

J. Dairy Sci. 101:1–11 https://doi.org/10.3168/jds.2017-13936 © American Dairy Science Association[®]. 2018.

Genetic background in partitioning of metabolizable energy efficiency in dairy cows

T. Mehtiö,¹ E. Negussie, P. Mäntysaari, E. A. Mäntysaari, and M. H. Lidauer Natural Resources Institute Finland (Luke), 31600 Jokioinen, Finland

ABSTRACT

The main objective of this study was to assess the genetic differences in metabolizable energy efficiency and efficiency in partitioning metabolizable energy in different pathways: maintenance, milk production, and growth in primiparous dairy cows. Repeatability models for residual energy intake (REI) and metabolizable energy intake (MEI) were compared and the genetic and permanent environmental variations in MEI were partitioned into its energy sinks using random regression models. We proposed 2 new feed efficiency traits: metabolizable energy efficiency (MEE), which is formed by modeling MEI fitting regressions on energy sinks [metabolic body weight (BW^{0.75}), energy-corrected milk, body weight gain, and body weight loss] directly; and partial MEE (pMEE), where the model for MEE is extended with regressions on energy sinks nested within additive genetic and permanent environmental effects. The data used were collected from Luke's experimental farms Rehtijärvi and Minkiö between 1998 and 2014. There were altogether 12,350 weekly MEI records on 495 primiparous Nordic Red dairy cows from wk 2 to 40 of lactation. Heritability estimates for REI and MEE were moderate, 0.33 and 0.26, respectively. The estimate of the residual variance was smaller for MEE than for REI, indicating that analyzing weekly MEI observations simultaneously with energy sinks is preferable. Model validation based on Akaike's information criterion showed that pMEE models fitted the data even better and also resulted in smaller residual variance estimates. However, models that included random regression on BW^{0.75} converged slowly. The resulting genetic standard deviation estimate from the pMEE coefficient for milk production was 0.75 MJ of MEI/kg of energy-corrected milk. The derived partial heritabilities for energy efficiency in maintenance, milk production, and growth were 0.02, 0.06, and 0.04, respectively, indicating that some genetic variation may exist in the efficiency of using metabolizable energy for different pathways in dairy cows.

Key words: feed efficiency, partitioning metabolizable energy, energy sink, heritability

INTRODUCTION

Milk production, maintenance, and growth are the most important factors for energy use of lactating primiparous dairy cows. Maintenance requirements consist of the energy necessary to conduct voluntary body activity and to maintain the basal metabolism and body temperature. Traditionally, calorimetric chambers have been used to estimate partial efficiencies in converting energy intake to the energy sinks of the different physiological pathways. These partial efficiencies are defined as a ratio between the ME utilization for product and the energy requirement for production. So far no strong evidence has been found to assume genetic differences in the partial efficiencies, but it has been shown that high genetic merit cows are more efficient because they partition the available energy differently from low genetic merit cows (Veerkamp and Emmans, 1995; Agnew and Yan, 2000; Yan et al., 2006). Mäntysaari et al. (2012) also observed differences in the mobilization of body energy reserves between cows with different energy efficiency when efficiency was measured as energy conversion efficiency [ECM/metabolizable energy intake (MEI)] but not when measured as residual energy intake (**REI**).

The most studied traits related to feed efficiency in dairy cows at the moment are DMI, REI, and residual feed intake (**RFI**), and different kinds of ratio traits, which are usually defined as the ratio of output over input or its inverse. Heritability estimates for DMI range from 0.27 to 0.63 in different studies (Spurlock et al., 2012; Berry et al., 2014; Liinamo et al., 2015). Residual traits such as REI and RFI can be calculated as the residual from a linear regression of energy or feed intake on various energy sinks, such as milk production, metabolic BW (for maintenance requirements), and BW change. Alternatively, these residual traits

Received October 4, 2017.

Accepted January 8, 2018.

¹Corresponding author: terhi.mehtio@luke.fi

2

ARTICLE IN PRESS

MEHTIÖ ET AL.

can be calculated as the difference between actual MEI or DMI and MEI or DMI predicted from animal performance. In recent studies, the heritability estimates for RFI have varied from 0.01 to 0.32 (Pryce et al., 2014; Tempelman et al., 2015) and for REI from 0.07 to 0.09 (Liinamo et al., 2015; Hurley et al., 2018). However, some concerns in using RFI and REI have been addressed as well. The observations of these residual traits accumulate measurement errors that are associated with the component traits. Additionally, unknown genetic correlations may exist between residual traits and the regressors that are used to predict those (Pryce et al., 2014; Manzanilla-Pech et al., 2016). High phenotypic correlation between REI and energy balance was reported by Liinamo et al. (2015) and Hurley et al. (2018) and they argued that selecting for REI might also lead to greater negative energy balance. However, Hurley et al. (2018) concluded that REI could be used as a breeding objective for feed efficiency, but at the same time traits such as health and fertility need to be considered in the breeding program.

Residual energy intake is describing the general efficiency of a cow in using ME. However, from a breeding point of view, it might be desirable to put more selection weight on efficiency with respect to a certain metabolic function. Therefore, models that are capable of partitioning a cow's efficiency with respect to different pathways may be of interest. Such models would give more comprehensive information as to why some cows are more efficient than others. To establish the required efficiency trait analogous to REI, a model that directly includes regressions on energy sinks is fitted for MEI observations. This model is hereafter referred as metabolizable energy efficiency (MEE). In the usual derivation of REI, the MEI is first corrected with respect to the energy requirements for assumed needs, and the resulting REI is further analyzed by genetic models. Instead the effect of animal breeding values could be directly added into the model of MEI, and thereafter the breeding values should become estimated more accurately. Such a model can be extended with random regressions on energy sinks nested within the additive genetic effect, which would provide partial efficiencies for use of ME (**pMEE**), given genetic variation exists in the efficiency of using ME for different pathways.

The objectives of this study were to assess the genetic variations in MEE and in its energy sink-specific components (pMEE) by fitting random regression models on weekly MEI measurements from Nordic Red dairy cattle, and further to compare the results with those from analyses of REI, which was used as a reference trait.

Research Data

The data used in this study were collected from Luke's experimental farms Rehtijärvi (tiestall) and Minkiö (loose housing) in Jokioinen between 1998 and 2014. The early data were from several consecutive and continuous feeding trials carried out between 1998 and 2008. Since 2009, the data collection was continued in Minkiö barn with automated feed intake, BW, and milk production data collection, with the main purpose of studying the animal variation in the components of feed efficiency. All cows in the data were fed grass silage and home blend concentrate mix. The proportion of concentrates in the diet depended on the experimental plan (1998–2008), stage of lactation, and digestibility of the grass silage (2009–2014). On average the proportion of concentrate in the diet of the cows in the data was 48.3%. To calculate energy and nutrient intake of the cows' weekly representative subsamples of feeds were collected and combined to 4- to 8-wk samples for analyses based on the study. The silage samples were analyzed for pepsin-cellulase solubility and the solubility values were converted to digestible organic matter content in DM (D-values; Huhtanen et al., 2006). The ME content for grass silage was calculated as 0.016 \times D-value (MAFF, 1975, 1984). The ME concentration of the concentrate was calculated from digestible nutrients (MAFF, 1975, 1984). The digestibility coefficients for the components of the concentrates were taken from the Finnish feed tables (Luke, 2015). The daily MEI was corrected by the total DMI and concentration of ME and protein in the diet according to the correction equation given by Luke (2015). More detailed explanation of data collection and feeding of the cows as well as feed sampling and analyses during years 1998 to 2008 are described in Mäntysaari et al. (2003, 2004, 2005, 2012) and during years 2009 to 2014 in Mäntysaari and Mäntysaari (2015).

Data were from 495 primiparous Nordic Red dairy cows, of which 291 were from different feeding trials and 204 had been measured since changing to routine measuring of feed intake since 2009. The data from wk 1 were excluded due to the big variability in studied traits, which complicated genetic analyses. The analyzed data included 12,350 weekly observations from wk 2 to 40 of lactation. Feed intake was not recorded during the pasture period, which resulted in gaps in the feed intake for animals that were in lactation during summer months. Cows were mainly calving during fall and therefore most gaps were at the end of recording period (lactation wk 31 to 40). Milk yield was recorded Download English Version:

https://daneshyari.com/en/article/8501298

Download Persian Version:

https://daneshyari.com/article/8501298

Daneshyari.com