ARTICLE IN PRESS



J. Dairy Sci. 100:1–12 https://doi.org/10.3168/jds.2016-12031 © American Dairy Science Association[®]. 2017.

A reaction norm sire model to study the effect of metabolic challenge in early lactation on the functional longevity of dairy cows

N.-T. Ha,*^{†1} A. R. Sharifi,* J. Heise,* M. Schlather,[‡] U. Schnyder,[§] J. J. Gross,[†] F. Schmitz-Hsu,[#] R. M. Bruckmaier,[†] and H. Simianer^{*}

*Animal Breeding and Genetics Group, Department of Animal Sciences, Georg-August University Goettingen, 37075 Goettingen, Germany †Veterinary Physiology, Vetsuisse Faculty University of Bern, 3001 Bern, Switzerland

‡Chair of Stochastics and Their Applications, University of Mannheim, 68131 Mannheim, Germany

§Qualitas AG, 6300 Zug, Switzerland

#Swissgenetics, 3052 Zollikofen, Switzerland

ABSTRACT

Due to the discrepancy of the high energy demand for rapidly increasing milk production and limited feed intake in the transition period around parturition, dairy cows require considerable metabolic adaptations. We hypothesize that some cows are genetically less suited to cope with these metabolic needs than others, leading to adverse follow-up effects on longevity. To test this, we designed a reaction norm model in which functional lifetime was linked to the metabolic challenge in the beginning of the first lactation. As challenge variables, we used either the sum of milk yield or the accumulated fat-to-protein ratio of the first 3 test-days (<120d in milk), pre-adjusted for herd-test-day variance. We defined a random regression sire model, in which a random slope was estimated for each sire to assess whether a bull had robust (neutral or positive slopes) or non-robust (negative slopes) daughters. We fitted the model to data of \sim 580,000 daughters of \sim 5,000 Brown Swiss bulls with suitable observations available (≥ 10 daughters per bull). To validate our proposed model and assess the reliability of the estimated (co)variance components, we conducted an extensive bootstrap approach. For both challenge variables, we found the sire variance for the slope of the random regression to be significantly different from zero, suggesting a genetic component for metabolic adaptability. The results of the study show that the ability to cope with metabolic stress in the transition period has a genetic component, which can be used to breed metabolically robust dairy cows.

Key words: metabolic challenge, transition period, reaction norm model, functional lifetime

INTRODUCTION

The inevitable phase of a negative energy balance of dairy cows during early lactation has posed a major challenge for dairy science in the last decades. The substantial increment of energy demand due to the onset of lactation coupled with inadequate feed intake make dairy cows susceptible to major production-related diseases and infections in the early lactation phase (Bobe et al., 2004; Gross et al., 2011, 2013). Hence, optimizing the metabolic adaptation of dairy cows would help to overcome this phase (Sundrum, 2015). Despite the growing interest and the number of studies performed to unveil the complex mechanisms of this adaptation driven by the liver (Greenfield et al., 2000; Reynolds et al., 2003; Loor et al., 2005; Graber et al., 2010; Ha et al., 2015), practical breeding and management strategies to effectively reduce the frequency of disorder cases during early lactation remain limited.

Even under the same conditions and similar production levels, the variability of how individual dairy cows deal with this situation is substantial (Kessel et al., 2008; Gross and Bruckmaier, 2015). This can range from a successful metabolic adaptation without any manifestation of clinical health problems to the development of production-related diseases, such as fatty liver and ketosis, going along with a weakening of the immune system. This has led to the hypothesis that the metabolic adaptability may have a genetic basis (Ingvartsen et al., 2003; Drackley et al., 2005; Graber et al., 2010; Gross and Bruckmaier, 2015; Ha et al., 2015). If existent, capturing this genetically determined metabolic robustness of dairy cows would allow breeding for robust dairy cows that are better suited to cope with excessive energy demand during the transition period. This goal, however, has not been reached so far, not least because there is no general definition of what metabolic robustness is and how it can be measured on a phenotypic scale.

Received September 22, 2016.

Accepted January 20, 2017.

¹Corresponding author: nha@gwdg.de

2

ARTICLE IN PRESS

HA ET AL.

In this study, we suggest defining the metabolic robustness of a dairy cow based on her reaction to a given metabolic load during early lactation. We further define metabolically robust cows as those able to cope with metabolic stress during early lactation. This ability is reflected by a general greater fitness of the cow, which will result in a longer functional lifetime. Figure 1 presents a schematic representation of metabolic robustness and illustrates the difference between a robust and non-robust dairy cow. Robust dairy cows are expected to have, in general, high fitness regardless of the extent of their metabolic load, whereas for nonrobust dairy cows, the extent of metabolic stress has a negative effect on their fitness.

In animal breeding, these kinds of models are referred to as reaction norm models and have been successfully applied for the analysis of genotype \times environment interaction effects (Kolmodin and Bijma, 2004; Streit et al., 2012, 2013). In the context of the present study, the challenge variable was the metabolic load that a cow must face during her early lactation and the response variable is her fitness. Metabolic robustness then is defined as the slope of the fitted linear regression line of the response variable on the challenge variable. To fit such a model, repeated observations of the challenge and response variable would be required for each genotype; that is, for each dairy cow. However, each dairy cow is subjected to an individual metabolic load in each lactation; thus, fitting a regression line at the cow level is not possible. Hence, we suggest the use of a reaction norm sire model, in which a regression line is estimated for each bull using the data of his daughters that are exposed to different challenges and, thus, exhibit different reactions. For our analysis, we assumed that the fitness of a certain cow is reflected by her functional lifetime, whereas the challenge is represented by her energy deficit in the early part of her first lactation, which is quantified by either the cumulated milk yield or the fat-to-protein ratio, which are suitable indicators of negative energy balance, as we will discuss later.

The aims of the present study were (1) to estimate breeding values for the ability to cope with metabolic stress during early lactation (slopes) using a reaction norm sire model, and (2) to assess the accuracy of the proposed model and relevant estimators by means of an extensive bootstrap approach, in which both the random effects and residuals are resampled.

MATERIALS AND METHODS

Raw Data and Data Filtering

In the present study, around 38 million test-day records of ~ 1.4 million Brown Swiss dairy cows were



Figure 1. Schematic representation of metabolic robustness. Color version available online.

available for the traits milk, fat, and protein yields. These test-day records were pre-adjusted for herd-testday variance as well as length of gestation, which was done in the routine genetic evaluation system (https:// wiki.interbull.org/public/Nat_GE_Forms?action=At tachFile&do=get&target=CHEBSWpro.pdf). Among these cows, around 1.4 million cows also had records for the functional lifetime trait obtained from the routine animal genetic evaluation (https://wiki.interbull.org/ public/Nat_GE_Forms?action=AttachFile&do=get& target=CHEBSW10.rtf) as pseudo-records and their corresponding weights from Survival Kit V5.0 (Mészáros et al., 2013), based on dead and living animals born between 1976 and 2014. In general, the pseudo-record should reflect the longevity of an animal corrected for all nongenetic effects, and the corresponding weight should reflect the reliability of the pseudo-records (Tarrés et al., 2006). In the following, the term "functional lifetime" is defined as the logarithmized pseudo-records. For our analysis, we filtered these data by considering only (1) cows that were born before 2011 and have died to have a reliable own record for longevity, (2) animals with pseudo-records having weights greater than 0.0005 to remove unreliable pseudo-records, and (3) animals with at least 3 test-day records within the first 120 DIM of the first lactation to be able to calculate the challenge variable.

Challenge and Response Variables

For each dairy cow, we defined functional lifetime as the response variable and used the sum of the first 3 test-day records in the first lactation for milk yield (kg) Download English Version:

https://daneshyari.com/en/article/5542170

Download Persian Version:

https://daneshyari.com/article/5542170

Daneshyari.com