

Innovative Breeding Schemes: Best Combinations of Genomics, Semen Type, and Culling

Albert De Vries
Associate Professor
Department of Animal Sciences, IFAS, University of Florida
2250 Shealy Drive, Gainesville, FL 32608
Phone: (352) 392-5594 ext. 227
Email: devries@ufl.edu

Introduction

Commercially affordable sexed semen (since 2006) and genomic testing (since 2009) have added to the options dairy farmers should consider when looking to increase profitability on the farm. These technologies, combined with good overall management, and older technologies such as embryo transfer or beef semen, lead to an expanded number of choices regarding genomic testing, breeding and culling. It is not quite obvious what the best combinations of these practices are. This paper attempts to describe the value of some of these combinations and shows some work on discovering new breeding schemes that lead to greater profitability.

Based on NAAB-reported semen sales, USDA reported that the use of (female) sexed-semen in heifers has increased from 9% in 2007 to 31% in 2015 (Hutchison and Bickhart, 2016). In cows, 0.2% of all breedings were with sexed semen in 2007, and this had increased to 1% in 2015. While sexed semen results in more heifer calves, it is also more expensive than conventional semen and reduces conception rates. USDA also reported that average conception rates for heifer sexed-semen breedings has recently increased due to improved technology (42% in 2007 compared to 49% in 2015). Comparable conception rates for heifer conventional breedings were 56% in 2007 and 59% in 2015. Conception rates for sexed-semen breedings to cows were 26% in 2007, and 30% in 2015 compared to 30, and 32% for conventional breedings during the same years. These conception rates are likely affected by the preferred use of sexed semen on more fertile animals.

Average reproductive performance has also increased considerably in the last 15 years due to improvements in management and technologies such as timed-AI and estrus detection gadgets. Characteristics of 7,032 Holstein herds (≥ 50 cows per herd) that participate in the DHIA Program showed an average pregnancy rate of 19% (records processed by DRMS by September 8, 2016) (De Vries, 2016). However, 11% of the herds had pregnancy rates of at least 28% and these herds accounted for 21% of the cows. These improvements in reproductive performance also allow for the creation of more dairy heifer calves.

The 7,032 DHIA herds had an average annual cow cull rate of 37%, which was independent of the pregnancy rate group (which varied from 6% to 37%). Annual cow cull rates have remained fairly constant in the last decade although the average cow breeding value for productive life has increased by 6 months since 2000, and has been increasing for 50 years (De Vries, 2017). Given that the national dairy herd is fairly constant at about 9 million cows, cow cull rates in the US are mostly

decided by the number of dairy calves that are being raised to replace cows. When more heifer calves are created, the larger supply of heifers may force cows out of the herd that otherwise might have stayed. Other factors also play a role, such as cow health and performance, beef prices, the cost to raise or purchase heifers, and markets for dairy heifer calves and crossbred calves.

The availability of these technologies and good quality of management on many farms is leading to the ability to create more heifer calves than are needed to replace cows. Among the options to consider are now on which animals to use sexed semen, which dairy calves to raise as herd replacements, and which cows to cull. Other options in the decision mix are the use of beef semen to create crossbred calves, embryo production and transfer, and whether to use genomic testing.

The use of genomic testing has changed from use in primarily males in 2009 to now in females. The Council of Dairy Cattle Breeding (CDCB) national genetic evaluation of December 2016 shows that more than 1.67 million animals in the national database have been genomically tested since 2009. Of these, 1.28 million were genotyped in the US. In the 35 days from November to December 2006, the increase was 40,000 (30,800 Holstein females and 3,200 Holstein males, the remainder other breeds). Almost always young calves are tested. If 4.5 million dairy heifer calves are born every year, then this means that approximately 9% of these calves are genomically tested. Genomic test results are useful to better rank animals for genetic merit of individual traits or based on an index such as Net Merit (NM\$), identify parentage misidentifications, and detect carriers of recessive alleles. Test results should improve culling and breeding decisions.

This paper first describes some basic genetic concepts that are needed to evaluate breeding schemes. Secondly, major factors are described that affect breeding schemes and these factors are tied together in a herd budget model to calculate a bottom line profitability. Third, several analyses show how the value of genomic testing depends on user-defined breeding schemes. Fourth, other analyses show how the optimal breeding scheme depends on genomic testing, the premium for crossbred calves, and the level of reproduction. The fifth part describes separate analysis not evaluated with the herd budget model such as the value of fixing misidentification and changing the cow cull rate. Part six contains some final thoughts and part seven has some take home messages.

Genetics and Genomic Testing 101

Genomic testing results provide better estimates of the genetic merit of animals and can be performed at a young age. Influenced by genomic test results, an often recommended policy is to sell the surplus heifer calves that are not needed to replace culled cows. These would typically be the genetically worst heifers, assuming health is fine. An additional use of genomic test results is to breed the top animals with sexed semen, the middle animals with conventional semen, and the bottom category with beef semen. When embryo transfer is employed, the top animals could be donors and the worst animals could be recipients.

Genomic test reports contain (categories) of predicted transmitting abilities and reliabilities for individual traits such as milk yield, daughter pregnancy rate, and production life, as well as their reliabilities (among other information). Table 1 is a part of a genomic test report for 9 calves tested at the University of Florida Dairy Unit. Results are expressed in Predicted Transmitting abilities (PTA) on the left with their reliabilities in percentages (%) on the right. NM\$ and TPI are indices that combine multiple traits weighted by their relative importance.

The PTAs on the test report (called Parent Averages if no information from the animal itself is available) are the genetic merit that the animal is expected (predicted) to transmit to its offspring (the next generation). Expression of genetic merit in PTAs made sense when looking at proofs of sires, because the primary interest is in the genetic merit of the daughters. The daughter is expected to obtain half of her genetic merit from the sire while the other half comes from her dam. However, when genomic testing a calf we are primarily interested in the genetic merit of the tested animal itself. The expected genetic merit of the animal itself is the estimated breeding value (EBV), which is $PTA \times 2 = EBV$. This matters when interpreting the difference in the genomic test results between the calves. In table 1, the best calf has a PTA of NM\$ of \$530 whereas the worst calf has a PTA of NM\$ of \$253. This is a difference of \$277 PTA. However, the expected genetic difference is $2 \times \$530 - 2 \times \$253 = \$554$. The NM\$ index is a lifetime measure, say 3 lactations. The best calf is therefore expected to be \$554 more profitable than the worst calf, or \$185 per lactation. These are larger differences than they appear when the PTAs are compared. The multiplication of the PTA by 2 does not change the ranking of the calves, of course.

Table 1. Partial genomic test results for 9 heifer calves at the University of Florida Dairy Unit.

On-farm ID (Herd Management #)	Birth Date	Sex	Breed	NM\$	TPI	Milk	DPR	PL	NM\$	TPA	Milk	DPR	PL
9598	2015/12/09	F	HO	253	1785	777	0.8	4	71%	NA	74%	66%	68%
9615	2015/12/23	F	HO	480	2159	747	2.8	6.4	71%	NA	75%	67%	69%
9605	2015/12/17	F	HO	358	2031	72	2.3	4.5	75%	NA	77%	71%	72%
9592	2015/12/02	F	HO	530	2249	593	3.7	7.3	70%	NA	74%	65%	67%
9593	2015/12/03	F	HO	484	2169	347	2.8	5.2	71%	NA	74%	66%	68%
9610	2015/12/22	F	HO	410	2041	619	2.9	5.4	69%	NA	73%	62%	65%
9590	2015/12/01	F	HO	365	2045	700	0.7	3.9	73%	NA	76%	67%	70%
9594	2015/12/05	F	HO	273	1907	410	2	4.3	73%	NA	76%	67%	70%

NM\$ = Net Merit, TPI = Total Performance Index, milk = milk yield (in lbs/lactation), DPR = daughter pregnancy rate (in %), PL = productive life (in months). Results are expressed in Predicted Transmitting abilities (PTA) with reliabilities in percentages (%) on the right.

The reliabilities show the uncertainty, both positive and negative, of the PTA to predict the true transmitting ability of the trait (the true genetic merit as determined by the DNA of the animal). The higher the reliability, the more information has been used, and the more certain we are that the true transmitting ability is near the PTA (or equivalently that the true breeding value is near the EBV). Without genomic testing, the reliabilities of the parent averages are around 20% when the sire is identified, and just over 30% when both sire and dam are identified. The PTAs will be more similar when reliabilities are low. Genomic testing therefore widens the distribution of the PTAs. Reliabilities for NM\$ are on average a little greater than 70% in table 1. These higher reliabilities provide more confidence in the rankings of animals, for example to make culling or breeding decisions. Ideally, animals are ranked by their true breeding values (or true transmitting abilities) but they are unknown.

The quality of the genomic testing technology to predict actual future performance is constantly improving as a result of better statistical methods and a bigger dataset of genomically tested animals that also have performance data. Weigel et al. (2015) presented some of the evidence that genomic testing works and helps predict future phenotypic performance.

When not all animals are needed to create the next generation, a useful formula to estimate the genetic progress from one generation to the next is the “breeder’s” equation. One of the simplest forms of this formula is: genetic progress/year = genetic variation x selection differential x $\sqrt{\text{reliability}}$ / generation interval. This formula is at least 80 years old and was mentioned by dairy genetics pioneer Jay Lush in 1937.

Genetic variation is the natural genetic difference that exists among the animals in the population. This would be the distribution of the true breeding values. USDA calculated the standard deviation (a measure of this variation) of the true breeding value of NM\$ in the US herd at \$388. One can estimate the genetic variation in a herd based on the PTAs, but this estimated variation is generally less than the true genetic variation that exists, because the reliabilities of the PTAs are less than 100%.

Selection differential is a mathematical function of the fraction of animals that are used (the selecting intensity). The value varies from 0 to more than 3 and increases when a smaller fraction is selected. For example, if 90% of the animals are used, the selection differential is 0.20. When 80% are selected, it is 0.35. At 10% it is 1.76. At 1% it is 2.67 and so on.

The square root of the reliability is the accuracy. It represents how well all animals can be ranked for true breeding value. When the reliability is low, genetic progress is minimal even when the selection intensity is high because we have little information about each animal’s true genetic merit. We’d more often select animals that in reality have lower true breeding values. Genomic testing can be seen as increasing the reliability of the ranking and thus the genetic progress in the animals that are kept is increased (if the goal is to select the best ones). The generation interval is the average age of the parents when the offspring is born.

The first part of table 2 shows how the average NM\$ of the selected animals increases from \$0 (the herd average) based on the selection intensity and the reliability in the breeder’s equation. For example, if 90% of the animals are selected and the reliability of the ranking the animals on their true breeding values is 30%, then the average true breeding value for NM\$ of the selected animals is \$37 greater than the population they were selected from. On the other hand, the bottom 10% in this case has an average true breeding value of -\$336 because the average of all animals is \$0. The average increase in NM\$ is the greatest when the reliability is high and a few best animals are selected such as with embryo donors after genomic testing.

The second part of table 2 is the net monetary gain after all animals (selected and not selected) are tested with a test that costs \$50 and delivers a reliability different from 0%. For example, if the reliability is 70% and the best 90% of the animals are selected, then the gain in profit of those 90% is only \$1. The gain in average true breeding value is offset by the testing cost to obtain the 70% reliability. This assumes that without the test, the reliability is 0%. In practice, the reliability is greater than 0% because the performance of the sire and dam are probably known.

Table 2. The breeder's equation applied to selection based on NM\$ and a \$50 cost of testing per animal. All animals are tested. The standard deviation is \$350.

Average true breeding value, per selected animal					
←Animals selected→					
Reliability ↓	10%	30%	50%	70%	90%
10%	\$194	\$128	\$88	\$55	\$22
30%	\$336	\$222	\$153	\$95	\$37
50%	\$434	\$287	\$197	\$123	\$48
70%	\$514	\$339	\$234	\$145	\$57
90%	\$583	\$385	\$265	\$165	\$65

Net gain after \$50 testing cost, per average selected animal					
←Animals selected→					
Reliability ↓	10%	30%	50%	70%	90%
10%	-\$306	-\$39	-\$12	-\$16	-\$34
30%	-\$164	\$55	\$53	\$24	-\$19
50%	-\$66	\$120	\$97	\$52	-\$8
70%	\$14	\$172	\$134	\$74	\$1
90%	\$83	\$218	\$165	\$94	\$9

Typical applications of the breeder's equation use reliabilities as seen in table 1 to show how genetic progress in the herd increases if animals are selected based on genomic test results vs. traditional PTAs. But some recent genetics theory says that the reliabilities used in the breeder's equation are often too high, especially with low parent average reliabilities (Calus et al., 2015). The theory is difficult, but the implication is that the reliabilities without genomic testing in the breeder's equation should be a lot lower, and with genomic testing should be somewhat lower. The result is that the value of genomic testing is actually greater than when calculated by the breeder's equation with the reliabilities in table 1 and traditional reliabilities of 10 to 30%.

The ideas in table 2 can be used to value selling the genetically worst surplus calves (reducing the number of animals selected from 100% to fewer, and indirectly when breeding the better animals with sexed semen (or as embryo donors) to propagate the better genetics. The data in table 2 is not sufficient, however, to design and evaluate breeding schemes on farms because too many factors are left out.

Using the breeder's equation idea as part of the analysis, a Dutch study by Calus et al. (2015) and a Danish study by Hjørtø et al. (2015) showed conflicting results of the economic value of genomic testing. In the Danish study, net gain was negative in most cases and the Dutch study showed a positive net gain. The Dutch study looked at all or nothing use of sexed semen, different cull rates and hence a varying fraction of surplus heifers that were sold, but they did not include all relevant costs such as the cost to raise heifers, cow cull prices, or reductions in conception rate when sexed semen was used. The Danish study, on the other hand, used beef semen in the herd so there was no

surplus of dairy heifer calves to sell. The value of genomic testing came from better identification of animals to breed with sexed, conventional, or beef semen. Optimization of breeding schemes was not pursued in both studies. Comprehensive analysis that looked at combinations of genomics, semen type and culling in the US and abroad appear not to be available.

How to Evaluate Breeding Schemes

At the University of Florida, a herd budget model was put together to evaluate breeding schemes and even find the optimal scheme given all kinds of herd specific data and prices. The bottom line is profit per milking cow per year. The budget moves animals from birth to culling over time and observes revenues and expenses such as feed costs, breeding costs, labor and other variable cost, and genomic testing cost (if applicable). Revenues come from milk sales, cow and heifer culling, sold calves, and kept dairy calves. Animal performance depends on reproductive efficiency, lactation and feed intake curves, body weights, and involuntary risk of culling, among many other inputs. This herd budget model was earlier used to evaluate stall stocking density (De Vries et al., 2016) and the economics of using natural service sires. New was the addition of genetics of the NM\$ trait as a comprehensive index of the value of genetic merit.

Kept dairy calves were valued based on their genetic merit. The breeder's equation was part of the analysis. This genetic merit depends on the genetic merit of the dams and sires of the calves and on the sale of surplus dairy heifer calves. The value created through the sale of surplus calves depends on the reliabilities, which increase with age and can be increased through genomic testing. A greater surplus of dairy calves can be created with sexed semen, but at a higher cost than conventional semen breeding and at lower conception rates. Sexed, conventional and beef semen can be applied to different groups of cattle, for example sexed semen on the genetically better heifers and beef semen in some of the genetically worse older cows. Younger dams are genetically better than older dams. The genetic variation decreases a little with age as a result of involuntary culling, which is associated with poorer genetics.

Reasonable prices and other assumptions (not shown) were chosen for the analyses that follow. The standard deviation of the true breeding value of NM\$ in calves was set at \$350 and the genetic trend in the herd was \$70 EBV per year. The cost of genomic testing was set at \$50 per tested calf which included extra labor cost. All born alive dairy calves were tested if genomic testing was applied. Culled cows were sold at approximately half the cost of raising heifers. Dairy bull calves and surplus dairy heifer calves were sold at a young age at a profit of \$150 after their expenses. This price for surplus dairy calves was assumed to be independent of the genetic merit of these calves. As table 2 shows, the greater the reliability and the smaller the fraction of the surplus dairy heifer calves that are sold, the lower their genetic merit will be. In other words, the market is assumed to be naïve about the genetic merit of the sold dairy heifer calves. The initial premium for a crossbred calf was \$75 over the price of a dairy bull calf. The cow cull rate was fixed and did not vary with the breeding scheme.

User-Defined Breeding Schemes

In **scenario 1**, only conventional semen was used which led to 12% surplus of calves given a fixed cull rate of 36% and a pregnancy rate of 21%. Four reliabilities for selecting the surplus calves were set. They were set at 0%, or 6%, or 20% (all at \$0 cost, traditional evaluation), or 57% (at \$50

cost, genomic test). These reliabilities may seem low but they are likely more correct to use in the breeder's equation (Calus et al., 2015). The higher the reliability, the better the 88% genetically truly best heifer calves are selected to remain in the herd.

Increases in revenues compared to the profit per milking cow at 0% reliability (0%) were \$14 (at 6% reliability), \$26 (at 20%) and \$42 (at 57%) per milking cow per year. However, genomic testing all heifer calves born alive in the herd cost \$27 per milking cow per year. The increases in profit per milking cow per year were therefore \$14 (at 6%), \$26 (at 20%) and $\$42 - \$27 = \$15$ (at 57%). Expressed per born alive dairy calf, the increases in profit were \$26 (at 6%), \$47 (at 20%) and again \$26 (at 57%). In this scenario, genomic testing was not profitable when the farm had some reliability for free through the traditional genetic evaluation. Because only conventional semen was used, the reliability information was not used when breeding heifers and cows. Thus, the genomic test information was only used to identify the 12% dairy heifer calves to be sold.

In **scenario 2**, the top 50% of heifers were bred with sexed semen twice. All other breedings in heifers and cows were with conventional semen. As a result, 18% surplus dairy heifer calves were created. The genomic test information was now used to identify the 82% of dairy heifer calves that were kept, and also to identify the 50% genetically best heifers to breed with sexed semen. The increases in profit (over the 0% reliability setting) were \$22 (at 6%), \$41 (at 20%) and \$37 (at 57%) per milking cow per year. In scenario 2, the higher reliability was more valuable because it was used twice. As a result, genomic testing was more likely to be profitable. The increase in profit per milking cow in scenario 2, compared to using only conventional semen (scenario 1), was \$18 when reliability was set at 0% and \$40 when reliability was 57%. The use of sexed semen on the better heifers was profitable regardless of the reliability of the genetic information.

In **scenario 3**, all heifers and the top 50% of first parity cows were bred with sexed semen twice. This extended use of sexed semen led to a 25% surplus of dairy heifer calves. The increases in profit (over the 0% reliability setting) were \$25 (at 6%), \$49 (at 20%) and \$58 (at 57%) per milking cow per year (reliabilities for cows were set slightly greater). The value of genomic testing therefore increased compared to scenarios 2 and 1. Scenario 3 was also more profitable than scenario 2 and 1 at any level of reliability.

In **scenario 4**, the top 50% of heifers were bred with sexed semen twice and the bottom 20% of older cows were bred with beef semen. This scenario led to only 11% surplus dairy heifer calves because crossbred calves were created. Thus there was less genetic progress because the selection intensity among the dairy calves was lower but crossbred calves were sold at a premium of +\$75. The increases in profit (over the 0% reliability setting) were \$14 (at 6%), \$31 (at 20%) and \$28 (at 57%) per milking cow per year. Profit was slightly lower than in scenario 3 but greater than in scenarios 2 and 1 at any level of reliability.

These four scenarios show that profit of the breeding scheme depends on the interaction between reliability of genetic testing and semen type. The results also depend on many other assumptions that were set and not varied such as the genetic variation of the selection index.

A genetic standard variation of \$350 for NM\$ was used in scenarios 1 to 4. A selection index can have a greater genetic variation, for example when new, economically important traits are included. For example, if the genetic standard deviation is increased to \$450, then the increases in profit (over

the 0% reliability) were \$29 (at 6%), \$53 (at 20%) and \$56 (at 57%) per milking cow per year in scenario 2 (50% sexed semen in heifers). The value of the greater reliability of genetic testing is greater when there is more genetic variation. Genomic testing is now the most profitable of the 4 reliabilities that were evaluated. On the other hand, a greater reliability of genetic testing is less valuable when there is less genetic variation in the herd, for example as a result of more inbreeding.

Another consideration is the use of the genetic merit of the service sires. Instead of using genomic testing to capture value from better selection of surplus calves and from better breeding decisions, service sires with greater genetic merit could be used. Again using scenario 2, the PTA of the service sires was varied for the 0%, 6% and 20% reliabilities to obtain the same profit per milking cow per year as with using genomic testing (57% reliability). These changes in PTA were assumed to be free. Changes in the PTAs to obtain the same profit were +\$50 (0% reliability), +\$20 (6%), and -\$6 (20%). In this last case, a sire with a slightly lower PTA could be used than when genomic testing was used. These changes are not large and confirm the importance of first selecting good service sires.

Optimal Breeding Schemes

The breeding schemes in the scenarios 1 to 4 were user-defined based on strategies that seem reasonable, but they are not likely to be optimal. Of interest is the identification of breeding schemes that result in the greatest profitability, given the prices and other inputs. The best breeding scheme generates the greatest profitability. This means finding the optimal combinations of semen type (sexed, conventional, beef) per service number and per parity. The herd budget model can search for these best breeding schemes. A constraint is that at least enough dairy heifer calves must be created to replace culled cows. Cow cull rate was kept at 35%.

Figure 1 shows results from an analysis where the premium for crossbred calves was set at +\$75, +\$150 and +\$225 over the sale price of purebred dairy calves. The top part has a user-defined breeding scheme where the top 60% of heifers were bred with sexed semen (se). The bottom 50% of second parity and older cows were bred with beef semen (be). All other breedings in heifers and cows were with conventional semen (co). This scheme resulted in the creation of just enough dairy heifer calves to replace culled cows but there was no surplus.

Profit per milking cow per year increased with a greater premium for crossbred calves as expected. Genomic testing resulted in a loss of \$5 per milking cow per year for all three premiums. Genomic testing results were used to identify the top 60% heifers to breed with sexed semen, and the bottom 50% of older cows to breed with beef semen, but not for calf selection.

The bottom part shows results for better breeding schemes. The schemes depend on the premium of crossbred calves and use more sexed semen. Conventional semen is not used at all. The schemes also depend a little on the use of genomic testing or not. Profit per milking cow is increased by \$13 to \$81 compared to the user-defined scheme in the top part of the figure. The better breeding schemes are clearly more profitable than a reasonable user-defined breeding scheme. Genomic testing now adds additional value compared to relying on traditional genetic reliabilities, but the value appears to decrease with the size of the premium.

Crossbred calf premiums

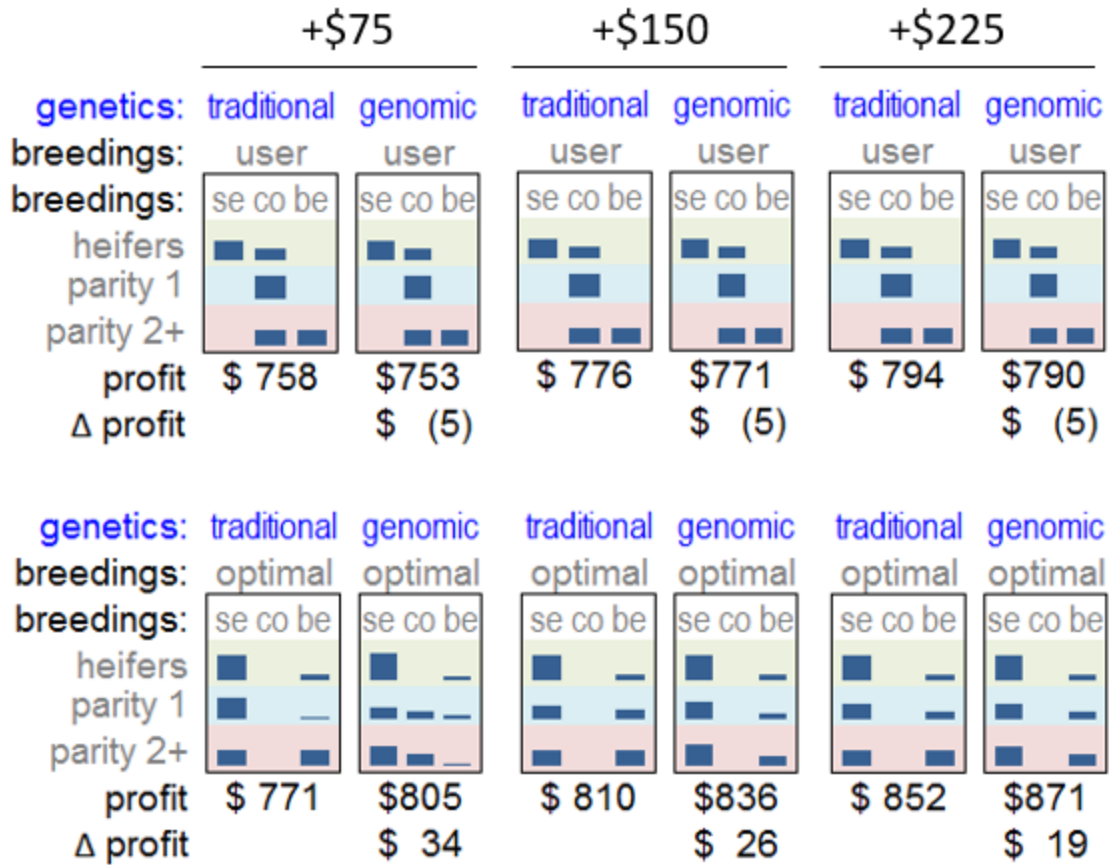


Figure 1. User-defined and optimal breeding schemes and profitability depending on the premiums paid for crossbred calves and the use of genomic testing or traditional genetic reliabilities. The top part has a user-defined breeding scheme where the top 60% of heifers were bred with sexed semen (*se*). The bottom 50% of second parity and older cows were bred with beef semen (*be*). All other breedings in heifers and cows were with conventional semen (*co*). In the bottom part no conventional semen is used although this was an option. Profit is profit per milking cow per year.

Figure 2 shows the effect of greater pregnancy rates ($\approx 14\%$, $\approx 20\%$, $\approx 28\%$) on the profitability and optimal breeding schemes. The set-up is the same as in figure 1. The user-defined breeding scheme used 50% sexed semen in the top heifers and conventional semen elsewhere. The pregnancy rates changed some when more or less sexed semen was used.

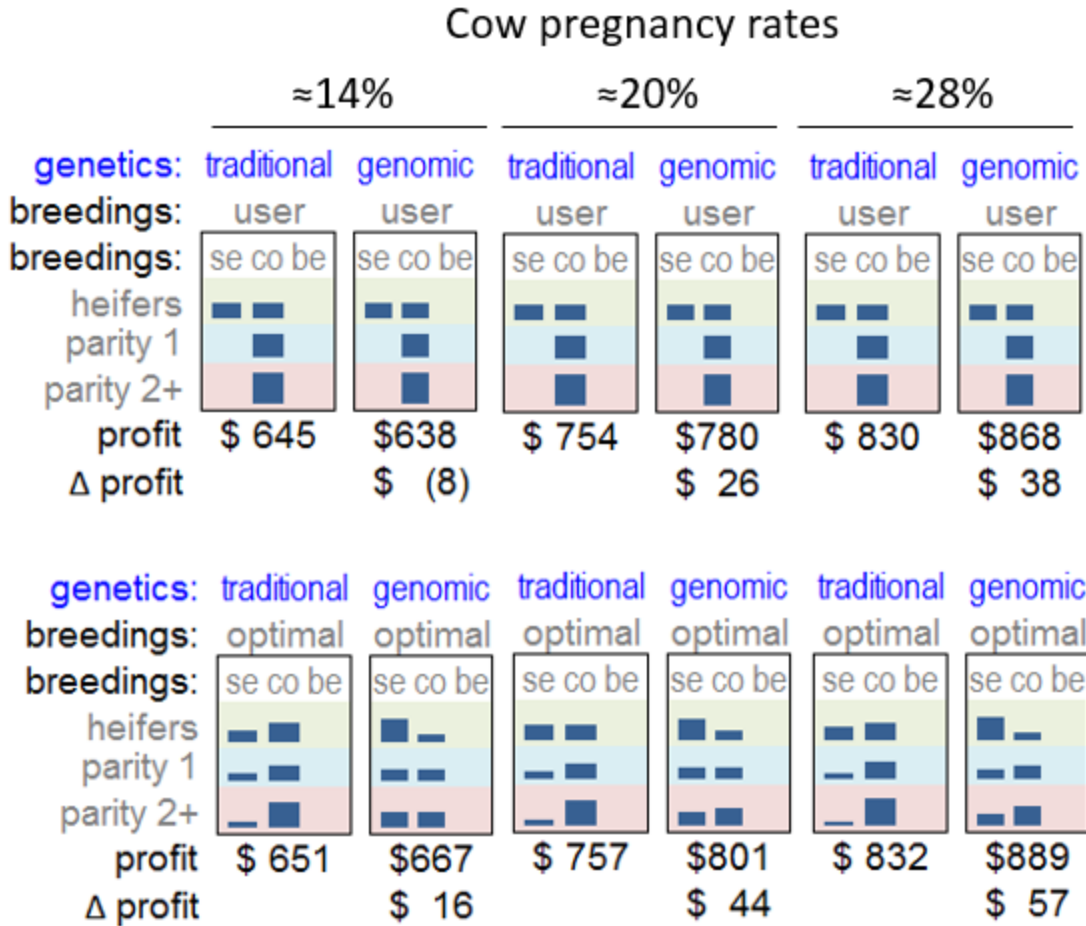


Figure 2. User-defined and optimal breeding schemes and profitability depending on pregnancy rates and the use of genomic testing or traditional genetic reliabilities. The top part has a user-defined breeding scheme where the top 50% of heifers were bred with sexed semen (se). All other breedings in heifers and cows were with conventional semen (co). Beef semen (be) was not allowed to be used. Profit is profit per milking cow per year.

The user-defined schemes show increases in profitability with greater pregnancy rates, as might be expected. Genomic testing was not profitable when pregnancy rate was ≈14% but generates \$38 more profit per milking cow per year when pregnancy rate is ≈28%. At the low pregnancy rate, no surplus calves are available so genomic testing results are only used to select the top 50% of heifers. At the high pregnancy rate, genomic testing is used to select the surplus calves (26% surplus when pregnancy rate is ≈28%) and again to identify the top heifers to breed with sexed semen. There is clearly a strong interaction between the value of genomic testing and the level of reproduction in the herd.

The bottom part of figure 2 shows again increases in profitability over the user-defined scheme in the same situation. Genomic testing results in the use of more sexed semen. Genomic testing is now profitable even at the low pregnancy rate in combination with the use of more sexed semen, which results in a small surplus of dairy calves. At the highest pregnancy rate, genomic testing results in a \$57 increase in profit per milking cow per year compared to no genomic testing.

The optimal breeding schemes were limited to the use of only sexed and conventional semen in figure 2. Beef semen was not allowed to be used to help the comparison with the user-defined scheme. This means that even better breeding schemes are possible when all three breeding types are available at these varying levels of pregnancy rates.

Figure 3 is a first attempt to show when the \$57 increase in profitability with genomic testing and a change in breeding scheme is realized over time. Genomic testing costs are in year 0. Return from genomic testing is realized from a better selection of the dairy heifer calves that are kept in the herd (own extra value), and the offspring from these dairy heifer calves (kept dairy calf value (current)) and even their future offspring (kept dairy calf value (future)). There are also small differences in the number of bull calves (other calves) that are sold when breeding schemes are sold. The small differences in operational profit are the results of the use of more sexed semen, such as the higher cost and lower conception rates. The profit line becomes positive between years 3 and 4 after genomic testing. The genomic test has at that point paid for itself.

Genomic testing costs are in year 0. Return from genomic testing is realized from a better selection of the dairy heifer calves that are kept in the herd (own extra value), and the offspring from these dairy heifer calves (kept dairy calf value (current)) and even their future offspring (kept dairy calf value (future)). Small effects are differences in the number of bull calves (other calves) that are sold. Differences in operational profit are the results of the use of more sexed semen, such as the higher cost and results from lower conception rates. The profit line becomes positive between years 3 and 4 after genomic testing.

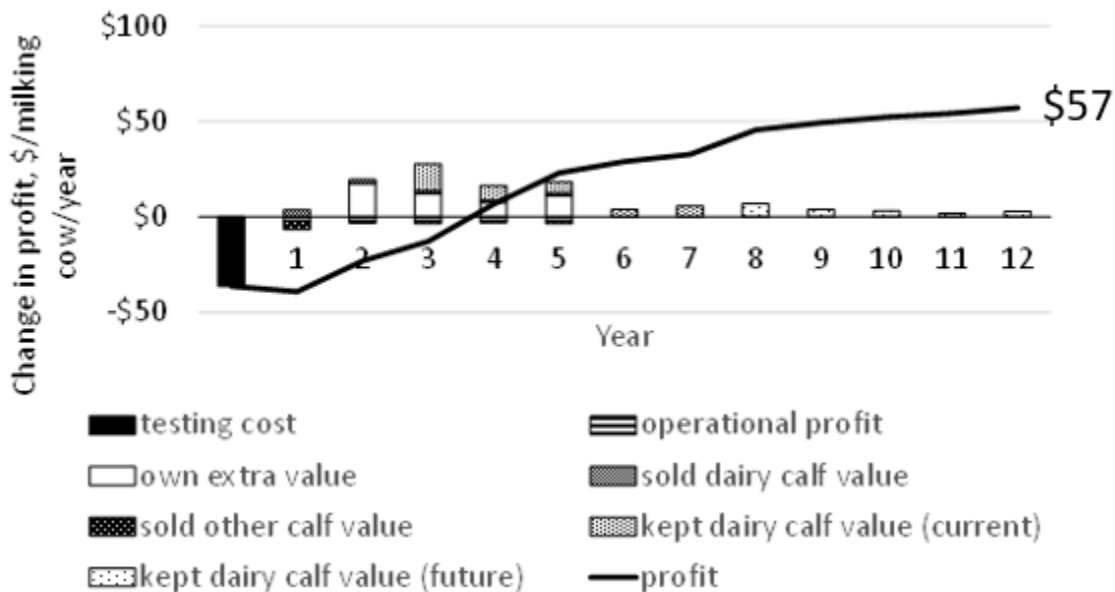


Figure 3. Decomposition of the \$57 increase in profit per milking cow per year from the use of genomic testing and the optimal breeding scheme compared to the optimal breeding scheme used with traditional reliabilities. Pregnancy rate is $\approx 28\%$.

Avoiding Inbreeding

Another value of genomic testing, not included in the breeding schemes above, is the ability to correct parent misidentification errors. The DNA analysis of the genomic test flags animals that are reported to have one or both different parents. The average national misidentification rate is thought to be around 15% but large variations exist between farms. Misidentified females could more likely be mated to closely related sires which increases inbreeding. Cassell (1999) estimated the economic loss per 1% greater inbreeding in a cow at approximately \$25 in her lifetime. This value was recently also obtained by USDA. This value is likely underestimated because inbreeding might lead to earlier losses such as a lower calving rate following a mating of related animals. The calculation in table 3 assumes that 80% of the misidentified cases are resolved with genomic testing. On the left is the level of misidentification before and after the genomic test. All animals are tested because it is not known which animals are misidentified. Genomic test costs are not included. In the center block is the economic loss per tested animal that is avoided depending on the amount of inbreeding that is avoided. For example, if 15% of the dairy calves are misidentified, and these 12% now correctly identified calves are mated to sires that are less related, resulting in offspring that is 1% less inbred, the economic loss avoided is \$3 per tested calf. These values are generally too low to warrant genomic testing only for correction of misidentification errors.

Table 3. *Avoided lifetime economic loss per calf from correcting misidentification errors in the herd. Results are per tested animal and all animals are tested.*

<u>misidentification</u>		\$25 : reduction in lifetime profit per 1% inbreeding				
before	after	80% : misidentification resolved by genomic test				
genomic	genomic	1 : number of female calves born during lifetime				
test	test	inbreeding avoided				
		4%	3%	2%	1%	0%
5%	1%	\$4	\$3	\$2	\$1	\$0
10%	2%	\$8	\$6	\$4	\$2	\$0
15%	3%	\$12	\$9	\$6	\$3	\$0
20%	4%	\$16	\$12	\$8	\$4	\$0
25%	5%	\$20	\$15	\$10	\$5	\$0
30%	6%	\$24	\$18	\$12	\$6	\$0
50%	10%	\$40	\$30	\$20	\$10	\$0
100%	20%	\$80	\$60	\$40	\$20	\$0

Culling and Genetic Improvement

The analyses above assumed a fixed annual cull rate to avoid the complicated effects of more or less voluntary culling. There is an economic trade-off between genetic improvement and cull rate in dairy cattle (reviewed in De Vries (2015, 2017) and partly restated here). Primarily as a result of genomic testing and shortening of the generation interval, the genetic improvement in sires used for AI is increasing faster compared to a decade ago. The genetic merit of replacement heifers is also

increasing faster and the genetic lag with older cows in the herd increases. Asset replacement theory says that this should trigger greater cow culling to capture this greater genetic improvement in heifers. On the other hand, lower culling rates are often viewed favorably because the costs and environmental impact to maintain herd size are generally lower.

The annual increase in average EBV of NM\$ of Holstein sires is accelerating from \$70/year when the sire entered AI around 2002 to \$171/year for sires that entered AI around 2012. The expectation is therefore that heifers born in 2015 are at least \$50 more profitable per lactation than heifers born in 2014.

Few studies have investigated the direct effects of genetic improvement on optimal cull rates. A 35-yr old study found that the economically optimal cull rates were in the range of 25% to 27%, compared to the lowest possible involuntary cull rate of 20%. There was only a small effect of using the best surviving dams to generate the replacement heifer calves. Genetic improvement from sires had little effect on the economically optimal cull rate. Another study that optimized culling decisions for individual cows also showed that the effect of changes in genetic improvement on optimal annual cull rates was relatively small. Reduced involuntary cull rates improved profitability, but also increased optimal voluntary culling. Finally, an economic optimal culling model with prices from 2015 confirmed that optimal annual cull rates were fairly insensitive to genetic improvement in heifers (De Vries, 2015). These studies concluded that the economic optimal cull rates continue to depend more on cow depreciation than on accelerated genetic improvement in heifers.

A point of consideration is the true cost of raising additional heifers, assuming the breeding scheme and good management are able to generate more heifers. Heifer purchase prices in 2015 in the 8 western regions in the US ranged from \$1,719 to \$2,251 (Frazer LLP, 2016). The cost of raising a heifer is often said to be more than \$2,000 in the eastern US. However, when raising the farm's own heifers, the raising cost for additional (marginal) heifers should not include fixed costs when there is room in the facilities and labor supply to raise these heifers with no extra expenses than feed, health care, and breeding. In some cases, raising more heifers may not be very expensive and might warrant a higher cow cull rate, especially when beef prices are strong. This would reduce the number of surplus dairy heifer calves.

A preliminary analysis with the herd budget model looked at the economics of raising all heifers and a variable cow cull rate vs. selling surplus heifer calves and a fixed cow cull rate (De Vries, 2016). Genetics was included. The analysis also included increases in pregnancy rate from 15% to 35% and some sexed semen. More heifer calves were born when pregnancy rates were increased. The results showed that selling surplus dairy heifer calves while maintaining a fixed cull rate was a more profitable strategy than forcing all heifers into the herd by increasing cow cull rate. The advantage of the fixed cull rate strategy was greater when pregnancy rates increased. The higher the pregnancy rate, the higher the cow cull rate in the variable cull rate strategy. This also resulted in more first parity cows and therefore fewer older but higher producing cows. On the other hand, the genetic level was higher in the variable cull rate strategy.

These results are preliminary because results will depend greatly on heifer raising and selling prices, and cow cull prices. Also, average cows within the parity were culled in the analysis where in practice the worst cows will be culled which raises the average performance of the remaining cows that stay in the herd. These comprehensive analyses are difficult to do well.

Discussion

A proper exploration of the value of innovative breeding schemes has proven to be challenging. In part this is because it is difficult to put all important factors correctly in a model so they can be analyzed together and a bottom line profitability can be calculated. Further, the best combinations are not always absolutely best because the optimization software that was used struggles with non-linear models. More capable (and expensive) optimizers should be used. But practical decision making aids are being developed. What is also not yet completed is a structured sensitivity analysis to find which factors affect the best breeding schemes the most. We are only recently learning how to do this well.

More importantly, the best combination of genomics, semen type and culling depends on many factors that are farm dependent such as the level of reproduction efficiency and health of the herd. Prices also play a major role, such as the sale and purchase prices of heifers, cow cull prices, and premiums for crossbred calves. These prices are volatile and may have changed greatly from the time when breeding decisions were made to the time when calves are born 9 months later. What was best then is likely no longer best. Difficult to quantify is the importance of having enough own raised heifers for biosecurity, risk aversion, and expansion reasons. Other options that should be considered are the use of embryo transfer and breeding policy in terms of voluntary waiting period and do-not-breed. This is currently work in progress.

Take Home Messages

- Genomic testing of females on the farm can be profitable, depending on the fraction surplus heifers that can be created and smart breeding decisions regarding the use of sexed and beef semen.
- Better reproduction makes innovative breeding schemes more profitable.
- Best breeding schemes are dependent on prices that are volatile, unfortunately.
- Recent increases in annual genetic progress in sires compared to a decade ago should increase cow culling by a few percentage points at most.
- The opportunity cost of not innovating breeding schemes is greater than a decade ago.
- Seek professional help to discover and implement an innovative breeding scheme that combines components of genomics, various semen types, and voluntary culling while protecting the farm's risk.

Acknowledgment

The model development and analyses in this study were financially supported by USDA NIFA AFRI grant award 2013-68004-20365 titled "Improving Fertility of Dairy Cattle Using Translational Genomics".

References

Calus, M. P. L, P. Bijma, and R. F. Veerkamp. 2015. Evaluation of genomic selection for replacement strategies using selection index theory. *Journal of Dairy Science* 98:6499-6509.

- Cassell, B. G. 1999. Effect of inbreeding on lifetime performance of dairy cows. WCDS Advances in Dairy Technology 11:13-23. Available at <http://www.wcds.ca/proc/1999/>
- De Vries, A. 2015. Culling/longevity versus genetic progress from heifers. WCDS Advances in Dairy Technology 27:345-355. Available at <http://www.wcds.ca/proc/2015/>
- De Vries, A. 2016. What is the optimal pregnancy rate? Is being too efficient a benefit or hindrance? Pages 5-13 in: Proceedings Dairy Cattle Reproduction Council, Columbus, OH.
- De Vries, A., H. Dechassa, and H. Hogeveen. 2016. Economic evaluation of stall stocking density of lactating dairy cows. Journal of Dairy Science 99:3848–3857.
- De Vries, A. 2017. Economic trade-offs between genetic improvement and longevity in dairy cattle. Journal of Dairy Science (in press)
- Frazer LLP. 2016. Dairy Farm Operating Trends. December 31, 2015. Available at <http://frazerllp.com/resources/dairy-farm-operating-trends/>
- Hjorto, L., J. F. Ettema, M. Kargo, and A. C. Sorensen. 2015. Genomic testing interacts with reproductive surplus in reducing genetic lag and increasing economic net returns. Journal of Dairy Science 98:646-658.
- Hutchison, J. L., D. M. Bickhart. 2016. Sexed-semen usage for Holstein AI in the United States. Journal of Dairy Science. 99(E-Suppl. 1)/Journal of Animal Science. 94(E-Suppl. 5):176(abstr. 0372). Available at <https://www.ars.usda.gov/research/publications/publication/?seqNo115=327370>
- Weigel, K. A., A. A. Mikshovsky, and V. E. Cabrera. 2015. Effective use of genomics in sire selection and replacement heifer management. Proceedings Western Dairy Management Conference, Reno, NV. Available at <http://wdmc.org/2015/Weigel.pdf>

Notes:

Notes: