Behind the Scenes of a Dairy Cattle Genetic Evaluation: From Information to Prediction

- Genetics Tools
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In the previous article, we saw how genetic evaluations combine information from an animal's own performance, relatives, pedigree, and genomic data to improve predictions of genetic merit. However, not every animal has the same amount or quality of data available. As a result, not all predictions are made with the same level of confidence. Understanding the outputs of an evaluation therefore means considering not only the breeding value itself, but also how strongly that prediction is supported.

Estimated Breeding Values

One of the main outputs of a genetic evaluation is an Estimated Breeding Value (EBV), which represents the best prediction of an animal's genetic merit for a particular trait. An EBV is not solely a reflection of

performance. As we learned in Article 2, differences between animals may also result from management, environment, or chance. By accounting for these non-genetic influences, the evaluation aims to identify the genetic component that can be passed to the next generation.

With an understanding of what a breeding value represents, we can now look at three important concepts that influence its estimation and interpretation: heritability, reliability, and shrinkage.

Understanding Heritability

The heritability of a trait helps us understand how much of an animal's performance records is due to its genetics rather than its environment. For some traits, genetics accounts for a larger portion of the differences we see between animals, while for others, environment, management, disease exposure, and chance play a greater role. For traits with higher heritability (greater than 25%), an animal's own performance record generally provides more information about its genetic merit. For traits with lower heritability (less than 10%), such as many health and fertility traits, an individual phenotype provides less information about an animal's underlying genetics. Low heritability does not mean genetic improvement is impossible or that a trait should receive little emphasis in selection. It simply means more information is generally needed to confidently identify genetic differences among animals. Genetic progress can still be achieved for these traits by combining large numbers of records. However, heritability is only one piece of the puzzle. The amount of information available also affects how confident we can be in the resulting breeding value.

Confidence in the Prediction

The amount of confidence we can have in a breeding value is expressed through reliability. Animals with multiple performance records, extensive information from relatives or progeny, and genomic data generally have more reliable evaluations than animals with limited information. As

reliability increases, there is greater confidence that the EBV is close to the animal's true genetic merit and is less likely to change substantially as new information becomes available. Lower reliability means there is greater uncertainty in the prediction, not that an animal has poor genetic merit or that its evaluation is incorrect. Every April, Lactanet publishes the average gain in LPI and Pro$ reliability due to genomics.

Accounting for Uncertainty

Genetic evaluations account for this uncertainty through a concept known as shrinkage. When an animal has limited supporting information, its breeding value is pulled, or shrunk, toward the population average. As more information becomes available, there is stronger evidence to support values farther from the average and less shrinkage is required. For example, consider two cows that each produce 2,000 kg more milk than their herd average. The first has only a few DHI test-day records and little information available from relatives. The second has several completed lactations, many well-recorded relatives and offspring, and genomic information. Although their observed performance is similar compared to their herd averages, the supporting evidence is very different. For the first cow, it is harder to determine whether her exceptional performance reflects genetics, environment, or chance, so her EBV may be pulled more toward the population average. For the second cow, consistent information from several sources provides greater evidence to support an EBV farther from the average. This does not mean the first cow is genetically inferior. There is simply less evidence available to confidently support an extreme estimate. Shrinkage is therefore not a penalty; it protects genetic evaluations from overconfidence when information is limited.

Why Evaluations Can Change

Since breeding values are based on the information available at a given point in time, they are not fixed. As new records, progeny information, or genomic data become available, evaluations are updated and breeding

values may change. An EBV should therefore be viewed as the best prediction based on the information available today.

A bull with a high breeding value and low reliability may still be an excellent prospect, but his evaluation is more likely to change with additional information. A bull with a slightly lower value and very high reliability is more predictable. This is why evaluations of young genomic bulls often change as daughter records accumulate, while evaluations of proven sires tend to be more stable. Both play valuable roles in breeding programs with young sires offering greater genetic potential and shorter generation intervals, while proven sires offer greater certainty.

Since breeding values can change, ensuring the accuracy of each evaluation is critical. Before results are published, extensive quality control and validation is done to identify unexpected trends and verify that changes are supported by the new data. Large or unexpected changes may be investigated to determine whether they reflect new daughter records, pedigree or genomic updates, or improvements to the evaluation system. Models may also be tested by withholding recent information and evaluating how well predictions based on older data agree with predictions based on newer data. These checks help ensure that published evaluations are unbiased and supported by the data.

Key Takeaway

The genetic evaluation process therefore does more than rank animals according to their observed performance. Phenotypes provide the starting information, environmental effects are accounted for, and pedigree and genomic relationships connect information across animals. Together, this information produces an estimated breeding value, while reliability describes the confidence surrounding it and shrinkage prevents uncertain estimates from being overvalued. With increased evidence, uncertainty decreases and evaluations become more stable. Understanding these outputs is essential because producing a breeding value is only part of the story. In the next article, we will look at how these predictions can be

used to make breeding decisions and drive genetic improvement.

For further information, please feel free to contact Lactanet Canada staff.

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