Feasibility of MACE for Longevity Traits

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1. Introduction

Many dairy breeders want to compare top bulls from all over the world objectively. They therefore greatly benefit from international estimated breeding values (EBVs) for milk production and conformation traits. However, for functional traits like longevity international EBVs from other countries are only available for somatic cell count. Functional traits become increasingly important when making selection decisions and therefore there is a clear need for Multiple Across Country Evaluation (MACE) for functional traits. MACE for functional traits also will encourage harmonisation of trait definition and statistical models by publishing genetic correlations between countries.

Many countries already have a genetic evaluation for longevity and include longevity in their total merit index because of the great economic importance. Therefore there is an increasing demand for an international genetic evaluation for longevity.

Longevity can be measured by using culling data only (direct longevity) or by using culling data and predictive traits as conformation or functional traits (combined longevity). Some studies are carried out to estimate genetic correlations between longevity traits in different countries. Powell *et al.* (1997) estimated a genetic correlation between the longevity traits in the USA and Canada of 0.69. A more recent study of Grignola and Schaeffer (2000) showed a genetic correlation, estimated by MACE, between Herdlife (Canada) and Productive Life (USA) of 0.91. Harbers (1999) used longevity EBVs of France, Germany, the Netherlands and the USA to estimate correlations for longevity traits between these countries. All correlations between countries ranged from 0.61 to 0.81. These correlations are moderate to high and should be high enough for an international evaluation of longevity traits. Mark *et al.* (2000) showed feasible results of a MACE evaluation for the functional traits somatic cell count and clinical mastitis. This means that MACE is feasible for low heritable traits.

The aim of this study is to review the national genetic evaluation procedures of longevity traits in the 11 participating countries and to estimate parameters (variances components and genetic correlations) of the traits needed for the MACE evaluation.

2. Material and Methods

Breeding values for longevity traits of (Red) Holstein bulls were obtained from Canada (CAN), the United States (USA), France (FRA), the Netherlands (NLD), Germany (DEU), Denmark (DNK), Sweden (SWE), Switzerland (CHE), Italy (ITA), Israel (ISR) and New Zealand (NZL). 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 determined 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 obtained from the participating countries, except for NZL where number of daughters was used. No selection on year of birth was applied.

Two analyses were carried for direct longevity and combined longevity each as described above. Genetic correlations were estimated with a copy of the MACE-system used in the Interbull evaluation for type of May 2001, obtained from Holstein Association, USA.

Proofs were deregressed using EDC. CAN and NZL bulls had 1 EDC for every daughter in the evaluation, but CAN only included cows in the genetic evaluation for longevity if cows have had their first calving at least 2 years before the date of evaluation. The USA calculated EDC based on age of daughters. Countries using survival analysis (FRA, NLD, DEU, DNK, CHE and ITA) and SWE and ISR used number of culled daughters for EDC.

SWE sent in data for direct longevity and residual longevity adjusted for milk production, daughter fertility, calving performance and diseases. Most countries provided longevity traits with higher EBVs being desirable except DEU for both direct and combined longevity and ITA for direct longevity, EBVs of these countries were multiplied with factor –1. In case direct or combined longevity was not available for a country, the available trait was used for the parameter estimation of both direct and combined longevity.

3. Results and Discussion

3.1 Description of national genetic evaluation systems

The main characteristics of the national evaluation systems are summarised in Table 4. FRA, NLD, DEU, DNK, CHE and ITA use survival analysis to evaluate longevity. USA and ISR use predicted or realised life span of cows in a single-trait model until cows are 7 years old. CAN uses a multiple-trait model with three binary traits which are survival in the first three lactations. SWE uses a single-trait model with ability to survive the second lactation. 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.

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[1]	
	Direct	Combined	Direct	Combined
Canada	6543	6543	3762	3762
USA	28,074	28,074	16,522	16,522
France	13,873	13,536	7745	7730
The Netherlands	11,464	11,464	4026	4026
Germany	12,402	6899	5532	4055
Denmark	5457	-	3144	3144
Sweden	1900	-	710	710
Switzerland	833	-	381	381
Italy	4457	4457	2964	2964
Israel	685	-	46	46
New Zealand	-	14,149	1310	1310
Total	85,688	85,122	46,142	44,650

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

Most countries use all lactations of cows, USA and ISR include cows until 7 years of age which is in practice most of the available lactations. CAN uses three and SWE two lactations. Heritabilities for longevity traits used in the various 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). Taking into account this requirement and the genetic ties (Table 2), all countries have enough genetic ties with each other, except ISR. This will probably result in large standard errors for the genetic correlation of longevity between ISR and other countries. But standard errors of estimated genetic correlations are not yet available, as software does not include this.

Table 2. Average number of common bulls per country.

CAN	292	SWE	112
USA	473	CHE	98
FRA	365	ITA	267
NLD	320	ISR	16
DEU	346	NZL	220
DNK	118		

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 (AV1) and combined longevity (AV3) of one country with all other countries and the average estimated genetic correlation of one country with all other countries except ISR for direct (AV2) and combined longevity (AV4). ISR was excluded from AV2 and AV4 because of weak genetic ties with other countries.

Table 3. Genetic correlations between countries for direct longevity (below diagonal) and combined longevity (above diagonal). AV1 gives the average correlation with all other countries for direct longevity and AV3 for combined longevity, AV2 is AV1 without ISR and AV4 is AV3 without ISR. MAX is the maximum genetic correlation with another country for direct longevity.

	CAN	USA	FRA	NLD	DEU	DNK	SWE	CHE	ITA	ISR	NZL
CAN		0.90	0.73	0.86	0.77	0.76	0.68	0.74	0.84	0.52	0.54
USA	0.92		0.69	0.82	0.79	0.77	0.72	0.70	0.73	0.46	0.62
FRA	0.67	0.70		0.75	0.73	0.86	0.49	0.67	0.59	0.29	0.40
NLD	0.84	0.80	0.69		0.79	0.85	0.66	0.73	0.77	0.16	0.55
DEU	0.71	0.69	0.60	0.72		0.79	0.59	0.69	0.64	0.29	0.51
DNK	0.57	0.67	0.84	0.77	0.64		0.52	0.71	0.57	0.25	0.59
SWE	0.78	0.72	0.59	0.65	0.45	0.48		0.50	0.71	0.05	0.48
CHE	0.65	0.65	0.66	0.71	0.69	0.72	0.47		0.64	0.14	0.57
ITA	0.85	0.71	0.51	0.75	0.59	0.45	0.71	0.59		0.19	0.47
ISR	0.37	0.44	0.16	0.09	0.36	0.15	-0.06	0.04	0.14		0.32
NZL	0.56	0.61	0.42	0.56	0.49	0.55	0.45	0.52	0.46	0.31	
AV1	0.69	0.69	0.58	0.66	0.59	0.58	0.52	0.57	0.58	0.20	0.49
AV2	0.73	0.72	0.63	0.72	0.62	0.63	0.59	0.63	0.62	0.20	0.51
AV3	0.73	0.72	0.62	0.69	0.66	0.67	0.54	0.61	0.62	0.27	0.51
AV4	0.76	0.75	0.66	0.75	0.70	0.71	0.59	0.66	0.66	0.27	0.53
MAX	0.92	0.92	0.84	0.84	0.72	0.84	0.78	0.72	0.85	0.44	0.61

3.3.1 Direct longevity

The EBVs for combined longevity were used for NZL as direct longevity was not available. Average genetic correlations between countries for direct longevity were 0.56 for AV1 and 0.64 for AV2. AV2 ranged from 0.73 for CAN to 0.51 for NZL. ISR had an average genetic correlation with the other countries of 0.21. Besides the average genetic correlation with other countries, maximum genetic correlation with the other countries also can be a measure for the genetic relationship of a country with the other countries. Maximum genetic correlation with other countries ranged from 0.92 for CAN and USA to 0.44 for ISR. CAN and USA had the highest genetic correlation with each other. The European countries using the survival analysis to analyse longevity (FRA, NLD, DEU, DNK, CHE and ITA) had genetic correlations with each other ranging from 0.47 to 0.84. ISR had genetic correlations with the other countries ranging from 0.44 to –0.06. NZL had genetic correlations with the other countries ranging from 0.61 to 0.42 (FRA) or 0.31 (ISR).

3.3.2 Combined longevity

The EBVs for direct longevity for DNK, SWE, CHE and ISR were used as combined longevity was not available. Average genetic correlation for combined longevity was 0.60 for AV3 and 0.68 for AV4. Average genetic correlation per country for combined longevity (AV4) was on average 0.04 higher compared to direct longevity (AV2) and ranged per country from 0.00 for SWE to 0.08 for DEU and DNK.

4. Discussion

4.1 Genetic correlations between countries

Genetic correlations for longevity traits between countries lower than unity may have several reasons:

- use of different statistical models;
- use of different culling data (2, 3 or all lactations);
- adjustment for production or not;
- different production circumstances per country (husbandry system, seasonal calving, quota system or not etc.);
- data quality;
- genetic ties.

The national statistical models are survival analysis (FRA, NLD, DEU, DNK, CHE and ITA), single-trait linear models (USA, SWE and ISR) or multiple-trait linear models (CAN and NZL).

Most countries use all data except CAN (3 lactations) and SWE (2 lactations). Most countries adjust longevity records for production of the cow except USA, ISR and NZL. Production circumstances in the participating countries are quite different as European countries, USA and Canada, Israel and New Zealand are included in this study.

The genetic correlation of ISR with the other countries for direct longevity was 0.20 on average, ranging from 0.44 (USA) to –0.06 (SWE). These moderate to low genetic correlations can probably be explained by the weak genetic ties of ISR with the other countries. Due to these weak genetic ties with other countries, ISR will not be taken into account in this discussion.

CAN, USA and NLD have the highest average genetic correlations per country with the other countries ranging from 0.72 to 0.73 for direct longevity. European countries except NLD have an average genetic correlation for direct longevity ranging from 0.59 to 0.63. Of these countries SWE has a slightly lower average genetic correlation which might be due to the different trait definition for longevity traits of SWE. The lowest average correlation with other countries was found for NZL, which might be explained by the quite different production circumstances in NZL compared to the other countries.

The genetic correlations of NZL with the other countries are consistently moderate ranging from 0.42 with FRA to 0.61 with USA.

4.2 Combined and residual longevity

The average correlation for combined longevity is on average 0.04 higher compared to direct longevity. For deregression of combined longevity, the same EDCs were used as for direct longevity. In most cases this is not correct, 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.

4.3 Outlook

Many countries already include longevity traits in their total merit index because of the great economic importance of longevity traits. Results from this study indicate that MACE for longevity is feasible. But genetic correlations range from moderate to high. Concerning the wide range of correlations, there is still room for improvement of correlations by harmonizing data and trait definition.

Another point of discussion will be which of the analysed longevity traits should be implemented in MACE for longevity traits. Theoretically, direct longevity would be better because of more uniform trait definitions whereas for combined longevity every country has different ways to calculate it. Direct longevity would be also preferable as long as an improved method to deregress proofs for combined longevity is not available. But genetic correlations between countries for combined longevity are on average slightly higher than for direct longevity. The participating countries should investigate how to get the most reliable breeding values for longevity traits in their country. As far as countries have combined longevity they have two possibilities: using MACE combined longevity or MACE direct longevity and afterwards combining with predictive breeding values into domestic combined longevity. For theoretical reason, the last option may be preferred.

5. Conclusions

- There is much variation in models and methods to evaluate longevity traits genetically.
- Enough genetic ties exist between countries except for Israel.
- Genetic correlations for direct longevity are moderate to high (0.42 - 0.92) between countries.
- Combined longevity gives slightly higher genetic correlations between countries compared to direct longevity (0.04 on average), but more research is needed if MACE for combined longevity is useful and how to deal with combined longevity using MACE.
- Much attention should be paid to the improvement of genetic correlations for longevity traits between countries.
- MACE for longevity traits is feasible.

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Table 4. Characteristics of the national evaluation systems of the participating countries.

Country	Direct longevity	Combined longevity	h^2 direct longevity / combined longevity	Records included	Adjustment for milk production	Survival analysis parameters rho/gamma	Data inclusion
CAN	AM MT	Direct + indirect (6 predictors)[1]	0.030 / 0.080[4]	First 3 lactations	yes	-	1980 >
USA	AM ST	Direct + 7 predictors	0.085	Cows until age of 7 years	no	-	1960 >
FRA	SM SA[2]	Direct + 10 predictors	0.200	All lactations	yes	2.00 / 4.00	1985 >
NLD	SM SA[2]	Direct + 6 predictors	0.110	All lactations	yes	1.49 / 4.19	1988 >
DEU	SM SA[2]	Direct + 5 predictors	0.180	All lactations	yes	2.00 / 4.00	1985 >
DNK	SM SA[2]	-	0.100	All lactations	yes	1.07 / 6.12	1984 >
SWE	SM ST RES[3]	SM ST	0.020	First 2 lactations	yes	-	1982 >
CHE	SM SA[2]	-	0.184	All lactations	yes	1.53 / 3.75	1980 >
ITA	SM SA[2]	Direct + 2 predictors	0.080	All lactations	yes	2.00 / 2.20	1980 >
ISR	AM ST	-	0.143	Cows until age of 7 years	no	-	??
NZL	-	AM MT	0.072	All lactations	no	-	1985 >

1) Canada combines direct longevity and indirect longevity (index of 6 traits) with a MACE procedure into combined longevity (herd life).
2) SA = survival analysis
3) RES = residual longevity (longevity adjusted for milk production, daughter fertility, calving performance and diseases).
4) Heritability for CAN for direct longevity is 0.03 and for combined longevity 0.08.