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Stochastic dynamic simulation modeling including multitrait genetics to estimate genetic, technical, and financial consequences of dairy farm reproduction and selection strategies

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ABSTRACT

The objective of this study was to develop a daily stochastic dynamic dairy simulation model that included multitrait genetics and to evaluate the effects of reduced genetic models and various reproduction and selection strategies on the genetic, technical, and financial performance of a dairy herd. The 12 correlated genetic traits included in the 2014 lifetime net merit (NM$) index were modeled for each animal. For each animal, a true breeding value (TBV) for each trait was calculated as the average of the sire's and dam's TBV, plus a fraction of the inbreeding and Mendelian sampling variability. Similarly, an environmental component for each trait was calculated and was partitioned into a permanent and a daily (temporary) effect. The combined TBV and environmental effects were converted into the phenotypic performance of each animal. Hence, genetics and phenotypic performances were associated. Estimated breeding values (EBV) were also simulated. Genetic trends for each trait for the service sire were based on expected trends in US Holsteins. Surplus heifers were culled based on various ranking criteria to maintain a herd size of 1,000 milking cows. In the first 8 scenarios, culling of surplus heifers was either random or based on the EBV of NM$. Four different genetic models, depending on the presence or absence of genetic trends or genetic and environmental correlations, or both, were evaluated to measure the effect of excluding multitrait genetics on animal performance. In the last 5 scenarios, the full genetic model was used and culling of surplus heifers was either random or based on the EBV of NM$ or the EBV of milk. Sexed semen use and reliability of the EBV were also varied. Each scenario was simulated for 15 yr into the future. Results showed that genetic models without all 12 genetic trends and genetic and environmental correlations provided biased estimates of the genetic, technical, and financial performance of the dairy herd. Average TBV of NM$ of all cows in the herd was $263 greater in yr 15 in a scenario that combined sexed semen use in heifers and culling of surplus heifers with the lowest EBV of NM$, compared with a scenario that used only conventional semen and surplus heifers were culled randomly. The average TBV of daughter pregnancy rate of all cows in the herd was 1.25 percentage points greater in yr 15 in a scenario that combined using sexed semen in heifers as well as culling of surplus heifers ranked by EBV of NM$, compared with a scenario using conventional semen only as well as culling surplus heifers ranked by EBV of milk. In conclusion, the multitrait genetics model resulted in improved estimates of genetic, technical, and financial effects and appears useful to evaluate consequences of various reproduction and selection strategies within a dairy farm.

Key words: multitrait genetics, modeling, selection, profit

INTRODUCTION

Reproductive technologies such as automated estrus detection, ovulation synchronization, sexed semen, and in vitro produced embryo transfer may allow for the creation of more dairy heifer calves than are needed to replace culled cows. Another recent technology is genomic testing to obtain more reliable breeding values, which may assist with culling and breeding decisions, among other uses (Schrooten et al., 2005; Weigel et al., 2012; Calus et al., 2015).

The combination of reproductive and genomic technologies creates options and allows for various synergistic strategies on dairy farms (Georges and Massey, 1991; Pryce and Daetwyler, 2012). For example, sexed semen might be used on the genetically better heifers and cows, and beef semen could be used on genetically worse cows. Genomic testing might be applied to some animals but not all. In some cases, the best strategy might be to raise many dairy calves and increase

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cow culling. The outcome of these strategies may be measured by farm profitability, combined with desired changes in the genetics of the herd. Optimal or near optimal strategies are not readily evident and depend on many farm specific factors. Our interest is in finding such strategies.

Several simulation studies have evaluated the economic benefits of some strategies, such as the combined use of sexed and conventional semen (Olynk and Wolf, 2007; De Vries, 2008) or combinations of estrus detection and ovulation synchronization (Galvão et al., 2013). Heikkilä and Peippo (2012) used linear programming to maximize profitability of milk production by finding an optimal combination for simultaneous use of different reproductive technologies in a dairy herd. None of these studies considered genetic changes over time, however.

Ettema et al. (2011) showed that including genetic progress in milk production was necessary when studying reproductive strategies in dairy herds. Studies that included genetic functions and explored genetic trends dependent on management decisions are scarce, however. Van Arendonk (1985), Dijkhuizen et al. (1986), Ghavi Hossein-Zadeh et al. (2010), and Ettema et al. (2011) incorporated some genetic progress while studying reproductive or replacement management decisions, but only for milk component traits. Genetic changes in functional traits were not considered.

Hjortø et al. (2015) and Calus et al. (2015) explored the value of genomic testing of females for either different breeding strategies or for selecting different proportions of available replacement heifers, respectively. These studies used selection index theory and a single composite trait such as a selection index. Hjortø et al. (2015) combined a simulation model without genetics with another model that mimicked genetic selection over time. Genetic merit did not affect the phenotypic performance of animals in their herd directly.

Our hypothesis is that studies that include genetic change in a single trait, but do not consider correlated changes in other traits, will yield biased results because genetic change and ensuing phenotypic change in the correlated traits are unaccounted for. For example, increased focus on milk yield that is negatively genetically correlated with fertility will result in reduced gains in fertility. To study the genetic, technical, and financial consequences over time of selection focused on individual traits, it is necessary that such traits affect the phenotypic performance of the animal. Each of the individual traits ideally is modeled separately and affects the phenotype. The model should also account for genetic and environmental correlations among traits. VanRaden and Cole (2014) described 12 such correlated traits included in the lifetime net merit (**NM$**) index.

Our objectives in this study were to (1) create and describe a model that incorporates genetics of 12 correlated traits included in the NM$ index, with the capability to estimate the genetic, technical, and financial performance of a dairy herd over time, (2) illustrate how a multitrait genetics model produces different technical and financial results than models that do not consider genetic trends in some traits or ignore genetic and environmental correlations, and (3) illustrate differences in trends in genetic, technical, and financial performance of herds using different selection criteria for culling of surplus heifers. Some sexed semen is used to increase selection intensity. An evaluation of many plausible management strategies, which include for example in vitro fertilization and embryo transfer or the use of beef semen, was beyond the scope of this study.

MATERIALS AND METHODS

Overview of the Model

Our purpose was to develop a model that would mimic the behavior and technical and financial results of a herd of females on a dairy farm over time. The performance of these females was subject to biological variation, herd management, and genetic changes in multiple traits in the herd. Genetic changes resulted from breeding heifers and cows to genetically better sires and selection of genetically better females to become dams to produce the next generation of females. Hence, reproduction and female selection strategies within the herd affected the genetics of future generations. Changes in genetics affected the performance of the individual animals and consequently the herd's technical results over time, such as, for example, milk production, feed intake, reproduction success, and culling. The financial results were calculated from the technical results.

Detailed modeling of biological performance was desired to mimic the behavior and outputs of the herd over time as realistic as possible. Therefore, a stochastic, dynamic Monte Carlo simulation model based on event-scheduling principles in an earlier model (De Vries and Conlin, 2003) was built in JAVA SE 8 (Oracle Corp., Redwood Shores, CA). Each individual animal in the herd was simulated on a daily basis over time. An animal existed in the model from its creation as an embryo to its removal from the herd, either by death or culling. Animals were embryos, heifers, or cows.

Each animal had 55 attributes that remained unchanged throughout its life (e.g., its genetic traits). Each animal also had 72 attributes that either could change daily (e.g., age, BW, milk yield) or when a particular event happened (e.g., abortion, estrus, conception, calving). The model was stochastic because the occurrence of events such as estrus detection, conception, abortion, sex, and viability of the calf, involuntary culling, and death were decided based on random variates drawn from relevant probability distributions obtained from the literature and described later. These probability distributions were originally developed to mimic the performance of similar dairy females as modeled in our study. Some unchanged attributes, such as the value of genetic traits, were also partly based on random variates when the embryo was created.

Some user inputs directed the phenotypic performance of animals over time, such as probabilities of conception, lactation curves, and BW functions. Seasonal effects were excluded to maintain simplicity as much as possible. Other user inputs directed herd management, such as herd size, voluntary waiting period for first insemination, and voluntary culling decisions. Inputs were chosen to represent a Holstein dairy farm in the United States in 2015. Management decisions, for example culling of older cows to accommodate calving heifers, were not dependent on prices. Instead, prices were applied to model outputs, such as the amount of milk produced and the number of cows sold, which allows for rapid and convenient sensitivity analyses because running the model was time consuming.

Actual daily phenotypic performance of an animal was the sum of standard phenotypic functions, and genetic and environmental deviations. Standard phenotypic functions describe the biological performance of an animal when all its genetic and environmental deviations are 0. Standard phenotypic functions for reproduction, culling, milk production, BW, and DMI were taken from previous studies of similar dairy models. The new genetic and environmental methods that produced genetic and environmental deviations are described in greater detail below. Simulations were run for 30 yr from d −5,475 (−15 yr) to d 5,475 (+15 yr) to calculate the genetic, technical, and financial performance of the herd over time.

Standard Phenotypic Functions

Reproduction. The reproductive process involved a cycle of events that included estrus, insemination, ovulation, conception, embryonic loss, abortion, and calving. In heifers, first ovulation occurred randomly between 300 and 320 d of age. Time to first ovulation after calving occurred randomly between 20 and 50 d. Voluntary waiting periods for first insemination were set at 400 d of age for heifers and 50 DIM for cows (Galvão et al., 2013). The length of all estrus cycles were set by a truncated normal distribution with high, mean, low, and standard deviation values of 28, 21.5, 14, and 2.5 d, respectively (De Vries and Conlin, 2003). Probability of estrus detection after the voluntary waiting period was 50% for heifers and cows. Inseminations continued in nonpregnant heifers until 200 d after the end of the voluntary waiting period. Nonpregnant cows that passed the peak day of milk production were inseminated until they became pregnant or milk yield excluding the daily temporary environmental effect was <20 kg above the average genetic deviation for daily milk yield in the herd, after which they were assigned a known reproduction status of “do not breed.” This moving cutoff based on increasing amounts of milk yield was used to account for the genetic increase of milk production over time.

The standard phenotypic probability of conception, defined as probability of pregnancy at 35 d after insemination, was 60% in heifers at first insemination, and decreased by 5 percentage points with each subsequent insemination, with a minimum probability of conception of 45% for conventional semen. For cows, the probability of conception was set to 35% for all inseminations (Galvão et al., 2013). When sexed semen was used, the probability of conception was set at 80% of the probability of conception of conventional semen based on Seidel (2007).

A new embryo was created at conception and the estrus cycle was suspended. A new ovulation was scheduled if conception did not occur or abortion occurred. The daily risk of abortion (loss of the conceptus after d 35 since conception) in pregnant heifers and cows was set at 0.029 and 0.042%, respectively, to ensure that approximately 5% of heifers and 10% of cows aborted (Santos et al., 2004). A stillbirth rate of 3% was assumed based on Meyer et al. (2001). Gestation length was set to 280 d. Pregnancy diagnosis occurred at 42, 60, and 220 d after insemination. Heifers and cows were known to be “bred” after insemination, until pregnancy diagnosis qualified cows as “open” or “pregnant.” Known pregnancy status was used for making culling decisions. For simplicity, we assumed 100% accuracy of pregnancy diagnosis.

Culling. The standard phenotypic daily death and live culling probabilities were calculated separately for open and pregnant animals. The daily risk of death and live culling for pregnant heifers was 0.005 and 0.008% respectively, based on Pinedo and De Vries (2010). The daily probability of death for open heifers was 0.007% until d 46 of age and 0.006% thereafter. The daily probability of live culling for open heifers was 0% until 123 d of age and 0.009% thereafter. Probabilities of live culling and death were modeled separately for parities 1 and 2 based on Pinedo et al. (2010). Daily culling probabilities for parities greater than 2 increased with parity, that is, by 25% for parity 3 up to an increase of 98% for parity 6 when compared with the culling probabilities for parity 2.

Male calves were sold on the day after they were born. Heifers not pregnant at 600 d of age were culled immediately. Cows assigned "do not breed" status were kept until they were culled as a result of rebalance culling as described later. Cows that were not pregnant at 1,000 d after last calving were culled. Cows that calved for the seventh time were culled. All born-alive female calves were initially kept to be raised but some female calves were culled as surplus heifers as described later.

Body Weight. Standard BW functions for Holsteins were based on growth curves for young stock (Pennsylvania State University Dairy Extension, 2013) and cows (Galvão et al., 2013), which depended on parity, age, days since calving, and days pregnant.

Milk Production and Components. Standard phenotypic functions for daily milk, fat, and protein production were calculated based on modified Wood (1967) lactation curves (De Vries and Conlin, 2003) with parameters taken from Dematawewa et al. (2007) for parities 1, 2, and $\geq$3. The 305-d milk yields for these curves were 9,472, 10,819, and 11,136 kg for parities 1 to $\geq$3. Average 305-d fat yield and protein yields were 414 and 315 kg, respectively. The arithmetic average of 305-d SCS for the first 3 parities was 3.35, based on functions in Morant and Gnanasakthy (1989). Cows were dried off on d 220 of pregnancy if known to be pregnant.

Dry Matter Intake. Standard phenotypic DMI was calculated daily for heifers based on data provided by Pennsylvania State University Dairy Extension (2013) and for cows based on NRC (2001) equations, which depended on DIM, milk yield, fat yield, and BW. Dry cows consumed 12.5 kg of DM daily.

Genetic and Environmental Functions

General Approach. The standard phenotypic probabilities of conception and culling, milk yield, fat, protein, and SCS were affected by genetic and permanent and temporary environmental deviations from 0. An animal's genetic deviations were based on the animal's true breeding values (**TBV**) of the traits. Genetic and permanent environmental deviations stayed the same during an animal's life. Temporary environmental deviations changed daily.

Each animal had 12 genetic traits included in the NM$ index 2014 (VanRaden and Cole, 2014). The traits, standard deviations, phenotypic and genetic and phenotypic correlations, and economic values were taken from the same research report. It was assumed that the genetic standard deviations and correlations of the TBV were the same as those reported for the EBV with high reliabilities in VanRaden and Cole (2014).

Using matrix notation, $\mathbf{P} = \mathbf{G} + \mathbf{E}$, where $\mathbf{P}$ is the phenotypic (co)variance matrix, $\mathbf{G}$ is the genetic (co)variance matrix, and $\mathbf{E}$ is the environmental (co)variance matrix (Mrode, 2014) of the 12 traits. The $\mathbf{P}$ and $\mathbf{G}$ matrices were calculated directly from data in VanRaden and Cole (2014). It was assumed that $\mathbf{E} = \mathbf{Ep} + \mathbf{Et}$ where $\mathbf{Ep}$ is the permanent environmental (co)variance matrix and $\mathbf{Et}$ is the temporary environmental (co)variance matrix. The partition of $\mathbf{E}$ into $\mathbf{Ep}$ and $\mathbf{Et}$ was constructed as follows. The diagonal elements of $\mathbf{Ep}$ (permanent environmental variances) were computed as t × phenotypic variance − genetic variance for each trait, where t is the intra-class correlation (Mrode, 2014), which we assumed to be equal to the square root of the heritability of each trait, given by VanRaden and Cole (2014). The off-diagonal elements of $\mathbf{Ep}$ (permanent environmental covariances between pairs of traits) were computed as the product of the permanent environmental correlation between 2 traits times the square root of the product of the permanent environmental variances of these 2 traits. Permanent environmental correlations for $\mathbf{Ep}$ and $\mathbf{E}$ were assumed to be the same. Finally, $\mathbf{Et} = \mathbf{E} - \mathbf{Ep}$.

The 12 traits were assumed to be 12-dimensional multivariate normally distributed with a mean vector equal to 0 and covariance matrices of $\mathbf{G}$, $\mathbf{Ep}$, or $\mathbf{Et}$. A vector of 12 genetic ($\boldsymbol{\Delta}\mathbf{G}$), permanent environmental ($\boldsymbol{\Delta}\mathbf{Ep}$), or temporary environmental ($\boldsymbol{\Delta}\mathbf{Et}$) deviations from 0 were generated for an animal by multiplying the Cholesky decomposition of the respective matrix by a vector of uncorrelated standard normal random variates (Kelton and Law, 2000).

Genetics of Females in the Herd. At the start of a simulation on d −5,475, a herd of unrelated 280-d pregnant heifers was generated. For each heifer, a vector of 12 genetic deviations ΔG_{ik} was generated, where i is animal and k is trait. The TBV were calculated as $TBV_{ik} = \mu_k + \Delta G_{ik}$, where μ_k is a fixed vector of constants such that after 5,475 d of simulation and genetic increase driven by the genetic trends in the service sires, the average TBV of the 12 genetic traits of the cows in the herd in yr 0 were approximately 0.

The TBV of the unborn calves, and of any future embryo in the model, were calculated for each trait k as follows (Ghavi Hossein-Zadeh et al., 2010; de Roos et al., 2011; Eikje et al., 2012): $TBV_{ik} = 1/2\ (TBV_{sk} + TBV_{dk}) + \sqrt{}\ (0.5 \times [1 - (F_s + F_d)/2)] \times MS_{ik}$, where TBV_{ik}, TBV_{sk}, and TBV_{dk} are the TBV of animal i with sire s and dam d, respectively, for trait k, and MS_{ik} is the Mendelian sampling effect for the kth trait. The Mendelian sampling effect was calculated the same way as ΔG. Dominance and epistasis effects were assumed to be 0. The F_s and F_d are the inbreeding coefficients of the sire and dam, respectively. Both F_s and F_d at the start of the simulation were set at 3.5%, to represent the inbreeding level in Holstein cows approximately 15 yr before today based on data from CDCB (2015), with a linear daily increase in inbreeding of 0.0004 percentage units for both cows and sires as per the observed trend in US Holsteins. By d 5,475 (end of simulation), the average inbreeding was 8.45%, which is within range of predicted inbreeding percentage for the Holstein breed in 2030 (Caraviello, 2004).

Genetics of Service Sires. Each day a new service sire was generated and used to mate with eligible females that day. The sire's TBV for each of the 12 traits were generated using the same method as for the pregnant heifers at the start of the simulation. A constant was added to each TBV daily, based on the expected linear trend in genetic change for that trait. From d −5,475 to d 0 of the simulation, 52% of the expected linear trends in VanRaden and Cole (2014) was used to mimic the earlier genetic trend predictions in Cole et al. (2009). The linear trends after d 0 were taken from VanRaden and Cole (2014). Each day the service sire was assigned a sire conception rate randomly taken from a normal distribution with mean 0 and standard deviation 2.7. The sire conception rate affected the probability of conception in each mating as described below.

Phenotypic Performance Affected by Genetic and Environmental Deviations

For each animal i, its daily phenotypic deviations $(\boldsymbol{\Delta}\mathbf{P})_{ik}$ from the values given by the standard phenotypic functions were calculated as $\mathrm{TBV}_{ik} + (\Delta \mathrm{Ep})_{ik} + (\Delta \mathrm{Et})_{ik}$ for the 8 genetic traits of milk yield, fat yield, protein yield, SCS, productive life, daughter pregnancy rate, heifer conception rate, and cow conception rate. Each day, the $(\Delta P)_{ik}$ modified the values from the standard phenotypic functions to mimic each animal's observed phenotypic performance as follows.

The daily (ΔP) for milk, fat, protein, and SCS were added to each standard phenotypic function. The (ΔP) for productive life, expressed in months (VanRaden and Cole, 2014), was converted to a multiplier calculated as $36/(36 + \Delta P)$, which assumes that the standard productive life was 36 mo (3 yr). This value was then multiplied with the probability of culling from the standard phenotypic function. The dam's phenotypic probability of conception could be affected by heifer conception rate, cow conception rate, daughter pregnancy rate, and sire conception rate. Phenotypic deviations for heifer conception rate or cow conception rate were added to the standard functions for probability of conception of heifers and cows, respectively. The (ΔP) for daughter pregnancy rate divided by 0.5 was also added to the standard probability of conception for cows. Here 0.5 was a proxy for the probability of estrus detection. It was assumed that (ΔP) for daughter pregnancy rate did not affect the probability of conception for heifers. Finally, the sire conception rate was added to the probability of conception for both heifers and cows.

The (ΔP) for the remaining 4 composite traits udder, feet and legs, body size, and calving ability in the NM$ index did not directly affect animal performance because it was not clear how those should be modeled. Changes in these traits over time should still be included because they are correlated with the 8 traits that were directly modeled. Therefore, a daily revenue adjustment for each trait for each animal, which was the product of TBV and its economic value divided by 1,095, was calculated. It was assumed that the effects of differences in genetics were expressed during the productive life of an animal which is approximately 1,095 d (3 yr). These revenue adjustments were added to the herd's revenue calculation.

Estimated Breeding Values

Estimated breeding values were calculated for the 12 traits and represented what was known about the genetic merit of the animal for management decisions such as culling of surplus heifers. For each trait k, EBV_k was calculated from a normal distribution with mean $[\mu_k + \sqrt{(\mathrm{reliability}_k)} \times (\mathrm{TBV}_{i,k} - \mu_k)]$ and variance $[(1 - \mathrm{reliability}_k) \times \sigma_k^2]$, and multiplied by $\sqrt{(\mathrm{reliability}_k)}$, where μ_k is the average TBV for the trait k, of all animals in the same parity at the start of the day, $\mathrm{reliability}_k$ is the square of the correlation of the TBV with the EBV for each trait k, and σ_k is the genetic standard deviation.

The reliabilities for young stock EBV were calculated as the sum of the parents' reliabilities for each trait divided by 4 (VanRaden and Wiggans, 1991). Sire reliabilities ranged from a low of 52% for calving ability to a high of 72% for milk, fat and protein based on typical young sire reliabilities (CDCB, 2015). Parent average reliabilities for a calf born out of a nongenotyped heifer ranged from 20% for calving ability to 27% for milk, fat and protein. Genomic reliabilities for heifers ranged from 52% for calving ability to 72% for milk, fat, and protein. In addition, reliabilities were increased for cows based on their parity (Weigel et al., 2012). The increase in reliabilities was added to the existing reliabilities every time the EBV were recalculated.

The EBV of the 12 traits were recalculated every 4 mo during the simulation for all animals to mimic the frequency of the current national genetic evaluation system (CDCB, 2015). The new EBV were autocorrelated with the previous EBV to mimic the likely bias of EBV over time. The EBV of NM$ was calculated as the sum of the multiplication of the EBV of each trait with its economic value (VanRaden and Cole, 2014).

Herd Management

Heifer Selection. Every day, cows might leave the lactating herd through death or involuntary live culling, lactating cows might be dried off, and heifers might enter the herd through calving. Every month a total of 40 heifer calves born in the herd were selected to be raised to replace culled cows. The surplus of heifer calves were culled at an age of 3 to 4 mo after ranking all calves based on genetic criteria such as their EBV of milk or EBV of NM$. Approximately 70% of the total heifer calves born entered the herd as calving heifers. If no calving was expected within 30 d after a cow was culled, then a replacement heifer was purchased from outside the herd. The TBV of the 12 traits of purchased heifers were simulated to be on average similar to those of an average springing heifer in the herd on that day.

Rebalance Culling. The objective of rebalance culling was to maintain approximately 1,000 milking cows in the herd each day. Where there was a surplus of calving heifers on any day, an equal number of nonpregnant cows >90 DIM were sold based on a ranking for the lowest milk yield. The annual cull rate was kept near constant at 33%. Therefore, as involuntary culling in the herd decreased over time due to an increase in the average TBV of productive life, the number of calvings increased due to an increase in the TBV of fertility traits and the amount of involuntary culling in the herd decreased and the rebalance culling increased.

Prices. All input costs and prices are given in Table 1. Prices for milk, feed, labor, supplies, and so on did not affect herd management. This assumption allowed for quick evaluations of effects of changes in prices and costs on the herd's financial performance without the need to rerun the model. The input costs and prices were kept the same across time.

Genetic, Technical, and Financial Outputs. Genetic and technical results were collected daily and summarized by year. Technical and financial outputs were calculated such as pregnancy rates, milk yield per cow per year, number of calves born, and profitability. Genetic lag was defined as the difference between the average TBV of 2 animal classes such as sires, calves, heifers, and cows at the same point in time. Revenue per cow per year was the sum of revenues for milk, fat, protein, SCS penalty or premium, cow and calf sales, and profit deviations calculated for the average TBV of the 4 composite traits body size, feet and legs, calving ability and udder. Variable costs included feed costs, breeding related costs, heifer raising and purchasing costs, and other daily variable costs associated with milking and dry cows. Fixed costs per milking slot were added to obtain a realistic profit per milking cow per year.

Experimental Design

Scenarios. Thirteen scenarios divided into 3 groups were simulated (Table 2). In the first group of 4 scenarios, the effects of the structure of the genetic model on the genetic, technical, and financial performance of the herd were investigated. The first genetic model included the predicted genetic trends, and genetic and environmental correlations in all 12 traits (VanRaden and Cole, 2014) [trends and genetic and environmental correlations: (**T,C**)]. This is the full model described earlier. The second genetic model included predicted genetic trends in all 12 traits but no genetic and environmental correlations between traits (**T,NC**). The third model included genetic trends only for milk, fat, and protein and included genetic and environmental correlations among all 12 traits (**NT,C**). The fourth genetic model included genetic trends only for milk, fat, and protein yields and no genetic and environmental correlations among the 12 traits (**NT,NC**). Expected genetic trends were an input for the service sires but observed genetic changes were a result for the females in the herd depending on reproduction and selection

Table 1. Input prices and costs used for calculating the financial results from the simulation model

Item	$
Milk price per kg of milk	0.07
Fat price per kg of fat	4.30
Protein price per kg of protein	5.47
SCC penalty[1]	−0.019
Cull cow value	800.00
Sold male calf value (at birth)	150.00
Sold female calf value (3–4 mo of age)	600.00
Feed price per kg of DMI (lactating cow)	0.30
Feed price per kg of DMI (dry cow)	0.20
Estrus detection labor per eligible day per animal	0.05
Conventional semen insemination	15.00
Sexed semen insemination	30.00
Pregnancy diagnosis	5.00
Genomic test	40.00
Other variable cost per milking cow per day	0.50
Other variable cost per dry cow per day	0.50
Fixed cost per stall per day	2.00
Purchased replacement heifer cost	2,000.00
Heifer raising cost per day	2.00
Cull price per kg of BW	2.00

[1] Premium or penalty calculated per 1,000 SCC above or below 200,000 cells per kg of milk.

Table 2. Description of 13 scenarios conducted to illustrate the model and to test different reproductive and selection scenarios

Scenario name[1]	Sexed semen use[2]	Rank criteria[3]	Reliability[4]	Genetic trends[5]	Correlations[6]	Group
CRAND_L(T,C)	False	Random	Low	Yes	Yes	1
CRAND_L(T,NC)	False	Random	Low	Yes	No	1
CRAND_L(NT,C)	False	Random	Low	No	Yes	1
CRAND_L(NT,NC)	False	Random	Low	No	No	1
CNM_L(T,C)	False	EBV of NM$	Low	Yes	Yes	2
CNM_L(T,NC)	False	EBV of NM$	Low	Yes	No	2
CNM_L(NT,C)	False	EBV of NM$	Low	No	Yes	2
CNM_L(NT,NC)	False	EBV of NM$	Low	No	No	2
CRAND_H(T,C)	False	EBV of NM$	High	Yes	Yes	3
CNM_H(T,NC)	False	EBV of NM$	High	Yes	Yes	3
CMILK_H(T,C)	False	EBV of milk	High	Yes	Yes	3
SNM_H(T,C)	True	EBV of NM$	High	Yes	Yes	3
SMILK_H(T,C)	True	EBV of milk	High	Yes	Yes	3

[1] Scenario name. C = use of conventional semen in all heifers and cows, S = use of sexed semen in heifers for the first 2 inseminations and conventional semen for all other inseminations. RAND, NM$, and MILK is the rank criteria for selection, where RAND = culling of surplus heifers based on random criteria, NM = culling of surplus heifers based on the lowest EBV of NM$, and MILK = culling of surplus heifers based on the lowest EBV of milk. H, L = high (genomic) or low (parent average) reliabilities with which EBV are calculated.

[2] Sexed semen use. False = no use of sexed semen, true = use of sexed semen only in heifers in the first 2 inseminations.

[3] Rank criteria for heifer ranking and culling.

[4] Reliability of the EBV: low = no use of genomic testing, or high = use of genomic testing.

[5] Genetic trend: yes = presence of genetic trends in all 12 traits; no = absence of genetic trends in 9 traits except for milk, fat, and protein.

[6] Correlations: Yes = presence of genetic and environmental correlations among the 12 traits used in the model, No = no genetic and environmental correlations among 12 traits used in the model.

strategies. The absence or presence of genetic and environmental correlations was an input for both service sires and females. In these 4 scenarios, only conventional semen was used, surplus heifers were ranked randomly before culling, and low parent average reliabilities were used for EBV calculations (conventional, random, low: **CRAND_L**).

The second group of 4 scenarios included the same 4 genetic models as in the first group. Surplus heifers were ranked based on their EBV of NM$, calculated with low reliabilities, before culling. Only conventional semen was used (**CNM_L**). The difference between the first 2 groups might show an interaction between the genetic model and the way surplus heifers were ranked and sold.

In the third group of scenarios, 5 reproductive and replacement strategies were simulated with the full [i.e., (T,C)] genetic model. These 5 scenarios aimed to illustrate the effect of surplus heifer culling and reproduction strategy on genetic composition, and technical and financial performance of the herd over time. Surplus heifers were identified by ranking them by 1 of 5 different ways. First, ranking was random along with the use of conventional semen and genomic reliabilities (**CRAND_H**). This is similar to CRAND_L except that heifers had greater EBV reliabilities in this scenario. No decisions were affected by genomic testing in this scenario, but costs increased. Second, ranking was based on the EBV of NM$ with genomic reliabilities along with the use of conventional semen (**CNM_H**). Third, ranking was based on the EBV of milk with genomic reliabilities along with use of conventional semen (**CMILK_H**). Fourth, ranking was based on the EBV of NM$ with genomic reliabilities along with the use of sexed semen in heifers for the first 2 inseminations and conventional semen for all other inseminations (**SNM_H**). Fifth, ranking was based on the EBV of milk with genomic reliabilities along with the use of sexed semen in heifers for the first 2 inseminations (**SMILK_H**). These scenarios which use the EBV of NM$ or milk to cull surplus heifers are analogous to scenarios where the farmer's breeding goal is to maximize the TBV of NM$ or milk through heifer culling, respectively.

Simulations

The first stage, d −5,475 to −1,825 (10 yr), were used as burn-in time to create a steady-state herd from the arbitrarily set starting herd with the CRAND_L(T,C) scenario. This is the default scenario. Herd demographics on d −1,825 were visually inspected and judged to be independent of the herd demographics at the start of the simulation. The second stage, from d −1,824 to 0 (5 yr), continued the default scenario while herd output statistics were obtained. In the third stage, from d 1 to 5,475 (15 yr), the 13 scenarios shown in Table 2 were simulated and herd output statistics were obtained. One hundred replicates were simulated in the second and third stages for each scenario so that the standard error for all herd output statistics was <0.1% of the absolute value observed and simulation time was still manageable. One hundred simulations of one scenario took on average 32 h on the University of Florida's HiPerGator computer.

The procedure GLM in SAS version 9.4 (SAS Institute Inc., Cary, NC) was used for one-way ANOVA of output statistics among the scenarios. Scenario was included as a fixed effect.

RESULTS

The average TBV and standard deviation of the 12 genetic traits and NM$ for sires and cows across all parities in year 0 (d −364 to d 0) for the default CRAND_L(T,C) scenario are shown in Table 3. Average TBV for cows were not exactly 0 for any trait, because the starting TBV at d −5,475 had to be estimated for each trait. A genetic lag of $556 in the TBV of NM$ between sires and the average cow in the herd was observed in yr 0. The genetic lag of TBV of NM$ between sires and average heifers at birth and at calving was $289 and $421, respectively. Likewise, the genetic lag with the sires for the other 12 genetic traits increased with the age of the animals. Cow pregnancy rate was 21%, average days open was 154, average DIM was 222, milk yield was 10,394 kg/cow per yr and the annual cull rate was 30% in yr 0.

Effect of Genetic Models

The 4 genetic models affected the average TBV of the 12 traits (Tables 4 and 5). The differences depended on the criteria used to rank and cull heifers. When there were no genetic trends in traits except for milk, fat, and protein [the (NT,C) and (NT,NC) genetic models], the average TBV of the 9 traits without genetic trends in cows increased to the level of the sire's TBV for those traits in yr 0. Technical and financial outputs (Tables 4 and 5) followed the same trends as the average TBV of the 12 traits. Genetic models without genetic trends (other than in milk, fat, and protein) had lower cow pregnancy rate, milk yield, annual cull rate, surplus female calves sold, and profit compared with genetic models that included all genetic trends. Days open in cows and age of dam at creation of the embryo were greater with these incomplete genetic models. The average DIM was 13 d lower for genetic models that had 12 genetic trends [(T,C) and (T,NC)] when compared with genetic models that did not have genetic trends in 9 of the 12 traits [(NT,C) and (NT,NC)].

Genetic models with no genetic and environmental correlations [(T,NC) and (NT,NC)] had lower average TBV of the 12 traits (indicated by different subscripts in Tables 4 and 5). They also had lower profit per cow per year, milk yield, annual cull rate, percent surplus female calves sold, and age of dam at creation of the embryo. Again days open in cows was greater when compared with the full genetic model (T,C).

Effects of Reliability and Ranking Criteria for Surplus Heifers

Among scenarios with the full genetic model, (T,C), the trait for which the surplus heifers were culled resulted in the strongest response after 15 yr. The greatest

Table 3. Average true breeding values (TBV) and standard deviations of 13 traits for sires and cows in the model in yr 0 just before the start of experiments, under a scenario where surplus heifers were culled randomly with a genetic model that included genetic trends, genetic and environmental correlations among the traits [CRAND_L(T,C)]

		Average TBV[1]		Average SD[1] of TBV	
Genetic trait	Unit	Sires	Cows	Sires	Cows
Milk	kg/305 d	458	−68	614	609
Fat	kg/305 d	25	−4	23	23
Protein	kg/305 d	16	−1	16	16
Productive life	mo	5.08	0.97	4.82	4.83
SCS	log	−0.27	0.00	0.42	0.43
Body size	composite	−0.68	−0.01	2.06	2.06
Udder	composite	0.28	0.15	1.80	1.80
Feet and legs	composite	0.44	0.16	2.08	2.06
Daughter pregnancy rate	%	1.72	1.17	4.61	4.62
Heifer conception rate	%	0.64	0.78	5.54	5.62
Cow conception rate	%	2.51	1.08	4.82	4.85
Calving ability	$	21	3	36	36
Net merit	$	571	15	392	389

[1] Standard errors of the average TBV and average of within-herd SD of all traits were less than 0.1% of the absolute value in all cases.

Table 4. Genetic, technical, and financial performance of the cows in yr 15 under a scenario where surplus heifers were culled randomly under 4 different genetic models[1]

Item	CRAND_L(T,C)	CRAND_L(T,NC)	CRAND_L(NT,C)	CRAND_L(NT,NC)	SEM
Average TBV (all cows)					
Milk (kg/305 d)	1,358^{a}	1,361^{a}	1,327^{b}	1,324^{b}	2.31
Fat (kg/305 d)	71.5^{a}	70.7^{b}	70.6^{b}	69.9^{c}	0.08
Protein (kg/305 d)	46.4^{a}	45.6^{b}	45.7^{b}	44.9^{c}	0.06
Productive life (mo)	13.65^{a}	13.32^{b}	5.22^{c}	4.95^{d}	0.02
SCS (log cells/mL)	−0.78^{d}	−0.75^{c}	−0.06^{b}	−0.03^{a}	2×10^{-3}
Body size composite	−1.99^{d}	−1.89^{c}	−0.80^{b}	−0.69^{a}	0.01
Udder composite	0.64^{a}	0.62^{a}	0.19^{b}	0.14^{c}	0.01
Feet and legs composite	1.01^{a}	0.99^{a}	0.32^{b}	0.28^{c}	0.01
Daughter pregnancy rate (%)	4.26^{a}	3.87^{b}	1.51^{c}	0.97^{d}	0.02
Heifer conception rate (%)	1.83^{a}	1.40^{b}	0.67^{c}	0.24^{d}	0.02
Cow conception rate (%)	6.63^{a}	6.08^{b}	2.42^{c}	1.77^{d}	0.02
Calving ability ($)	60.0^{a}	56.6^{b}	23.0^{c}	19.4^{d}	0.12
Net merit ($)	1,592^{a}	1,552^{b}	1,128^{c}	1,088^{d}	1.35
Technical and financial outputs					
Cow pregnancy rate (%)	30.6^{a}	30.4^{a}	26.3^{b}	25.5^{c}	2×10^{-3}
Cow days open (d)	113.5^{d}	115.4^{c}	131.8^{b}	134.9^{a}	0.41
Milk yield (kg/cow per yr)	12,901^{a}	12,897^{a}	12,615^{b}	12,589^{b}	7.57
Annual cow cull rate (%)	34.7^{a}	34.4^{a}	33.1^{b}	32.8^{b}	2×10^{-3}
Surplus calves sold (%)	17.7^{a}	17.3^{a}	13.2^{b}	12.7^{b}	3×10^{-3}
Age of dam at creation of embryo (d)	1,125^{c}	1,119^{c}	1,165^{a}	1,158^{b}	1.81
Profit ($/cow per yr)	1,464^{a}	1,433^{b}	1,244^{c}	1,205^{d}	2.98

[a–d]Means with different superscripts within a row differ ($P < 0.05$).

[1] Name of scenario: CRAND_L = use of conventional semen in heifers and cows for all inseminations, culling of surplus heifers is random and reliability is low. (T,C) = genetic trend, genetic and environmental correlations in the 12 traits, (T,NC) = genetic trends in all 12 traits and no genetic and environmental correlations among the 12 traits, (NT,C) = no trends in 9 traits except milk, fat, protein, and genetic and environmental correlations among the 12 traits, (NT,NC) = no trends in 9 traits except milk, fat, and protein, and no genetic and environmental correlations among the 12 traits.

Table 5. Genetic, technical, and financial performance of the cows in yr 15, under a scenario where surplus heifers were culled based on the lowest EBV of NM$ under 4 different genetic models[1]

Item	CNM_L(T,C)	CNM_L(T,NC)	CNM_L(NT,C)	CNM_L(NT,NC)	SEM
Average TBV (all cows)					
Milk (kg/305 d)	1,376^{a}	1,369^{a}	1,345^{b}	1,331^{c}	2.26
Fat (kg/305 d)	72.8^{a}	71.6^{b}	71.5^{b}	70.4^{c}	0.09
Protein (kg/305 d)	47.2^{a}	45.9^{c}	46.2^{b}	45.3^{d}	0.06
Productive life (mo)	13.8^{a}	13.4^{b}	5.40^{c}	5.01^{d}	0.02
SCS (log cells/mL)	−0.79^{d}	−0.75^{c}	−0.07^{b}	−0.03^{a}	1×10^{-3}
Body size composite	−2.02^{d}	−1.90^{c}	−0.84^{b}	−0.69^{a}	0.01
Udder composite	0.64^{a}	0.63^{a}	0.19^{b}	0.14^{c}	0.01
Feet and legs composite	1.04^{a}	0.99^{b}	0.33^{c}	0.28^{d}	0.01
Daughter pregnancy rate (%)	4.35^{a}	3.93^{b}	1.60^{c}	1.02^{d}	0.02
Heifer conception rate (%)	1.92^{a}	1.41^{b}	0.75^{c}	0.23^{d}	0.02
Cow conception rate (%)	6.72^{a}	6.08^{b}	2.52^{c}	1.74^{d}	0.02
Calving ability ($)	61.0^{a}	57.0^{b}	23.7^{c}	19.7^{d}	0.13
Net merit ($)	1,617^{a}	1,567^{b}	1,148^{c}	1,099^{d}	1.33
Technical and financial outputs					
Cow pregnancy rate (%)	30.6^{a}	30.3^{a}	26.2^{b}	25.6^{c}	1×10^{-3}
Cow days open (d)	114.0^{c}	115.0^{c}	131.8^{b}	134.9^{a}	0.39
Milk yield (kg/cow per yr)	12,932^{a}	12,915^{a}	12,648^{b}	12,597^{c}	7.44
Annual cow cull rate (%)	34.5^{a}	34.6^{a}	33.4^{b}	33.0^{b}	2×10^{-3}
Surplus female calves sold (%)	17.6^{a}	17.1^{a}	13.8^{b}	12.9^{b}	3×10^{-3}
Age of dam at creation of embryo (d)	1,117^{b}	1,110^{b}	1,154^{a}	1,155^{a}	1.89
Profit ($/cow per yr)	1,475^{a}	1,442^{b}	1,259^{c}	1,208^{d}	2.96

[a–d]Means with different superscripts within a row differ ($P < 0.05$).

[1] Name of the scenario: CNM_L = use of conventional semen in heifers and cows for all inseminations, culling of surplus heifers is based on the lowest EBV of net merit with low reliability. (T,C) = genetic trend, genetic and environmental correlations in the 12 traits, (T,NC) = genetic trends in all 12 traits and no genetic and environmental correlations among the 12 traits, (NT,C) = no trends in 9 traits except milk, fat, protein, and genetic and environmental correlations among the 12 traits, (NT,NC) = no trends in 9 traits except milk, fat, and protein, and no genetic and environmental correlations among the 12 traits.

average TBV of milk and protein, as well as the lowest TBV of daughter pregnancy rate and cow conception rate, were obtained with the SMILK_H(T,C) scenario (Table 6). The scenario SNM_H(T,C) had the greatest average TBV for fat (83.7 kg), daughter pregnancy rate (4.99%), heifer conception rate (2.48%), cow conception rate (7.51%), and NM$ ($1,856). Selection for NM$ in both conventional and sexed semen scenarios produced the second greatest and the greatest TBV for productive life, udder composite, feet and legs composite, and calving ability (Table 6). Selection for NM$ in both conventional and sexed semen scenarios produced the second lowest and the lowest TBV for SCS and body size composite. Low TBV are desirable for both traits.

Figures 1, 2, and 3 show genetic trends in TBV for NM$, milk, and daughter pregnancy rate in response to selection for the 5 scenarios in the third group. Because we simulated a doubled genetic trend in the sire compared with the sire genetic trend before d 0, the genetic lags initially increased after d 0. By yr 15 the genetic lags appeared to be constant again.

The genetic lag in NM$ decreased when surplus heifers were selected for milk or NM$, compared with random selection of surplus heifers (Figure 1). The greatest genetic lag in NM$ ($1,170) was for the CRAND_H(T,C) scenario in yr 15. The smallest genetic lag in NM$ was for the SNM_H(T,C) scenario in yr 15 ($907) as well as in the previous 14 yr. Thus a gain of $263 in average TBV of NM$ was made in yr 15 as a result of combining sexed semen and culling of surplus heifers based on the lowest EBV of NM$, compared with a scenario that only used conventional semen and culled the surplus heifers randomly.

Figure 2 shows the genetic lag in TBV of milk for the same 5 strategies in the third group. The greatest genetic lag in milk (966 kg) was for the CRAND_H(T,C) scenario in yr 15. The smallest genetic lag in TBV of milk (590 kg) was for the SMILK_H(T,C) scenario in yr 15. Therefore the gain in TBV of milk was 376 kg through using sexed semen as well as culling the worst surplus heifers ranked by their EBV of milk when compared with the CRAND_H(T,C) scenario.

Figure 3 shows the genetic lag in TBV of daughter pregnancy rate. The greatest genetic lag in TBV of daughter pregnancy rate (3.22%) was for the SMILK_H(T,C) scenario in yr 15. The smallest genetic lag in TBV of daughter pregnancy rate (1.97%) was for the SNM_H(T,C) scenario in yr 15, because the genetic correlation between the TBV of daughter pregnancy rate and NM$ was greater than the genetic correlation

Table 6. Genetic, technical, and financial performance of the cows in yr 15 from the multitrait model with genetic trends, genetic and environmental correlations in all 12 traits, under 5 different scenarios that are combinations of 3 surplus heifers culling strategies based on random criteria, lowest EBV of NM$, or lowest EBV of milk, and 2 reproductive strategies that use either only conventional semen or use sexed semen in all heifers for the first 2 inseminations and conventional semen for all other inseminations[1]

Item	CRAND_H(T,C)	CNM_H(T,C)	CMILK_H(T,C)	SNM_H(T,C)	SMILK_H(T,C)	SEM
Average TBV (all cows)						
Milk (kg/305 d)	1,358^{e}	1,453^{d}	1,526^{c}	1,587^{b}	1,737^{a}	2.35
Fat (kg/305 d)	71.5^{e}	76.7^{c}	74.5^{d}	83.7^{a}	79.1^{b}	0.08
Protein (kg/305 d)	46.4^{e}	49.8^{d}	50.3^{c}	54.5^{b}	55.3^{a}	0.06
Productive life (mo)	13.6^{e}	14.5^{b}	13.8^{d}	15.7^{a}	14.2^{c}	0.01
SCS (log cells/mL)	−0.78^{a}	−0.82^{c}	−0.77^{a}	−0.89^{d}	−0.78^{b}	2×10^{-3}
Body size composite	−1.99^{a}	−2.11^{c}	−2.05^{b}	−2.28^{e}	−2.15^{d}	0.01
Udder composite	0.64^{c}	0.70^{b}	0.60^{d}	0.80^{a}	0.56^{e}	0.01
Feet and legs composite	1.01^{c}	1.10^{b}	1.01^{c}	1.21^{a}	1.02^{c}	0.01
Daughter pregnancy rate (%)	4.26^{c}	4.59^{b}	3.97^{d}	4.99^{a}	3.74^{e}	0.02
Heifer conception rate (%)	1.83^{c}	2.10^{b}	1.78^{c}	2.48^{a}	1.79^{c}	0.02
Cow conception rate (%)	6.63^{c}	7.00^{b}	6.41^{d}	7.51^{a}	6.33^{e}	0.02
Calving ability ($)	60.0^{e}	64.3^{c}	61.9^{d}	70.0^{a}	65.2^{b}	0.13
Net merit ($)	1,592^{e}	1,703^{c}	1,648^{d}	1,856^{a}	1,739^{b}	1.52
Technical and financial measures						
Cow pregnancy rate (%)	30.7^{c}	31.2^{b}	30.1^{d}	31.6^{a}	30.0^{d}	1×10^{-3}
Cow days open (d)	113.5^{b}	112.9^{bc}	114.0^{ab}	111.9^{c}	114.8^{a}	0.33
Milk yield (kg/cow per yr)	12,901^{e}	13,007^{d}	13,091^{c}	13,160^{b}	13,291^{a}	6.68
Annual cow cull rate (%)	34.7^{ab}	34.5^{b}	35.2^{a}	34.5^{b}	34.3^{b}	2×10^{-3}
Surplus female calves sold (%)	17.8^{b}	18.0^{b}	17.0^{b}	33.2^{a}	32.2^{a}	3×10^{-3}
Age of dam at creation of embryo (d)	1,125^{a}	1,080^{c}	1,101^{b}	911^{e}	952^{d}	1.68
Profit ($/cow per yr)	1,444^{d}	1,488^{c}	1,484^{c}	1,552^{a}	1,525^{b}	2.72

$^{a–e}$Means with different superscripts within a row differ ($P < 0.05$).

[1] Name of the scenario: C = use of conventional semen in heifers and cows for all the inseminations, S = use of sexed semen in all heifers for the first 2 inseminations and conventional semen for all other inseminations, H = high (genomic) reliability used when calculating the EBV, RAND = culling of surplus heifers is based on random criteria, NM = culling of surplus heifers based on the lowest EBV of NM$, MILK = culling of surplus heifers based on the lowest EBV of milk. (T,C) denotes a genetic model with genetic trends, genetic and environmental correlations among all 12 traits.

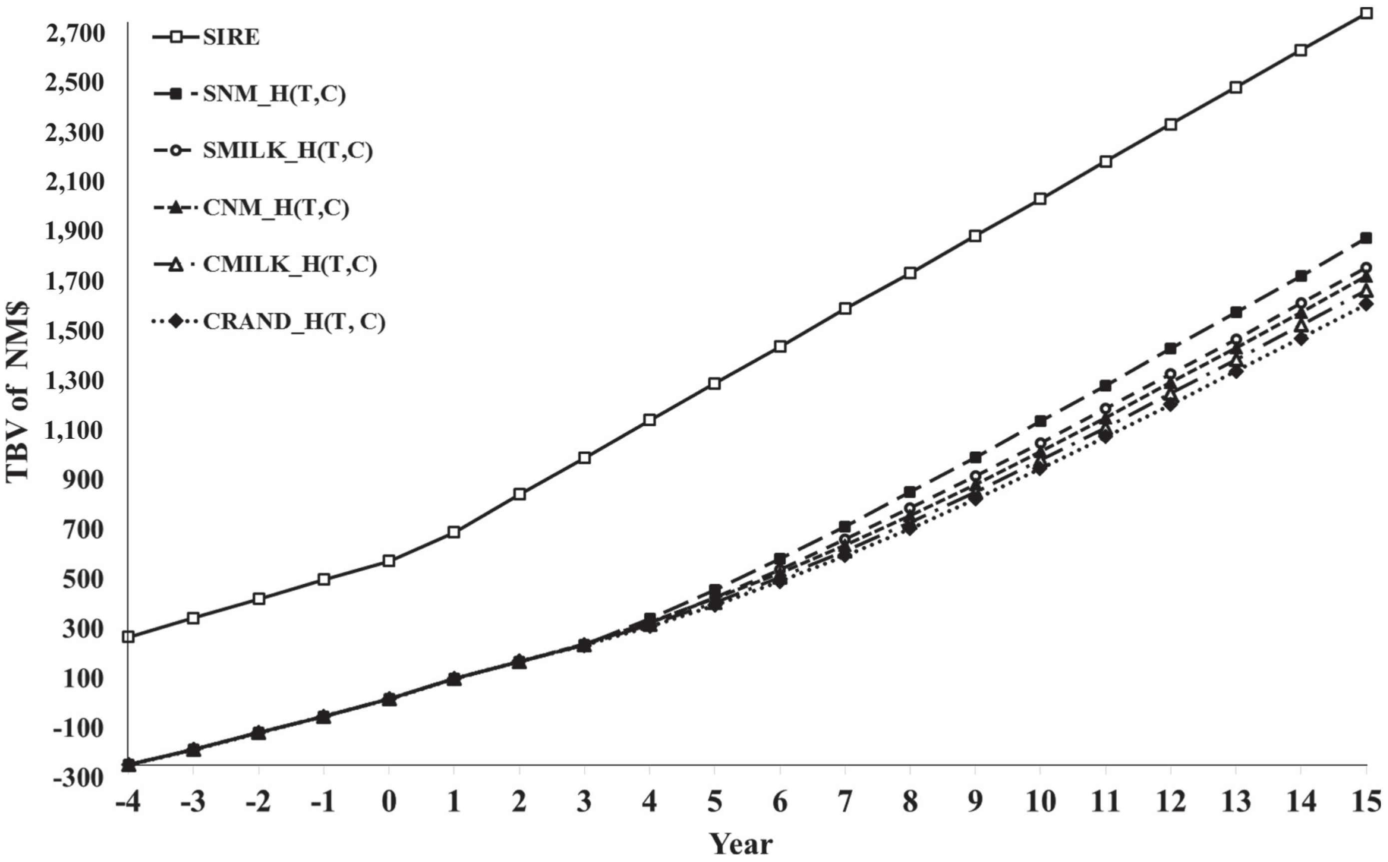

Figure 1. Genetic trends for true breeding value of net merit (TBV of NM$) in sires and cows estimated by the full genetic model that includes genetic trends, and genetic and environmental correlations (T,C) from yr −4 to +15, in 5 scenarios where surplus heifers were culled: randomly [CRAND_H(T,C)], or based on the EBV of NM$ [CNM_H(T,C)], EBV of milk [CMILK_H(T,C)], EBV of NM$ along with sexed semen used twice in heifers [SNM_H(T,C)], or EBV of milk along with sexed semen used twice in heifers [SMILK_H(T,C)]. All EBV were calculated with high (genomic) reliability, which is indicated by H. The TBV of the sires is the expected genetic trends in NM$ (VanRaden and Cole, 2014).

between daughter pregnancy rate and milk. Therefore, a gain of 1.25 percentage units was made in the average TBV of daughter pregnancy rate in yr 15 by using sexed semen as well as culling surplus heifers ranked by EBV of NM$ when compared with using the lowest EBV of milk to cull the surplus heifers.

Technical and financial performance outputs were associated with the genetic results. Table 6 shows that the greatest and second greatest cow pregnancy rate was obtained when surplus heifer culling was based on the EBV of NM$ along with or without the use of sexed semen. The average number of days open was the lowest (112 d) for the SNM_H(T,C) scenario followed by the CNM_H(T,C) scenario (113 d). Milk yield was the greatest in the SMILK_H(T,C) scenario with 13,291 kg/cow per yr due to sole selection for milk when identifying surplus heifers.

Annual cow cull rates were similar in all scenarios by design (Tables 4, 5, and 6). Because involuntary culling had declined from 29% in yr 0 to 18% in yr 15, the amount of rebalance culling increased from 1% in yr 0 to 16% in yr 15. The percent of heifer calves culled was the greatest for the SNM_H(T,C) scenario followed by the SMILK_H(T,C) scenario. Age of dam at creation of the embryo was the lowest (911 d) in the SNM_H(T,C) scenario because sexed semen use generated more calves from heifers.

Profitability was the greatest for scenario SNM_H(T,C) in yr 15 at $1,552/cow per yr (Table 6). This scenario had the greatest revenues ($5,867 per cow per yr) toward which milk components, calf sales, and profit deviations from the traits feet and legs composite, body size composite, udder composite, and calving ability contributed. Among the scenarios where EBV of NM$ was used to rank and cull heifers, CNM_L(T,C) and CNM_H(T,C) differed by only $13/cow per yr, whereas the difference in profit between SNM_H(T,C) and CNM_H(T,C) was $52 (Tables 5 and 6). Profits for scenarios CNM_H(T,C) and CMILK_H(T,C) were not significantly different.

No significant change was observed for the within-herd standard deviation for all 12 traits in each of the last 15 yr in the scenarios CRAND_L(T,C) and CNM_L(T,C). Across the 5 scenarios in the third group, the standard deviation decreased for the trait for which surplus heifers were selected and sold. For example, the standard deviation of NM$ in the scenarios SMILK_H(T,C) and SNM_H(T,C) were $432 and $388 in yr 15, with standard errors of 0.83 and 0.80 of the standard deviation, respectively. The standard deviations of milk in the scenarios SNM_H(T,C) and SMILK_H(T,C) were 591 and 522 in yr 15, with standard errors of 1.26 and 1.25 of the standard deviation, respectively.

DISCUSSION

Model Development and Input Choices

Our objectives were to create and describe a stochastic dynamic dairy herd simulation model with multitrait genetics, illustrate how such a model would generate different results compared with a model with fewer genetic traits, and illustrate the genetic, technical, and financial performance of a herd using various selection criteria for culling of surplus heifers. Various model development and input choices had to be made, which affected our results.

Changes in the TBV of body size composite, feet and legs composite, udder composite, and calving ability did not affect the phenotypic performance of the animals because their effects could not be easily and realistically modeled. For example, body size composite is not equivalent to BW (Holstein Association USA, 2015). Low calving ability means increased risk of dystocia, which affects health and metabolic problems, reduces fertility, and lowers milk yield. Instead, changes in these traits were accounted for indirectly by adding their profit deviations from the economic weights in the NM$ formula to the revenues.

A heifer's phenotypic DMI was solely affected by her BW. Therefore, there was no genetic effect on DMI of

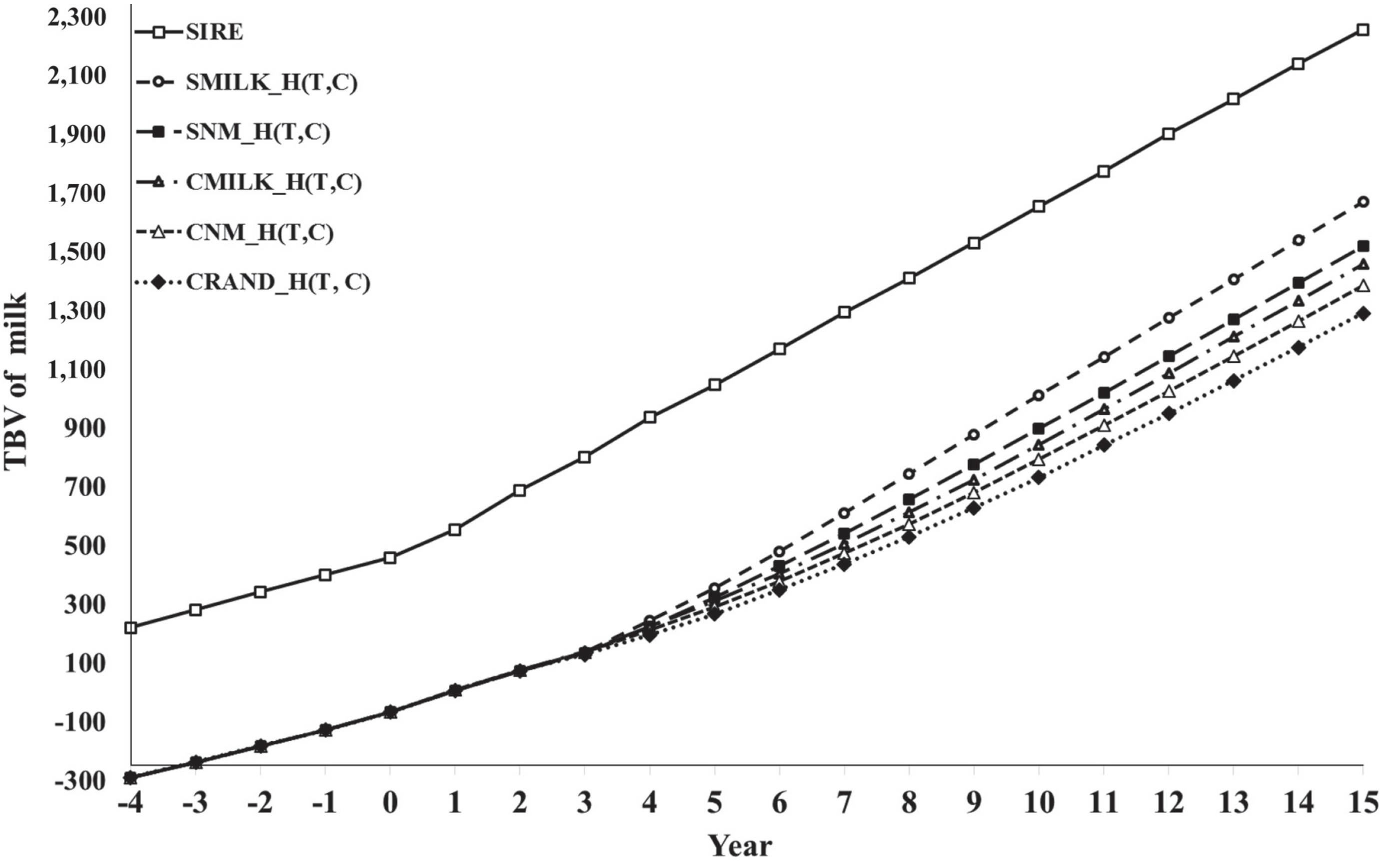

Figure 2. Genetic trends for true breeding value of milk (TBV of milk) in sires and cows estimated by the full genetic model that includes genetic trends, and genetic and environmental correlations (T,C) from yr −4 to +15, in 5 scenarios where surplus heifers were culled: randomly [CRAND_H(T,C)], or based on the EBV of NM$ [CNM_H(T,C)], EBV of milk [CMILK_H(T,C)], EBV of NM$ along with sexed semen used twice in heifers [SNM_H(T,C)], or EBV of milk along with sexed semen used twice in heifers [SMILK_H(T,C)]. All EBV were calculated with high (genomic) reliability, which is indicated by H. The TBV of the sires is the expected genetic trends in NM$ (VanRaden and Cole, 2014).

heifers. The DMI in cows was affected by phenotypic milk and fat production, which were directly affected by their genetic traits. The daily DMI of cows was therefore indirectly under the influence of genetic selection. Relationships between diets and animal performance were not directly modeled. To include the effect of a change in diet on animal performance, the user would have to manually adjust the inputs for the standard phenotypic functions that might be affected, such as those for reproduction.

While the model has the capability to simulate reproductive programs such as timed AI and embryo transfer, we chose to use only inseminations based on estrus detection for simplicity. We did not model individual diseases such as lameness, mastitis, and ketosis, other than the related traits of SCS and productive life. The main reason was to keep the model as parsimonious as possible. In addition, the association between the 12 genetic traits and disease incidence and effects was not clear. Further research might investigate the importance of detailed modeling of diseases to estimate genetic, technical, and financial consequences of reproduction and selection strategies.

Our method of calculating EBV was based on the Falconer et al. (1996) definition of accuracy of selection as the correlation between the TBV and EBV. More recently, Calus et al. (2015) distinguished between the accuracy of selection and the accuracy as the correlation between TBV and EBV. Their study suggests that the reliabilities without genomic testing used in our study may be overestimated.

In our study, genetic trends in the service sires were user inputs and independent of selection and mating strategies within the herd. These genetic trends followed expected trends as reported by Cole et al. (2009) and VanRaden and Cole (2014). The increase in genetic lag in yr 15 versus 0 is explained by the higher rate of genetic progress predicted after 2014 compared with

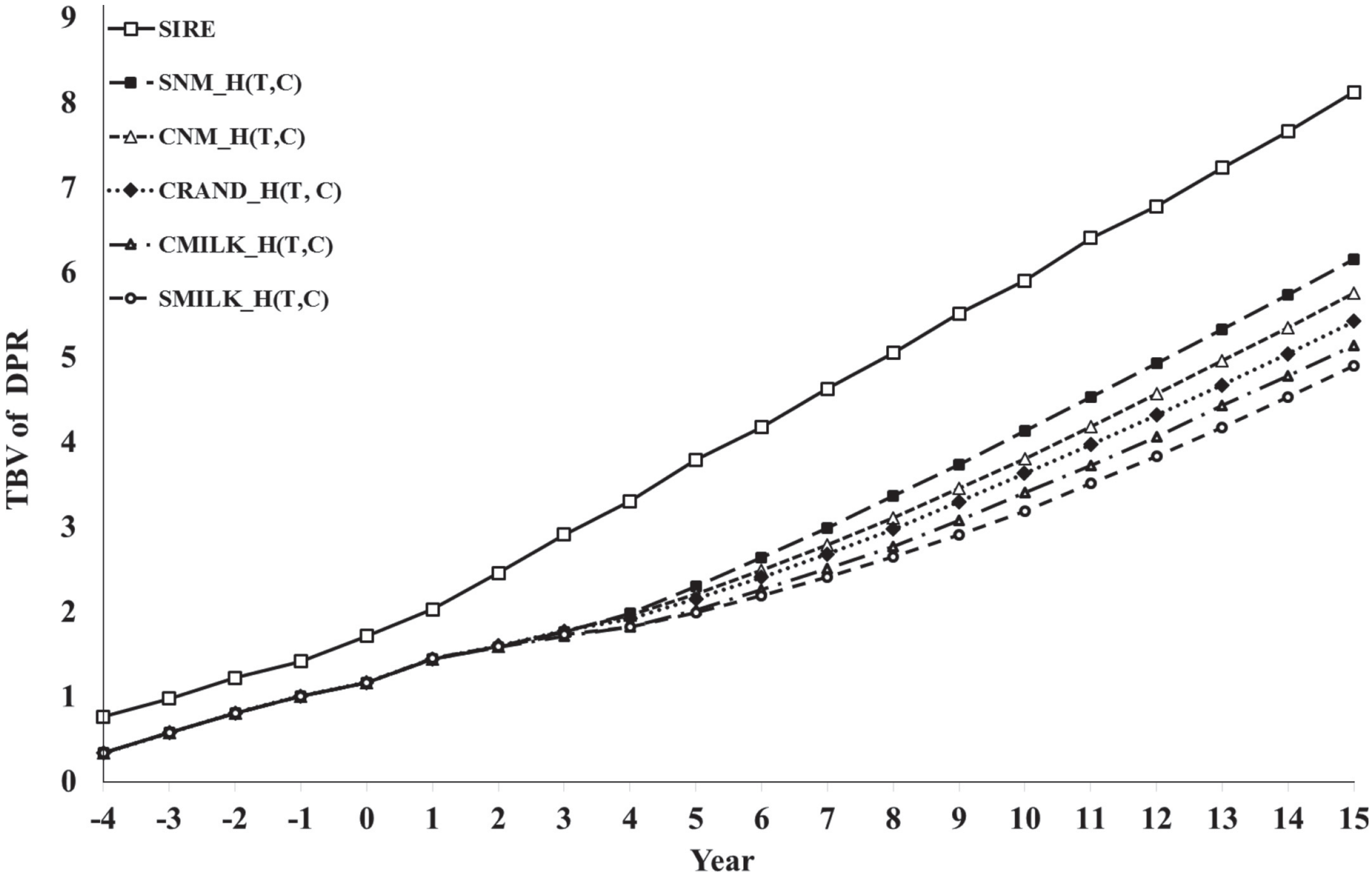

Figure 3. Genetic trends for true breeding value of daughter pregnancy rate (TBV of DPR) in sires and cows estimated by the full genetic model that includes genetic trends, genetic and environmental correlations (T,C) from yr −4 to +15, in 5 scenarios where surplus heifers were culled: randomly [CRAND_H(T,C)], or based on the EBV of NM$ [CNM_H(T,C)], EBV of milk [CMILK_H(T,C)], EBV of NM$ along with sexed semen used twice in heifers [SNM_H(T,C)], or EBV of milk along with sexed semen used twice in heifers [SMILK_H(T,C)]. All EBV were calculated with high (genomic) reliability, which is indicated by H. The TBV of the sires is the expected genetic trends in NM$ (VanRaden and Cole, 2014).

earlier years as a result of the wider use of genomically tested young sires (VanRaden and Multi-State Project S-1008, 2006; Cole et al., 2009; VanRaden and Cole, 2014). We chose to use the lower genetic trends before d 0 and the greater genetic trends after d 0 for all 12 traits. Genetic trends in the sire TBV affect the differences in genetic merit between younger and older females in the herd.

We used an inbreeding increase per year based on Weigel (2001) and assumed that the farm would consider inbreeding when making mating decisions, for example through computerized mating programs (Weigel and Lin, 2000). More detail in sire choice is possible with the model, for example by using different sires for heifers and for cows, or by implementing a mating program based on EBV of individual traits of females and expected level of inbreeding. Inbreeding reduced the genetic variances in our model, but we did not include any effect of inbreeding on phenotypic performance.

The assumed linear trends in sire genetic merits and constant application of the same reproduction selection strategy is expected to lead to near linear genetic lags between sires and cows over time. However, exact linear genetic increases are not expected because constant changes in fertility and culling result in nonconstant herd demographics. As is evident from Figures 1, 2, and 3, genetic lag in yr 15 was near constant but could continue to change in yr 16 and beyond.

Verification and Validation of the Full Genetic Model

The purpose of verification is to check that the model functions as intended. The purpose of validation is to check that the model sufficiently mimics the real system behavior of interest (Sorensen, 1990). Complete verification and validation cannot be obtained in practice.

We verified our full genetic model (T,C) based on over 120 different herd output statistics (most not shown). The herd output statistics were compared with herd statistics available from CDCB (2015), DRMS (2015), and Holstein Association USA (2015), as well as our own expertise. Inputs were chosen such that the herd performance in yr 0 was similar to that of a US Holstein dairy farm where possible. For example, milk, fat, and protein production in yr 0 in the default scenario CRAND_L(T,C) was 10,394, 376, and 315 kg/cow per yr, respectively, which is comparable to average milk component production by US Holsteins presently.

To help judge the validity of the model, we compared the genetic trends in NM$. The actual genetic lag between the TBV of NM$ for sires (98th percentile) and cows (50th percentile) was $555 in December 2014 (CDCB, 2015), which is realistically close to the $556 calculated with our model (Table 3). When scenarios CRAND_L(T,C) and CNM_L(T,C) were compared for average TBV of NM$, a difference of $25/cow per yr was observed (Tables 4 and 5) as a result of selection for NM$ but with the lower reliabilities. About one third of that difference ($8) might be observed in profit per cow per year because NM$ is expressed for the animal's expected lifetime, which is approximately 3 yr. We observed a difference in profit of $11 (SE was $2.72), which was not significantly different from $8. These verification and validation results provide confidence in the model's ability to generate realistic genetic, technical, and financial responses of herds adopting various combinations of reproduction and selection strategies.

Other Genetic Models

Recent studies that analyzed the benefits of using genomic testing and sexed semen used stochastic models with single traits. Whereas Ettema et al. (2011) only used milk production traits to study genetic gain, Hjortø et al. (2015) used a total merit trait similar to the NM$ but this trait didn't affect the phenotypic performance of animals directly. Tables 4 and 5 showed that the full genetic models of 12 traits with genetic trends, genetic and environmental correlations led to different results than the reduced genetic models where genetic trends, and genetic and environmental correlations for all traits except milk components were ignored. Genetic models that do not account for the genetic trends of some traits, for example in the CRAND_L(NT,C) and CNM_L(NT,NC) scenarios, have lower TBV for all traits than the genetic models that included genetic trends as well as genetic and environmental correlations. Therefore, previous studies that assumed genetic progress in only milk component traits (e.g., Ettema et al., 2011) may not have captured the full technical and financial performance as a result of genetic selection. Whereas our model includes many correlated genetic traits, inclusion of other genetic traits would further improve estimates of genetic, technical, and financial consequences of reproduction and selection strategies.

Effects of Reliability and Ranking Criteria for Culling of Surplus Heifers

In all scenarios, we decided to keep only the minimum number of heifers required in yr 1 to replace the involuntary culled cows and cull the remaining surplus heifers after ranking them based on various criteria. The use of sexed semen increased the availability of dairy heifers and hence the selection intensity. There was a greater gain in average TBV of milk and NM$ when surplus heifers were ranked and sold based on EBV of milk and NM$, respectively. Negative genetic correlations of milk with fertility traits resulted in lower TBV of fertility traits in the SMILK(T,C) and CMILK_H(T, C) scenarios (Table 6). Because the TBV of daughter pregnancy rate and cow conception rate affected the phenotypic pregnancy rate, the scenario SNM_H(T,C) had the greatest cow pregnancy rate of 31.6% in yr 15. Increased emphasis on selection directly for fertility traits would further accelerate increases in pregnancy rate.

As shown in Figure 1, the SNM_H(T,C) scenario led to an additional gain of $263 in TBV of NM$ over the CRAND_H(T,C) scenario in yr 15. The differences is the result of both the greater selection intensity from sexed semen use in the previous 14 yr, as well as continuous increases in fertility due to selection for NM$ that led to a younger herd, as evident from the lowest age of dam at creation of the embryo of 911 d (Table 6). We estimated a reduction in genetic lag for NM$ of 0.67 standard deviation ($263/$392) when comparing the scenarios SNM_H(T,C) to CNM_L(T,C) in yr 15. Recently Hjortø et al. (2015) showed that using sexed semen in conjunction with genomic testing reduced the genetic lag by 0.30 standard deviation of the breeding goal. Hjortø et al. (2015) used selective sexed semen and beef semen and avoided creating surplus heifers in the herd.

Profitability of the SNM_H(T,C) scenario was greater than profitability of the SMILK_H(T,C) scenario, which shows that surplus heifer selection based on the NM$ index was more profitable than selection based on the single trait milk yield. The economic values of the 8 genetic traits that directly affected phenotype, such as fat and protein prices, were set slightly different than the economic weights used in the NM$ index, however. Therefore, a selection index exists that would increase profitability more than the NM$ index in our herd.

Sexed semen was used in all heifers, independent of their genetic merit. Genetic lag and profitability might be increased if sexed semen was used selectively, for example on the genetically better animals. Using more aggressive reproductive technologies such as in vitro produced embryo transfer may reduce the genetic lag more than the artificial insemination strategies shown in this study (Hansen and Block, 2004; Pedersen et al., 2012), but economic consequences of such strategies are not immediately clear.

CONCLUSIONS

Genetic trends and genetic and environmental correlations of 12 individual traits were directly or indirectly built into a daily stochastic dynamic dairy simulation model. Verification and validation results provided confidence in the ability of the model to generate realistic genetic, technical, and financial outputs of herds adopting different reproduction and selection strategies. Results showed that genetic models without genetic trends in some of the traits, or without genetic and environmental correlations, resulted in biased estimates of genetic, technical, and financial outputs. The scenario that used sexed semen in heifers along with culling of surplus heifers based on their EBV of NM$ resulted in the greatest progress into the desired direction of change for 10 traits of interest, except for milk and protein. Among 5 scenarios evaluated, this scenario also resulted in the greatest profit per cow per year.

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