



Genetic parameters between feed-intake-related traits and conformation in 2 separate dairy populations—the Netherlands and United States

C. I. V. Manzanilla-Pech,*†‡¹ R. F. Veerkamp,*† R. J. Tempelman,§ M. L. van Pelt,*# K. A. Weigel,|| M. VandeHaar,§ T. J. Lawlor,¶|| D. M. Spurlock,** L. E. Armentano,|| C. R. Staples,†† M. Hanigan,‡‡ and Y. De Haas*

*Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, PO Box 338, 6700 AH Wageningen, the Netherlands

†Animal Breeding and Genomics Centre, Wageningen University, PO Box 338, 6700 AH Wageningen, the Netherlands

‡Mococho Research Station, National Institute of Forestry, Agriculture and Livestock Research, 97454 Mococho, Yucatan, Mexico

§Department of Animal Science, Michigan State University, East Lansing 48824

#CRV BV, Animal Evaluation Unit, PO Box 454, 6800 AL Arnhem, the Netherlands

||Department of Dairy Science, University of Wisconsin, Madison 53706

¶||Holstein Association, Brattleboro, VT 05301

**Department of Animal Science, Iowa State University, Ames 50011

††Department of Animal Sciences, University of Florida, Gainesville 32611

‡‡Department of Dairy Science, Virginia Tech, Blacksburg 24061

ABSTRACT

To include feed-intake-related traits in the breeding goal, accurate estimates of genetic parameters of feed intake, and its correlations with other related traits (i.e., production, conformation) are required to compare different options. However, the correlations between feed intake and conformation traits can vary depending on the population. Therefore, the objective was to estimate genetic correlations between 6 feed-intake-related traits and 7 conformation traits within dairy cattle from 2 countries, the Netherlands (NL) and the United States (US). The feed-intake-related traits were dry matter intake (DMI), residual feed intake (RFI), milk energy output (MilkE), milk yield (MY), body weight (BW), and metabolic body weight (MBW). The conformation traits were stature (ST), chest width (CW), body depth (BD), angularity (ANG), rump angle (RA), rump width (RW), and body condition score (BCS). Feed intake data were available for 1,665 cows in NL and for 1,920 cows in US, from 83 nutritional experiments (48 in NL and 35 in US) conducted between 1991 and 2011 in NL and between 2007 and 2013 in US. Additional conformation records from relatives of the animals with DMI records were added to the database, giving a total of 37,241 cows in NL and 28,809 in US with conformation trait information. Genetic parameters were estimated using bivariate animal model analyses. The model included the following fixed effects for feed-intake-related traits: location by experiment-ration, age of cow at

calving modeled with a second order polynomial by parity class, location by year-season, and days in milk, and these fixed effects for the conformation traits: herd by classification date, age of cow at classification, and lactation stage at classification. Both models included additive genetic and residual random effects. The highest estimated genetic correlations involving DMI were with CW in both countries (NL = 0.45 and US = 0.61), followed by ST (NL = 0.33 and US = 0.57), BD (NL = 0.26 and US = 0.49), and BCS (NL = 0.24 and US = 0.46). The MilkE and MY were moderately correlated with ANG in both countries (0.33 and 0.47 in NL, and 0.36 and 0.48 in US). Finally, BW was highly correlated with CW (0.77 in NL and 0.84 in US) and with BCS (0.83 in NL and 0.85 in US). Feed-intake-related traits were moderately to highly genetically correlated with conformation traits (ST, CW, BD, and BCS) in both countries, making them potentially useful as predictors of DMI.

Key words: feed intake, conformation trait, genetic correlation

INTRODUCTION

Feed intake accounts for approximately 50% of variable costs in dairy production in Europe (EU, 2011). Including feed intake or feed efficiency in the selection index is worthwhile to reduce feed costs (Kennedy et al., 1993; de Haas et al., 2012; Veerkamp et al., 2012). Reducing feed intake, while increasing production in the breeding objective, should improve feed efficiency and hence farmer profit, provided that other economically important traits, such as fertility and health, are maintained. To be able to include feed intake in the

Received April 20, 2015.

Accepted September 15, 2015.

¹Corresponding author: coralia.manzanillapech@wur.nl

selection index, specialized equipment is required to obtain individual DMI records. This equipment is expensive to buy and labor intensive to use. Therefore, it is unrealistic that large numbers of records will be obtained to allow accurate estimation of genetic parameters to predict breeding values in a progeny testing scheme.

Another option is to use other traits as predictors, such as production traits (e.g., milk, fat, and protein content) that have been shown to have strong genetic correlations with DMI (Veerkamp and Emmans, 1995; Veerkamp and Brotherstone, 1997; Manzanilla-Pech et al., 2014). Other possible predictor traits are conformation traits or linear type traits, which describe a range of visual characteristics of an animal (Berry et al., 2004), or BCS, which is an estimate of the fat storage (Waltner et al., 1993). Body condition score and chest width (**CW**) are highly correlated with BW and have moderate to high heritabilities (Short and Lawlor, 1992). Several studies have already demonstrated that conformation traits are indeed useful as genetic predictors of DMI and feed efficiency in Holsteins (Veerkamp et al., 1994; Parke et al., 1999; Battagin et al., 2012).

Accurate estimates of genetic and residual correlations between feed-intake-related traits and conformation traits are required to compare the different options of including the latter as predictor traits for DMI within a selection index. However, estimated genetic parameters can vary depending on the population in which they are estimated (van Oers and Sinn, 2011). For instance, due to different selection history, genetic correlations between type and feed intake might differ. The objective of this study was to estimate genetic correlations between 6 feed-intake-related traits and 7 conformation traits for dairy cattle from 2 different countries: the Netherlands (**NL**) and the United States (**US**).

MATERIALS AND METHODS

Selection of the Traits

A careful selection of traits was conducted based on both nutritional and genetic perspectives. Some of the traits are obviously related together because of the trait definition [e.g., milk yield (**MY**) with milk energy (**MilkE**), and BW with metabolic BW (**MBW**)]. Some other traits include part-whole relationships [e.g., DMI with residual feed intake (**RFI**), MilkE with protein and fat content]. The purpose of this paper was to estimate the genetic correlations between all feed-intake-related traits (i.e., DMI, RFI, MY, MilkE, BW, and MBW) and various conformation traits to be able to

determine which traits might be most useful to include in a selection index.

Data Collection and Editing: Feed Intake Traits

The Netherlands. Weekly data on MY, DMI, and BW were available from 2,283 cows that participated in nutritional experiments that were conducted on several Dutch farms during 1986 to 2010. A description of the methodology of most experiments and of the content of the diets has been summarized previously (Veerkamp et al., 2000; Beerda et al., 2007; Zom et al., 2012). Diets primarily included grass silage, fresh grass, dehydrated grass, corn, corn silage, cereal, concentrates or beet pulp. Average DM of the diets was 53 g/100 g. All cows were kept indoors in conventional cubicle housing and they were offered completely mixed diets ad libitum. They were milked twice a day, except for half of the cows in one of the locations ($n = 50$) that were milked 3 times per day. Recording frequencies of the individual feed-intake-related traits varied by experiment: DMI was recorded 1, 2, 3, or 5 times per week (Veerkamp et al., 2000; Beerda et al., 2007; Zom et al., 2012), whereas BW was measured with weighing platforms 3 times per week or daily.

Additional feed-intake-related traits were calculated: MilkE, MBW, and RFI. A full description of the data editing strategies can be found in Tempelman et al. (2015). Milk energy output is expressed in megacalories and was calculated from weekly MY plus the fat % (**FP**), protein % (**PP**), and lactose % (**LP**), using the following formula according to National Research Dairy Council (2001):

$$\text{MilkE} = (0.0929 \times \text{FP} + 0.0563 \times \text{PP} + 0.0395 \times \text{LP}) \times \text{MY}/100.$$

Weekly MBW was computed as the weekly average $\text{BW}^{0.75}$. Kleiber (1932) determined MBW to be proportional to the basal metabolic rate of animals and to be representative of maintenance nutrient requirements for animals as a function of their BW. Residual feed intake is defined as the estimated residual from an energy sink model (Berry et al., 2014), whereby weekly DMI was modeled as a linear function of MilkE, MBW, and BW. The following 6 feed-intake-related traits were analyzed: DMI, RFI, MilkE, MY, BW, and MBW. Twenty-eight-day-average traits were calculated based on the records obtained in the first period of 28 d between 50 and 200 DIM (Tempelman et al., 2015). This restriction was imposed because BW changes are more stable in this interval, resulting in more robust RFI

Download English Version:

<https://daneshyari.com/en/article/10974028>

Download Persian Version:

<https://daneshyari.com/article/10974028>

[Daneshyari.com](https://daneshyari.com)