



## Deriving estimates of individual variability in genetic potentials of performance traits for 3 dairy breeds, using a model of lifetime nutrient partitioning

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### ABSTRACT

This study explored the ability of an existing lifetime nutrient partitioning model for simulating individual variability in genetic potentials of dairy cows. Generally, the model assumes a universal trajectory of dynamic partitioning of priority between life functions and genetic scaling parameters are then incorporated to simulate individual difference in performance. Data of 102 cows including 180 lactations of 3 breeds: Danish Red, Danish Holstein, and Jersey, which were completely independent from those used previously for model development, were used. Individual cow performance records through sequential lactations were used to derive genetic scaling parameters for each animal by calibrating the model to achieve best fit, cow by cow. The model was able to fit individual curves of body weight, and milk fat, milk protein, and milk lactose concentrations with a high degree of accuracy. Daily milk yield and dry matter intake were satisfactorily predicted in early and mid lactation, but underpredictions were found in late lactation. Breeds and parities did not significantly affect the prediction accuracy. The means of genetic scaling parameters between Danish Red and Danish Holstein were similar but significantly different from those of Jersey. The extent of correlations between the genetic scaling parameters was consistent with that reported in the literature. In conclusion, this model is of value as a tool to derive estimates of genetic potentials of milk yield, milk composition, body reserve usage, and growth for different genotypes of cow. Moreover, it can be used to separate genetic variability in performance between individual cows from environmental noise. The model enables simulation of the effects of a genetic selection strategy on lifetime efficiency of individual cows, which has a main advantage of including the rearing costs, and thus, can be used to explore the

impact of future selection on animal performance and efficiency.

**Key words:** nutrient partitioning, dairy cow, genetic variability, dynamic model

### INTRODUCTION

Milk production efficiency is affected by the way in which dairy cows partition obtained nutrients between life functions. Generally, an efficient cow should allocate a greater proportion of nutrients toward the mammary gland, for milk synthesis (Linn et al., 2009). This traditional view of efficiency is based on the concept of dilution of maintenance; that is, when a cow eats more feed to support milk production a smaller proportion is used for maintenance and is thus more efficient (Bauman et al., 1985). However, if efficiency is considered over the lifespan of an animal, the extent to which nutrients are partitioned to vital functions such as health and fertility is important because the longer the productive life the smaller is the rearing phase as a proportion, and thus greater the lifetime efficiency. These vital functions are not only related to economic (Collard et al., 2000) and environmental issues (Garnsworthy, 2004), but animal welfare (Oltenucu and Algers, 2005). Thus, being able to predict the nutrient partitioning process of cows can help improve animal efficiency and farm profitability, and reduce environmental impact.

Pioneering works of Baldwin et al. (1987a,b) and Oldham and Emmans (1989) show that mathematical models can be used to explore concepts and hypotheses, regarding nutrient partitioning in dairy cows, and have potential for predicting long-term efficiency (Dumas et al., 2008; Friggens et al., 2013). Clear genetic differences exist in nutrient partitioning between cows (Yan et al., 2006) and physiological states (Kirkland and Gordon, 2001). Thus, prediction of nutrient partitioning should consider genetic variability between cows and differences in expression of their genotypes through time. By capturing these ideas, the model of Martin and Sauvant (2010a) is able to simulate the average

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pattern of dynamic partitioning of energy intake and performance through lifespan of cows of different yield levels, and thus allows genetic variability to be incorporated in prediction of lifetime efficiency. This model assumes a general trajectory of dynamic partitioning of a cow's relative priority between life functions, and genetic scaling parameters are then incorporated to scale individual performance, and to simulate variability between genotypes in, for example, milk production. In other words, it assumes that performance of animals differs only in terms of scaling but not in terms of the dynamic shape.

At this moment, however, the appropriateness of the model to realistically simulate individual variability in nutrient partitioning trajectories is untested. Though the model shows a good fit to the mean values of various population data from literature (Schutz et al., 1990; Hoffman, 1997), the extent to which the assumption of one general trajectory of dynamic partitioning of relative priority still holds when comparing different genotypes should be validated. Does the trajectory of dynamic partitioning of relative priority differ between breeds kept in the same environment? It is also important to evaluate the individual variation in genetic scaling parameters and their possible correlations and factors affecting them. Such information is necessary for setting up realistic population simulations and, in the wider context, for using the model to simulate the effects on lifetime efficiency of possible selection and management strategies.

The aim of this study was, therefore, to examine the model of Martin and Sauvant (2010a) for its capability of simulating individual variability in genetic potentials of milk yield (MY), milk composition, growth, and body reserve usage of different genotypes of cow.

## MATERIALS AND METHODS

For clarity, it should be noted that this paper dealt with the situation where cows are managed in a non-constraint environment (i.e., unlimited access to a high quality feed, water or neutral ambient temperature), and thus, the performance profiles that a given cow would achieve in such an environment is referred to as genetic potential, in accordance with literature definitions of genetic potential (e.g., Oldham and Emmans, 1989).

### Teleonomic Model (GARUNS)

This section presents a brief introduction to the teleonomic model of Martin and Sauvant (2010a). This teleonomic model, referred to here as **GARUNS**, consists of a regulating submodel providing a driving force

to control the function of an operating submodel. An adapted scheme of GARUNS is presented in Figure 1. The regulating submodel describes the dynamic partitioning of a female mammal's priority between life functions: growth (**G**), aging (**A**), regaining of body reserves (**R**), and energy supply of the unborn (**U**), newborn (**N**), and suckling (**S**) calf over a lifespan. This dynamic pattern of priorities is assumed to be general for all individual cows. The sum of these relative priorities is always equal to one. The operating submodel uses the relative priorities to partition energy intake between fetal growth, BW and body composition, MY, and milk composition over the lifespan and during repeated reproductive cycles. Genetic scaling parameters are incorporated in the operating submodel to scale individual performance potentials of, for example, mature body size or milk production. It should be noted that these genetic scaling parameters are not simply related to the widely reported breeding values commonly used in the animal genetics literature. They act as multipliers on the different dynamic priorities and thus provide the means to create different levels of genetic potential performance for different cows. A general principle is that the higher the value genetic scaling parameter, the higher the genetic potential. In this context, the variation in genetic scaling parameters describes the variation in genetic potential between animals. In the model, an animal is described in terms of its genotype for growth, capacity to store and mobilize reserves, and milk production using the following genetic scaling parameters: nonlabile body mass at maturity ( $W_M$ ), rate of regaining body reserves per day ( $b_0$ ), labile body mass mobilization index ( $\nu_X$ ), peak MY potential ( $\nu_Y$ ), milk fat secretion ( $\nu_F$ ), milk protein secretion ( $\nu_P$ ), and milk lactose secretion ( $\nu_L$ ). The unit of  $W_M$  is kilograms, whereas the remaining parameters are fractions and, therefore, have no unit. For example, for a reference Holstein cow ( $W_M = 500$ ), the value of  $\nu_Y$  of 1 represents peak MY of 24, 29, and 32 kg/d in first, second, and third parities, respectively. Thus, to describe each genotype, a specific set of these genetic scaling parameters is needed, and noticeably they were the same throughout the lifespan of the animal. External triggers of successful insemination (i.e., conception) drive the changes between nonreproductive and reproductive states of the animal, cueing in the dynamic priority trajectories described in the regulating submodel. As shown in Figure 1, the combination between dynamic priority and genetic scaling parameters makes it possible to quantify the total amount of energy required to fulfill all functions ( $\Sigma_E$ ). The resulting DMI is quantified by multiplying  $\Sigma_E$  with the predetermined dietary energy density ( $e_D$ ). The coefficients of energy partition to different life functions ( $E_G/\Sigma_E$ ,  $E_R/\Sigma_E$ ,  $E_{MY}/$

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