Official Genetic Evaluation for Mastitis Resistance

Réseau laitier canadien

CDN

Canadian Dairy Network

Producers recording health data can give themselves a pat on the back and soon reap the first benefit of their efforts. In December 2013, a routine evaluation for Mastitis Resistance will officially be implemented for Holstein, Ayrshire and Jersey breeds. The development of this novel trait was made possible through on-farm data voluntarily recorded by Canadian producers.
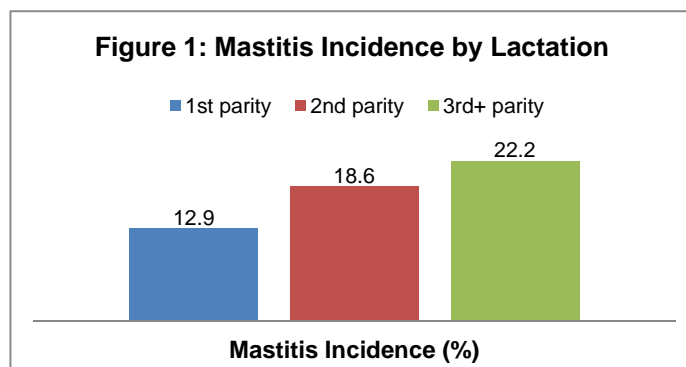
Health Recording

Mastitis Resistance is the product of a nation-wide effort to collect health and disease data, which began in 2007. The objective of the Canadian National Health Project was to provide information to dairy producers and their veterinarians for herd management, and to establish a national genetic evaluation system for selection to improve disease resistance.

Health events, including mastitis, are recorded by producers using on-farm management software or record books. This information is collected by milk recording technicians and then forwarded to the DHI association for the region. In the province of Quebec, a very significant portion of the health data is recorded by veterinarians offering herd health services through the "DSA" (i.e.: Dossier Santé Animale/Animal Health Record) Program and then forwarded to Valacta. Once all recorded health events are processed within the national milk recording database, they are sent to Canadian Dairy Network (CDN) for the purposes of research and genetic evaluation. After six years, over 40% of all herds enrolled in milk recording are providing health event data for eight diseases on voluntary basis. In addition to clinical mastitis, the other recorded diseases include metritis, retained placenta, cystic ovaries, lameness, milk fever, ketosis and displaced abomasum.

Mastitis Recording and Incidence

Of the eight diseases, clinical mastitis is the most frequent and most often reported, highlighting the economic importance of this trait. As seen in Figure 1, the frequency of mastitis increases with each parity and is estimated to be 12.9% in first lactation, 18.6% in second lactation and 22.2% in third and later lactation cows.

Figure 1: Mastitis Incidence by Lactation

■ 1st parity ■ 2nd parity ■ 3rd+ parity

12.9   18.6   22.2

Mastitis Incidence (%)

Genetic Evaluation of Mastitis Resistance

Traits producers commonly use for selection to promote udder health include Somatic Cell Score, Udder Depth and Fore Udder Attachment. However, together these traits only explain 46% of the genetic variation in resistance to mastitis. The new genetic evaluation for Mastitis Resistance incorporates these three predictors as well as recorded mastitis, Body Condition Score and several other measurements associated with somatic cell count. This approach results in an evaluation that explains as much as 72% of the genetic variation in Mastitis Resistance and increases the accuracy of genetic evaluations provided by CDN.

Since Mastitis Resistance is considered as a functional trait, genetic evaluations will be expressed as Relative Breeding Values (RBV) and they will be displayed in that manner on the CDN web site. An average bull in any breed will have a rating of 100 and higher evaluations reflect bulls that have daughters that are genetically more resistant to mastitis.

Despite the relatively low heritability of 4% for Mastitis Resistance, large differences exist between daughter groups. Table 1 shows that the percentage of diseased daughters varies between

Table 1: Percentage of Diseased Daughters for the 10 Best and 10 Worst Holstein Sires for Mastitis Resistance		
No. Sires Evaluated	**% of Diseased Daughters**	
	10 Best Sires	**10 Worst Sires**
Mastitis Resistance 220	6.3	22.0

6.3% and 22.0% among the group of ten sires with the best and worst proofs for Mastitis Resistance, respectively. In other words, for the worst bulls, one out of five daughters had a case of mastitis whereas only one out of 15 daughters of the best sires was affected by mastitis.

Comparing average incidence rates of mastitis in daughters of sires that are highly or poorly ranked clearly shows value in genetic evaluation and selection programs to improve disease resistance in dairy cattle. However, concern is occasionally voiced in regards to selection for low heritability traits. It is important to note that when correlated traits that have a lot of historical data are included in a genetic evaluation model (like Somatic Cell and Udder Depth in the case of Mastitis Resistance), the accuracy of the resulting evaluations increases. This means progress can be made, even for low heritability traits, with the best strategy being the combination of genetic selection alongside the use of best herd health management practices.

More Disease Recording, More Disease Resistance Traits
Although 40% of herds on milk recording are reporting health information for some or all of the eight identified diseases, there is substantial room for improvement. Many herds are not consistently recording or keeping track of each of the eight diseases of interest and many that are may not be providing them to the milk recording service provider. With increased on-farm recording and subsequent reporting to the CanWest DHI or Valacta personnel (or to the DSA veterinarians in Quebec), the accuracy of the Mastitis Resistance evaluation will undoubtedly improve and new health traits, such as resistance to metabolic disorders, could be developed. To ensure accurate and consistent diagnosis, standardized disease definitions are available on CDN's web site.

Summary
Starting December 2013, a routine evaluation for Mastitis Resistance will officially be implemented by CDN for the Holstein, Ayrshire and Jersey breeds. This evaluation is the first product of the Canadian National Health initiative started in 2007. While herd health management and disease prevention must remain priorities, genetic evaluations for Mastitis Resistance can be a useful tool for any mastitis control strategy. Producers are strongly encouraged to record complete health information in order to yield more accurate genetic evaluations and allow for the development of new disease resistance traits in the future.

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