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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

K. Kaniyamattam,* M. A. Elzo,* J. B. Cole,† and A. De Vries*[1]
*Department of Animal Sciences, University of Florida, Gainesville 32611
†Animal Improvement Program, Animal Genomics and Improvement Laboratory, ARS-USDA, Beltsville, MD 20705-2350

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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[1] Corresponding author: devries@ufl.edu

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, concep-

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