52	0,52	0,53	0,51	
SWE	0,63	0,63	0,62	0,62	0,63	0,65	0,65	0,64	0,63	0,62	0,61	0,62	0,61	0,61	0,60	0,60	0,58	0,53	0,55	0,58	0,57	0,55	0,55	
CR cows																								
DNK	0,45	0,44	0,44	0,45	0,45	0,46	0,47	0,46	0,48	0,48	0,46	0,46	0,46	0,45	0,45	0,44	0,44	0,46	0,47	0,47	0,46			
FIN	0,41	0,42	0,42	0,41	0,41	0,40	0,39	0,40	0,40	0,39	0,39	0,40	0,40	0,40	0,40	0,39	0,38	0,39	0,41	0,42	0,42			
SWE	0,47	0,47	0,46	0,46	0,46	0,47	0,46	0,46	0,46	0,46	0,45	0,45	0,46	0,46	0,46	0,45	0,44	0,46	0,48	0,48	0,47			
AIS heifers																								
DNK	1,53	1,51	1,52	1,51	1,50	1,49	1,48	1,51	1,49	1,48	1,52	1,51	1,54	1,59	1,63	1,60	1,64	1,72	1,65	1,62	1,65	1,69	1,64	
FIN	1,64	1,64	1,61	1,61	1,61	1,58	1,61	1,61	1,64	1,63	1,64	1,65	1,63	1,66	1,65	1,65	1,73	1,83	1,78	1,71	1,70	1,68	1,69	
SWE	1,50	1,49	1,49	1,48	1,47	1,43	1,42	1,47	1,50	1,51	1,54	1,52	1,54	1,55	1,55	1,58	1,60	1,75	1,69	1,62	1,62	1,64	1,65	
AIS cows																								
DNK	1,85	1,88	1,86	1,84	1,84	1,80	1,78	1,81	1,76	1,78	1,82	1,84	1,85	1,88	1,90	1,92	1,94	1,89	1,88	1,88	1,91			
FIN	1,93	1,91	1,91	1,94	1,95	1,97	2,01	1,99	2,01	2,02	2,04	2,02	2,05	2,04	2,07	2,10	2,14	2,12	2,06	2,03	2,02			
SWE	1,78	1,79	1,80	1,80	1,81	1,80	1,81	1,84	1,82	1,83	1,85	1,87	1,85	1,84	1,86	1,88	1,93	1,87	1,84	1,82	1,82			

**Table 13.** Phenotypic means of Jersey females by birth years before pre-correction. For cows, observations from parities 1 to 3 are combined. The last birth years included end up earlier in cows than in heifers to obtain the average number of yearly observations.

Traits	Phenotypic means of Jersey females born in:																							
	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	
ICF cows	68,5	69,8	71,3	71,8	72,2	75,5	77,4	77,6	78,6	78,4	78,0	78,4	76,6	74,9	74,3	73,0	71,3	70,7	70,9	71,6	72,1			
NRR heifers	75,7	76,7	78,1	77,8	77,2	78,4	77,0	77,6	76,7	76,0	73,8	71,7	71,4	68,6	65,9	67,0	66,9	66,8	67,4	65,0	66,1	64,5	64,8	
NRR cows	62,4	63,5	64,1	64,7	65,7	67,7	66,6	66,2	67,9	67,6	66,7	64,9	63,7	61,4	61,9	61,0	59,8	60,1	60,1	59,3	58,7			
IFL heifers	18,5	17,8	17,1	17,2	19,1	18,7	19,1	20,0	21,0	20,7	22,8	24,6	26,0	26,9	29,3	27,6	27,7	28,1	27,3	28,8	28,9	29,2	27,3	
IFL cows	38,1	38,1	39,5	38,9	37,9	38,1	39,9	40,1	38,6	39,9	40,9	42,5	43,0	44,3	42,7	43,8	43,3	41,2	40,3	41,1	40,8			
CR heifers	0,61	0,63	0,64	0,64	0,62	0,63	0,62	0,61	0,60	0,60	0,58	0,57	0,55	0,54	0,52	0,54	0,54	0,54	0,55	0,53	0,53	0,52	0,53	
CR cows	0,46	0,47	0,47	0,47	0,48	0,49	0,48	0,48	0,49	0,49	0,49	0,47	0,47	0,45	0,46	0,46	0,46	0,47	0,47	0,47	0,47			
AIS heifers	1,51	1,48	1,45	1,45	1,47	1,46	1,48	1,47	1,50	1,50	1,54	1,59	1,62	1,66	1,72	1,68	1,67	1,69	1,66	1,73	1,70	1,73	1,73	
AIS cows	1,83	1,80	1,81	1,80	1,77	1,74	1,78	1,79	1,75	1,77	1,80	1,85	1,87	1,93	1,89	1,91	1,92	1,90	1,89	1,90	1,91			

### Amount of total heterosis in female fertility

Results show that the amount of total heterosis in RDC is larger than that in HOL and JER, in accordance with the more heterogeneous genetic background of RDC compared to HOL or JER (Table 14). Level of total heterosis in CR and IFL is very similar in cows, but larger differences were found in heifers.

**Table 14.** Total heterosis by breeds, parities and traits, expressed relative to the phenotypic mean.

	Total heterosis, % of the mean		
	HOL	RDC	JER
<b>Heifers</b>			
NRR	2.1	2.9	2.2
IFL	-9.9	-15.7	-6.7
CR	3.6	7.4	3.3
AIS	-3.5	-5.3	-3.4
<b>Parity 1</b>			
ICF	-1.3	-1.3	-0.5
NRR	2.0	3.8	2.8
IFL	-8.0	-11.0	-8.6
CR	7.7	10.9	7.7
AIS	-3.0	-4.6	-3.7
<b>Parity 2</b>			
ICF	-1.3	-1.0	0.7
NRR	1.7	3.4	0.6
IFL	-7.8	-11.5	-5.5
CR	9.1	11.9	4.4
AIS	-2.6	-4.1	-0.8
<b>Parity 3</b>			
ICF	-1.5	-0.9	0.9
NRR	1.3	2.7	2.7
IFL	-5.5	-9.5	-6.7
CR	7.6	10.4	5.4
AIS	-2.2	-2.9	-2.8

### Consequences of the use of sexed semen

On average, the effect of use of sexed semen was 11% units in the Nordic data for all breeds and parities while the model update was carried out. However, the deteriorating effect of the use of sexed semen is decreasing with the years to come since techniques and skills related to this practice will improve. It is important therefore to model the year interaction also as was done for CR and NRR. However, a fixed value of 11% is used for pre-correcting the effect of use of sexed semen for IFL and AIS and the pre-correction step should be changed to take account the year effect, when the difference between conventional and sexed semen is diminishing more.

**Table 15.** Comparison of conception rate indices of 6 Jersey bulls born in 2009 and differing most in the prevalence of daughters inseminated with sexed semen. The first model is the current national evaluation model with the semen type effect included (Included). In the second model the semen type effect was not accounted for (Excluded). Numbers after CR refer to parities from 1 to 3, zero to heifers, and 1-3 to combined index of cow traits through parities 1 to 3.

	Prop., % <sup>A</sup>	CR0	CR1	CR2	CR3	CR1-3
<b>Bull A</b>						
Included	8,9	92	95	93	92	93
Excluded		94	96	94	93	95
<b>Bull B</b>						
Included	9,4	110	103	101	101	102
Excluded		111	104	101	101	103
<b>Bull C</b>						
Included	10,1	103	100	101	103	101
Excluded		103	101	102	104	102
<b>Bull D</b>						
Included	40,3	101	82	79	78	80
Excluded		99	81	78	77	79
<b>Bull E</b>						
Included	50,7	133	127	129	128	128
Excluded		129	124	126	125	125
<b>Bull F</b>						
Included	53,0	148	120	121	120	121
Excluded		142	117	118	118	118

<sup>A</sup>Proportion of daughters inseminated with sexed semen in first service.

Comparison of 2 different CR models clearly indicated that the semen type effect should be taken into account in the populations that commonly use sexed semen. We studied EBV of JER bulls differing in the proportion of daughters inseminated with sexed semen at the first service. Six extreme types of bulls were selected in Table 15; 3 bulls having less than or equal to 10% of daughters inseminated with sexed semen at first service and 3 bulls having more than or equal to 40% of such daughters. The difference of CR EBV from 2 different models was on average -0.9 units for the first 3 bulls, but for the latter visibly more. Their heifer CR EBV improved from +2 to +6 units, and the increase was consistent with the increase in proportion of daughters with sexed semen. The latter bulls' EBV for cow CR improved from +1 to +3 units (Table 15).

Further, the genetic trends of JER and HOL bulls differed between the 2 models (semen type effect included or excluded) for heifer and cow CR in JER, and for heifer CR in HOL (Tyrisevä et al. 2017). The latter population is dominated by Danish heifers, for which the prevalence of use of sexed semen at first service was around 30% in later years in the data (Table 1). Thus, results illustrate that not considering the semen type effect in the prediction of EBV in the populations using commonly sexed semen lead to biased EBV and genetic trends.

### Correlation between fertility index and underlying traits

The expected progress in each individual fertility trait as the selection target is the fertility index, expressed as a percentage of maximum progress for that trait, is shown in Table 16. Maximum progress is obtained if selection is based solely on the trait in question.

**Table 16.** Correlations between fertility index and fertility traits for bulls born in 2005-2010 and with minimum reliability of 75% (50 % for JER).

Index	RDC	HOL	JER
ICF1-3	0.53	0.55	0.55
IFL0	0.56	0.59	0.63
IFL1-3	0.99	0.99	0.99
AISO	0.55	0.59	0.70
AIS1-3	0.88	0.90	0.89
CRO	0.58	0.67	0.73
CR1-3	0.91	0.92	0.88

### Effect of 10 index units

The effect of fertility indices expressed on the original scale is shown in Table 17. 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 17.** Effect of +10 fertility index units in the sire on performance of ICF, IFL, AIS, and CR in daughter group. Only results for cows are shown.

Trait	RDC	HOL	JER	High values mean
ICF1-3	-1.1	-1.6	-1.1	Longer interval
IFL1-3	-3.8	-4.0	-2.9	Longer interval
AIS1-3	-0.06	-0.06	-0.05	More inseminations
CR1-3	-0.03	-0.03	-0.02	More failures

### Genetic trends of female fertility in Nordic countries

Currently, genetic trends of bulls for female fertility are improving or have stabilized for all breeds and traits, but the pattern of trends and rate of genetic gain differ between breeds and somewhat between heifers and cows. Nordic HOL faced a steep decline in female fertility especially in cow traits that reached their nadir at the early 2000's, in accordance with the global trends, despite the fact that female fertility has been one of the breeding goals in Nordic HOL populations for a long time. This is because many of the AI bulls used earlier have been of foreign origin, from countries which did not consider fertility in their breeding goal. After reaching the nadir, female fertility in HOL bulls is increasing steeply both in heifer and cow fertility traits, in accordance with the global trends. AIS is the only exception, showing hardly any progress.

Patterns of genetic trends of HOL bulls differ among Nordic countries in early birth year classes. The genetic level of Finnish and Swedish HOL was clearly higher than that for Danish HOL. The reason for this lies in the rate of holsteinization that has been more rapid in Danish HOL than in Finnish and Swedish HOL. The latter two maintained longer the old Friesian genetics in their populations. The old Friesian type black-and-white dairy cattle have been shown to have better fertility than North-American HOL.

RDC has been one of the exceptions among breeds worldwide that has been able to maintain its genetic level in female fertility for decades. This is because female fertility has been included among the breeding goals long time ago and RDC has been one of the world's leading red dairy cattle populations with strong own genetics. However, there is hardly any genetic gain seen in RDC bulls for cow traits, whereas heifer fertility is clearly improving in RDC bulls. In accordance with the HOL, the pattern for AIS differs somewhat from other fertility traits.

Genetic trends of JER are between HOL and RDC. As with HOL genetic trends of JER bulls declined for ICF13 and IFL13 in 80's and 90's, but more modestly. Currently, the genetic progress is largest in CR0 and CR13.

Genetic trends of all breeds and traits can be found from the additional Excel files, see the list in the Appendix.

### Interbull validation

CR has replaced NRR as a trait that is sent to Interbull for international bull evaluation. Table 18 shows overall results from IB3 test; more detailed information are given in separate log-files (tt3\_DFSHOL.log, tt3\_DFSJER.log, tt3\_DFSRDC.log).

**Table 18.** Combined results from IB3-test sent to Interbull in September 2016.

	HOL	JER	RDC
hco = CR0	pass	pass	fail
crc = ICF1-3	pass	pass	pass
cc1 = CR1-3	pass	fail	pass
cc2 = IFL1-3	pass	fail	pass
interval = ICF+IFL1-3	pass	pass	pass

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## Appendix

### List of attachments:

- 1) Editing rules: Nordic fertility editing rules\_19022018.docx
- 2) Reliability study: Heinonen\_reliability\_approximation\_fertility.pdf
- 3) Genetic trends:  
HOL\_bulls\_genetic\_trends\_08082017.xls, RDC\_bulls\_genetic\_trends\_08082017.xls,  
JER\_bulls\_genetic\_trends\_08082017
- 4) Log-files from Interbull test 3: tt3\_DFSHOL.log, tt3\_DFSJER.log, tt3\_DFSRDC.log

**Things having probably minor effect but could still be tested:**

- 1) Modeling AI technician. Sweden has, however, not provided this information. The effect has been included in the data for Denmark and Finland (AI technician and AI technician × year class).
- 2) Modeling double services. This has been included in the data. Preliminary tests showed only minor effects, but it has not been tested from the final models.
- 3) Following practice from the sire model, forage years have been used for herd year effects and for the calving year × month effects, but for insemination year × month effects normal calendar years. It has not been tested, does this have any impact on calving/insemination year × month effects. However, there is already a class for calving year × month effect in the data for which normal calendar years are used according to insemination year × month effect.
- 4) For Finland, fixed effects are nested within breeds, as all breeds from Finland are included in breed-specific evaluation data sets. Following practice from the sire model, Finncattle has been combined with RDC for some fixed effects but for some other fixed effects it is in its own group. This could be unified and Finncattle could be combined with RDC in all fixed effects as it has rather small population size.
- 5) In Nordic evaluation, open cases for CR get a value of 0.7. France has very complicated probability calculations for such cases, although they have no pregnancy check results to ease the phenotyping. This could be fine-tuned for Nordic countries as well. However, it is very unlikely that it has a large effect because all data is used for defining phenotypes and after that 150 d of the most recent data is cut away. Therefore, there are only very few open cases that are the most probably pregnant females not calved yet.
- 6) Modeling service sire effect. According to literature, the effect has been minor.