

Genetic Selection for Improved Longevity

Starting in February 2006, bull proofs for longevity will reflect more actual daughter survival information and less predicted herd life. This advancement is the fruit of an extensive research effort at Canadian Dairy Network (CDN) during the past few years and reflects the desire of Canadian producers for accurate Herd Life evaluations as early as possible.

Two-Step Research Approach

The first area of research to ensure the highest degree of accuracy was an analysis of the methodology used in Canada compared to other countries that provide bull proofs for a measure of daughter survival. Currently, the international bull evaluations for longevity, calculated and distributed by the Interbull Centre, are based on domestic proofs from 18 different Holstein populations, including Canada. The methods used to compute domestic bull proofs for longevity vary from country to country so CDN researchers examined the strengths and weaknesses of each to optimize the national system used currently in Canada for all dairy breeds.

The basic conclusions of this initial phase were three-fold:

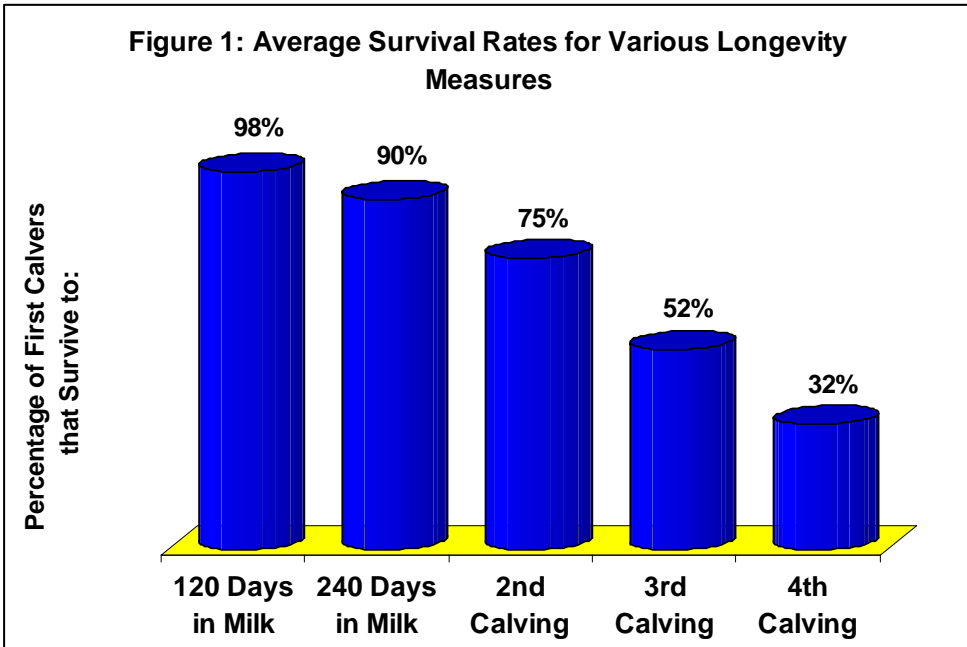
- (1) The animal model methodology currently used in Canada yielded high genetic relationships with other countries and more reasonable genetic trends compared to other methods of evaluation.
- (2) Partitioning longevity into separate but related measures of daughter survival (i.e.: through first, second and third lactation) was an effective way to analyze this trait instead of waiting to the end of each daughter's productive life.
- (3) The required waiting period of two years after calving before considering any survival data was too long and prevented newly proven bulls from having actual daughter survival data until at least 1.5 years after receiving their first official production and type proof. Methods used in other countries were able to include actual daughter survival data earlier in their sire's life, therefore relying less on the indirect prediction formulae that are used in each country.

Enhanced Methods

The second stage of the CDN research effort was to modify the current genetic evaluation system for Herd Life to address two areas of weakness. Firstly, bull proofs for Herd Life are calculated after accounting for production yields of each daughter relative to their herdmates. To do this, a herdmate deviation must be available, which was not always the case in the current system. As an improvement, a method was developed to maximize the number of cows within each breed population that have a BCA for each of

milk, fat and protein yield in order to compute a BCA deviation relative to herd mates. This procedure increased the number of records used for Herd Life evaluations by 36 percent, which simply translates to more daughter information per sire.

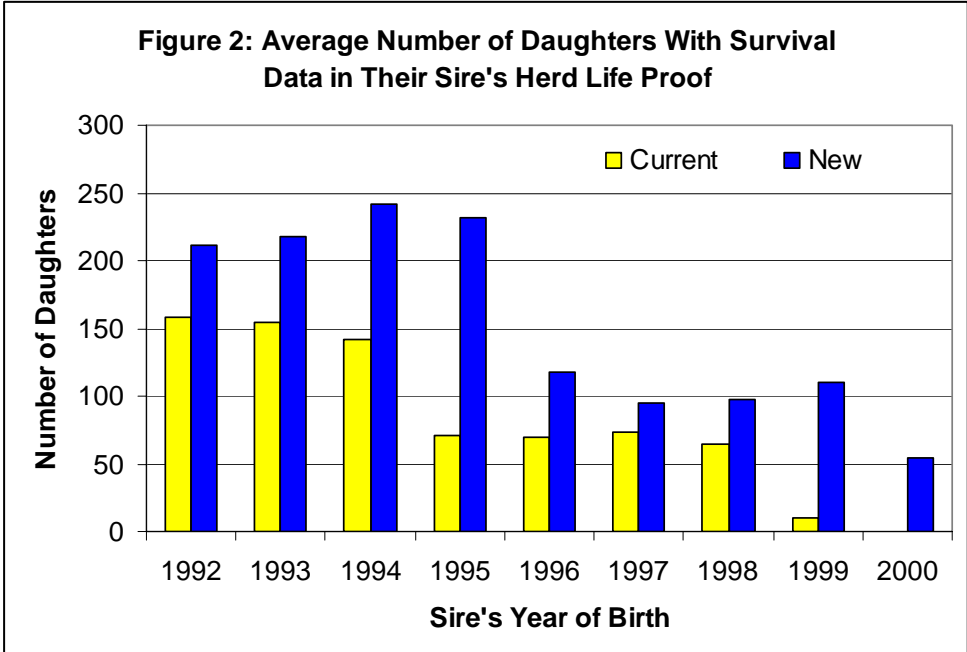
While increasing the volume of data that contributes to Herd Life evaluations is very important from a general perspective, the second area of enhancement was the genetic evaluation model, focusing mainly on improving the accuracy of Herd Life proofs for younger proven bulls. Basically, the new system partitions the definition of daughter survival into five critical points that act as separate but genetically related measures of longevity. These five “traits” can be described as (1) survival from first calving to 120 days in milk in first lactation, (2) survival from 120 to 240 days in milk in first lactation, (3) survival from 240 days in milk in first lactation to a second calving, (4) survival through second lactation to a third calving, and (5) survival through third lactation to a fourth calving. As shown in Figure 1, the average survival rate from first calving to each of these critical points is 98%, 90%, 75%, 52% and 32% respectively.



For genetic evaluations, the new Herd Life system will consider actual survival and culling data as daughters have the opportunity to pass 120 days in milk and then 240 days in milk in first lactation. As before, survival to a second, third and fourth calving are also used as daughters progress through their productive life. Even though relatively few animals are culled prior to 120 and 240 days in milk in first lactation, genetic differences across sires for these early measures are 78 percent correlated to genetic differences for the longer term measure of survival to fourth calving.

For sires with little or no daughter survival data available, currently published Herd Life proofs are dominated by a predicted value based on their proofs for female fertility, somatic cell score, milking speed, mammary system, rump angle, feet & legs and dairy strength. With this new methodology, less emphasis will be placed on these predicted values with the actual daughter survival data having a greater contribution, which increases the accuracy of the published Herd Life proofs. Figure 2 compares the average number of daughters with survival data contributing to their sire’s Herd Life proof, within year of birth, based on the current and new approaches. The increased

amount of daughter survival data that is included in published bull proofs is clearly an important improvement, especially for bulls born in 1999/2000 and 1994/1995 since they have many daughters still in first lactation (first and second crops, respectively).



Summary

Genetic selection for a prolonged productive life is a key goal for many dairy producers and can be achieved by considering Herd Life proofs in sire selection decisions. With an enhanced genetic evaluation system for Herd Life, planned for introduction in February 2006, sires will have more daughter survival data in their published Herd Life proof and newly proven sires will have this data available much earlier than before, therefore improving their proof accuracy. Published bull proofs will show a greater variation across sires than currently, which will also be reflected in the LPI formula.