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Combining genetic and physiological data to identify predictors of lifetime reproductive success and the effect of selection on these predictors on underlying fertility traits

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ABSTRACT

Fertility of the dairy cow relies on complex interactions between genetics, physiology, and management. Mathematical modeling can combine a range of information sources to facilitate informed predictions of cow fertility in scenarios that are difficult to evaluate empirically. We have developed a stochastic model that incorporates genetic and physiological data from more than 70 published reports on a wide range of fertility-related traits in dairy cattle. The model simulates pedigree, random mating, genetically correlated traits (in the form of breeding values for traits such as hours in estrus, estrous cycle length, age at puberty, milk yield, and so on), and interacting environmental variables. This model was used to generate a large simulated data set (200,000 cows replicated 100 times) of herd records within a seasonal dairy production system (based on an average New Zealand system). Using these simulated data, we investigated the genetic component of lifetime reproductive success (LRS), which, in reality, would be impractical to assess empirically. We defined LRS as the total number of times, during her lifetime, a cow calved within the first 42 d of the calving season. Sire estimated breeding values for LRS and other traits were calculated using simulated daughter records. Daughter pregnancy rate in the first lactation (PD₁) was the strongest single predictor of a sire's genetic merit for LRS ($R^2 = 0.81$). A simple predictive model containing PD₁, calving date for the second season and calving rate in the first season provided a good estimate of sire LRS ($R^2 = 0.97$). Daughters from sires

with extremely high ($n = 99,995$ daughters, sire LRS = +0.70) or low ($n = 99,635$ daughters, sire LRS = -0.73) LRS estimated breeding values were compared over a single generation. Of the 14 underlying component traits of fertility, 12 were divergent between the 2 lines. This suggests that genetic variation in female fertility has a complex and multifactorial genetic basis. When simulated phenotypes were compared, daughters of the high LRS sires (HiFERT) reached puberty 44.5 d younger and calved ~14 d younger at each parity than daughters from low LRS sires (LoFERT). Despite having a much lower genetic potential for milk production (-400 L/lactation) than LoFERT cows, HiFERT cows produced 33% more milk over their lifetime due to additional lactations before culling. In summary, this simulation model suggests that LRS contributes substantially to cow productivity, and novel selection criteria would facilitate a more accurate prediction at a younger age.

Key words: reproduction, genetic evaluation, simulation model

INTRODUCTION

Reproduction is a key driver of the profitability of dairy farming. Regardless of geography or production system, improving female fertility in dairy cattle improves profitability by reducing costs associated with mating and early culling and by increasing the length of the cow's productive lifetime (Veerkamp et al., 2002; González-Recio et al., 2004; Meadows et al., 2005; De Vries, 2006). Genetic selection is an effective method for producing long-term and compounding improvements in dairy cow fertility (Pryce and Veerkamp, 2001; Pryce et al., 2014). However, evaluating many traits for genetic selection via on-farm recording can be cost prohibitive and time consuming. Typically, phenotypes

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derived from existing industry records (e.g., gestation length and mating submission rate) are used as genetic selection criteria, but these can be highly variable due to random and systematic environmental effects and inaccurate recording. Manipulative experimentation with novel selection criteria (e.g., hormone assays, behavioral data) is extremely costly, particularly in the context of genetic evaluation because thousands of records are required. An alternative, or supplementary approach, is to use mathematical modeling to simulate the recording of novel selection phenotypes in an industry setting. This method combines existing knowledge of the genetic and environmental contributions to variation in female fertility into a stochastic simulation that can predict the outcomes of different scenarios.

Reproductive success relies on complex interactions between genetics, physiology, and management. For example, the inter-calving interval is affected by how soon the postpartum cow resumes ovulation and displaying overt estrus, the strength and regularity of her estrus events, milk yield, body fat, the probabilities of conception and pregnancy loss, and the length of gestation. Many of these underlying drivers of fertility are heritable and modified by management and environmental factors (reviewed in Royal et al., 2000a). In addition, a cow's previous history such as growth as a heifer, age at puberty, calving difficulty, and hormonal treatments can affect subsequent fertility.

Here, we describe the development of a stochastic simulation model driven by genetic, physiological, and management parameters derived from over 70 published studies. This model is based on the average seasonal-pastoral system in New Zealand, where, to match feed demand with pasture growth, the whole herd calves in early spring and is rebred within a fixed period (generally 12 wk) to maintain an annual calving cycle. Cows that conceive early in the mating season (and therefore calve early in the calving season) are the most desirable because they have a greater number of DIM and a longer recovery period between calving and the beginning of the next mating season. Cows that are not successfully bred in this fixed mating season represent a net cost to the seasonal-pastoral system and are culled.

We used this model to generate a large simulated data set (200,000 cows per simulation with simulations replicated 100 times) and investigated a range of combinations of measurements for predicting the genetic merit of sires for lifetime reproductive success (**LRS**).

During this simulation, we also investigated the effect that sires with extreme genetic merit (either very high or very low) for fertility can have on daughter production and reproduction.

MATERIALS AND METHODS

Model Description

A stochastic fertility model was developed to simulate detailed lifetime phenotypic herd records (up to 5 parities) for dairy cattle in a New Zealand seasonal calving herd. The model is composed of 3 modules (Figure 1). A genetic module with specified genetic variance and covariance inputs is used to parameterize a simple pedigree with correlated genetic drivers of fertility, a heifer development module simulates outcomes from birth until first calving, and the milking cow module simulates outcomes from first calving until death or culling.

The model has been programmed in R (R Core Team, 2016) using add-on packages: “corpcor” (Schäfer et al., 2015), “data.table” (Dowle et al., 2015), “gdata” (Warnes et al., 2015), “MASS” (Venables and Ripley, 2002), “plyr” (Wickham, 2011), “reshape” (Wickham, 2007), and “runuran” (Leydold and Hörmann, 2015).

Model Parameters

Important management and environmental parameters in a seasonal pastoral system are listed in Table 1. We conducted a literature review to obtain estimates of 14 underlying drivers of fertility, with a focus on New Zealand cattle (Table 2). We used published genetic correlations to emulate genetic relationships among underlying fertility driving traits (Table 3). Where necessary, inputs were adjusted to reflect the high proportion of Holstein-Friesian \times Jersey crossbreeds present in New Zealand systems.

Genetic Module: Simulation of Driving Variable Values

A key component of the model is the simulation of underlying genetic variation in fertility for a set of cows organized in a simple pedigree structure (1 generation). This pedigree structure is important for simulating the underlying genetic variation among cows and also facilitates a genetic analysis of simulated data to infer genetic properties for aggregate genetic traits. The structure was chosen to facilitate efficient computation of accurate genetic merit of aggregate genetic traits. Thus, unrelated sires and dams were simulated in each replicate to generate a single generation of cows with phenotypes in 200 paternal half sib groups of 1,000. The sire and dam genetic variables along with a Mendelian sampling term are combined to generate a true breeding value (**TBV**) as follows:

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