Understanding and Using Genomic Selection in Dairy Herds

Abstract

This publication discusses genomic selection, including how it may be used within a dairy cattle herd, and provides information on different testing and submission options to determine how genomic selection may be implemented for different herds and various genetic and management goals. Additionally, consultants and veterinarians can learn more about genomic selection to better answer questions from clients and discuss it more knowledgeably.

Introduction

Genomic selection uses DNA information to make informed decisions on which females to keep in the breeding herd, choosing sires to mate with heifers and cows, and determining parentage. Genomic selection was commercially introduced to the dairy industry in 2009, allowing for a more accurate selection of traits important to producers (Erf 2020). Selecting animals that excel in milk production, reproduction, and health traits can be used to advance the genetic merit of individual herds, specific breeds, and the industry as a whole. Producers select specific traits or indexes to make progress on, depending on the specific goals for an individual herd. Identifying elite animals and using them to meet specific production and management goals is one tool that dairymen can use to advance their current herd and breeding objectives.

What Is Genomic Selection?

Genomic selection evaluates an individual's genetic makeup (DNA) and compares it to a reference population of the same breed. An offspring's performance can be predicted using genetic variants associated with traits of interest. These predictions are termed predicted transmitting abilities (PTAs) and measure differences expected in the offspring of one individual compared to the herd average. This "herd average" comprises production data from the national dairy herd for each breed and is maintained through the Council on Dairy Cattle Breeding (CDCB). These breed-specific base values are updated routinely to accurately represent where the national average truly lies.

Genetic variants that are used to determine PTAs are called SNPs (**single nucleotide polymorphism**). A **nucleotide** is part of DNA's molecular structure, and there are four nucleotides. The nucleotides are abbreviated as A (adenine), T (thymine), C (cytosine), and G (guanine). When one nucleotide is replaced with another, it is termed a SNP. Figure 1 highlights an example of a SNP within the DNA sequences of three heifers. The example in Figure 1 shows that the SNP is associated with a trait for milk fat production. By identifying the SNP at this location, the milk fat production in the heifer's offspring can be estimated. Heifer 3, with a "T," would be predicted to have offspring that produce an average amount of milk fat compared to the breed average, in contrast to the offspring of Heifer 1, with a "C," which would be predicted to produce 100 pounds more milk fat than average. The offspring of Heifer 2, with an "A," would be predicted to produce 25 pounds more milk fat than average.

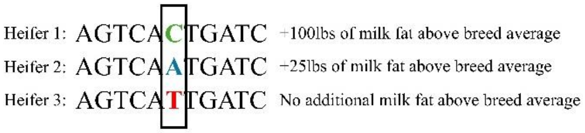

Figure 1. Example of a single nucleotide polymorphism (SNP), when one DNA nucleotide is changed. In this example, each of the three SNPs represents different estimates of milk fat production in the offspring. Figure credit: Allison Herrick.

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Predicted transmitting abilities are available for fluid milk yield, fat and protein production, reproductive abilities, and disease risk. DNA can be analyzed at any time in the animal's life and can be collected from nasal or oral swabs, semen, a blood sample, ear punch, or hair sample that includes an intact root bulb. Genomic selection provides a tool for a producer to know their cattle's estimated potential in the form of PTAs months before the traits would be expressed. These estimates can then be used to make management decisions early in the production cycle with the potential to reduce financial risk and maintain a genetically superior herd.

One way to consider genomic selection is as another "tool in the toolbox." If the data and information gathered from the testing are used effectively for mating decisions, culling, and refining herd goals and benchmarks, producers may see improvements to many aspects of their dairy. Heifer inventories can be sorted using their genomic rank for whatever trait(s) the producer selects (e.g., **net merit dollars** [NM$]), and if a culling opportunity presents itself, those ranked in the bottom proportion of the herd can be selected to sell. Furthermore, those remaining at breeding age can be selectively mated to improve the next generation of calves from top-ranked parents or can add a potential revenue stream by mating some of the bottom proportion to beef, resulting in a higher value crossbred calf to sell.

Selection Without Genomics

Selecting cattle to remain in the breeding herd occurred long before genomic technology became available. Traditional selection methods encompassed selection based on visual information or with data collected from related individuals. Offspring performance is typically estimated using parental information, including the parental genomic predictions and the performance of current progeny. Some dairies will base estimates on the average of the sire's performance and the dam's performance within the herd. If dam information is unavailable, many producers utilize performance averages of the sire and maternal grandsire. If only sire information is used, it is important to acknowledge that the dam's genetic contribution of half of the genetic merit of the calf is overlooked. A lack of information on the dam will reduce the accuracy of the prediction for the calf's future performance. When using information from both parents, the predicted values are more representative but still do not identify the actual DNA that the calf inherited. Only by evaluating the calf's DNA can an accurate performance prediction be made.

Traditional selection has been used for decades, leading to significant improvements throughout the dairy industry. However, because genomic selection increases the predicted performance accuracy for future calves, it has increased the rate of genetic progress in the dairy industry. The accuracy (reliability) of pedigree-based predictions ranges from 46% to 72%, compared to genomic prediction reliability that ranges from 73% to 93.5% (Gutierrez-Reinoso et al. 2021). While several years and large numbers of progeny are needed to reach high-reliability values using traditional methods, genomic selection has higher reliabilities due to SNP information being continually updated on sires and dams.

How to Start

Sampling Method

Different options are available to choose from when selecting which genetic sampling method works best for your operation. The most common sample types include blood, tissue, or hair follicles. Semen collection or nasal or oral swabs can also be used. Genotyping from blood samples is widely used, and different options are available. Figure 2 (left panel) shows a blood card, otherwise known as an **FTA (fast technology for analysis of nucleic acids) card**, an absorbent paper that requires only a few drops of blood. FTA cards preserve the sample's quality without deterioration and can be refrigerated or stored at room temperature before testing (Burt 2009). Another blood sampling option is collecting whole blood in vacutainers; however, more blood is required (approximately two teaspoons), and samples must be refrigerated in a collection tube with a nonclotting agent. A third option involves collecting hair with the root bulb intact, shown in the right panel of Figure 2. Commonly, hair samples are collected by removing a few tail hairs. It is important to ensure the hair bulb remains intact when taking the sample, as this is where the genetic material is contained. Samples are then placed in an envelope or stuck to adhesive on a card (similar to the right panel of Figure 2) (Burt 2009).

Other tissues, including ear, semen, or oral tissues, can also be used for genetic testing. Figure 3 demonstrates ear tissue collection for genomic analysis. This is commonly done on-farm using a **tissue sampling unit** (TSU) to take an ear punch. The tissue sample is pushed into a tube containing preservatives, and the top is sealed immediately after the sample is collected. The sample can be kept at room temperature and also contains an individual identification code to assist with record-keeping. Semen straws can be used for genetic testing, as can nasal or oral swabs that scrape the skin surface, removing cells that can be used for DNA evaluation.

Figure 2. Two means of collecting samples for DNA testing. On the right, hair is collected and attached to the fast technology for analysis of nucleic acids (FTA) card produced by Flinders Technology Associates with follicle bulbs intact. On the left is an FTA card used for collecting blood samples. Photo credit: Allison Herrick.

Figure 3. Collecting a tissue sample with a tissue sampling unit (TSU). On the right is the location where the tissue sample should be taken, in the middle to outer portion of the ear, with the TSU. The left picture shows the TSU applicator (in blue) and the TSU sample collector (in white and red). Photos: Allison Herrick.

Associated Costs

Testing costs depend upon the specific desired trait predictions and preferences for the company providing the test. Table 1 highlights some available options. Neogen and Zoetis offer many different tests that vary depending on the information the producer desires. Artificial insemination (AI) companies are also beginning to offer genomic testing options for their customers, creating an all-encompassing reproductive solutions package where producers can test their herds genomic profile, select bulls, and receive assistance with matings. A third option available to purebred cattle breeders is testing through their respective breed association. Table 1 also includes cost estimates for the different tests that are available through Neogen, Zoetis, or AI companies and additional information about each option (Neogen 2024; Zoetis 2024; ABS Global 2024; STgenetics 2024).

Costs shown within the table represent the submission and genotyping costs for each sample. Costs are not included for the two AI companies, as this service is marketed as a comprehensive solution or package, which can include genomic consultation, sire selection, and custom matings for each individual in the herd. Since this is customizable and can be altered based on herd size, the cost per animal is not included. Typically, costs for the sampling device and any other supplies are additional to the testing cost. Blood cards cost approximately one dollar each, and the cost of collecting hair samples is $1.50. On the other hand, Allflex TSUs are closer to $2.50 per sample, plus the $45 reusable applicator required to collect the tissue punch (Neogen 2020). Beyond the sampling utensils and the basic genotyping package selected, additional testing can be added to screen for phenotypes that the general tests do not include. Additional screening tests can look for lethal genetic conditions, potential disease risks, polled status, and milk protein determination for beta caseins, which cost an additional $10–$30 per add-on (Zoetis 2024).

Submitting Samples

Once the desired company and genomic package are selected and samples have been collected, samples must be sent to the company for processing. These samples are submitted via online forms, and information regarding identification numbers, birthdates, breeds, sex, sample type, and the genomic test you are performing is entered. This information will be included with the genotyping information when results are returned.

What Do You Get Back?

When deciding to implement genomic testing within your herd, it is important to understand the information types that are being provided. Outputs depend on the company and test selected and can also be “customized” based on the specific metrics each producer is interested in. Table 2 shows an example of the output that producers receive when the results are completed.

Each report will begin with basic information about each individual. This includes farm identification, individual identification, sex, breed, and birthdate. **Genomic predicted transmitting abilities** (GPTAs) for economically important traits are then reported in their respective units. Using this information, producers can compare animals within their herd and use the information to make mating and culling decisions, improve herd values for desired traits, and increase the rate of genetic progress. These comparisons are based on records from the CDCB, which estimate each breed’s genetic merit to establish breed-specific “base values” that represent the average performance for each trait being compared. The results may also include parentage results, allowing for accurate record-keeping and minimizing inbreeding. If additional traits or disease identification were added to the genomic analysis, results could be used for selective mating or culling in order to reduce undesirable traits.

Table 1. Different genomic tests for dairy cattle and corresponding information for each. The first two listed are offered through Zoetis, the next three are offered through Neogen, and the final two highlight options available through different AI companies.

Test Option	Base Price	Data Provided	Breeds Offered
CLARIFIDE	$37/sample	PTAs for most production traits and parentage verification	Holstein, Jersey, Brown Swiss, and Guernsey
CLARIFIDE Plus	$43/sample	PTAs for all CLARIFIDE Plus data, plus cow and calf wellness and fertility traits	Holstein and Jersey only
Igenity Basic	$26/sample	PTAs are described on a 1–10 scale for popular traits	Designed for crossbred cows
Igenity Essential	$33/sample	PTAs on 15 popular traits	Holstein, Jersey, Brown Swiss, Ayrshire, and Guernsey
Igenity Select	$42/sample	PTAs on Neogen’s complete suite of traits	Holstein, Jersey, Brown Swiss, Ayrshire, and Guernsey
GENEadvance	NA	PTAs on traits of specific interest to the producer	Holstein and Jersey
Vision+	NA	PTAs on 48 traits, 22 unique markers, and 4 indexes	Holstein and Jersey

Table 2. Example of genomic selection results. Basic information is included first, followed by performance traits and index estimates for each individual. The information provided in this table only highlights a small portion of the information that a producer would receive.

On-Farm ID	Breed	Sire	Dam	Birthdate	Sex	NM$	NM$ % Rank	CM$[*]	TPI[†]	Milk
818	HO	HO123A	1	9/19/2023	F	460	62	461	2574	1451
814	HO	HO123B	2	9/02/2023	F	770	93	775	2747	1784
799	HO	HO123C	3	8/25/2023	F	576	77	581	2538	1001
784	HO	HO123B	4	7/1/2023	F	646	85	657	2714	912
779	HO	HO123D	5	3/17/2023	F	592	79	595	2634	362
781	HO	HO123D	6	6/15/2023	F	449	61	458	2454	408
768	HO	HO123E	7	3/10/2023	F	544	74	547	2587	884

[*] CM$ = cheese merit dollars.
[†] TPI = total performance index.

Selection Indexes

Selection indexes have been developed for the dairy industry to provide a calculated value based on the sum of weighted traits included within it. These indexes can be economic, which involve a financial component to calculate a dollar amount attributable to how much more money an individual will generate over their lifetime compared to the average. An example is the NM$ index, shown in Figure 4.

There are many economic indexes beyond NM$; however, it is the most widely used throughout the industry. Producers can select one or multiple traits or indexes that best assist in accomplishing their herd goals or create their own index unique to their specific herd goals. Producers can also use genomic results to make progress specific to their herd in the most efficient manner by selecting replacements, making culling decisions, and selecting bulls for mating.

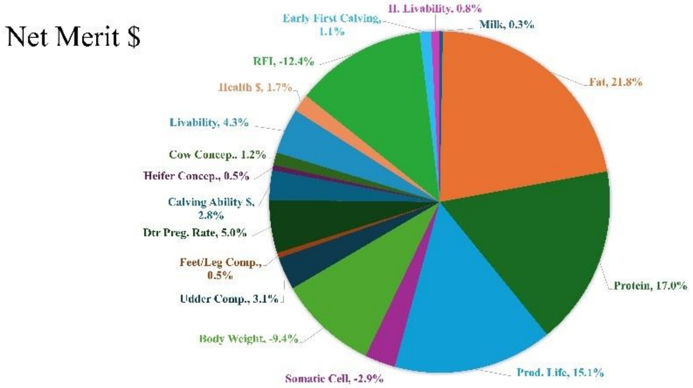

Figure 4. Net merit dollars breakdown. Included traits are defined with the respective weights for each trait. Figure adapted from CDCB NM$ formula.

Economic Benefits

When determining if genomic selection tools are best for your herd, it is important to understand the areas within your operation that can be impacted by its adoption. Genomic selection is the most cost-effective when the results are applied to multiple management areas. On average, heifer rearing costs range from $1,700 to $2,400, depending on the facility type, labor costs, and feed utilized (Overton and Dhuyvetter 2020). Utilizing genomic selection tools allows producers to select only the best individuals for their operations and selectively cull those who do not meet their criteria. This could save them thousands of dollars in rearing costs for genetically inferior individuals. By selecting individuals to cull from the bottom portion of the herd each year, the herd's genetic progress has the ability to improve at a faster rate.

When identifying heifers to keep or cull and the costs associated with that decision, the timeline for raising heifers must be mentioned. An optimal time to do genomic testing is right after birth. This allows the producer to send samples in at regular intervals, depending on the operation size and factoring in shipping costs. Ideally, if samples were sent biweekly, then samples could begin to be analyzed every two weeks. Within a month after submitting the samples, producers could see the genomic results for each individual. These results would be automatically integrated into the producer's online interface for their herd, as discussed in the What Do You Get Back? section above. This interface compares data against the national herd averages and compiles any individuals that were sampled to allow for management decisions. Though they would need to be reared until results were returned, producers could better estimate their future performance, cull those who do not meet their thresholds, and save costs associated with raising those heifers after 60–90 days.

Conclusions

When considering genomic selection, many factors should be considered, including financial implications, operation goals, and how the information will be utilized. Improving selection for specific traits and identifying elite individuals sooner may lead to cost savings for a producer and higher productivity for a herd.

Glossary

fast technology for analysis of nucleic acids (FTA) card—Cotton-based paper with chemicals present that rupture cells and denature proteins in order to preserve the DNA that is present without introducing diseases or pathogens. Created by Flinders Technology Associates (Santos 2018).

genome—Complete set of genetic material that is present in an organism.

genomic predicted transmitting ability (GPTA)—The difference from the individual's predicted performance from a genomic test from the average for the breed. Used for selective mating, culling, and genetic improvement.

net merit dollars (NM$)—A popular economic index used within the dairy industry to make genetic progress across production, health, and functional traits.

nucleotide—Building block of DNA. The possible options are A (adenine), T (thymine), C (cytosine), and G (guanine), and when in a sequence, encodes for bodily function.

single nucleotide polymorphism (SNP)—The substitution of one nucleotide for another at a specific location in the genome, which can alter the individual's performance.

tissue sampling unit (TSU)—Allows for rapid and clean tissue sample collection, typically from the ear in cattle, to be sent for processing.

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