CDCB
COUNCIL ON DAIRY CATTLE BREEDING

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Changes to evaluation system (April 2017)

Cow livability and revised body weight composite in net merit

By Paul VanRaden and Tom Lawlor

Cow livability (LIV) was introduced as a new trait in August 2016 and is now included in lifetime net merit dollars (NM$). Cows that die are assumed to generate $1,200 less income than those sold for beef. Relative emphasis on LIV in December 2016 NM$ is 7%, but is counteracted by decreasing the relative emphasis on productive life (PL) from 19% to 13%. This revision does not change the expected genetic progress for PL but will cause more progress for LIV and healthier cows.

Body size composite (BSC) was updated by Holstein USA in August 2016 to better predict actual body weights, and that change is now also used in NM$. The previous formula for BSC is replaced by the new formula for body weight composite (BWC):

BSC = .5 * stature + .25 * strength + .15 * body depth + .10 * rump width

BWC = .23 * stature + .72 * strength + .08 * body depth + .17 * rump width - .47 * dairy form

Major differences are that BWC is estimated from much more recent data, each unit of BWC is associated with larger differences in body weight than those of BSC, and BWC uses dairy form to account for presence or absence of fat in addition to skeletal size. Composites for other breeds were updated with this same formula except that Jerseys and Brown Swiss are not scored for body depth, so the .08 for body depth was added to the .72 for strength in those breeds. The standard deviation of predicted body weight has increased, and this causes more negative emphasis in NM$ (-6% on BWC vs. -5% previously on BSC). Genetic correlations of BWC with other traits also differ from those previously used for BSC:

Trait	BSC	BWC
Stature	0.96	0.64
Strength	0.87	0.94
Body depth	0.92	0.72
Rump width	0.75	0.59

Dairy form	0.45	-0.16

Therefore, use of BWC instead of BSC in NM$ reduces the selection against stature, body depth, rump width, and dairy form.

Economic values for other traits were updated with 2 additional years of price data, resulting in small reductions in milk price, a shift in value of fat relative to protein, and less emphasis on somatic cell score. For recent bulls, the 2017 and 2014 NM$ indexes were correlated by 0.99. Further details are provided HERE.

Revision of heterosis adjustments

By Paul VanRaden, Gary Fok, and Mel Tooker

Heterosis adjustments had been computed incorrectly for 14 of the 58 Montbeliarde bulls and 5 of the 34 Simmental bulls with US daughter records. Most Montbeliarde and Simmental bulls have pedigrees containing ancestors of more than 1 breed and their pedigree breed composition was stored in a table for crossbreds, but some have purebred pedigrees and were not in the table. For those bulls, the default heterosis value of 0 for purebreds had been used and was correct for the animal's own heterosis, but should have been 100% for the expected heterosis of progeny because the bull's breed differs from its breed of evaluation. Their predicted transmitting abilities (PTAs) will increase by 9 pounds protein, 20 pounds fat, and 2.7 daughter pregnancy rate (DPR) for example when their expected heterosis adjustment is corrected. None of the top 10 Montbeliarde or Simmental bulls were affected. This problem was detected while designing new programs to convert PTAs from the all-breed to within-breed scales.

Heterosis adjustments were also incorrect for traditional PTAs of crossbred cows. Those adjustments had been programmed separately and used the cow's own heterosis instead of the expected progeny heterosis as intended, which is usually only half as large, and therefore PTAs of crossbred cows received too much adjustment. Cows with maximum of 100% heterosis (F1 crossbreds) will have their traditional PTAs decreased by 4.5 pounds protein, 10 pounds fat, and 1.4 DPR, with proportionally smaller decreases for cows with less heterosis. Differences from this adjustment are fairly small because the expected future inbreeding (EFI) differences between crossbreds and purebreds account for most of the total heterosis effect, and the EFI adjustments were applied correctly. Genotyped cows will be much less affected by this heterosis adjustment because the marker effects receive more emphasis than the traditional PTA, and because genotypes for crossbred cows that do not pass the breed check edits are not evaluated.

Correction of SCS parent averages for non-genotyped heifers

By Ezequiel Nicolazzi, Gary Fok, and Paul VanRaden

A coding mistake introduced in the August 2016 evaluation caused females to receive a better SCS (traditional) evaluation than they should have and, as a consequence, also their other (traditional) evaluations that use SCS information such as multi-trait productive life and net merit were impacted. Some nongenotyped heifers had received net merit values that seemed to be incorrect. Upon investigation, the cause was determined to be a bug in one of the computer programs that handles cow unknown parent group contributions to SCS traditional evaluations. This bug was introduced just before the August 2016 evaluation. Please note that due to the nature of the group of animals involved, this issue affected mainly heifer parent averages that were not public, and therefore released only to Dairy Records Processing Centers. This, and the fact that genomic evaluations were not affected, is probably the reason why the bug went unnoticed for so long. We have now fixed the bug and tested the program in order to avoid this event from propagating further. We thank Bill Verboort for reporting this problem after the December triannual run, and we are sorry for the inconvenience.

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Revision of rear udder width for Brown Swiss

By Ezequiel Nicolazzi and Jan Wright

Interbull evaluations for rear udder width (RUW) will now be used for Brown Swiss, which is the only breed with RUW evaluations from Interbull. In April 2017, RUW for Brown Swiss will be published according to the following criteria:
1) if a bull has a traditional or Interbull evaluation, then the evaluation with the highest reliability - usually Interbull - will be considered as the official value for RUW.

2) if a bull does not have either of the above evaluations (please remember there is no direct genomic evaluation on this trait), then the official value of RUH will be used as the official value for RUW.

Other breeds are not affected by this change.