# **NAV** evaluation for calf survival

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## Introduction

Calves and young stock that die during the rearing period result in lost revenue, fewer heifers for replacement, higher veterinarian costs and deteriorating animal welfare. Today, Nordic Cattle Genetic Evaluation(NAV) aims at fewer stillbirths (death within one day after birth) and enhanced longevity. Probably, breeding for these two traits has contributed to the fact that the animals' genetic ability to survive the rearing period has not been impaired. The reason is favourable genetic correlations between the traits. However, it is more efficient to breed directly for lower mortality among calves and young stock.

The decision of NAV to develop the genetic evaluation of survival in calves and young animals was based on the results from a project conducted by Danish data by the Knowledge Centre for Agriculture, Cattle (project 2143) – the Danish title of the report is "Genetiske muligheder for at nedbringe ungdyrdødeligheden" (in the following the project is named the "Danish calf survival project").

## Summary of the Danish calf survival project

Knowledge Centre for Agriculture, Cattle has investigated the possibility to breed for more live calves and young stock. Before 1998 the exact date of dead or disposal of young stock was not always registered. Therefore, the study only used records on Danish calves born 1998 and later. Only calves that were alive after the first day after birth (liveborn calves) were included. The study is based on records on both heifer calves and bull calves such that all available information is used. Survival in calves and young animals were defined as different traits in the two sexes. Moreover, the rearing period is divided into two periods within each gender. Survival in calves and young stock is therefore described by means of four traits.

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

There are both computational and biological considerations behind the division of the rearing period. One of these considerations is that many calves are moved within the first month of their life. Some heifers are gathered in herds specialised in raising heifers and most bull calves are gathered in fattening herds until slaughter. Thus, they are no longer affected by the environment in the herd where they were born, and this fact has to be taken into account in the calculations.

In addition, previous studies have shown that survival in calves and young stock from a genetic point of view is not the same trait in calves that are few weeks old, and calves that are several months old. It can probably be explained by the fact that there are various reasons why calves die depending on how old they are. Thus, it is different parts of the calf's immune system, which ensures its survival, depending on how old it is. For instance, diarrhoea and pneumonia are the most

frequent reasons why calves die, whereas these diseases do not occur so frequently in older animals.

In a Dutch calf survival project nearly the same definition of periods was used except that the first period (day 1 to 30) was subdivided into 2 periods.

The fixed effects of the model were

- Herd at start of period x birth 2-year
- Birth year x birth month
- Parity of dam (1 or 2+) x calf size x calving ease

The estimated genetic parameters are shown in tables 1, 2 and 3. The heritabilities are much alike for RDM, Holstein and Jersey. The heritabilities for the four traits are low, but in line with the heritabilities of stillbirths, diseases and other health traits. The low heritabilities are due to the facts that the incidence is relatively low within each trait, that the environmental variation is relatively large and that there are several reasons why the calves die.

Tabel 1. Holstein. Genetic and residual variances, heritabilities (diagonal), genetic correlations (above diagonal) and residual correlations (below diagonal). Standard errors in parenthesis

|     | Gen. var. | Res. var. | HP1           | BP1           | HP2           | BP2           |
|-----|-----------|-----------|---------------|---------------|---------------|---------------|
| HP1 | 0,0003    | 0,0294    | 0,009 (0,001) | 0,90 (0,13)   | 0,51 (0,13)   | 0,40 (0,15)   |
| BP1 | 0,0002    | 0,0347    | 0,00          | 0,007 (0,001) | 0,42 (0,21)   | 0,44 (0,13)   |
| HP2 | 0,0004    | 0,0337    | 0,01 (0,004)  | 0,00          | 0,011 (0,002) | 0,95 (0,04)   |
| BP2 | 0,0011    | 0,0382    | 0,00          | -0,03 (0,004) | 0,00          | 0,027 (0,003) |

Tabel 2. RDC: Genetic and residual variances, heritabilities (diagonal), genetic correlations (above diagonal) and residual correlations (below diagonal). Standard errors in parenthesis.

|     | Gen. var. | Res. var. | HP1           | BP1           | HP2           | BP2           |
|-----|-----------|-----------|---------------|---------------|---------------|---------------|
| HP1 | 0,0002    | 0,0293    | 0,007 (0,001) | 0,95 (0,10)   | 0,75 (0,08)   | 0,61 (0,14)   |
| BP1 | 0,0002    | 0,0404    | 0,00          | 0,007 (0,001) | 0,78 (0,12)   | 0,58 (0,08)   |
| HP2 | 0,0010    | 0,0331    | -0,03 (0,003) | 0,00          | 0,023 (0,003) | 0,89 (0,05)   |
| BP2 | 0,0019    | 0,0543    | 0,00          | -0,03 (0,003) | 0,00          | 0,034 (0,004) |

Tabel 3. Jersey. Genetic and residual variances, heritabilities (diagonal), genetic correlations (above diagonal) and residual correlations (below diagonal). Standard errors in parenthesis

|     | Gen. var. | Res. var. | HP1           | BP1           | HP2           | BP2           |
|-----|-----------|-----------|---------------|---------------|---------------|---------------|
| HP1 | 0,0011    | 0,0605    | 0,018 (0,002) | 0,95 (0,05)   | 0,42 (0,12)   | 0,34 (0,18)   |
| BP1 | 0,0012    | 0,0820    | 0,00          | 0,015 (0,003) | 0,39 (0,18)   | 0,39 (0,17)   |
| HP2 | 0,0007    | 0,0582    | -0,08 (0,004) | 0,00          | 0,012 (0,002) | 0,99 (0,06)   |
| BP2 | 0,0008    | 0,0771    | 0,00          | -0,11 (0,005) | 0,00          | 0,010 (0,003) |

The genetic correlations are high within period and across gender and moderate across period. It supported the notion that there are various genes that control survival of calves and young stock over time, but these are the same genes in bull calves and heifer calves.

## Data and edit of data

The edit of data for the calf survival evaluation starts with 2 dataset from each country: Birth data and Where-about data

#### Birth data

Birth data include information on id, dam id, birth date, birth herd, parity of dam, sex of the calf, vitality and calving ease.

- The birth data from DNK and FIN are raw data extractions from the databases and include quite some calves that must be deleted (e.g. stillborn, ET-calves, twins, beef breeds, crossbred calves).
- The birth data from SWE is pre-edited and include only liveborn, female calves born in 1999 and up to now (RDC, HOL and JER)

The edit of birth data will delete information in the following cases:

- Stillborn
- Calves killed right after birth (killed up to day 7 after birth)
- Multiple birth (twins, triplets)
- Abortions and defect calves
- ET-calves, unknown sex, casterates
- Missing vitality, herd, birth date or invalid parity
- Calves with unknown dam
- Breed not RDC, HOL, JER, RED or FIC (crossbred calves are excluded)
- The calf has no identity in the NAV-pedigree file and sire is unknown (i.e. calves without identity in NAV pedigree but with known sire and dam are included)

Table 4. Survey of birth data at the end of 2012 (calves born 1998 to 2012)

| , , , , , , , , , , , , , , , , , , , | ,          | ,         |           |
|---------------------------------------|------------|-----------|-----------|
|                                       | DNK        | FIN       | SWE       |
| Before edit                           | 10,258,508 | 3,555,368 | 1,777,138 |
| After edit                            | 7,151,752  | 2,227,936 | 1,777,138 |
| Heifer calves                         | 3,716,403  | 1,091,390 | 1,777,138 |
| Bull calves                           | 3,435,349  | 1,136,546 | 0         |
| RDC (+FIC)                            | 676,682    | 1,435,182 | 846,223   |
| HOL (+RED)                            | 5,776,756  | 790,805   | 919,398   |
| JER                                   | 698,314    | 1,949     | 11,517    |

#### Where-about data

The setup of the initial where-about files differs somewhat between counties, probably due to the setup in the original databases.

Essentially, the where-about data include information on the where-abouts of the calves defined by a start date and an end date – and a herd. Besides, it includes a departure code defining the reason for leaving the herd (e.g. trade, slaughter, export, death).

From the original where-about file 2 separate datasets are created.

- A DSE-file (**D**eath, **S**laughter, **E**xport) with one record per animal. It includes information of date and a departure code (and of cause id of calf and birth date). The information on death is of cause essential in this project, but also information on slaughter and export is important because those calves must be excluded from the analyses
- A trade-file, that keep track of the herds where the calf has stayed. This file is used for definition of the fixed effect of trades. It might include several records per animal

## **Departure codes in DSE-file**

- In FIN the following code are defined: Death, Killed, Lost, Slaughtered, Exported
- In DNK the following codes are defined: Death, Killed, Slaughtered, Exported. However, we should beware:
  - Calves that never get an official id and where the exact death date are not registered. There are two groups (the farmer decides the departure code):
    - Calves that die within 7 days. Here the death date is defined as day 4. However, the date
      of death is not used in the model setup. Therefore, this assumption has no impact on the
      results.
    - Calves that are killed right after birth. (The frequency is very high among Jersey bull calves)
  - o For calves (and cows) with an official id, the departure code "Killed" has only existed since October 2008. Before that killed calves and cows were registered as dead.
- In SWE, the only departure codes in the DSE-file are: Dead and Slaughtered.
  - We should be aware that SWE calves that leave the herd without identity within the first 7
    days are not included in the dataset. The result is that the survival rate of SWE calves in the
    first period is higher compared to FIN and DNK.

If was decided to merge dead and killed calves into one group – except for calves killed within the first 7 days after birth.

## **Definition of calf survival traits**

Heifer period 1 (HP1): 1-30 days

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

## Heifer period 2 (HP2): 31-458 days

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

## Bull period 1 (BP1): 1-30 days

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

### Bull period 2 (BP2): 31-184 days

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

## Survival rates per year, breed and country

Figure 1 – figure 4 show the survival rates per year, breed and country.

### Finland

In general the survival rates are very high in FIN – both in period 1 and 2.

- Survival rates are highest for HOL
- Survival rates are highest for period 1
- Survival rates are highest for heifer calves

#### Sweden

- Survival rate is high in period 1, but lower in period 2. However, calves that died within the
  first week without being ear tagged are not included in SWE (they are included in DNK and
  FIN).
- The survival rate in HOL is higher than in RDC especially in period 2.

## Denmark

- In HOL survival rates are similar in period 1 and 2.
- Survival rates are highest for heifer calves

## Jersey (Denmark)

- The Jersey survival rates are much lower than in RDC and HOL.
- Opposite to RDC and HOL the survival rates are lowest in period 1
- Survival rates are highest for heifer calves

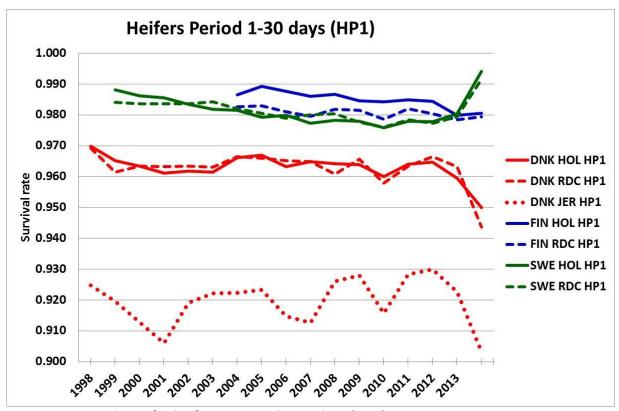


Figure 1. Survival rate for heifers in period 1-30 days (HP1)

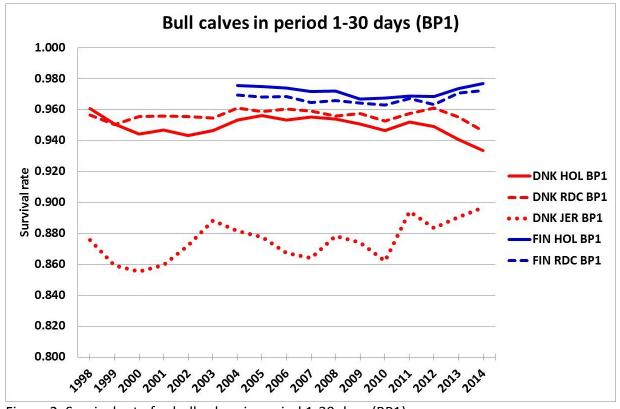


Figure 2. Survival rate for bull calves in period 1-30 days (BP1)

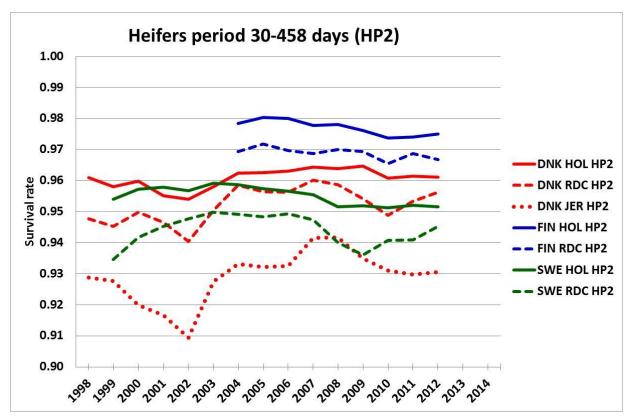


Figure 3. RDC bull calf survival rates

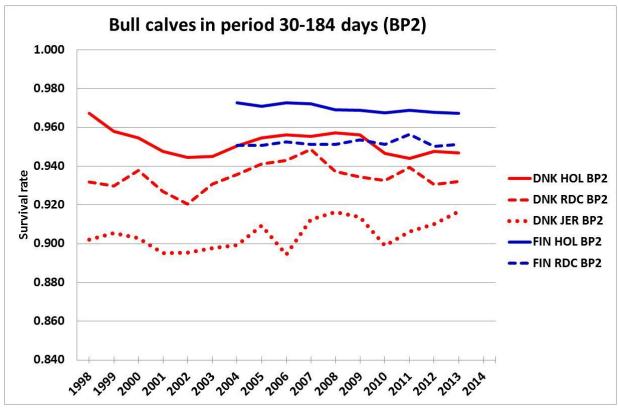


Figure 4. Survival rate for bull calves in period 30-184 days (BP2)

## The evaluation model

The evaluation model was adopted from the Danish calf Survival project with some modifications due to inclusion of Swedish and Finnish data

#### The effects of the model

The effects included in the NAV evaluation model are:

- Fixed herd x 5-year birth period
- Fixed country x year x birth month
- Fixed effect of country x transfer (0/1) x calendar month of transfer (only HP2 and BP2)
- Fixed effects of heterozygoty (described below)
- Random phantom parent groups (defined by birth year and original breed group)
- Random herd x year of birth
- Random genetic effect of animal

## Country effect

As NAV data consist of Danish, Swedish and Finnish data and because the effects probably are different from country to country an interaction with country was introduced for all effects

### Calf size and calving ease

In Swedish and Finnish data information on calf size is not recorded – and calving ease is recorded differently in the three countries. Therefore, it was decided to exclude these 2 factors from model.

### Effect of transfer to another herd

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

The effect of transfer on survival in period 2 is equally problematic – especially for heifer calves that are generally transferred late in period 2. It turn up that calves that are transferred have a high survival rate.

Up to now, it has been decided to exclude effect of transfer from the model for HP1 and BP1. For HP2 and BP2 the effect of transfers within the first 60 days is included.

#### Herd x year

As pointed out in the Danish calf survival project the herd x year effect constitutes a special problem: Due to the high survival rate many herd x years have a survival rate of 1.0, and therefore data from these herds are non-informative from a statistic point of view (in the linear model). This problem becomes larger when the data from the small Finnish herds are included. If we look at herd x 5-year periods the problem is reduced but still exists.

Therefore it was decided to redefine the herd x year effect to (The same setup is used in most NAV evaluation models):

- Random herd x year
- Fixed herd x 5-year

However, the herd x year variance was not estimated in the Danish calf survival project. Therefore the herds variance was estimated in a simple model (using a SAS GLM - eg HP1 = herdxyear). Then the estimated percent herd variance (10-15%) was added to the phenotypic variance estimated in the Danish calf survival project.

## Effect of heterozygoty

At the outset, the following effects were defined. In the final model some effects were later modified.

#### Holstein

- BW x HF
- RW x HF
- HOL x RDC (only Finland)
- Total heterosis

#### RDC

- RDM x ABS
- RDM x HF
- RDM x Nordic breeds (= SRB+FAY+NRF)
- ABS x HF
- ABS x Nordic breeds (= SRB+FAY+NRF)
- HF x Nordic (= SRB+FAY+NRF)
- Nordic heterosis (= SRB x FAY + SRB x NRF + FAY x NRF)
- CAY x Nordic breeds (= SRB+FAY+NRF)
- FAY x FIC
- Total heterosis

#### Jersey

- DJ x USJ
- DJ x NZJ
- Total heterosis

Note: Total heterosis includes more combinations than those specified.

#### The final model includes

- HOL:
  - O BW x HF + RW x HF
  - HOL x RDC (only Finland)
- RDC:
  - ABShet = RDM x ABS + ABS x HF + ABS x (SRB+FAY+NRF)
  - NORhet = Nordic heterosis + CAY x NOR + FAY x FIC
  - RDCxHF = RDM x HF + HF x (SRB+FAY+NRF)
  - RDMxNordic breeds = RDM x (SRB+FAY+NRF)
- JER:
  - o DJ x USJ

#### Phantom parent groups

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

## **Genetic parameters**

The genetic parameters reported in the Danish calf survival project were adapted. However, the inclusion of Swedish and Finnish data required some modifications to the model and parameters. That was due to the large difference in survival rates between countries and because a linear model was used to evaluate a binary trait. In that case the heritability (genetic and environmental variance) will depend on the survival rate. Because Finland has much higher survival rates the Finnish heritability measured on a binary scale will be lower than estimated in the Danish calf survival project.

In table 5, the average survival rate per country and breed is shown together with the average of standard deviations (SD).

Table 5. Average survival rate and standard deviation of survival rate (both calculated as average of yearly results in the period 2008-2012)

|                | Average survival rate |       |       | Average SD on survival rate |       |       |       |       |
|----------------|-----------------------|-------|-------|-----------------------------|-------|-------|-------|-------|
|                | HP1                   | HP2   | BP1   | BP2                         | HP1   | HP2   | BP1   | BP2   |
| DNK HOL        | 0.963                 | 0.962 | 0.950 | 0.950                       | 0.188 | 0.190 | 0.217 | 0.217 |
| <b>FIN HOL</b> | 0.985                 | 0.975 | 0.969 | 0.968                       | 0.122 | 0.155 | 0.174 | 0.175 |
| SWE HOL        | 0.978                 | 0.952 |       |                             | 0.148 | 0.214 |       |       |
| DNK RDC        | 0.963                 | 0.954 | 0.957 | 0.935                       | 0.189 | 0.209 | 0.203 | 0.247 |
| <b>FIN RDC</b> | 0.981                 | 0.968 | 0.965 | 0.952                       | 0.137 | 0.176 | 0.184 | 0.213 |
| SWE RDC        | 0.978                 | 0.941 |       |                             | 0.147 | 0.236 |       |       |
| DNK JER        | 0.926                 | 0.934 | 0.878 | 0.909                       | 0.262 | 0.249 | 0.327 | 0.287 |

Table 6 is showns the heritabilities per country obtained using the transformation of Dempster&Lerner(1949). The assumption is that the heritability on the underlying normal scale is the same in all three countries. The Dempster&Lerner(1949) transformation is (p is the survival rates shown in table 5):

- $h^2$ -underlying =  $h^2$ -observed \*p \*(1-p) /  $z^2$  or
- $h^2$ -observed =  $h^2$ -underlying \*  $z^2/(p*(1-p))$

The difference in survival rates and in heritabilities is taken into account by scaling of input variable and by using weights in the model. The scaling factors and weights are shown in table 7.

It is important to have in mind that a time trend in survival rate will change these parameters. If the time trend becomes very large the use of this approach might become quite complicated, and the shift to a survival or threshold model should be considered.

Table 6. Estimated heritabilites based on the assumption that the heritability on an underlying normal scale is the same in all three countries. The heritability on the underlying scale is based on the results obtained in the Danish calf survival project. Conversions between underlying and observed scale are made by the formula of Dempster&Lerner(1949)

|                          | HP1    | HP2    | BP1    | BP2    |
|--------------------------|--------|--------|--------|--------|
| DNK RDC underlying scale | 0.0359 | 0.0943 | 0.0293 | 0.1117 |
| DNK RDC observed scale   | 0.0066 | 0.0199 | 0.0060 | 0.0296 |
| FIN RDC observed scale   | 0.0042 | 0.0074 | 0.0045 | 0.0179 |
| SWE RDC observed scale   | 0.0056 | 0.0115 | -      | -      |
| DNK HOL underlying       | 0.0437 | 0.0527 | 0.0277 | 0.1079 |
| DNK HOL observed scale   | 0.0080 | 0.0098 | 0.0062 | 0.0241 |
| FIN HOL observed scale   | 0.0042 | 0.0074 | 0.0045 | 0.0179 |
| SWE HOL observed scale   | 0.0056 | 0.0115 | -      | -      |
| DNK JER underlying       | 0.0626 | 0.0560 | 0.0314 | 0.0309 |
| DNK JER observed scale   | 0.0180 | 0.0150 | 0.0120 | 0.0100 |

The DNK heritabilities on the observed scale are different from results in table 1-3 because heritability is defined as:  $h^2 = V(G)/(V(G) + V(HY) + V(E))$ 

Table 7. The phenotypic scaling factors and weights. Wanted SD(P) and V(E) calculated from Danish data. The observed SD(P) and V(E) are calculated from the results in table 5 and 6.

|         | Scaling factor: |            |            | Weights: |       |                           |       |       |  |
|---------|-----------------|------------|------------|----------|-------|---------------------------|-------|-------|--|
|         | Wante           | ed SD(P)/O | bserved SE | )(P)     | Wan   | Wanted V(E)/Observed V(E) |       |       |  |
|         | HP1             | HP2        | BP1        | BP2      | HP1   | HP2                       | BP1   | BP2   |  |
| DNK HOL | 1.000           | 1.000      | 1.000      | 1.000    | 1.000 | 1.000                     | 1.000 | 1.000 |  |
| FIN HOL | 2.111           | 1.412      | 1.459      | 1.437    | 0.530 | 0.753                     | 0.730 | 0.741 |  |
| SWE HOL | 1.515           | 0.818      | =          | =        | 0.700 | 1.177                     | -     | -     |  |
|         |                 |            |            |          |       |                           |       |       |  |
| DNK RDC | 1.000           | 1.000      | 1.000      | 1.000    | 1.000 | 1.000                     | 1.000 | 1.000 |  |
| FIN RDC | 1.744           | 1.337      | 1.183      | 1.281    | 0.624 | 0.784                     | 0.870 | 0.819 |  |
| SWE RDC | 1.542           | 0.815      | =          | =        | 0.694 | 1.182                     | =     | =     |  |
|         |                 |            |            |          |       |                           |       |       |  |
| DNK JER | 1.000           | 1.000      | 1.000      | 1.000    | 1.000 | 1.000                     | 1.000 | 1.000 |  |

## The economic value of calf survival traits

An economic evaluation of mortality of young stock has been included in the NTM-model that previously has been used for assessment of economic value of the traits included in the NTM-index.

## Effect of mortality in young stock

The problem is that the mortality rates in young stock assumed in the NTM-model up to now are quite low compared to the mortality rates found in the current analyses. Tables 8 and 9 shows a comparison of these results. For RDM and DH, the results of the current analyses showed mortabilty rates that are more than twice as large as the mortality rate assumed in the NTM-model. For Jersey, the mortality rate found in the current analysis is 4-5 times larger than used in the NTM-model

Table 8. Mortality of heifer calves – a comparison of current results (table5) and results used in the NTM-model

|        | (         | Current results (table 5) |         | Assumed in the NTM-model |
|--------|-----------|---------------------------|---------|--------------------------|
|        | Heifers   | Heifers                   | Total   | Total                    |
|        | 1-30 days | 31-458 days               | heifers | Heifers                  |
| RDM    | 3.7%      | 4.6%                      | 8.3%    | 3.0%                     |
| DH     | 3.7%      | 3.8%                      | 7.5%    | 3.0%                     |
| Jersey | 7.4%      | 6.6%                      | 14.0%   | 3.0%                     |

Table 9. Mortality of bull calves – a comparison of current results (table5) and results used in the NTM-model

|        | (                  | Current results (table 5 | 5)                 | Assumed in cur-<br>rent NTM-model |
|--------|--------------------|--------------------------|--------------------|-----------------------------------|
|        | <b>Bull calves</b> | Bull calves              | Total              | Total                             |
|        | 1-30 days          | 31-184 days              | <b>Bull calves</b> | <b>Bull calves</b>                |
| RDM    | 4.3%               | 6.5%                     | 10.8%              | 5.0%                              |
| DH     | 5.0%               | 5.0%                     | 10.0%              | 5.0%                              |
| Jersey | 12.2%              | 9.1%                     | 21.3%              | 5.0%                              |

However, we must be aware that mortality of young stock in general has some effect on the value of some other traits in the model. That is:

- Value of growth traits: If mortality of bull calves increases the value of growth rate and EUROP classification decreases because an increased growth rate or EUROP classification will be expressed in fewer animals per year
- Value of stillbirth rate: The value of stillbirth is mainly due to a higher output of heifer calves
  and bull calves for slaughter. If mortality of young stock is increased the output of heifers for
  replacement or sale and bull calves for sale will decrease. Consequently, the value of improved stillbirth rate will be lower

• Value of fertility traits: The value of fertility also depends – to some degree – on the general level of mortality of heifers. If the number of heifer available for AI decreases the value of improved fertility decreases.

## Other assumptions related to mortality of young stock

I table 10 the preliminary estimates of cost related to mortality of young stock is shown

Table 10. Costs related to mortality of young stock

|                                                          | Costs, € |
|----------------------------------------------------------|----------|
| Calves, destruction of dead, €/ap                        | 21.30    |
| Extra work related to dead heifers day 1-30, hours       | 0.25     |
| Extra work related to dead heifers day 31-458, hours     | 0.50     |
| Extra work related to dead bull calves day 1-30, hours   | 0.25     |
| Extra work related to dead bull calves day 31-184, hours | 0.50     |
| Extra costs related to dead heifers day 1-30, €/ap       | 5.00     |
| Extra costs related to dead heifers day day 31-458, €/ap | 10.00    |
| Extra costs related to dead bull calves day 1-30, €/ap   | 5.00     |
| Extra costs related to dead bull calves day 31-184, €/ap | 10.00    |
| Current NTM-model                                        |          |
| Calves, destruction of dead, €/ap                        | 21.30    |
| Extra work related to dead calf, hours                   | 0.25     |
| Extra costs related to dead calf, €/ap                   | 0.00     |

## Feed costs in relationship with mortality of young stock

The calculation of feed costs for young stock has been reworked according to the periods defined by Buch et al. (2011). However, for comparison it is also necessary to clarify how feed costs for the dead heifer and bull calves were allocated in the current NTM-model.

Up to now feed cost has only been estimated up to the average age at death (table 11).

Table 11. Average age at death, days

|        | Heifers<br>1-30 days | Heifers<br>31-458 days | Bull calves<br>1-30 days | Bull calves<br>31-184 days |
|--------|----------------------|------------------------|--------------------------|----------------------------|
| RDM    | 14                   | 142                    | 14                       | 97                         |
| DH     | 12                   | 152                    | 12                       | 93                         |
| Jersey | 13                   | 142                    | 13                       | 89                         |

Table 12 shows the results. It seems to be most logical to compare to value of stillbirth. However, this comparison is not quite easy. Stillbirth is expressed separately for 1<sup>st</sup> and later calvings, but across sexes – whereas mortality of young stock is expressed per sex, but across all lactations. As a starting point the sums of the economic values could be compared.

These preliminary results indicate that the economic values of mortality of young stock are 2.0-2.5 times larger than the economic value of stillbirth rate. Besides, the results also shown that it is the mortality of heifer calves that carries the largest value (table 12).

I table 12 both the current values of stillbirth and the new reduced values are shown

Table 12. Value of improving each of the 4 mortality traits (€/unit). The results are obtained using the assumptions listed in tables 10 and 11

| Trait                           | Unit    | HOL   | RDC   | JER   |
|---------------------------------|---------|-------|-------|-------|
| Mortality in young stock        |         |       |       |       |
| Mortality, heifers 1-30 days    | %-units | 3.445 | 3.550 | 2.004 |
| Mortality, heifers 31-458 days  | %-units | 4.050 | 4.151 | 2.406 |
| Mortality, bulls 1-30 days      | %-units | 1.288 | 1.431 | 0.272 |
| Mortality, bulls 31-184 days    | %-units | 1.793 | 2.021 | 0.791 |
| Stillbirth (new reduced values) |         |       |       |       |
| %stillborn, 1st                 | %-units | 1.568 | 1.533 | 0.647 |
| %stillborn, later               | %-units | 2.447 | 2.702 | 1.182 |
| Stillbirth (Current values)     |         |       |       |       |
| %stillborn, 1st                 | %-units | 1.712 | 1.711 | 0.793 |
| %stillborn, later               | %-units | 2.669 | 2.993 | 1.459 |

## Test of the evaluation model

## The calf survival indexes

Five Calf survival indexes are calculated

- HP1-index: Breeding value of heifer survival 1-30 days
- HP2-index: Breeding value of heifer survival 31-458 days
- BP1-index: Breeding value of bull calf survival 1-30 days
- BP2-index: Breeding value of bull calf survival 31-184 days
- CS-index: Total calf survival breeding value. The breeding value for calf survival (CS) is calculated by applying the economic weight described in the previous section (table 12) to the original solutions of the evaluation

The means of breeding values for the calf survival traits are standardized such that means of calves born in a rolling 2 year period (in this case, calves born 1.5.2009 - 1.5.2011) have average 100. The variation is standardized such that sires with at least 200 progeny, reliability >= 50 and born 2004-05 have a standard deviation of 10 index units.

Table 13. Factors for standardization of variation of index (= SD of sires born 2004-05, sires with at least 200 progeny and reliability of HP1 and of BP1 >= 50)

|     | ,             |              |        | •                            |
|-----|---------------|--------------|--------|------------------------------|
|     | HOL (and RED) | RDC(and FIC) | JER    | Unit                         |
| HP1 | 0.0098        | 0.0107       | 0.0259 | Survival rate/10 index units |
| HP2 | 0.0118        | 0.0192       | 0.0169 | Survival rate/10 index units |
| BP1 | 0.0097        | 0.0109       | 0.0275 | Survival rate/10 index units |
| BP2 | 0.0208        | 0.0283       | 0.0188 | Survival rate/10 index units |
| CS  | 11.29         | 17.65        | 9.82   | €/10 index units             |

## Correlations with NTM and NTM-traits

In table 14, the correlation with the NTM-index and the traits included in the NTM-index are shown. The correlations are generally low to NTM and the NTM-traits. Small positive correlations are found in all three breeds for the following traits:

- Birth
- Udder Health
- Health
- Longevity
- Claw Health
- Leg conformation
- NTM

For body conformation the correlation is negative in all three breeds.

Table 14. Correlations between the total calf survival index and the NTM-traits. Based on sires born 2005-2007. (Bold blue correlations are significantly different from 0 at 5% level)

|                          |       | , , ,, |       |
|--------------------------|-------|--------|-------|
|                          | HOL   | RDC    | JER   |
| yield                    | 0.02  | -0.01  | -0.09 |
| Growth                   | 0.01  | -0.12  | 0.08  |
| Fertility                | 0.04  | 0.11   | 0.04  |
| Birth                    | 0.07  | 0.27   | 0.08  |
| Calving                  | 0.06  | -0.04  | 0.10  |
| Udder health             | 0.04  | 0.03   | 0.21  |
| Health                   | 0.10  | 0.02   | 0.09  |
| Claw health              | 0.13  | 0.06   | 0.02  |
| Longevity                | 0.15  | 0.18   | 0.05  |
| <b>Body conformation</b> | -0.04 | -0.26  | -0.13 |
| Legs conformation        | 0.04  | 0.22   | 0.01  |
| Udder conformation       | -0.04 | -0.07  | 0.10  |
| Milking speed            | -0.04 | -0.11  | -0.02 |
| Temperament              | 0.01  | -0.07  | -0.09 |
| NTM                      | 0.09  | 0.07   | 0.08  |
| Number of sires          | 1050  | 650    | 148   |

## **Trend results**

### Jersey (Figure 5 and 6)

Figures 5 and 6 shows the trend results for Jersey calf survival including the individual indexes for heifer survival in period 1 and 2 and bull calf survival in period 1 and 2. Both figures clearly show that the results of period 1 is very similar in the 2 sexes, i.e. calf survival for heifers and bull calves is nearly the same trait in period 1. The same result was found for period 2.

The result for total calf survival (CS) is close to the average results for period 1 and 2.

In Jersey, the trend for the Calf Survival Index has been varying from year to year (probably random variation due to the low number of sires), but there has been no genetic development in the Calf Survival Index from 1996 to now.

#### **HOL and RDC**

The total calf survival (CS) trends for period 1 are shown in figure 7 and 8. Both figures show that the level of CS in Finnish Holstein is around 15 index units higher than the level of CS in RDC. This result is supported by the results for Danish RDC (figure 8) where the sires are subdivided into two groups: One with less than 25% Red Holstein genes and one with more than 25% Red Holstein genes. The level of DNK RDC sires with more than 25% Red Holstein genes is clearly larger than the level for the DNK RDC sires with less than 25% Red Holstein genes.

The RDC-evaluation has been run without Finnish Holstein included. That did not change the results for the two DNK RDC groups.

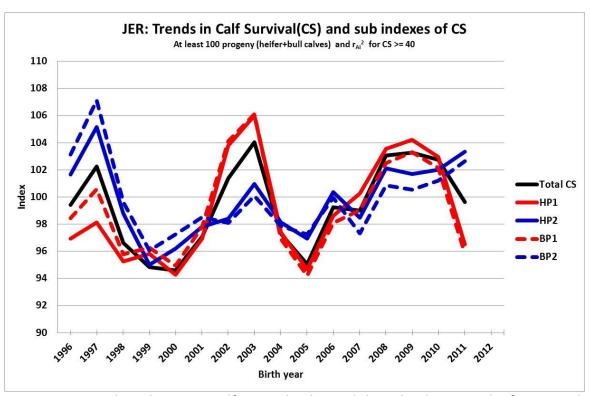


Figure 5. Trends in the Jersey calf survival index and the subindexes, i.e. heifer survival in period1 and 2 (HP1 and HP2) and bull calf survival in period1 and 2 (BP1 and BP2)

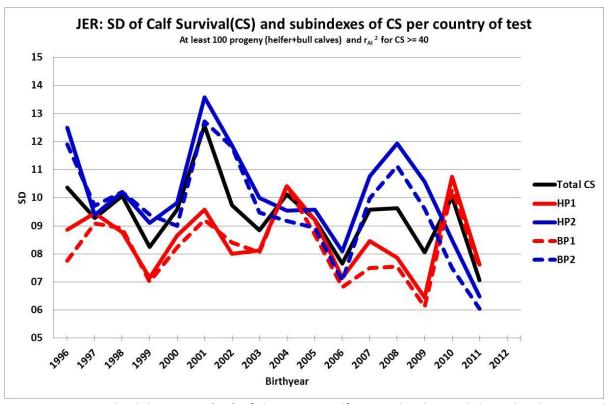


Figure 6. Standard deviations(SD) of the Jersey calf survival index and the subindexes, i.e. heifer survival in period1 and 2 (HP1 and HP2) – and bull calf survival in period 1 and 2(BP1 and BP2)

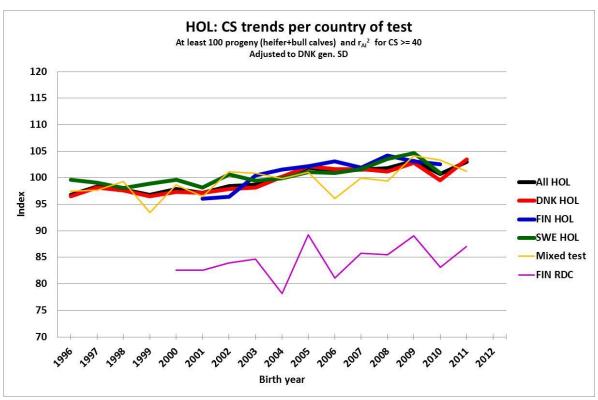


Figure 7. Trends in the Holstein calf survival index. Results for the Finnish RDC included in the Holstein evaluation are also shown

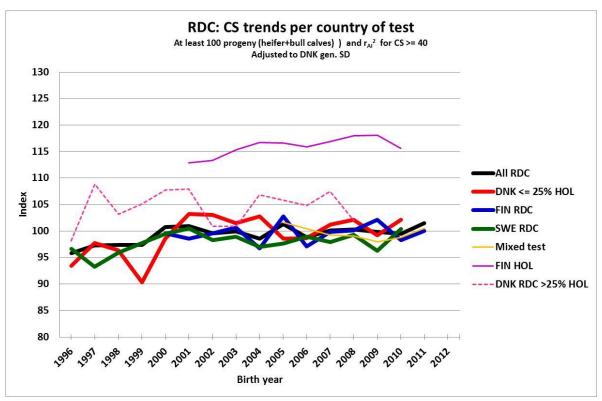


Figure 8. Trends in the RDC calf survival index. Results for the Finnish Holstein included in the RDC evaluation are also shown. The Danish RDC sires are subdivided into 2 groups:

Sires with less than 25% Red Holstein genes and sires with more than 25% Red Holstein genes.

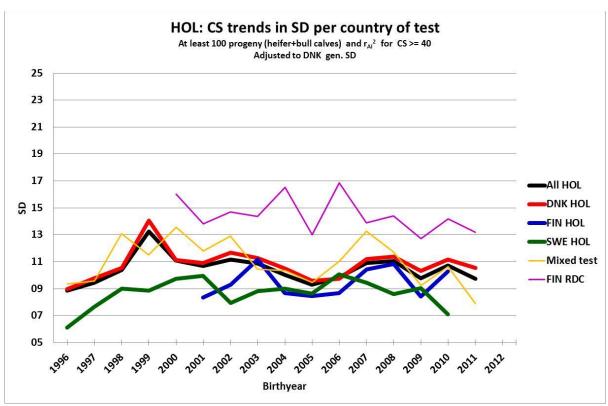


Figure 9. Standard deviations of the Holstein calf survival index. Results for the Finnish RDC included in the Holstein evaluation are also shown

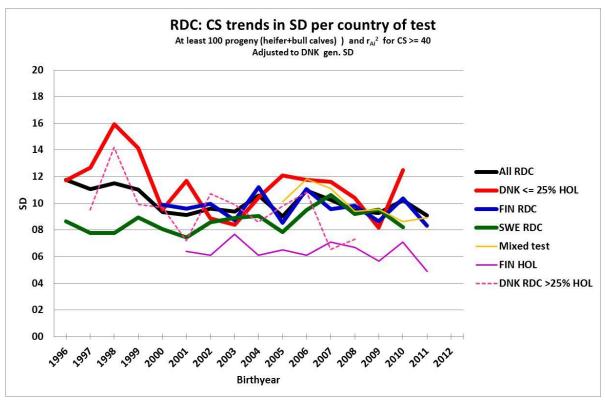


Figure 10. Standard deviation of RDC calf curvival index. Results for the Finnish Holstein included in the RDC evaluation are also shown. The Danish RDC sires are subdivided into 2 groups: Sires with less than 25% Red Holstein genes and sires with more than 25% Red Holstein genes.

## Standard deviation (SD) of HOL and RDC calf survival

The Holstein and RDC standard deviations are shown in figures 9 and 10. When the Holstein standardization factors are applied to the Finnish RDC sires then the standard deviation of Finnish RDC becomes very large (figure 9). Opposite, when the RDC standardization factors are applied to Finnish Holsteins the SD of Finnish Holstein becomes very small (figure 10). That is a natural consequence of the standardization factors for total calf survival shown in table 13.

## **IB3** test results

Table 15 showns the results of an Interbull test 3. For most traits the result are within the required 2% limit. However, all result outside the 2%-limit are far away from being statistical significant. The conclusion is that Interbull test 3 is passed for all traits and breeds.

Table 15. Interbull test 3 results

|        | No of | Reg. on  | Regression. | SD of re- |         |       | t in % of |  |  |  |  |
|--------|-------|----------|-------------|-----------|---------|-------|-----------|--|--|--|--|
|        | sires | red. EBV | on t        | gression  | Pr >  t | SD(G) | SD(G)     |  |  |  |  |
|        |       |          |             |           |         |       |           |  |  |  |  |
| HOL    |       |          |             |           |         |       |           |  |  |  |  |
| HP1    | 1185  | 0.95     | 0.214       | 0.561     | 0.7027  | 17.5  | 1.22%     |  |  |  |  |
| HP2    | 1329  | 0.97     | 0.104       | 0.457     | 0.8199  | 16.9  | 0.62%     |  |  |  |  |
| BP1    | 999   | 0.43     | 0.010       | 0.681     | 0.9881  | 16.8  | 0.06%     |  |  |  |  |
| BP2    | 1083  | 0.96     | 0.026       | 0.662     | 0.9686  | 16.3  | 0.16%     |  |  |  |  |
|        |       |          |             |           |         |       |           |  |  |  |  |
| RDC    |       |          |             |           |         |       |           |  |  |  |  |
| HP1    | 684   | 0.98     | -0.245      | 0.757     | 0.7458  | 17.0  | -1.45%    |  |  |  |  |
| HP2    | 793   | 0.98     | -0.012      | 0.531     | 0.9815  | 17.6  | -0.07%    |  |  |  |  |
| BP1    | 517   | 0.99     | 0.615       | 1.055     | 0.5603  | 15.0  | 4.09%     |  |  |  |  |
| BP2    | 539   | 0.98     | 0.577       | 0.866     | 0.5051  | 17.1  | 3.37%     |  |  |  |  |
|        |       |          |             |           |         |       |           |  |  |  |  |
| Jersey |       |          |             |           |         |       |           |  |  |  |  |
| HP1    | 180   | 0.98     | -0.095      | 0.653     | 0.8846  | 12.5  | -0.76%    |  |  |  |  |
| HP2    | 182   | 0.91     | -0.307      | 0.752     | 0.6834  | 15.6  | -1.96%    |  |  |  |  |
| BP1    | 178   | 0.96     | 0.842       | 0.967     | 0.3853  | 12.6  | 6.66%     |  |  |  |  |
| BP2    | 138   | 0.91     | 0.076       | 1.380     | 0.9562  | 15.4  | 0.49%     |  |  |  |  |

# **Summary**

Nordic Cattle Genetic Evaluation(NAV) aims at fewer stillborn calves and enhanced longevity. There are favourable genetic correlations between these traits and the ability to survive the rearing period. However, it is more efficient to breed directly for higher survival rates among calves and young stock. The basic registration for an evaluation of calf survival is available in the NAV countries. A Danish project has demonstrated that in spite of the low heritability of calf survival it would be possible to improve this trait by breeding.

In this project an evaluation routine for calf survival has been developed. It is based on a simple linear model for four calf survival traits. The evaluation routine is ready for implementation.

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