Properties of International Longevity Evaluations and Correlations with Other Traits

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Abstract

Longevity evaluations from 11 countries were examined, and correlations with other traits on each country's scale were obtained. Correlations of longevity with somatic cell score and conformation traits were fairly uniform across countries. Correlations with yield traits varied for countries that reported functional longevity and for those that reported true longevity. Some correlations of yield with functional longevity were higher than correlations of yield with true longevity. Improved definitions of effective daughter contribution and heritability were suggested for different types of statistical analysis currently in use. Estimates of genetic correlations and standard deviations may be sensitive to incorrect values because fewer bulls have evaluations with high reliability. A goal is that national and international reliability reflect true reliability for all evaluations.

Keywords: Genetic evaluation; International ranking; Longevity; Dairy cattle

Introduction

National longevity evaluations are computed using a wide range of statistical methods (Van der Linde & de Jong, 2002). Different types of national analyses for longevity and parameter definitions were compared for 11 countries (Canada, Denmark, France, Germany, Israel, Italy, New Zealand, The Netherlands, Sweden, Switzerland, and the United States). Some simple changes in reported effective daughter contribution (EDC) and heritability could improve estimated genetic correlations and accuracy of proposed international evaluations. National, international, and true reliabilities (REL) of evaluations could be consistent and comparable even though national statistical methods differ.

Cows are culled for a variety of reasons, and those reasons may differ across time, management systems, and countries. Trait definitions also differ across countries; most adjust longevity for yield traits but others do not. Differences among trait definitions may be quantified by examining correlations of evaluations for longevity with those for yield, somatic cell score (SCS), and conformation within each country.

Materials and Methods

International longevity evaluations from the research study of Van der Linde and de Jong (2002) were examined. Longevity evaluations as of November 2000 for bulls born from 1985 through 1994 from 11 countries were included. Only evaluations on the scale of the country that reported the most daughter records for protein yield (home country) for a bull were used.

Longevity EDC were compared with number of daughters from the November 2000 Interbull protein evaluation in an attempt to understand the calculations of each country. In November 2000, a format for data exchange was developed by Van der Linde and de Jong (2002) that included a field for number of culled daughters. In October 2001, participating countries were given a chance to fill that field with the number of informative daughters or with EDC for longevity if those were more appropriate for the particular trait analyzed. For some countries such as Germany and New Zealand, the total number of daughters for yield was reported instead of the number of culled daughters or EDC. This practice probably caused some REL to be overestimated and some genetic correlations to be underestimated.

February 2002 Interbull yield (milk, fat, and protein), SCS, and conformation evaluations on the home country scale were matched with the longevity evaluations. Simple correlations among those traits were obtained on each country's scale. To allow correlations of the same sign to have the same interpretation, direct longevity evaluations from Germany and Italy were reversed to make positive values desirable, and SCS evaluations from France, Italy, Sweden, and The Netherlands were reversed to make positive values undesirable. Correlations of longevity evaluations with birth year provided a unitless measure of genetic trend.

Results and Discussion

Binomial trait analysis (Sweden). A binomial (yes/no) indicator of culling by third parity is analyzed in Sweden. The EDC appears to be the number of daughters culled before reaching third parity. Daughters that lived for three lactations or more were assumed to provide no information. In a binomial analysis, both "yes" and "no" responses provide information. A suggested improvement to analysis is to count every cow that has had the opportunity to survive to third parity as 1 EDC whether or not the cow was culled. Cows with shorter opportunity could receive a lower EDC. The REL for most Swedish bulls would increase, which would affect the genetic standard deviation (SD) and correlations in the multiple-trait, across-country evaluation (MACE) analysis.

Repeated binomial trait analysis (Canada). Binomial (yes/no) indicators of culling after each of first three lactations are analyzed in Canada. The EDC were the number of daughters with an observation in the longevity analysis. The reported heritability (3%) is a mean value per lactation, but cows with repeated chances to be culled did not get higher credit in EDC calculations. This lack of credit may explain why Canadian REL were low and MACE SD did not match Canadian national SD. A suggested improvement to analysis is to count a cow with the opportunity to survive from first to second parity as 1 EDC. Cows with additional parities would receive higher EDC (analogous to EDC calculations for additional parities in yield data). An alternative improvement is to report a multiple-parity heritability as some countries such as The Netherlands do for yield MACE.

Survival analysis (Germany). Variance for German estimated breeding values (EBV) decreased greatly from early to later birth years. Second-crop bulls had large variance of EBV and contributed a large percentage of both the top and bottom bulls for direct longevity (Table 1). A heritability of 10% on the log scale was reported initially and used in MACE whereas a heritability of 18% on the observed scale was reported later. German national REL were based on EDC computed from squared correlations between partial and completed longevity for censored cows. Thus, reporting those EDC in the field for number of culled daughters field is suggested.

Table 1. Proportion of second-crop bulls[1] in the top 50 and bottom 50 for direct longevity[2] within each country.

Country	Bulls (no.)	Proportion (%) of second-crop bulls among:		
		All bulls	Top 50	Bottom 50
Canada	3501	8	34	12
Denmark	3593	4	42	2
France	6774	8	50	2
Germany	6847	13	88	76
Israel	440	10	12	2
Italy	2751	13	16	30
New Zealand	2579	15	0	32
Sweden	907	13	62	22
Switzerland	360	18	40	8
The Netherlands	4622	10	36	6
United States	13,571	7	32	20

[1]Second-crop bulls were born before 1992 and had ≥ 500 total daughters with information available for evaluation of protein yield as of November 2000.

[2]Bulls with daughters in the country were ranked for direct longevity on that country's scale.

Survival analysis (France and Switzerland). The REL in France and Switzerland are high because of high heritabilities (20% and 18%, respectively) for the observed scale. If REL are overestimated, genetic correlations and SD may be underestimated. Ducrocq (1999) reported that approximate REL in France overestimated true REL by about 4%. Ducrocq's (1988) estimate of a heritability of 8.5% from U.S. data agreed with the 8.5% estimated and used in the United States (VanRaden & Klaaskate, 1993). Ducrocq (1988) also reported that most heritability estimates for stayability measures ranged from 2 to 8%. Although heritabilities used in survival analysis on the log scale may be accurate, those reported on the observed scale appeared to be too high. Ducrocq (1999) reported that the formula to transform heritability from log to observed scale "seems an obscure way to get larger heritabilities." Actual analyses of data on observed scales usually provide lower heritability estimates. If heritability is much higher on the observed than on the log scale, simple analyses on the observed scale may result in more accurate rankings than survival analysis.

Length of life (Israel, New Zealand, and the United States). Israel, New Zealand, and the United States report measures of true (unadjusted) longevity, whereas all other countries adjust for yield and report functional longevity. In Israel, predicted longevity includes a regression on protein yield, but final length of life is not adjusted for yield. The three length-of-life analyses as well as the binomial and repeated binomial analyses use linear models, whereas survival analyses use non-linear models.

In linear models, REL is a function of the incidence matrices for fixed and random effects and residual variance ($\mathbf{Z}$, $\mathbf{X}$, and $\mathbf{R}$, respectively), but not the data vector ($\mathbf{y}$). In non-linear models, the number of culled daughters may influence REL, but the connection is not direct. Suppose that many sires each have 100 daughters, with a mean of 25 daughters culled before second parity. The sire with the lowest genetic merit might have 50 daughters culled, and the sire with the highest merit might have no daughters culled. The sire with no culled daughters would receive a high EBV, and that EBV contains information and has positive REL. In that case, using the standard EDC formulas that are functions of $\mathbf{Z}$, $\mathbf{X}$, and $\mathbf{R}$ (and not $\mathbf{y}$) may be more accurate than using number of culled daughters, which assumes that this best sire has no information and no REL.

The U.S. EDC for longevity are calculated with the same formulas as for yield and with adjustment for number of contemporaries and REL of mates. A daughter with the opportunity to reach 7 yr of age is a completed observation and receives full credit. Cows with less opportunity receive less credit regardless of whether they are culled or alive. Thus, EDC are based on mean culling rates, and sires with culling rates above or below this mean receive the same REL. Weighting factors are 0.35 at 36 mo of age, 0.67 at 48 mo, 0.88 at 60 mo, and 0.98 at 72 mo (VanRaden & Klaaskate, 1993). The EDC from progeny are added to EDC from parents to calculate direct REL, and then information from other traits is combined by selection index to obtain combined REL as reported by VanRaden (2001).

Correlations with other traits. Correlations on each country's scale for evaluations of yield, udder health (SCS), and conformation traits with longevity are in Table 2. Correlations of longevity with SCS were uniform across countries. Correlations with conformation traits were fairly uniform except for New Zealand. Those correlations among EBV only approximate true genetic correlations. Correlations with birth year (genetic trends) were small but higher for countries in which longevity was favorably correlated with yield.

Correlations for yield traits were not uniform, and adjustments for yield may deserve more attention. Correlations of functional longevity with milk yield ranged from −0.22 for Italy to 0.26 for France. The U.S. correlations of true longevity with yield were similar to those of France even though France removes yield whereas the United States does not. New Zealand does not adjust for yield, and yet the EBV correlation of longevity with milk yield was negative and correlation with protein was near 0. In the United States, correlations with yield have declined over time.

Countries that adjust for yield usually remove phenotypic correlations. Perhaps a more important goal is to remove genetic correlations, which could be done by regressing on yield EBV within each country before MACE and then adding yield back after MACE. This strategy might be easier than convincing all countries to do, undo, or redo yield adjustments in released evaluations.

Table 2. Correlations on bull's home country[1] scale of direct longevity[2] with other traits[3].

Country	Combined longevity	Birth year	Yield traits		
			Milk	Fat	Protein
Canada	0.86	0.10	0.09	−0.01	0.03
Denmark	1.00	0.36	0.06	0.10	0.09
France	0.95	0.26	0.26	0.11	0.17
Germany	0.93	0.07	0.10	0.07	0.11
Israel	1.00	0.24	0.51	0.30	0.51
Italy	0.98	−0.11	−0.22	−0.15	−0.27
New Zealand	1.00	−0.14	−0.18	0.28	0.02
Sweden	0.99	0.07	0.19	0.13	0.15
Switzerland	1.00	0.09	−0.04	−0.08	−0.04
The Netherlands	0.98	0.14	0.11	−0.17	0.04
United States	0.97	0.19	0.25	0.19	0.27
	Somatic cell score	Conformation traits			
		Overall Udder	Udder depth	Foot angle	Stature
Canada	−0.27	0.28	0.25	0.18	0.02
Denmark	−0.28	0.41	0.43	0.09	0.16
France	−0.34	0.40	0.39	0.07	0.08
Germany	−0.31	0.22	0.26	0.09	−0.02
Israel	−0.22	. . .	. . .	. . .	. . .
Italy	−0.17	0.14	0.27	0.07	−0.08
New Zealand	. . .	−0.26	. . .	. . .	−0.47
Sweden	−0.26	0.23	0.34	0.04	0.06
Switzerland	−0.46	0.36	0.37	0.06	0.14
The Netherlands	−0.27	0.34	0.35	0.13	−0.01
United States	−0.30	0.26	0.28	0.13	−0.07

[1]Country that reported the most daughter records for protein yield for a bull as of November 2000.

[2]Evaluations on home country scale from van der Linde and de Jong (2002).

[3]February 2002 Interbull evaluations on home country scale.

Conclusions

Longevity is an indicator of overall health of the cow and overall satisfaction of the owner, but the trait is defined and analyzed differently among countries. Correlations of yield traits with longevity ranged from −0.27 to 0.51 and were higher for some countries that reported functional (yield-adjusted) longevity than for others that reported true (unadjusted) longevity. Correlations of conformation traits and SCS with longevity were consistent across countries with few exceptions. More uniform trait and parameter definitions could increase correlations among and value of potential international longevity evaluations. Further research on national and international evaluations should have high priority because most national indexes assign high economic value to longevity.

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