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Genetic Analysis of Milk Urea Nitrogen and Lactose and Their Relationships with Other Production Traits in Canadian Holstein Cattle

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ABSTRACT

The objective of this research was to estimate heritabilities of milk urea nitrogen (MUN) and lactose in the first 3 parities and their genetic relationships with milk, fat, protein, and SCS in Canadian Holsteins. Data were a random sample of complete herds (60,645 test day records of 5,022 cows from 91 herds) extracted from the edited data set, which included 892,039 test-day records of 144,622 Holstein cows from 4,570 herds. A test-day animal model with multiple-trait random regression and the Gibbs sampling method were used for parameter estimation. Regression curves were modeled using Legendre polynomials of order 4. A total of 6 separate 4-trait analyses, which included MUN, lactose, or both (yield or percentage) with different combinations of production traits (milk, fat and protein yield, fat and protein percentages, and somatic cell score) were performed. Average daily heritabilities were moderately high for MUN (from 0.384 to 0.414), lactose kilograms (from 0.466 to 0.539), and lactose percentage (from 0.478 to 0.508). Lactose yield was highly correlated with milk yield (0.979). Lactose percentage and MUN were not genetically correlated with milk yield. However, lactose percentage was significantly correlated with somatic cell score (–0.202). The MUN was correlated with fat (0.425) and protein percentages (0.20). Genetic correlations among parities were high for MUN, lactose percentage, and yield. Estimated breeding values (EBV) of bulls for MUN were correlated with fat percentage EBV (0.287) and EBV of lactose percentage were correlated with lactation persistency EBV (0.329). Correlations between lactose percentage and MUN with fertility traits were close to zero, thus diminishing the potential of using those traits as possible indicators of fertility.

Key words: lactose, milk urea nitrogen, genetic parameter

INTRODUCTION

Valacta, the DHI organization responsible for milk recording in the province of Quebec, has been collecting data for MUN since 1997 in approximately two-thirds of herds enrolled in traditional milk recording. In 2001, Valacta also started collecting data for lactose in approximately one-third of milk-recorded farms. Phenotypic information of MUN and lactose is sent back to farmers for management purposes. The MUN is generally used as a noninvasive approach to monitor the animal's protein status and the efficiency of nitrogen utilization (Moore and Varga, 1986; Broderick and Clayton, 1997; Jonker et al., 1998; Eicher et al., 1999). Analysis of lactose was introduced by Valacta to include this trait in the calculation of the energy value of milk for the purpose of establishing energy requirements for feeding recommendations.

Literature regarding genetic parameters for MUN and lactose, and their relationships with other production traits in dairy cattle, is scarce. Concentration of MUN in Ontario herds has been shown to be heritable with low genetic correlations with production traits (Wood et al., 2003). In the study by Wood et al. (2003), heritabilities of MUN for the first 3 parities ranged between 0.44 to 0.59, and genetic correlations with production traits were close to zero in parities 1 and 3 and slightly positive in parity 2. Lower heritabilities for MUN have been found in 2 US studies (Vallimont et al., 2003; Mitchell et al., 2005). Both studies found greater heritabilities when MUN was analyzed by midinfrared spectroscopy than with wet chemistry. Wet chemistry methods directly measure urea nitrogen in milk, whereas infrared MUN values are calculated with prediction equations that use spectrum analyses. Mitchell et al. (2005) found a low positive genetic correlation between wet chemistry and midinfrared MUN (0.38

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and 0.23, in first and second parity, respectively). Two recent investigations from the Netherlands found heritability values for midinfrared MUN of 0.14 (Stoop et al., 2006) and of 0.22 (de Roos and de Jong, 2006). Stoop et al. (2006) used a fixed regression test-day model on a relatively small data set of first parity cows, whereas de Roos and de Jong (2006) used a random regression test-day model on a much larger data set of multiparous cows. Heritability of 0.23 was found for MUN by Gredler et al. (2006), using a multiple-trait animal model for MUN, BCS, days to first service, and fat:protein ratio.

Lactose percent has been reported to be highly heritable (0.53), according to a study in Holstein cows from Michigan (Welper and Freeman, 1992). The Michigan study included a relative large number of first-lactation cows (>5,000), and a lactation sire model was implemented to estimate variance components. Welper and Freeman (1992) found that lactose yield was less heritable (0.26) than, but highly correlated with, milk yield traits, and negatively correlated with milk content traits, whereas lactose percentage followed the opposite pattern. Stoop et al. (2006) found a higher heritability for lactose yield (0.47). They also estimated genetic correlations among various production traits. Lactose yield was highly correlated with fat and protein yield (0.58 and 0.86, respectively) and less correlated with MUN (0.22).

Miglior et al. (2006) found a statistically significant association between lactose percentage and MUN in first lactation with functional survival in Canadian Ayrshire and Holstein cows. In particular, Holstein cows were at a decreasing relative risk of being culled with increasing levels of MUN or lactose percentage. Miglior et al. (2006) concluded that the significant association between longevity with MUN and lactose was likely indirect because both traits have been found to be statistically associated with health and fertility status of cows, both of which are associated with longevity.

The underlying motivation for the study was the desire to assess the feasibility of routine estimation EBV for lactose and MUN and to explore their potential as indicator traits for female fertility by estimating their relationship with EBV of other economically important traits. In addition, we wanted to confirm previous findings on MUN by Wood et al. (2003) by using a larger data set and an improved model, as well as to estimate genetic parameters for lactose (yield and percentage), a trait for which literature is scarce. Therefore, the specific objectives of this research were to estimate a) heritabilities of MUN and lactose (yield and percentage) in the first 3 parities, b) their genetic relationships with milk, fat, protein, and SCS, c) breeding values for MUN and lactose percentage in Canadian Holsteins, and d) correlations between bull EBV for MUN and lactose with other traits of interest.

MATERIALS AND METHODS

Test-day records collected from 2001 to 2004 were provided by Valacta for Holstein cows from Quebec farms. The data included animal registration number, herd, calving date, test date, milk yield, fat, protein and lactose percentages, SCC, MUN concentration, number of milkings per day, and a flag indicating supervised/unsupervised control. Full pedigree records were provided by Canadian Dairy Network (Guelph, Canada). All samples were analyzed by midinfrared spectroscopy using Fossomatic 4000 milk analysers (Foss Electric, Hillerød, Denmark) calibrated (wavelength = 9.6 μm) weekly. Calibration samples were analyzed for anhydrous lactose by HPLC (IDF Standard 198/ISO 22662) and for MUN by pH difference (IDF Standard 195/ISO 14637; International Committee for Animal Recording, 2006).

Records from DIM <5 and >305 d were eliminated. The SCC were log-transformed to SCS. Only records from the first 3 parities that had data for all production traits on a given test day, including lactose and MUN, were kept. Within cow, if parity 3 was present, parities 1 and 2 were also present, and if parity 2 was present, parity 1 was also present. Herds were required to have a minimum of 20 cows in the data set to be included in the analysis (~5 cows per year). The final edited data set included 892,039 test day records from 144,622 cows from 4,570 herds. To estimate variance components, a random sample of complete herds was extracted from the edited data set. A total of 5,022 cows from 91 herds (average 55 cows/herd) with 60,645 test-day records were randomly selected. The total number of animals (cows with own records + pedigree) included 15,532 animals.

Covariance components were estimated by Bayesian methods with Gibbs sampling using 6 separate 4-trait random regression test-day models. Custom-written software was used for the analysis. Analyzing all 9 traits in one model was computationally very demanding, and the option of several analyses using smaller number of traits was therefore chosen. The six 4-trait analyses were performed for the following group of traits: 1) Milk, lactose percentage, MUN, SCS; 2) Milk, lactose (kg), MUN, SCS; 3) Fat percentage, lactose percentage, MUN, SCS; 4) Protein percentage, lactose percentage, MUN, SCS; 5) Milk, fat (kg), protein (kg), SCS; and 6) Milk, fat percentage, protein percentage, SCS.

The model for a single trait (milk, fat, protein, SCS, MUN, or lactose) can be expressed in matrix notation by the equation