

Farm Management Decisions in the Era of Genomics

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■ Take Home Messages

- ▶ Genomics has had a major impact in terms of sire selection by A.I. organizations due to the increased accuracy of selection of young bulls for entry into A.I.
- ▶ Given the high genetic merit of A.I. – genomic young bulls with significantly higher levels of Reliability compared to traditional Parent Averages – 70% of semen used by Canadian dairy producers is from genomic young bulls while 30% is from progeny proven sires.
- ▶ The full adoption of genomics on the sire side has more than doubled the realized rate of genetic progress for LPI in Canadian Holsteins and Brown Swiss with a rate of 1.7 fold in Ayrshire and 1.5 fold in Jersey.
- ▶ Genomic testing of females provides significant opportunity for more accurate herd management decisions to boost rates of genetic gain in the herd, especially in conjunction with the use of sexed semen to breed elite heifers and first lactation cows.
- ▶ The return on investment (ROI) associated with genomic testing, with or without the use of sexed semen, is dependent upon several variables that are different from herd to herd.
- ▶ Genomic testing of females is the only accurate way to manage the impact of genetic recessive characteristics, including haplotypes affecting fertility in all breeds and cholesterol deficiency in Holsteins.
- ▶ CDN and Holstein Canada will jointly launch a new software tool in 2018 to help Canadian producers assess the economic benefit of genomic testing and/or sexed semen for herd management decisions

■ Introduction

Canadian Dairy Network (CDN) introduced official genomic evaluations for the Holstein breed in August 2009, which has now proven to be a very significant event that has permanently changed the genetic selection scheme for dairy cattle improvement in Canada and internationally. Realized genetic progress in a population or breed of dairy cattle is primarily driven by the selection of A.I. sires having semen offered to producers. Due to the competitive nature of the A.I. sector, with each organization striving to offer the highest level of genetics, the adoption of genomics for sire selection was very rapid and has already had a significant impact within the first few years. Today, essentially every A.I. bull with semen actively marketed in Canada to Holstein, Ayrshire, Jersey, Brown Swiss and Guernsey breeders has a genomic evaluation.

The adoption of genomic testing of females by Canadian producers has not seen the same dramatic uptake, compared to how the A.I. sector has embraced the technology. While this is true on an overall basis, some herd owners have recognized the value of heifer genotyping as a cost effective herd management tool and routinely collect a DNA tissue sample at the time of ear tagging newborn heifers. In reality, hundreds of Canadian Holstein breeders today have over half of their herd genotyped, but across all Holstein heifers born each year, less than 10% are genotyped. Canadian producers need the proper tools available to them to assess the economic benefit of genomic testing to the overall profitability of their herd. Currently, CDN and Holstein Canada are collaborating to develop such a software tool, in partnership with Zoetis Canada, which will be launched in 2018 and freely available to all Canadian breeders for their registered animals. This software tool will also help producers assess the economic benefits associated with investing in semen from the highest ranking A.I. sires, as well as the use of sexed semen either on its own or in conjunction with genomic testing of heifers. While the benefits of these tools vary from herd to herd, a growing percentage of Canadian producers are expected to adopt some level of genomic testing in their herd to assist with various herd management decisions.

■ Impact of Genomics

The rate of genetic progress achieved in a population, breed or herd is determined by the following formula.

$$\text{Genetic Gain per Year} = \frac{\text{Genetic Variation} \times \text{Selection Intensity} \times \text{Accuracy}}{\text{Generation Interval}}$$

Genetic variation may gradually change over several generations, but for practical purposes this component of the formula can be considered as a constant value. With genomic selection, however, there has been a significant impact on the other three variables, mainly due to the important gain in the accuracy level of genetic evaluations used for making selection decisions.

Accuracy of genomic evaluations are a function of the size of the reference population used to estimate them. In Canada, the reference population for the Holstein breed in December 2017 includes over 33,000 genotyped sires that are progeny proven for both production and type. For the other breeds, even though genotyped cows with performance data in Canada are also included, the relative size of their reference population, in terms of proven sire equivalents, is significantly smaller, at approximately 6,800 for Brown Swiss, 5,300 for Jersey, 1,500 for Ayrshire and 400 for Guernsey. Figure 1 presents the average Reliability value for LPI, which is the same for Pro\$ in the Holstein and Jersey breeds, for Parent Average (PA) in heifers before genomics and for the Genomic Parent Average (GPA) that results after including the heifer's genomic information.

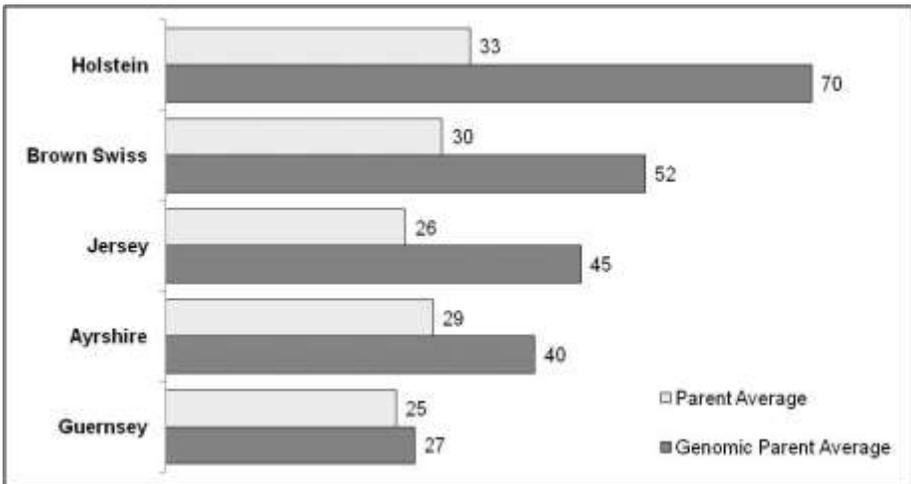


Figure 1: Average Reliability (%) for LPI (and Pro\$) of genotyped heifers based on Parent Average before genomics versus Genomic Parent Average with genomics.

With Parent Average information, which was the only tool available for the selection of young bulls for entry into A.I. and for replacement heifers on the farm before the arrival of genomics, the average Reliability ranged from 25% to 33% depending on the breed. Today, for genotyped heifers and young bulls with genomic information included, the average LPI Reliability reaches 70% in Holsteins, which represents a gain of 37 percentage points. For the Brown Swiss, Jersey and Ayrshire breeds, the Reliability gain due to genomics is 22,

19 and 11 percentage points, respectively. For the Guernsey breed, the reference population is not currently large enough to yield any substantial benefit with genomics but this may be possible in the future through the international exchange of bull genotypes and increased adoption of female genotyping by Guernsey breeders.

During the first few years with genomic evaluations, the A.I. organizations gained confidence in the improved level of accuracy offered by this technology, which has now resulted in its full adoption. Not only does every A.I. bull with semen available to Canadian producers have an official genomic evaluation, but those bulls were pre-selected by the various A.I. organizations based on genomic results for a broader group of young bull candidates. Figure 2 shows the increase in the number of young Holstein bulls genotyped in North America for birth years since 2005. Based on this genotyping activity in recent years, which surpassed 30,000 bulls annually, compared to approximately 1,500 bulls being progeny proven each year, A.I. companies in Canada and United States are currently purchasing and proving one bull out of every 20-25 that are being genotyped. In the equation presented earlier for calculating genetic gain per year, this pre-selection step based on genomics has significantly increased the selection intensity in terms of young bulls entering A.I. in North America.

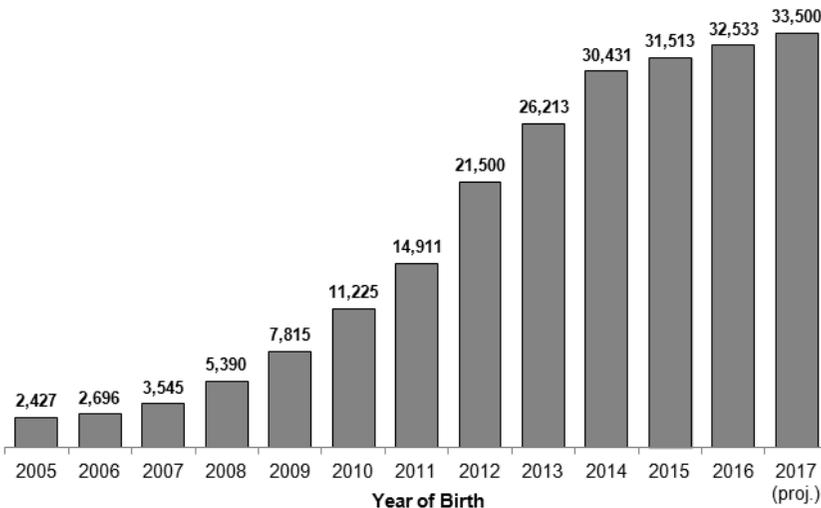


Figure 2: Number of young Holstein bulls genotyped in North America

The third variable significantly affecting genetic gain per year with genomics is generation interval, which is measured by the average age of parents when their progeny are born. Figure 3 shows the trend in age of the sires and dams of the Holstein candidate young bulls genotyped each year. Prior to the introduction of genomics in 2009, the average age of sires of young bulls

entering A.I. consistently exceeded 6 years since they generally first needed to be progeny proven. The dams of the same young bulls were approximately 4 years of age, on average, suggesting they had completed one or more lactations. In recent years, the generation interval for both parental sides has reduced to less than 3 years and continues to gradually decrease to below 30 months of age (Figure 3). This major trend, which translates to faster rates of genetic progress, is a consequence of the high level of confidence and selection intensity that A.I. organizations are now placing in genomic evaluations of very young animals, without a significant loss of accuracy.

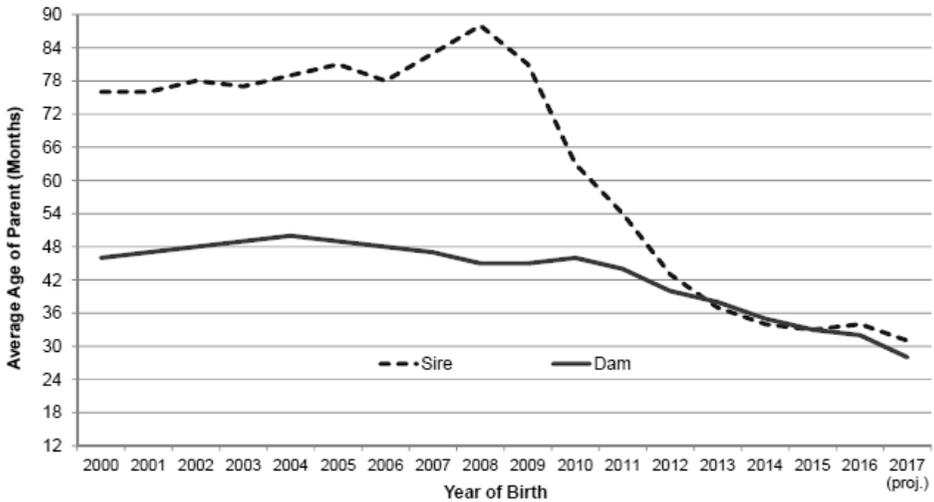


Figure 3: Average age of parents (i.e.: generation interval) of young Holstein bulls genotyped in North America

Canadian dairy producers also have a high sense of confidence in genomic evaluations when making their sire selection decisions. Figure 4 shows the increased usage of young sire semen since the introduction of genomics in 2009. After an initial spike in interest towards genomic young bulls in 2010, the national semen market share occupied by genomic young bulls settled back to normal levels in 2011, but has steadily increased to reach the 70% mark in 2017. This means that only 30% of all Holstein sire semen used in Canada is from progeny proven bulls – a percentage that is expected to gradually decrease further in the coming years.

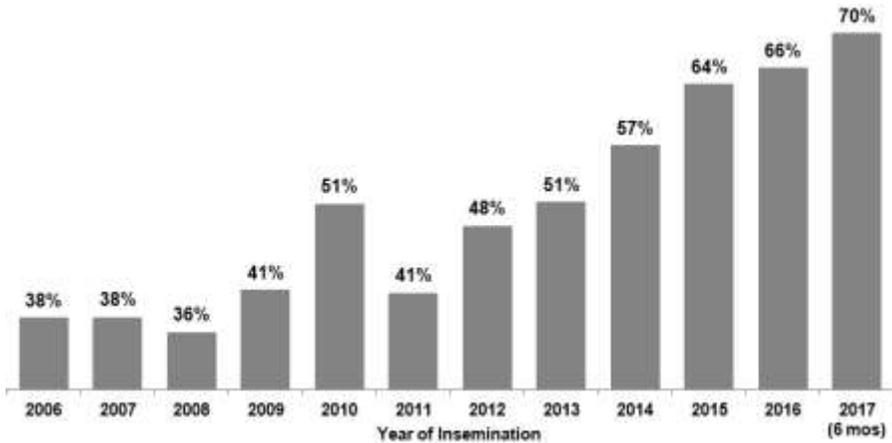


Figure 4: Trend in Holstein young sire usage in Canada

With the full adoption of genomics by the A.I. sector and the increased market demand by producers for semen from genomic young bulls, rates of genetic progress realized in various breeds have significantly increased. Figure 5 shows the genetic trend achieved for both LPI and Pro\$ in the Canadian Holstein population for females born since 2000. Prior to genomics, genetic gain was quite steady at 45 LPI points per year and \$69 annually for Pro\$. Over the past five years, however, after genomics has been fully adopted by A.I. organizations, these rates for genetic progress have reached an average of 106 LPI points and \$176 Pro\$ per year in Canadian Holsteins. These faster rates of genetic gain with genomics translate to an increase of 2.4 and 2.6 fold, respectively. While the adoption rate and impact of genomics has varied by breed, a consistent result has been faster rates of realized genetic gain, which has increased for LPI by 1.7 fold in Ayrshire, 1.5 fold in Jersey and 2.8 fold in Brown Swiss.

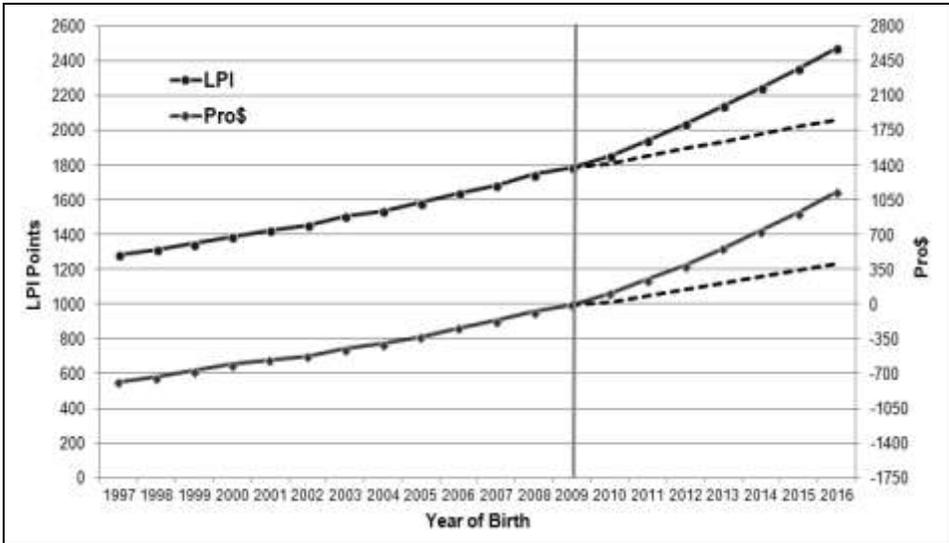


Figure 5: Genetic Trend Realized for LPI and Pro\$ in Canadian Holsteins Before and After Genomics

■ Genomics for Herd Management

While sire selection decisions are critical for achieving significant rates of genetic progress in a breed and within each specific herd, breeders also have an opportunity to achieve their breeding goals through improved female selection decisions. Traditionally, Canadian dairy producers have had a strong tendency to keep all heifer calves born on the farm, raise them and breed them to achieve a first calving, and then make herd replacement selection decisions once in first lactation and with type classified. Given the strong export market usually available to Canadian producers, and the relatively low accuracy of Parent Average information for young heifers, this strategy made sense. The arrival of genomics now provides dairy producers with new opportunities to make herd management decisions related to genetic improvement. This is especially the case for most herds in conjunction with the increased availability of sexed semen.

Economically speaking, there are three main areas of potential benefit that result from the use of genomic information for herd management decisions:

1. The opportunity to identify young calves that do not have the level of genetics that warrant keeping them as potential heifer replacements.
2. The opportunity to make improved genetic selection and mating decisions to increase the genetic potential of future heifer replacements for the herd.

3. The opportunity to identify females that are carriers of undesirable genetic traits in order to manage the potential impact on the herd.

In addition, genotyping also provides the benefit of accurate parentage verification when the recorded parents have been genotyped, which is the case for essentially all daughters of A.I. sires.

In reality, the potential return on investment associated with heifer genotyping varies from herd to herd. There are several factors that affect the economics of heifer genotyping, including the:

- ▶ cost of genomic testing
- ▶ number of heifers born relative to the number of replacements required for the milking herd
- ▶ expected change in size of the milking herd during the next two years
- ▶ sale value of young heifer calves, bred heifers and/or fresh cows in first lactation
- ▶ genetic variability of heifer calves born in the herd
- ▶ gain in Reliability of genomic evaluations compared to Parent Average

For herds using sexed semen to breed a significant proportion of their heifers and/or cows, the economics of heifer genotyping is also affected. In this case, a higher number of heifer calves are subsequently born potentially resulting in a greater opportunity to sell heifers not required as herd replacements. Once the combined use of sexed semen and heifer genotyping have been incorporated into the herd management strategy, then it may also be beneficial to incorporate the use of beef sire semen as well. Table 1 provides a summary of the common herd management actions that are likely in herds that adopt a longer term strategy involving both heifer genotyping and sexed semen.

Table 1: Common herd management actions by age group associated with an economical strategy involving heifer genotyping and use of sexed semen

Herd Management Action	Young Calves	Yearling Heifers	1st Lactation Cows	Later Lactation Cows
Genomic test	✓	✓		
Breed with conventional semen		✓	✓	✓
Breed with sexed semen ¹		✓	✓	
Breed with beef sire semen ²				✓
Sell (remove from herd)	✓			

¹Use of sexed semen may be replaced by use as a donor for embryo transfer.

²Candidates to be bred with beef sire semen may also be used as embryo transfer recipients.

The various herd management actions are somewhat dependent upon the group of females in the herd, with four likely categories being: (a) young calves, usually under 12 months of age, (b) yearling heifers to be bred as replacements for the milking herd, (c) cows in first lactation, and (d) cows with two or more calvings. Within each group the females should be ranked by Pro\$, LPI or a custom index defined by the breeder. For specific herds, actions for managing the young calves would be to either genomic test them or to sell those that are genetically inferior when a surplus of heifer calves exists. Those calves identified for genomic testing are targeted to improve the accuracy of the herd owner's decisions to keep or sell each one, as well as later decisions like sire selection and mating. For yearling heifers, some degree of genomic testing may still be beneficial since the primary herd management decision for this group is to identify those to be bred using sexed semen instead of conventional semen. Similar decisions need to be made for the milking herd, recognizing that sexed semen is mainly an option for younger, first lactation cows, but can also be used to some degree to breed older cows. In a herd achieving steady genetic progress, the females that fall into the bottom group genetically will mainly include older cows beyond first lactation, so fewer will be identified for breeding with sexed semen regardless. Once the highest yearling heifers and milking cows have been accurately ranked based on their genetic/genomic evaluations, the economic decision to use sexed semen is highly dependent upon the increased semen cost versus the genetic sacrifice that must be made given that not all of the highest A.I. sires have sexed semen available to Canadian producers. If herd owners are interested in using embryo transfer (ET) as a means of producing more replacement heifers from their genetically superior

dams, the highest candidates recommended for breeding with sexed semen could be considered as ET donors. Either approach ends up generating more heifer calves born in the herd, which then alters the genomic testing strategy and economics the following year and boosts the genetic potential of the milking herd in future years. In addition, for some herds, it may be economically beneficial to breed the genetically inferior cows with beef sire semen to produce a crossbred calf that generates a higher sale value at birth. This economic decision should primarily be driven by the expected increase in sale price of crossbred beef versus purebred dairy calves, but a lower average blend price and a higher average conception rate for beef sire semen could also be considered.

For each herd, the frequency of each herd management action (i.e. genomic testing, sell or breed with conventional, sexed or beef sire semen) will vary and will not be consistent over time as the herd evolves. This reality makes it difficult for herd owners to identify and apply the most profitable strategy for genomic testing, either on its own or in conjunction with the use of sexed semen. For this reason, the new software to be jointly launched by CDN and Holstein Canada in 2018 is being developed. This tool will allow Canadian dairy producers to:

- ▶ assess the genetic progress realised with past breeding decisions
- ▶ compare past genetic progress across traits to identify those that have received the most and least emphasis
- ▶ assess the ranking of the herd on a trait-by-trait basis compared to other herds of the same breed nationally
- ▶ understand the expected genetic progress achievable in the herd resulting from selection based on Pro\$, LPI or a customized index
- ▶ manage the herd inventory of heifers and cows
- ▶ view genetic evaluation results for each female and generate individual animal reports and/or group reports
- ▶ generate printable herd plots based on a wide variety of variables/traits
- ▶ compare the relative ranking of the herd based on both genetics and performance for key traits
- ▶ assess the estimated return on investment (ROI) associated with various strategies involving (a) the use of the best A.I. sires possible, (b) genomic testing of heifers, (c) use of sexed semen, or (d) heifer genotyping combined with use of sexed semen
- ▶ select and apply a preferred strategy involving genomic testing and/or use of sexed semen, which generates a list of herd management actions for specific females in the herd

- ▶ rank A.I. sires according to the custom selection index to identify those that would maximize future genetic progress of the herd
- ▶ identify matings to avoid in order to minimize the impact on the herd of genetic recessives, like cholesterol deficiency in Holsteins and haplotypes affecting fertility

■ Genetic Variability and Genomics Reliability Gain

Figure 1 presented the average gain in Reliability for LPI that results from genomic testing, which also applies to Pro\$. For example, for Holsteins, the average Reliability increases from 33% for a heifer's Parent Average to 70% once she is genotyped. Figure 6 helps explain this concept further. Without genomic testing, the typical Holstein heifer is born with a Parent Average (PA) that has a Reliability of 33%, which generally increases to 36% by the time it becomes a yearling heifer. This gain in PA Reliability results from its dam adding more accuracy as a lactating cow, and often, the sire adding more daughter data to its proof. Once calved, the typical Holstein cow receives an LPI with a 55% Reliability, which gradually increases to 59%, 62% and 64% with each additional lactation, respectively. Only dams with a high number of lactating daughters, usually resulting from embryo transfer, end up with an LPI Reliability of 65% or higher without being genotyped. The advantage of genomic testing is that it can be done immediately after birth and the resulting Genomic Parent Average (GPA) achieves, on average, a 70% Reliability level. Basically, with genomic testing, Holstein breeders can now have more confidence in the genomic evaluations of their heifers and cows than they had in the genetic evaluations they traditionally received for their lactating cows, including their own milk recording and type classification performance data. For Brown Swiss, Jersey and Ayrshire breeders, this conclusion is not as obvious (see Figure 1). Still, they can surely have increased confidence in the genetic information they receive for genotyped heifers compared to only having Parent Averages.

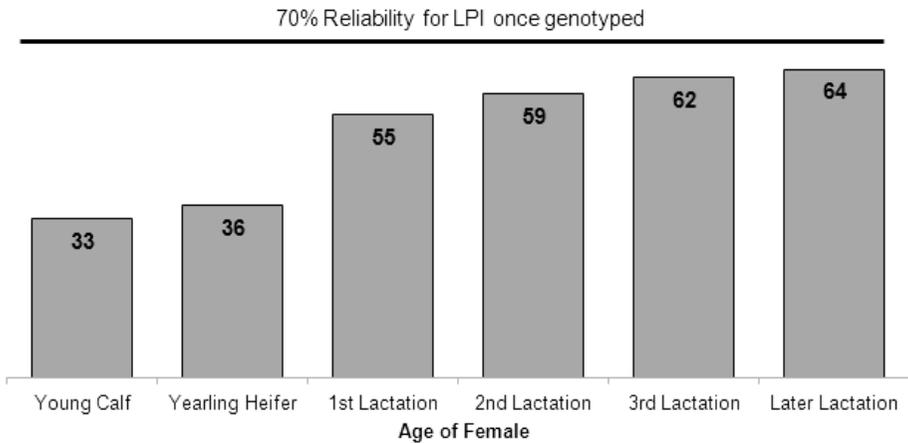


Figure 6: Average LPI Reliability for Holstein females without genomics compared to 70% level achieved once genotyped

In addition to the increased accuracy of evaluations for genotyped heifers compared to only having a Parent Average, genomic testing will also increase the degree of variability of genetic evaluations among the heifers born in a herd. Increasing this genetic variability spreads them out across a wider range and results in some degree of re-ranking. Figure 7 shows actual results for three Holstein herds (i.e.: Herds A, B and C) that each genotyped more than 100 heifer calves. For each herd, the distribution of LPI based on Parent Average is compared to that based on Genomic Parent Average which resulted from genomic testing. Although these are actual results, these three herds were selected based on the fact that they each have a different degree of change between Parent Averages and Genomic Parent Averages.

For Herd A, the Parent Averages for LPI have a narrow distribution and genomic testing the heifers resulted in a much wider range in terms of their genetic evaluation, which also yields a significant re-ranking among the heifers. In this herd, genomic testing clearly helps to separate the genetically superior heifers from the poorer ones. Also of interest with the results for this herd is a downward shift in the average LPI of the heifers, which was 85 points in this case. In most herds, however, the average Genomic Parent Average is expected to be very close to the average Parent Average, which is what is observed for example herds B and C in Figure 7.

For Herd B, genomic testing resulted in a moderate increase in the genetic variability and spread of the heifers. In this herd, genomic testing also created some degree of re-ranking, which would translate to improved genetic selection and mating decisions. For herds like this one, a well-planned strategy for heifer genotyping is expected to yield a good return on

investment, especially if there is a surplus of heifer calves available and herd management decisions involve the sale of those heifer below a specific genetic level for an index like LPI or Pro\$.

In Herd C, genomic testing did not have a significant impact on the spread of the heifers for LPI based on Genomic Parent Average versus traditional Parent Average. In this case, the degree of re-ranking would be significantly less compared to herds A and B, however, it must be noted that individual heifers do end up with varying results with genomic testing, so some degree of re-ranking occurs in all herds.

In reality, herd owners do not know in advance the degree to which genomic testing will spread out the genetic evaluations of their heifers and cause re-ranking. This result varies from herd to herd, but the new software tool to be launched by CDN and Holstein Canada will help advise producers on the degree of genomic testing that makes economic sense for their herd.

■ Managing Genetic Recessives

As the volume of genotypes in each dairy cattle breed has increased, which now totals more than 2 million at CDN across all breeds, research scientists have been able to discover genetic anomalies in each of the Holstein, Ayrshire, Jersey and Brown Swiss breeds. Technically speaking, the specific genes underlying these anomalies were not discovered, but haplotypes, which are short sections of DNA, were identified. All of the original haplotypes found were negatively associated with fertility by either resulting in early embryonic mortality or stillborn calves. For this reason, they were simply named as Haplotypes Affecting Fertility and labelled as HH1 (i.e.: Holstein Haplotype 1), HH2, HH3, HH4 and HH5 in Holsteins, AH1 and AH2 in Ayrshires, JH1 and JH2 in Jerseys and BH1 and BH2 in Brown Swiss. In recent years, another haplotype – for cholesterol deficiency (i.e.: HCD) – was discovered in Holsteins, for which a gene test was later developed. Table 2 shows the evolution of the estimated frequency for each haplotype within the Canadian population. These frequencies are population averages, but will vary significantly from herd to herd depending on the sire lines used. The only way a herd owner can know the actual frequency of these undesirable genetic recessives is by genotyping all animals in the herd. In Holsteins, it is HCD that requires the most attention in terms of mating carrier sires to carrier females, since its frequency exceeds 10% for heifers born in 2015-2017; this is also true for both AH1 (19.3%) and AH2 (24.1%) in Ayrshire, JH1 (19.2%) in Jersey as well as both BH1 (13.3%) and BH2 (15.6%) in Brown Swiss. Genomic testing helps producers manage these genetic recessives by avoiding the use of carrier sires to breed known carrier females in the herd. For some herds and breeds, depending on the frequency of carriers, managing these genetic recessives can contribute significantly to the economic return on investment associated with genomic testing.

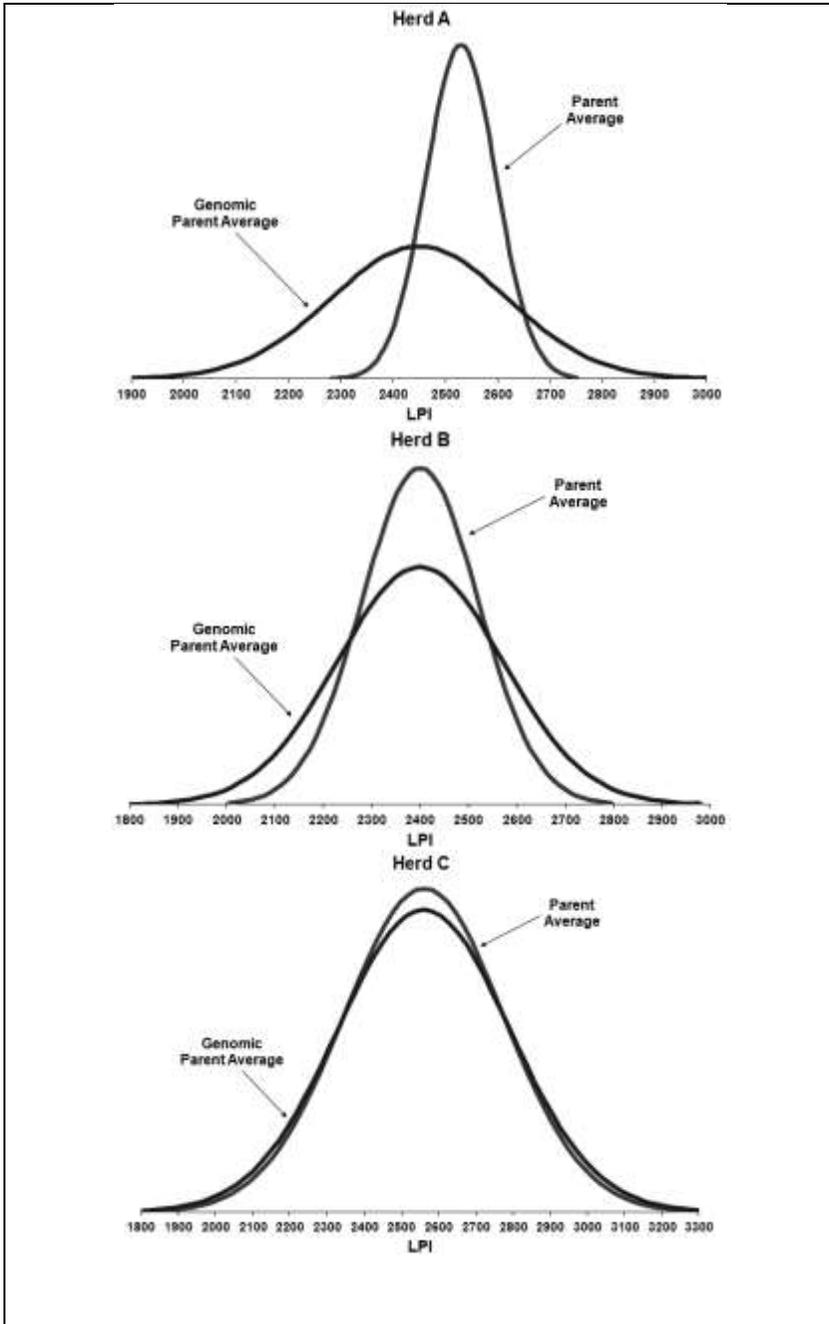


Figure 7: Comparison of the distribution of heifers based on Parent Average and Genomic Parent Average for LPI - Results from three actual Holstein herds with over 100 genotyped heifer calves

Table 2: Evolution of Frequencies for Known Haplotypes in Canadian Dairy Breeds

Birth Year	HH1	HH2	HH3	HH4	HH5	HCD	AH1	AH2	JH1	JH2	BH1	BH2
1970-1974	0.0	0.0	0.0	0.0	0.4	0.0	23.8	1.0	0.2	0.2	0.0	0.2
1975-1979	0.1	0.0	0.0	0.0	0.4	0.0	27.5	2.3	0.4	0.4	0.2	0.2
1980-1984	0.9	0.5	0.2	0.4	0.3	0.0	25.0	2.9	0.7	2.5	2.3	0.3
1985-1989	1.3	1.5	1.4	1.0	0.6	0.0	21.0	4.2	4.1	7.7	2.7	0.5
1990-1994	3.7	1.7	1.4	0.8	0.5	0.0	20.2	4.4	4.6	9.2	6.2	8.4
1995-1999	8.3	2.3	1.1	0.5	0.3	1.9	26.4	6.3	6.8	10.4	6.7	8.8
2000-2004	9.3	4.1	1.3	0.3	0.2	3.6	27.9	13.4	11.0	12.5	9.4	11.0
2005-2009	8.2	2.9	1.5	0.3	0.7	10.6	22.6	19.6	18.2	15.3	10.4	11.9
2010-2014	5.2	3.3	3.6	0.3	3.8	14.2	24.4	22.1	21.4	10.8	15.5	19.5
2015-2017	2.9	2.2	4.4	0.3	5.4	10.3	19.3	24.1	19.2	6.1	13.3	15.6

■ Conclusions

The era of genomics in the Canadian dairy cattle industry began in 2009 when the Canadian Dairy Network (CDN) introduced the first official genomic evaluations for the Holstein breed. In the following year, the same was done for the Jersey breed; genomic evaluations for the Brown Swiss, Ayrshire and Guernsey breeds were also introduced during this time. The general benefits of genomics are directly related to the size of the reference population available for each breed, which gives Holsteins a significant advantage, but it is important for all breeds to establish international exchange agreements for access to the highest possible number of genotypes for progeny proven sires. Breeds with genomic evaluations based on a reference population with thousands of genotyped animals have a distinct advantage over those that do not since annual rates of genetic progress are significantly improved with genomics, as exemplified by the realised rates of gain in all such Canadian dairy breeds.

On the female side, the same statement can be made. Herd owners that decide to genomically test selected females in their herd will be able to make improved herd management decisions compared to others that decide not to adopt this new technology. In most herds, the optimal economic long-term strategy is a combined use of sexed semen to breed the genetically superior heifers and cows along with genomic testing of selected heifer calves that are subsequently born in the herd. The optimal usage level of sexed semen and/or genomic testing is dependent upon several variables specific to each herd, which means that it is difficult for herd owners to determine if it is economically beneficial to use either or both of these technologies to make better herd management decisions, and if so, to what degree they should be used. In 2018, CDN and Holstein Canada will be jointly launching a new software tool to help all Canadian dairy producers assess the return on

investment (ROI) in their herd associated with the adoption of genomic testing and/or usage of sexed semen.

■ References

Canadian Dairy Network (CDN), 2017. Various extension articles authored by Brian Van Doormaal available on the Internet at: <http://www.cdn.ca/articles.php>



