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Considerations when combining data from multiple nutrition experiments to estimate genetic parameters for feed efficiency

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ABSTRACT

Prior to genomic selection on a trait, a reference population needs to be established to link marker genotypes with phenotypes. For costly and difficult-to-measure traits, international collaboration and sharing of data between disciplines may be necessary. Our aim was to characterize the combining of data from nutrition studies carried out under similar climate and management conditions to estimate genetic parameters for feed efficiency. Furthermore, we postulated that data from the experimental cohorts within these studies can be used to estimate the net energy of lactation (NE_L) densities of diets, which can provide estimates of energy intakes for use in the calculation of the feed efficiency metric, residual feed intake (RFI), and potentially reduce the effect of variation in energy density of diets. Individual feed intakes and corresponding production and body measurements were obtained from 13 Midwestern nutrition experiments. Two measures of RFI were considered, RFI_{Mcal} and RFI_{kg}, which involved the regression of NE_L intake (Mcal/d) or dry matter intake (DMI; kg/d) on 3 expenditures: milk energy, energy gained or lost in body weight change, and energy for maintenance. In total, 677 records from 600 lactating cows between 50 and 275 d in milk were used. Cows were divided into 46 cohorts based on dietary or nondietary treatments as dictated by the nutrition experiments. The realized NE_L densities of the diets (Mcal/kg of DMI) were estimated for each cohort by totaling the average daily energy used in the 3 expenditures for cohort members and dividing by the cohort's total average daily DMI. The NE_L intake for each cow was then calculated by multiplying her DMI by her cohort's realized energy density. Mean energy density was 1.58 Mcal/kg. Heritability estimates for RFI_{kg}, and RFI_{Mcal} in a single-trait animal model did not differ at 0.04 for both measures. Information about realized energy density could be useful in standardizing intake data from different climate conditions or management systems, as well as investigating potential genotype by diet interactions.

Key words: feed efficiency, residual feed intake, energy density, genetic selection

INTRODUCTION

Feed costs are a major expense for US dairy producers, accounting for 56% of total costs of producing milk and offering potential for increased feed efficiency to improve the economic position of dairy producers (USDA-NASS, 2013). Additionally, a general rise in concern over its carbon footprint has led the US dairy industry to establish a goal of reducing greenhouse gas emissions by 25% by 2020 (Connor et al., 2012). Feed efficiency is a major source of variation in the carbon footprint associated with milk production; thus, its improvement could offer substantial reductions in greenhouse gas emissions (Connor et al., 2012).

An increasingly common measure of feed efficiency is residual feed intake (**RFI**), which is defined as the difference between the actual intake and predicted intake after adjusting for level of production, usually through linear regression. A cow with negative RFI is expected to convert feed to energy more efficiently than a cow with neutral or positive RFI. Residual feed intake was first used as a measure of feed efficiency in cattle by Koch et al. (1963) when they regressed DMI on live weight and daily gain in growing beef cattle. In lactating dairy cattle, intake is typically regressed on milk yield, BW, and change in BW or body condition (Buttazzoni and Mao, 1989; Van Arendonk et al., 1991; Veerkamp et al., 1995; Vallimont et al., 2011).

Statistically, the phenotype for RFI is a residual term that includes the variation associated with feed efficiency, but it also includes errors associated with measurements of its component traits (Koch et al., 1963). If the coefficients used to compute RFI are gen-

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erated through least squares means, it is phenotypically independent from its component traits (Koch et al., 1963; Korver, 1988; Korver et al., 1991; Arthur et al., 2001b). However, an adverse effect on the component traits could occur if genetic correlations are not zero (Kennedy et al., 1993). Furthermore, the presence of BW in the regression for RFI forgives large cows for the extra feed required to satisfy their higher maintenance costs, and their increased salvage values may not be large enough to compensate the added maintenance costs incurred over their lifetimes.

The expenses and difficulties associated with measuring individual animal feed intakes, which are necessary for calculating measures of feed efficiency, are considerable. Genomic selection offers a relatively inexpensive solution, as compared with conventional progeny testing. However, before genomic selection for any trait, a reference population of animals with phenotypes and genotypes must be established so that the genetic variation associated with a particular polymorphism can be assigned (Hayes et al., 2009). Subsequent generations can then be genotyped and selected based on genomic EBV derived solely from markers in the absence of phenotypic data (Meuwissen et al., 2001).

The key to effective genomic selection for a trait is the establishment of a reference population that is large enough to provide accurate estimates of SNP effects. Hayes et al. (2009) demonstrated that if a trait is moderately heritable, 0.35 for example, a reference population of approximately 8,000 animals is needed to predict genomic breeding values with an accuracy of 80%. Furthermore, continued collection of phenotypes over time is necessary because linkage disequilibrium dissipates over generations. These requirements are difficult to meet when recording of phenotypes is very expensive, such as for RFI, so collaboration across disciplines, experimental sites, and countries is important (Banos et al., 2012). de Haas et al. (2012) demonstrated that the accuracy of genomic prediction for DMI can increase by up to 5.5% when using a trivariate model that incorporated feed intake data from 3 countries, as compared with univariate models implemented within each country.

Nutrition studies carried out in experimental herds represent a potential source of individual feed intake data from lactating dairy cattle. These studies are characterized by meticulous record keeping, and diets generally meet or exceed the animals' nutritional requirements, but variation in feedstuffs tested and levels of nutrients provided could add variation to RFI measurements. One way to combat this is with the Net Energy System (NRC, 2001). Fan et al. (1995) cites the convenience of calculating dietary requirements in terms of net energy, such that animal requirements are independent of diet, and feed requirements for maintenance are estimated separately from the requirements for productive functions. The NE_L of a diet refers to the energy produced in milk, expended as maintenance, and stored in or mobilized from body tissues after consumption of that diet. The calculation of NE_L typically uses nutrient analyses of TMR samples, but, if data are sourced from many different collaborators and experiments, this information may be difficult to acquire. Therefore, we propose to calculate NE_L within each cohort based on total feed consumed and total energy expended. The objective of our study was to consider the use of phenotypic data from nutrition studies for genetic analyses of feed efficiency in lactating cows, more specifically: (1) evaluate estimates of genetic parameters for RFI and its component traits obtained from small cohorts and a wide array of diets used in nutrition studies, and (2) propose a method for estimating NE_L intake within each experimental cohort for the purpose of computing RFI.

MATERIALS AND METHODS

Data Collection

Data were pooled from 13 nutrition studies carried out between 2007 and 2012 in 3 Midwestern research herds, as summarized in Table 1 and depicted graphically in Figure 1. Eight studies were from the University of Wisconsin (**UW**)-Madison Integrated Dairy Facilities, with 6 at the Emmons Blaine Dairy Cattle Research Center (Arlington, WI) and 2 at the Dairy Cattle Instructional Center (Madison, WI). Four were from the USDA-Agricultural Research Service (**ARS**) Dairy Forage Research Center (Prairie du Sac, WI), and one was from the Cargill Innovation Center (Elk River, MN). All data were collected according to approved animal care and use protocols at the respective institutions. Individual intakes for the 6 studies at the Emmons Blaine Dairy Cattle Research Center were recorded via electronic gates (RIC system, Insentec, Marknesse, The Netherlands); see Chapinal et al. (2007) for a detailed description of the system. In the 2 remaining UW-Madison studies, as well as the studies carried out at the USDA-ARS Dairy Forage Research Center and the Cargill Innovation Center, daily intakes were recorded manually via weigh-backs in a tiestall setting. Eleven of the trials started on the same date for all cows, and for those trials cohorts were assigned based on dietary or nondietary treatments. In the 2 remaining trials, start dates were based on calving dates, and cohorts were assigned initially based on dietary or nondietary treatments followed by additional stratification based on time, such that the cows in each cohort