Value of Selecting for Cow and Calf Livability

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Abstract

Predicted transmitting abilities (PTAs) for cow livability (CL) were developed to measure a cow's ability to stay alive while on the farm, whereas PTA for productive life (PL) measures a cow's ability to avoid either dying on the farm or being culled. CL records for 69,710,392 lactations of 25,514,760 cows were evaluated with an all-breed animal model. The heritability of CL per lactation on the observed scale was 1.3%. Genomic PTAs for CL of young bulls were computed from 4-year truncated data and had squared correlations with future data about twice as high as from parent averages. Genomic reliability was 56% compared to 30% from parent average. For recent bulls with >80% reliability, CL PTAs are correlated favorably by about 0.70 to PL, 0.45 to daughter pregnancy rate, and −0.25 to somatic cell score PTAs, with low correlations to yield trait PTAs. The 0.70 correlation with PL seems sufficiently below 1 to add value from selecting for both CL and PL in an index. The relative emphasis on CL was estimated to be 7.4% of total emphasis, and the relative emphasis on PL value will decline from 19.1% relative value to 13.5% because the PL economic value will include only losses other than death. Thus, total emphasis on cow longevity and livability should increase from 19.1 to 20.9% but will be split across two correlated traits instead of just one trait. Future evaluations could also include calf livability. About 5% of heifers have termination codes reported, and >20,000 calf deaths were reported to the Council on Dairy Cattle Breeding database each year for about 10 years; however, heritability for calf loss is very low.

Key words: cow mortality, economic value, genomic evaluation, longevity

Introduction

Mortality of dairy cows is a growing concern for producers and consumers. Recent genetic and phenotypic studies investigated trends in the United States (Miller *et al.*, 2008; Tokuhisa *et al.*, 2014), United Kingdom (Pritchard *et al.*, 2013), Denmark (Maia *et al.*, 2014), and across many countries (Compton *et al.*, 2017). Reasons for cow disposal including death loss have been reported and stored in U.S. Dairy Herd Information records since about 1970; codes reported after day 305 of lactation were not always stored until about 2000. Across all breeds, 16.7% of cows die instead of being sold, with death losses averaging 6% per lactation but higher for later than earlier parities. Heritabilities for CL on the underlying scale were 6% for first parity, 6% for second, and 5% for third (Tokuhisa *et al.*, 2014). Because cows that die are a large expense compared to those sold for beef, two different traits can be defined with CL measuring only the rate of death loss or euthanasia on farms. Longevity includes both culling and death rates and is an important trait in dairy cattle; 20 countries now participate in Interbull multi-trait across-country evaluations for longevity.

Methods

Edits and methods of evaluation for CL were similar to a previous study of U.S. cow mortality (Miller *et al.*, 2008). A multi-trait model was developed to increase the reliability of CL, using individual lactation records for PL data instead of one lifetime PL record that is used officially. The CL PTAs from this two-trait model will be reported, but official PL PTAs will continue to use the lifetime record because further research is needed on the proposed trait definition for lactation PL. The scale for reporting CL is reversed from mortality so that positive PTAs are favorable (0 = died or 100 = lived for each lactation).

The binary records were pre-adjusted for parity-year variance and weighted based on heritability to account for changes in variance

with the mean. Heritabilities for each parity were estimated by sire model REML from >5 million daughters of 4,976 Holstein sires. Livability deviations from group mean were adjusted by multiplying by square root of the ratio of base group mean to parity-year group mean and by square root of ratio of base heritability to parity heritability. The evaluation uses a multitrait all-breed animal model with different weights for CL and PL, which made use of a threshold model difficult.

Economic values for CL and PL were derived using input and output prices assumed in the current version of the net merit index (VanRaden and Cole, 2014). Mature cows, which weigh around 1,500 pounds and had an average beef price of about $0.75 per pound over the last 4 years, had a value of $1,125. Mortality costs also include either on-farm disposal or collection fees for rendering that may average about $25 per mature cow and $10 per calf (Informa Economics, Inc., 2004). Another $25 of farm labor may be required for each cow that dies, and treatment costs incurred before the cow dies may be larger than the disposal expenses. Addition of $75 for treatment, labor, and disposal fees raises the total cost to $1,200, with lost beef value accounting for >90% of the mortality expense. A 1% increased death rate per lactation is worth $12 per lifetime (1,200 × 0.01). The standard deviation of true transmitting ability for CL is 2.3% per lactation and has a relative value of 7.4% (100 × 12 × 2.3/375) of the total emphasis in the net merit index, where 375 is the sum of economic values times standard deviation across all traits in the index.

After assigning a direct economic value to CL, the PL economic value includes only losses other than death. This reduces the PL value from $29 per month to $21 and from 19.1% relative value to 13.5%. Thus, total emphasis on cow longevity and mortality increases from 19.1 to 20.9% but is split across two correlated traits instead of just being on one trait. Total emphasis may actually decrease because reliability of CL is lower than for PL, but the multi-trait model should counteract the lower heritability. Correlations with PTAs for other traits such as daughter pregnancy rate and somatic cell score were also examined.

Heifer livability (HL) was examined from an initial data set of 10,757,993 records for heifers of all breeds born from 2001 through 2013 from the April 2016 Council on Dairy Cattle Breeding database. After matching with subsequent termination codes or calving dates, 6,343,337 records remained; about 4 million heifers had a birth record but no subsequent information. Months alive was defined as number of months from the birth date until the date that the heifer left the herd or until a maximum of 18 months of age. Individual herds were excluded if they reported <2 or ≥25% heifer deaths. A few herds had 100% death losses and apparently only reported the heifers that died. A total of 22,562 herds reported heifer births, with 9,213 reporting at least some death loss. After final edits, records from 2,826,534 heifers from 6,424 herds were used. Over 99% of the usable records were from Dairy Records Management Systems (Raleigh, NC).

A Holstein haplotype for cholesterol deficiency (HCD) causes young calves to die at a few months of age if homozygous (Kipp *et al.*, 2016). Death losses were examined using HCD carrier status of sire and maternal grandsire (MGS) of calves as described by Cole *et al.* (2016). Confirmed carriers were labeled "carrier"; possible carriers were labeled "not tested," and "not carrier" was assigned to bulls confirmed as not being a carrier. Genotypes for 418 HCD homozygous calves born >2 years ago also were available with confirmed inheritance on both sides of pedigree to Maughlin Storm with defective haplotype but not to Willowholme Mark Anthony with normal (before mutation) haplotype. Several genetic recessives affecting calf loss have been discovered recently (e.g. Pausch *et al.*, 2015), but most contribute little additive variance to HL.

Results and Discussion

Heritabilities of CL for the first 5 parities were 0.43, 0.70, 0.73, 0.74, and 0.74%; all were equivalent to about 3% on the underlying scale but lower than the previous estimate of 1.3% for heritability per parity on the observed scale from Miller *et al.* (2008), which was used in the initial August 2016 evaluation. The new, lower

estimates were introduced in December 2016. For comparison, heritability on the observed scale for overall culling rate per lactation is 3.0% and higher than for CL.

Correlations within breed were computed for recent Holstein (HO), Jersey (JE), and Brown Swiss (BS) bulls with > 80% reliability. PTAs for CL were correlated favorably to PTAs for PL (0.73 HO, 0.60 JE, 0.71 BS), daughter pregnancy rate (0.45 HO, 0.38 JE, 0.56 BS), and somatic cell score (−0.25 HO, −0.14 JE, −0.39 BS) PTAs, but unfavorably to protein in JE and BS (0.11 HO, −0.15 JE, −0.17). The correlations with PL seem sufficiently below 1 to add value from selecting for both PL and CL in an index. Correlations of CL with birth year were 0.31 in HO, 0.11 in JE and 0.05 in BS, indicating a more favorable genetic trend in HO than the other breeds. For comparison, PL in HO was correlated by 0.33 with birth year.

The CL PTAs from all-breed data and from JE-only data were correlated by 0.985 for 296 JE bulls that had >80% reliability for livability. The standard deviation of CL PTA was exactly the same for the all-breed and within-breed evaluations, and genetic trends were nearly the same. The correlation of CL with PL was also consistent for JE bulls and differed by only 0.01 between the all-breed and JE-only data. Statistics were not quite so consistent for JE bulls with >50% reliability, but those were more affected by crossbred daughters and HO herdmates. The heterosis estimate was 1.0% more CL per lactation for 100% heterosis, and 1% inbreeding caused 0.03% more mortality.

Genomic CL PTAs for young HO bulls from truncated data had squared correlations with future data about twice as high as from parent averages. Genomic reliability was 56% compared with 30% from parent averages. The multi-trait model included individual lactation records for PL instead of one lifetime record. The PTAs for the two PL definitions were correlated by only 0.92 for high reliability HO bulls, and further work on this proposed PL definition is needed. The standard deviation of true transmitting ability for CL is 0.82% per lactation or 2.3% per lifetime based on an average of 2.8 lactations per cow. Reporting CL on a lifetime instead of lactation basis should improve understanding because CL PTAs will express mortality differences as a percentage of all cows leaving the herd. Norman *et al.* (2016) provided further information on use of CL, and methods of calculation are outlined in Interbull Form GE (Council on Dairy Cattle Breeding, 2016). Genomic evaluations for CL are a good trait to add because so much historical data are already available for free.

Calf death loss was only 3% in the original data, but after excluding herds with low (<2%) or high (>25%) death loss, average death loss was 5%, with the majority of those losses during the first few months. Of the 495,871 heifers with termination codes reported, 158,045 (31%) were sold to another dairy farm with the heifer alive, 195,697 (40%) were sold for beef, and 142,129 (28%) were reported to have died while on the farm. Of those reported deaths, 42,260 (30%) occurred during the first 3 months. The heritability of HL was estimated by sire model REML to be only 0.5% on the observed scale.

Analysis of 3,426 HCD carrier sire × carrier MGS matings revealed 4% ($P < 0.0001$) higher death loss than normal matings, whereas 12% would be expected (0.125 × 95%). The lower observed frequency could be explained by under-reporting of death loss or by homozygous HCD calves that become sick and are sold before they die. Only 41 of the 418 homozygous HCD calves born during or before 2014 had any breedings, lactations, or progeny reported. Some of these apparent homozygotes probably inherited one copy of the normal haplotype from some other ancestor. Termination codes were provided for only 31 homozygous HCD heifer calves: 22 with code 6 (died) and 9 with code 2 (sold for dairy, perhaps to a heifer grower). These findings support the conclusion that HCD is usually lethal when homozygous.

Conclusions

Income averages about $1,200 less for cows that die than those sold for beef. Thus, CL is a very useful trait to select for, especially because millions of historical records are available for free in the national database, allowing accurate genomic PTAs to be computed. The United States in 1994 was the first country to evaluate PL and in August 2016 was the first to add cow mortality or livability as a specific economic trait. Economic value of CL is high and contributes 7% of total selection emphasis but

is balanced by a 6% reduction in emphasis on PL that previously included the CL economic value indirectly.

Heifer livability is of growing interest to dairy producers, but the lack of historical, national, and international data and the very low heritability of HL may not lend itself to routine evaluation at the present time. Calves have only 1 record, whereas repeated records across parities increase reliabilities for cow livability. Both traits depend on continued accurate reporting of mortality on farms.

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