**Simulation of Heifer Body Weight (BW) and Dry Matter Intake (DMI)**

The study employed a stochastic dynamic Monte Carlo model to simulate the performance of a 1,000-cow dairy herd over a 15-year period. The body weight (BW) of heifers was modeled using true breeding values (TBV) combined with permanent and temporary environmental deviations to account for genetic and environmental influences on growth. Additionally, the dry matter intake (DMI) of heifers was determined as a function of their body weight, lactation stage, and energy requirements, ensuring that feed intake adapted dynamically to physiological demands. The model accounted for the genetic variation in feed efficiency and how it influenced the energy available for growth and production.

**Simulation of Body Weight in Lactating and Pregnant Cows**

The body weight of lactating and pregnant cows was simulated based on genetic TBV for BW, adjusted by permanent and temporary environmental deviations. The weight gain or loss during lactation was modeled by considering metabolic factors such as milk production, energy balance, and pregnancy stage. The model integrated changes in energy reserves due to lactation stress, ensuring that cows with higher milk production experienced greater body weight loss in early lactation, followed by gradual weight recovery in mid and late lactation. Additionally, pregnancy was accounted for by modeling fetal growth and its impact on the cow’s overall body weight.

**Mathematical Logic for Simulating Lactation Curves**

The lactation curves of cows were simulated using standard phenotypic equations that describe milk yield as a function of days in milk (DIM). The model included peak milk yield, lactation persistency coefficients, and adjustments for genetic and environmental deviations. By incorporating genetic TBV for milk yield, the simulation ensured that individual cows had different lactation curves based on their genetic potential. Furthermore, the persistency of milk yield decline over time was determined using exponential decay functions that accounted for energy balance and metabolic stress.

**Simulation of Protein Curves**

Protein curves followed a similar modeling approach as lactation curves, where milk protein yield was influenced by genetic TBV for protein percentage, dietary effects on milk composition, and the stage of lactation. The model accounted for the natural increase in milk protein percentage toward the end of lactation, reflecting the physiological adaptation of cows. Additionally, feed efficiency and dietary crude protein levels influenced protein synthesis in the mammary gland, and these factors were included in the simulation equations.

**Simulation of Somatic Cell Count (SCC) Curves**

The simulation of somatic cell count (SCC) curves was based on the equation developed by Morant and Gnanasakthy (1989), where somatic cell score (SCS) was calculated as a function of lactation stage, genetic resistance to mastitis (TBV for SCC), and environmental deviations. The SCS equation was expressed as:

A math equations on a white background

AI-generated content may be incorrect.

where the parameters α, β, γ, and δ were estimated based on the US Holstein population, and ΔEp and ΔEt accounted for permanent and temporary environmental effects, respectively. The somatic cell score was then converted to SCC using Schutz’s (1994) transformation formula:



This approach ensured that genetic and environmental influences on mastitis susceptibility were accurately reflected in SCC dynamics.

**Simulation of Daily Live and Death Culling Risks**

The daily culling risk for cows was modeled as a function of productive life genetics, health status, milk production, and market conditions. The probability of voluntary culling was influenced by low milk yield, poor reproductive performance, and unfavorable economic conditions. In contrast, involuntary culling was determined by disease occurrence, particularly mastitis and metritis, which increased the likelihood of early removal from the herd. The mathematical model for culling probability incorporated TBV for longevity, environmental deviations, and disease incidence to simulate realistic herd turnover patterns.

**Mastitis Economics Simulation**

The economic impact of mastitis was simulated by integrating the SCC curves, culling risk equations, and treatment costs into a comprehensive economic model. Mastitis incidence was modeled based on genetic resistance (TBV for mastitis), environmental factors, and herd management practices. The economic losses associated with mastitis included direct treatment costs, estimated at $73.50 for gram-positive cases and $45.50 for other cases, along with indirect costs such as reduced milk yield, increased culling rates, and reproductive inefficiencies. The model also evaluated different genomic selection strategies, including AI-NM$, AI-MAST, AI-METR, and AI-HTH$, to determine their effectiveness in reducing mastitis prevalence while maintaining farm profitability.

By integrating these mathematical models, the study provided a comprehensive simulation of the interactions between genetics, health, and economics in a dairy herd. The dynamic modeling approach allowed for the evaluation of different breeding and management strategies, ultimately contributing to improved decision-making in dairy production.