

# MACE for Longevity Traits

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## 1. Introduction

At the Interbull meeting in May 2002 in Interlaken research was presented on MACE for longevity traits for (Red) Holstein with 11 participating countries (Van der Linde and De Jong, 2002). After that meeting another request for data was done and also Australia, Great Britain and Ireland joined the project with data. This report describes results of the second part of the research project on MACE for longevity traits.

The aim of this study is to review the national genetic evaluation procedures of longevity traits in the 14 participating countries and to estimate parameters (variances components and genetic correlations) of the traits needed for the MACE evaluation. This study also aims to compare results to the previous (2002) research and to identify potential problems for MACE for longevity traits.

## 2. Material and Methods

Breeding values for longevity traits of (Red) Holstein bulls were obtained from 14 countries, Australia (AUS), Canada (CAN), Switzerland (CHE), Germany (DEU), Denmark (DNK), France (FRA), Great Britain (GBR), Ireland (IRL), Israel (ISR), Italy (ITA), the Netherlands (NLD), New Zealand (NZL), Sweden (SWE) and the United States (USA). The numbers of sire proofs for longevity traits per country are in Table 1. Pedigree and cross-reference files were obtained from the Interbull Centre. The participating countries also answered questionnaires about their national genetic evaluation system for longevity traits.

Number of common bulls and common sire-maternal grandsire (mgs) combinations were de-

termined to indicate the amount of genetic ties between countries. Estimation of genetic correlations between countries included all bulls with evaluations in multiple countries and bulls that were members of common sire-mgs combinations with evaluations in multiple countries.

For the estimation of genetic parameters for direct and combined longevity, bulls should have at least daughters in 10 herds and 10 effective daughter contributions (EDC), both first crop and imported bulls. EDC were used as provided by the participating countries. No selection on year of birth was applied.

Genetic correlations were estimated both for direct longevity and combined longevity as described above.

Proofs were deregressed using EDC. For CAN and NZL bulls got 1 EDC for every daughter in the evaluation, but CAN only included cows in the longevity evaluation with their first calving at least 2 years ago. USA calculated EDC based on age of daughters. FRA, NLD, DEU, DNK, CHE, ITA, SWE and ISR used number of culled daughters for EDC. AUS en GBR calculated EDC like the Interbull routine evaluations for production, type and somatic cell count. IRL computed EDC as number of daughters in survival analysis + 0.67 \* total number of daughters, because all daughters with records contributed directly via survival and calving interval.

Most countries provided longevity proofs with higher EBVs being desirable except ITA for direct longevity, these EBVs were multiplied with factor -1. If direct or combined longevity was not available for a country, the available trait was used for the parameter estimation.

Table 1. Number of received and used sire proofs per country for direct and combined longevity.

| Country         | Number of received records |          | Number of used records <sup>1</sup> |          |
|-----------------|----------------------------|----------|-------------------------------------|----------|
|                 | Direct                     | Combined | Direct                              | Combined |
| Australia       | 6360                       | 6360     | 2161                                | 2161     |
| Canada          | 7246                       | 7246     | 4502                                | 4502     |
| Denmark         | 6118                       | -        | 3675                                | 3144     |
| France          | 14,293                     | 13,951   | 8376                                | 8041     |
| Germany         | 14,859                     | 14,859   | 6782                                | 6888     |
| Great Britain   | 3735                       | -        | 2432                                | 2432     |
| Ireland         | -                          | 786      | 619                                 | 619      |
| Israel          | 769                        | -        | 54                                  | 54       |
| Italy           | 4774                       | 4774     | 2941                                | 2941     |
| The Netherlands | 10,566                     | 10,566   | 4728                                | 4728     |
| New Zealand     | -                          | 14,149   | 1789                                | 1789     |
| Sweden          | 1900                       | -        | 710                                 | 710      |
| Switzerland     | 833                        | -        | 382                                 | 382      |
| USA             | 40,169                     | 41,008   | 18,749                              | 18,885   |
| Total           | 111,622                    | 113,699  | 57,900                              | 57,276   |

1) Number of records used for estimation of genetic correlations between countries.

### 3. Results and Discussion

#### 3.1 National genetic evaluation systems

The main characteristics of the national genetic evaluation systems for longevity traits are summarised in Table 7. FRA, NLD, DEU, DNK, CHE and ITA use survival analysis to evaluate longevity. USA and ISR use a single-trait model with predicted or realised life span of cows up to 7 years of age. GBR uses number of lactations completed or expected to complete based on survival probabilities analysed bivariate with phenotypic index scores computed from 4 type traits. CAN and IRL use a binary multiple-trait model with survival in the first three lactations. IRL includes milk yield, calving interval and 3 type traits in the model and afterwards adjust the breeding value for survival per lactation for the breeding value for milk yield in the respective lactation before combining them into one index. SWE uses a single-trait model with ability to survive the second lactation. AUS uses the probability of surviving from one year to the next with different years considered as repeated measurements. NZL uses a multiple-trait animal model. Each animal has a record for only one trait, depending on current lactation of the cow or her cohorts. Realised or predicted life span is evaluated in a 6-trait model. These traits are lactation 1 through 5 and lactation 6 and higher. Survival analysis is used to predict censored records (with

25 predictors) by using the mean residual life function.

Inclusion of data in the national longevity evaluations ranged from 2 to all lactations. USA and ISR include cows till 7 years of age. AUS includes 7 lactations, GBR 5 lactations, CAN and IRL 3 lactations and SWE 2 lactations, other countries include all lactations per cow. Heritabilities for longevity traits used in the national genetic evaluations ranged from 0.02 in SWE to 0.20 in FRA, both for direct and combined longevity.

#### 3.2 Genetic ties

The average number of common bulls with at least 10 daughters in two countries for direct longevity are in Table 2. To convert EBVs between countries, at least 20 bulls with regular AI-proofs based on daughters in at least 20 herds in each country and having proofs with repeatabilities of at least 75% in both countries are required according to Interbull recommendations (Interbull, 1990). All countries met this requirement on average, but genetic ties between ISR and some other countries were weak. This probably resulted in large standard errors for the genetic correlation of longevity between ISR and other countries. But standard errors of estimated genetic correlations were not available, as software did not include this.

Table 2. Average number of common bulls per country.

|     |     |     |     |
|-----|-----|-----|-----|
| AUS | 249 | IRL | 177 |
| CAN | 360 | ISR | 20  |
| CHE | 92  | ITA | 274 |
| DEU | 381 | NLD | 347 |
| DNK | 136 | NZL | 275 |
| FRA | 380 | SWE | 108 |
| GBR | 341 | USA | 511 |

### 3.3 Genetic correlations

Table 3 gives the estimated genetic correlations between countries for direct and combined longevity and the average estimated genetic correlations for direct (DIR) and combined longevity (COM) of one country with all other countries.

#### 3.3.1 Direct longevity

NZL and IRL did not provide breeding values for direct longevity. For these countries combined longevity is used in the direct longevity run.

Average genetic correlations between countries for direct longevity are moderately high

(mean 0.60). Average genetic correlations range from 0.72 for CAN and USA to 0.28 for ISR. Besides the average genetic correlation with other countries, also the maximum genetic correlation per country is a measure for the genetic relationship between countries. Maximum genetic correlations between countries ranged from 0.93 between CAN and USA to 0.46 between FRA and ISR. CAN and USA have the highest genetic correlation although using different models for evaluating longevity. The European countries using the survival kit to analyse longevity (FRA, NLD, DEU, DNK, CHE and ITA) have genetic correlation with each other ranging from 0.56 to 0.88. Genetic correlations between ISR and the other countries are low ranging from  $-0.03$  to 0.46.

#### 3.3.2 Combined longevity

The EBVs for direct longevity for CHE, DNK, GBR, ISR and SWE were used as combined longevity was not available. Average genetic correlation for combined longevity was 0.58. Average genetic correlations per country for combined longevity were similar to direct longevity, except for AUS (combined longevity 0.12 lower compared to direct longevity).

Table 3. Genetic correlations between countries for direct longevity (below diagonal) and combined longevity (above diagonal). DIR gives the average correlation with all other countries for direct longevity and COM for combined longevity. MAX is the maximum genetic correlation with another country for direct longevity.

|     | AUS  | CAN  | CHE  | DEU  | DNK  | FRA  | GBR  | IRL   | ISR   | ITA  | NLD  | NZL  | SWE  | USA  |
|-----|------|------|------|------|------|------|------|-------|-------|------|------|------|------|------|
| AUS |      | 0.42 | 0.46 | 0.51 | 0.55 | 0.67 | 0.33 | 0.21  | 0.35  | 0.40 | 0.49 | 0.36 | 0.53 | 0.44 |
| CAN | 0.58 |      | 0.77 | 0.83 | 0.80 | 0.68 | 0.88 | 0.79  | 0.35  | 0.87 | 0.82 | 0.50 | 0.67 | 0.92 |
| CHE | 0.55 | 0.75 |      | 0.79 | 0.79 | 0.72 | 0.82 | 0.72  | 0.13  | 0.70 | 0.75 | 0.43 | 0.44 | 0.70 |
| DEU | 0.50 | 0.84 | 0.78 |      | 0.85 | 0.66 | 0.78 | 0.61  | 0.41  | 0.79 | 0.86 | 0.50 | 0.48 | 0.80 |
| DNK | 0.63 | 0.75 | 0.79 | 0.85 |      | 0.83 | 0.69 | 0.54  | 0.33  | 0.71 | 0.90 | 0.47 | 0.59 | 0.82 |
| FRA | 0.78 | 0.65 | 0.67 | 0.66 | 0.81 |      | 0.56 | 0.44  | 0.45  | 0.60 | 0.74 | 0.32 | 0.49 | 0.65 |
| GBR | 0.51 | 0.89 | 0.82 | 0.78 | 0.67 | 0.52 |      | 0.78  | 0.23  | 0.85 | 0.74 | 0.53 | 0.58 | 0.82 |
| IRL | 0.43 | 0.77 | 0.69 | 0.60 | 0.52 | 0.41 | 0.77 |       | 0.05- | 0.64 | 0.65 | 0.46 | 0.60 | 0.76 |
| ISR | 0.42 | 0.40 | 0.17 | 0.31 | 0.35 | 0.46 | 0.31 | 0.03- |       | 0.17 | 0.07 | 0.39 | 0.17 | 0.36 |
| ITA | 0.44 | 0.88 | 0.70 | 0.79 | 0.70 | 0.56 | 0.83 | 0.59  | 0.23  |      | 0.78 | 0.42 | 0.59 | 0.77 |
| NLD | 0.53 | 0.81 | 0.74 | 0.86 | 0.88 | 0.69 | 0.72 | 0.63  | 0.12  | 0.77 |      | 0.38 | 0.57 | 0.80 |
| NZL | 0.58 | 0.49 | 0.46 | 0.49 | 0.47 | 0.37 | 0.53 | 0.47  | 0.32  | 0.41 | 0.38 |      | 0.40 | 0.52 |
| SWE | 0.66 | 0.68 | 0.46 | 0.47 | 0.56 | 0.56 | 0.59 | 0.60  | 0.15  | 0.60 | 0.55 | 0.35 |      | 0.70 |
| USA | 0.67 | 0.93 | 0.70 | 0.80 | 0.80 | 0.67 | 0.82 | 0.76  | 0.40  | 0.76 | 0.79 | 0.51 | 0.70 |      |
| DIR | 0.56 | 0.72 | 0.64 | 0.67 | 0.68 | 0.60 | 0.67 | 0.55  | 0.28  | 0.64 | 0.65 | 0.45 | 0.53 | 0.72 |
| COM | 0.44 | 0.72 | 0.63 | 0.68 | 0.68 | 0.60 | 0.66 | 0.55  | 0.26  | 0.64 | 0.66 | 0.44 | 0.52 | 0.70 |
| MAX | 0.78 | 0.93 | 0.82 | 0.86 | 0.88 | 0.81 | 0.89 | 0.77  | 0.46  | 0.88 | 0.88 | 0.58 | 0.70 | 0.93 |

### 3.4 Genetic correlations 2002 and 2003

Results of the 2002 and the 2003 research evaluation were compared for direct longevity. Table 4 gives the (absolute) average and absolute maximum difference of genetic correlations between both evaluations. Also the correlation between the breeding values provided for both evaluations was calculated to investigate the consistency of both data sets. Differences were calculated as genetic correlations of 2003 minus 2002.

Table 4. Average (AVG), absolute (ABS) average and absolute maximum (MAX) differences in genetic correlations of longevity between the 2002 and 2003 evaluation and the correlation (CORR) between breeding values provided for both evaluations for direct longevity.

|     | AVG   | ABS  | MAX  | CORR  |
|-----|-------|------|------|-------|
| CAN | 0.02  | 0.07 | 0.18 | 0.96  |
| CHE | 0.05  | 0.06 | 0.13 | 1.00  |
| DEU | 0.08  | 0.09 | 0.21 | -0.85 |
| DNK | 0.11  | 0.13 | 0.25 | 0.79  |
| FRA | 0.03  | 0.06 | 0.30 | 0.97  |
| ISR | 0.09  | 0.11 | 0.30 | 0.97  |
| ITA | 0.06  | 0.10 | 0.25 | 0.95  |
| NLD | 0.00  | 0.07 | 0.18 | 0.97  |
| NZL | -0.07 | 0.07 | 0.18 | 1.00  |
| SWE | -0.02 | 0.08 | 0.21 | 0.98  |
| USA | 0.02  | 0.06 | 0.13 | 1.00  |
| ALL | 0.03  |      |      |       |

The average genetic correlation was 0.03 higher for 2003 compared to 2002 for countries with data in both evaluations. The correlation between breeding values of both evaluations was higher than 0.95 for all countries except DEU (-0.85) and DNK (0.79). Largest differences in genetic correlations between both evaluations had DEU, DNK and ISR. The lower correlation between breeding values of both evaluations for DEU and DNK might explain the relative large differences in genetic correlations between both evaluations, for ISR the differences in genetic correlations between both evaluations might be due to weak connections with other counties. But also a better connected country as NZL showed relative large differences in genetic correlations between both evaluations with the same data.

## Discussion

### 4.1 Deregression of proofs

Standard deviations of estimated transmitting abilities (ETA) and deregressed proofs (DRPF EDC) and the correlations between both were estimated to investigate potential problems with deregression of proofs of traits with a low heritability. Proofs were also deregressed to 100 % reliability (DRPF REL) based on average reliability. The ratio (RAT) between proofs deregressed based on EDC and reliability is given.

Maximum ETA and DRPF are given in order to visualise to what extent proofs are deregressed. Bulls included had at least daughters in 10 herds and 10 effective daughter contributions (EDC). Results are in Table 5.

Table 5. Standard deviations of ETA and DRPF (based on EDC or REL), ratio (RAT) between DRPF EDC and DRPF REL, maximum ETA and DRPF and the correlation (CORR) between both per country for direct longevity.

|     | ETA  | DRPF<br>EDC | DRPF<br>REL | RAT | CORR | MAX<br>ETA | MAX<br>DRPF |
|-----|------|-------------|-------------|-----|------|------------|-------------|
| AUS | 2.22 | 3.28        | 3.42        | 96  | 0.87 | 6.7        | 14.8        |
| CAN | 0.59 | 1.93        | 0.72        | 268 | 0.82 | 2.3        | 9.3         |
| CHE | 0.48 | 0.64        | 0.59        | 108 | 0.95 | 1.6        | 2.8         |
| DEU | 0.39 | 0.50        | 0.49        | 102 | 0.96 | 1.6        | 3.5         |
| DNK | 0.49 | 0.79        | 0.66        | 120 | 0.93 | 2.1        | 3.7         |
| FRA | 0.37 | 0.51        | 0.47        | 109 | 0.94 | 1.5        | 6.3         |
| GBR | 0.40 | 0.75        | 0.55        | 136 | 0.87 | 1.2        | 3.1         |
| IRL | 1.38 | 2.52        | 2.55        | 99  | 0.85 | 4.0        | 7.8         |
| ISR | 0.54 | 0.80        | 0.65        | 123 | 0.92 | 1.1        | 4.1         |
| ITA | 0.92 | 1.89        | 1.29        | 147 | 0.85 | 3.0        | 10.1        |
| NLD | 0.46 | 0.71        | 0.61        | 116 | 0.93 | 1.7        | 4.1         |
| NZL | 1.03 | 1.72        | 1.72        | 100 | 0.88 | 3.3        | 9.1         |
| SWE | 0.45 | 4.02        | 1.09        | 369 | 0.48 | 2.6        | 90.2        |
| USA | 1.34 | 2.46        | 2.05        | 120 | 0.87 | 5.0        | 13.3        |

Results from Table 5 show that correlations between ETA and DRPF were in the range of 0.48 for SWE to 0.96 for DEU. The ratio between DRPF EDC and DRPF REL ranged from 96 for AUS to 369 for SWE. CAN and SWE did have the largest ratio between DRPF EDC and DRPF REL which might be due to the low heritability of

direct longevity in these countries, but AUS also had a low heritability for direct longevity and had the lowest ratio between DRPF EDC and DRPF REL. The maximum ETA and DRPF showed rather large differences for most countries.

#### 4.2 Genetic trends per country

Genetic trends per country were calculated by regression of the ETA on year of birth for direct and combined longevity (Table 6). ETA were calculated using the mean and standard deviation of expression of the breeding values. Not all these factors were available per country and therefore not all genetic trends per country. Genetic trends per country ranged from -0.02 to 0.08 genetic standard deviations per year for respectively CHE and USA. USA had the highest genetic trend for longevity traits which might to certain extent be explained by not adjusting longevity for production whereas all the other countries in Table 6 with a calculated genetic trend did adjust longevity for production.

Table 6. Genetic trends per country for direct and combined longevity expressed in genetic standard deviations per year.

|     | Direct | Combined |
|-----|--------|----------|
| AUS | -      | -        |
| CAN | 0.01   | 0.02     |
| CHE | -0.02  | -0.02    |
| DEU | -0.01  | 0.00     |
| DNK | 0.04   | 0.04     |
| FRA | 0.00   | 0.00     |
| GBR | 0.01   | 0.01     |
| IRL | -      | -        |
| ISR | -      | -        |
| ITA | 0.04   | -        |
| NLD | 0.03   | 0.03     |
| NZL | -      | -        |
| SWE | 0.01   | 0.01     |
| USA | 0.07   | 0.08     |

#### 4.3 National genetic evaluation systems

New in the 2003 research evaluation was the inclusion of data of AUS, GBR and IRL. The evaluation model of GBR was comparable to USA and ISR. IRL was the only country that directly included other traits in their longevity evaluation. AUS considered the first 7 lactations as repeatable traits. GBR included 5 and IRL 3 lactations. AUS did not adjust and GBR and IRL did adjust longevity for production.

#### 4.4 Direct and combined longevity

The average genetic correlation for combined longevity was 0.02 higher compared to direct longevity. In most cases the same EDC for deregression of proofs were used for direct and combined longevity. This is not optimal, because additional information on direct longevity has been combined into combined longevity. If countries would like to use information on combined longevity, more research should be carried out how MACE can deal with combined longevity.

#### 4.5 Outlook

Results from this study are in line with results from the 2002 report and show the feasibility of MACE for longevity traits. But genetic correlations ranged from low to high. This research has not shown the impact of EDC on genetic correlations between countries as the way countries calculated EDC was not changed between the 2002 and 2003 report. More research is needed to investigate the importance of method of calculation of EDC on genetic correlations.

## 5. Conclusions

- There is much variation in national longevity evaluation models and methods.
- Enough genetic ties exist between countries, but genetic ties between ISR and other countries are weak.
- Genetic correlations between countries for direct longevity are low to high (-0.03 - 0.93).
- Average genetic correlations of direct longevity are 0.02 higher compared to combined longevity, but more research is needed in case combined longevity will be included in MACE.
- Genetic trends per country vary from -0.02 to 0.08 genetic standard deviations per year.
- Much attention should be paid to the improvement of genetic correlations for longevity traits between countries.
- MACE for longevity traits is feasible.
- Implementation of MACE for longevity traits is catalysing the uniformization of evaluation procedures and trait definitions and therefore the improvement of genetic correlations between countries.

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## References

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Table 7. Characteristics of the national evaluation systems of the participating countries.

| Country | Direct longevity       | Combined longevity                                    | $h^2$ direct longevity | $h^2$ combined longevity | Records included          | Correction for milk production | Survival kit parameters rho/gamma | Data inclusion |
|---------|------------------------|-------------------------------------------------------|------------------------|--------------------------|---------------------------|--------------------------------|-----------------------------------|----------------|
| AUS     | AM ST                  | Index combining direct with 4 predictors              | 0.025                  | 0.025                    | First 7 lactations        | no                             |                                   | ??             |
| CAN     | AM MT                  | Index combining direct with 6 predictors <sup>1</sup> | 0.03                   | 0.08                     | First 3 lactations        | yes                            | -                                 | 1980 >         |
| CHE     | SM SA <sup>2</sup>     | -                                                     | 0.184                  | -                        | all lactations            | yes                            | 1.53 / 3.75                       | 1980 >         |
| DEU     | SM SA <sup>2</sup>     | Direct + 5 predictors                                 | 0.20                   | 0.20                     | all lactations            | yes                            | 2.00 / 4.00                       | 1985 >         |
| DNK     | SM SA <sup>2</sup>     | -                                                     | 0.10                   | -                        | all lactations            | yes                            | 1.07 / 6.12                       | 1984 >         |
| FRA     | SM SA <sup>2</sup>     | Direct + 10 predictors                                | 0.20                   | 0.20                     | all lactations            | yes                            | 2.00 / 4.00                       | 1985 >         |
| GBR     | AM ST                  |                                                       | 0.06                   |                          | First 5 lactations        | yes                            |                                   | ??             |
| IRL     |                        | SM MT combining 13 traits in one MT evaluation        |                        | 0.03                     | First 3 lactations        | yes                            |                                   | ??             |
| ISR     | AM ST                  | -                                                     | 0.143                  | -                        | Cows up to 7 years of age | no                             | -                                 | ??             |
| ITA     | SM SA <sup>2</sup>     | Direct + 2 predictors                                 | 0.08                   | 0.08                     | all lactations            | yes                            | 2.00 / 2.20                       | 1980 >         |
| NLD     | SM SA <sup>2</sup>     | Direct + 6 predictors                                 | 0.11                   | 0.11                     | all lactations            | yes                            | 1.49 / 4.19                       | 1988 >         |
| NZL     | -                      | AM MT                                                 | -                      | 0.072                    | all lactations            | no                             | -                                 | 1985 >         |
| SWE     | SM ST RES <sup>3</sup> | SM ST                                                 | 0.02                   | 0.02                     | First 2 lactations        | yes                            | -                                 | 1982 >         |
| USA     | AM ST                  | Direct + 7 predictors                                 | 0.085                  | 0.085                    | Cows up to 7 years of age | no                             | -                                 | 1960 >         |

<sup>1</sup>Canada combines direct longevity and indirect longevity (index of 6 traits) with a MACE procedure into combined longevity (herd life).

<sup>2</sup>SA = survival analysis

<sup>3</sup>RES = residual longevity (longevity corrected for milk production, daughter fertility, calving performance and diseases).