IDENTIFICATION OF GENETIC AND ENVIRONMENTAL INFLUENCES ON MILK UREA NITROGEN

G. Wood[1], P. Boettcher[2], D. Kelton[3], J. Jamrozik[1] and G.B. Jansen[1]

[1]CGIL, Animal & Poultry Science, University of Guelph, Ontario, Canada
[2]IDVGA-LITA, Via Fratelli Cervi 93, 20090 Segrate (MI), Italy
[3]Population Medicine, University of Guelph, Ontario, Canada

INTRODUCTION

Many dairy herd improvement associations now offer testing for urea nitrogen in milk to producers as part of their test-day analyses. Interest has developed in using milk urea nitrogen (MUN) levels as a method of monitoring the dietary efficiency and protein utilization of dairy herds. Automated infrared spectrophotometric methods were introduced in the early 1990s, making measurement of MUN concentrations fast and inexpensive (Godden *et al.* 2001). Urea is considered to be a normal component of the non-protein nitrogen found in milk. The breakdown of dietary protein for energy results in the production of ammonia. This highly toxic molecule is converted to urea by the liver and kidneys and urea may be present in body fluids at somewhat elevated levels without causing adverse health effects in the cow. At very high levels, however, urea may cause fertility problems (Larson *et al.* 1997). MUN levels are known to vary with the amount of protein in the diet, amount of urine excreted, amount of water intake, dry matter intake, sampling methods, breed, parity, days in milk, season and herd management (Godden *et al.* 2001). MUN concentrations may also differ amongst cows due to genetic differences in their ability to metabolize protein, although there have been no studies published which investigate this possibility. The objectives of this study were to determine the heritability of MUN concentration and its genetic correlations with the production traits milk, fat and protein yield.

MATERIALS AND METHODS

Data. The data for this study were collected from 202 registered Holstein dairy herds from southern Ontario. Milk urea nitrogen concentrations were measured by an automated infrared method on test-day milk samples routinely collected by the milk recording agency (Ontario DHI Corporation). The MUN data provided by Ontario DHI were exported from the on-farm software DairyComp305. In total, 288,785 test-day records from these herds were provided, of which 86,016 contained a valid MUN test score. MUN tests were recorded in all 202 herds between January and December, 1999, and a few herds had additional tests between July, 1997, and December, 1998. The data included herd number, cow registration, birth date, sire identification, lactation number, test-date, milk production and MUN scores for each record. The data were first edited to eliminate records with missing information for any of these variables except sire and birth date. Records with milk, fat and protein yields greater than 99 kg, 9 kg or 6 kg, respectively, were eliminated. A standard 305 day lactation length was imposed by excluding records outside 5 to 305 DIM. Only records for the first three lactations were retained. The average MUN concentration for primiparous cows was 12.41 mg/dl (SD= 3.31 mg/dl) and values ranged from 1.0 to 45.0 mg/dl. For 2nd lactation cows, the mean MUN

concentration was 12.80 mg/dl (SD=3.5 mg/dl) and ranged from 1.0-50.0 mg/dl. For cows in 3rd lactation, the mean MUN concentration was 12.74 mg/dl (SD= 3.45mg/dl) and values ranged from 1.0 to 29.0 mg/dl.
The test-day records were matched to complete Holstein pedigree information provided by the Canadian Dairy Network. Only cows with a known sire were retained and cows with either sire or birth date mismatches were removed. Age at calving was restricted to 18-40, 28-49 and 40-68 months in lactations 1, 2, and 3, respectively. In addition, all records from a lactation were excluded if the cow had less than 4 records in that lactation. The final data set contained 36,074 records on 6102 cows. Adding dams without records, 795 sires and four generations of ancestors of the sires resulted in 14,375 animals in the pedigree file.

Fixed Effect Analysis. A preliminary analysis of fixed effects was done using the GLM procedure of SAS (SAS Institute Inc., 1990). The model, applied to each lactation separately, included effects of herd-test-date (HTD), the interaction of age at calving by season of calving by DIM (AS*DIM), and linear regressions on test-day milk, fat and protein yield. There were three classes of age at calving in months for each lactation (1st: 18-24, 25-29, 30-40; 2nd: 28-38, 39-41, 42-49; 3rd: 40-50, 51-57, 58-68), two seasons of calving (April-September and November-March) and 31 DIM classes. There were 16030, 12196 and 7848 records and 1496, 1509 and 1419 HTD classes in lactation 1, 2 and 3, respectively.

Genetic Analysis. The genetic analysis of MUN was performed with a random regression model (Schaeffer and Dekkers 1994; Jamrozik *et al.* 1997). Random regression models (RRM) are ideal for the genetic analysis of test-day data because they are able to model separate, unique lactation curves for every animal. Linear functions of both random and fixed coefficients and a set of covariates are used to describe the shape of individual curves. The fixed regressions describe the general shape of the curve for all cows belonging to a particular subclass, while the random regressions describe the genetic deviations of each cow from the fixed regressions. The Canadian Test-Day Model (CTDM) (Schaeffer *et al.* 2000) was used as template for the analysis of these data. The CTDM analyzes four traits - milk, fat, protein, and somatic cell score (SCS) - in the first three lactations.

The genetic analysis was done using the same data as the fixed effect analysis. Because the data were collected over a relatively short period of time, there were not enough animals with records across lactations for the CTDM to be feasible. The trait SCS was replaced by MUN and each of the first three lactations was analyzed separately. The model equation for all four traits (milk, fat and protein yield and MUN concentration) in any one lactation was

$$y_{ht:ijk} = HTD_{h:i} + \sum_{m=1}^{q} \beta_{h:jm} z_{tm} + \sum_{m=1}^{q} a_{h:km} z_{tm} + \sum_{m=1}^{q} p_{h:km} z_{tm} + e_{ht:ijk}$$

where $y_{ht:ijk}$ is the test-day record of cow k, for trait h, at DIM t; $HTD_{h:i}$ is the herd-test-date effect; $\beta_{h:jm}$ are the fixed regression coefficients specific to each age-season subclass (j) and trait (h); $a_{h:km}$ are the additive genetic random regression coefficients specific to each trait (h) and animal (k); $p_{h:km}$ are the permanent environment random regression coefficients for each animal (k) and trait (h); z_{tm} represent the covariates associated with DIM; and $e_{ht:ijk}$ are the

residual effects for each record. Fourth order Legendre polynomials were used for both the fixed and random regressions on the scale from 5 to 305 DIM.

Gibbs sampling was used to generate variances and covariances from their respective marginal posterior distributions. For each lactation, 100,000 samples were generated and 10,000 burn-in samples were discarded. Heritabilities of average production and MUN levels were calculated from genetic and permanent environmental variances of the first Legendre coefficient, $V(a_{h:0})$ and $V(p_{h:0})$, and a weighted average residual variance, $V(e_{h:*})$, with weights proportional to the length of the four periods for the residual variance (41, 70, 150 and 40 d). Genetic correlations were calculated from the variances and the covariance of the first Legendre coefficients for all pairs of traits.

RESULTS AND DISCUSSION

The results of the fixed effect analysis are summarized in Table 1. The fixed effects were considered significant at the 0.05 level using the type III sums of squares.

Table 1. Significance of fixed effects for milk urea nitrogen level

Lactation	HTD	AS*DIM	Milk	Fat	Protein	R^2
1	✓	✓	✓	✓	✓	0.65
2	✓	✓		✓		0.62
3	✓	✓		✓	✓	0.65

In all three lactations, the herd-test-day and age-season effects had the strongest significance with Pr>F less than 0.0001. The R^2 for all three models was high, ranging from 0.62 to 0.65, indicating that the fixed effect model accounted for much of the observed variation in MUN.

Table 2. Heritabilities of milk production level and MUN concentration (posterior SD)

Lactation	Milk	Fat	Protein	MUN
1	0.46 (0.08)	0.37 (0.07)	0.41 (0.07)	0.44 (0.02)
2	0.44 (0.10)	0.58 (0.09)	0.46 (0.09)	0.59 (0.07)
3	0.34 (0.08)	0.50 (0.09)	0.36 (0.07)	0.48 (0.07)

Table 3. Genetic correlations between milk production level and MUN concentration (posterior SD)

Lactation	Milk - MUN	Fat - MUN	Protein – MUN
1	0.11 (0.04)	0.01 (0.05)	0.04 (0.04)
2	0.17 (0.14)	0.32 (0.10)	0.22 (0.12)
3	-0.05 (0.16)	0.20 (0.13)	0.06 (0.15)

Tables 2 and 3 summarize the results of the genetic study. Heritabilities of all production traits were in the range of 0.30 to 0.50, at the upper end of the general range of previous results

based on Canadian data (Jamrozik, *et al.*1997). The heritabilities obtained for MUN are very high, reaching the same magnitude as heritabilities of milk production traits, indicating that a very good possibility exists for selection on MUN. The genetic correlations of MUN to production traits is close to zero in lactations one and three, and only slightly positive in lactation two. These weak correlations do not contradict the potential for simultaneous selection for increased yield and reduced MUN concentrations.

CONCLUSIONS

Although various fixed effects such as herd and age explained a large proportion of the variance in MUN, estimates of heritabilities were also quite high (>0.40). Further study is needed to confirm these estimates with larger datasets, to determine the effect of MUN on health traits, particularly those related to fertility, and to evaluate the impact of MUN on economic efficiency of milk production in order to determine whether attention to MUN is warranted in a breeding program.

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