Genetic relationships between milk urea nitrogen increase in the early stage of lactation and reproduction traits in Japanese Holsteins

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Introduction

The Early recovery of an animal's ovary function after calving is important for efficient dairy management. Milk urea nitrogen (MUN) has been used as an indicator to monitor the protein energy balance of cows (Eicher *et al.* (1999)). In addition, the level of MUN has been used to evaluate nutrition levels of a dairy herd, and MUN in early lactation is believed to have a relationship to fertility. Many researchers have studied the genetic and phenotypic relationships between MUN and fertility traits (Butler *et al.* (1996); Mitchell *et al.* (2005); König *et al.* (2008)). The change of MUN periods of days in milk (DIM) might be an indicator of energy efficiency and metabolism status. Moreover, it might be adequate for means evaluating the relationship to fertility. In this study, MUN increases by certain interval of DIM were calculated from test day records in Japan to estimate their genetic parameters. Also, genetic correlations between the MUN increases and reproduction traits were calculated.

Material and methods

Data. Data used in this study were records of insemination, test days yields and pedigree records for first and second lactation cows calved between 2001 and 2007 in Hokkaido, Japan, and their pedigree records. The records of cows that had no sire identification, moved to a different herd, or had less than 6 test day records from 6 to 305 DIMs were eliminated. The method of multiple trait prediction (Schaeffer and Jamrozik (1996)) was used to calculate MUN increases from 6 to 35, 36 to 65, 66 to 95, 96 to 125 DIM (MUN_{6-35}, MUN_{36-65}, MUN_{66-95} and MUN_{96-125}) for each cow, respectively. In this study, days open (DO) and days from calving to first service (DFS) were used as reproduction traits, and the DO were defined as the days from the calving date to the last service date. For insemination records, first and second lactation cows were matched with DO between 21 and 410, DFS between 21 and 200, and the number of services were used for the analysis. After editing, 265,582 and 219,136 cows for first and second lactation were obtained, respectively.

Statistical analyses. Statistical model for both MUN increases and reproduction traits included fixed effect of herd-year of calving, calving year-month and age group at calving, and random additive genetic effect. Genetic parameters of MUN increases between DIMs and genetic correlations between them and reproductive traits were obtained by 2-trait animal model.

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The GIBBS2F90 program for 2-trait analysis was used to estimate genetic parameters (Misztal *et al.* (2002)). Length of Gibbs chain was 100,000, and the first 20,000 samples were discarded as burn-in. Thinning interval was set to 10, and the resulting 8,000 samples were used for calculating posterior means.

Results and discussion

Means and standard deviations of MUN_{6-35} were the highest values among the MUN increases between DIMs for both lactations (Table 1). This might have been caused by the individual difference of adaption of feeding environment after calving or difficulty of MUN prediction in the early stage of lactation. In the second lactation, MUN increased similarly to the first lactation. DO and DFS of the second lactation were slightly longer than the first lactation. The DO and DFS for both lactations were longer than the results of Abe *et al.* (2009) who used from the data from Japanese Holsteins. This could have been caused by the inclusion of more recent animals in this study.

Genetic parameter estimates of the MUN increases and reproduction traits for first and second lactation were shown in Table 2. Variance components of MUN increases for the first and second lactation had similar values for all corresponding periods between lactation. The additive genetic variances of all MUN increases were small compared to the residual variances. The residual variances of MUN_{6-35} were the largest among MUN increases. Generally, various factors influence production traits such as milk, somatic cell score and MUN in early lactation. The same factors may also influenced the MUN increases in this study. Thus, the residual variances of MUN increases earlier in lactation in this study were considered to be larger than later in lactation. The heritabilities of MUN_{6-35} and MUN_{36-65} for first lactation (0.01 and 0.02, respcetively) were lower than MUN_{66-95} and MUN_{96-125} (0.06 and 0.05, respcetively). The heritabilities for second lactation showed the same tendency to the first lactation. These results suggest that genetic factors of the MUN increases between DIMs are very small and to use genetics to improve fertility will be difficult. Heritabilities of DO (0.06 and 0.06 ,respectively) and DFS (0.06 and 0.05, respectively) for both lactations were low and were consistent with Mitchell *et al.* (2005) and Abe *et al.* (2009).

Genetic and phenotypic correlations between the MUN increases by DIM intervals and reproduction traits are shown in Table 3. For the first lactation, MUN_{6-35} and MUN_{36-65} were genetically related to DO (0.25 and 0.20, respcetively), whereas MUN_{66-95} and MUN_{96-125} were not related to it (0.10 and 0.03, respcetively). Genetic correlation between MUN and DO in the first lactation which Mitchell *et al.* (2005) estimated by using the repeatability model was 0.21, which was similar values to genetic relationships of MUN_{6-35} and MUN_{36-65} to DO in the current study. Although the levels of MUN for each cow were not considered in this analysis, these results indicate that there have a close genetic relationship to fertility. Therefore, the use of the MUN increase earlier in DIMs could be more useful for the evaluation of fertility if the levels of MUN for each individual are also used. Also, genetic correlatons between MUN_{6-35} or MUN_{36-65} with DFS in first lactation cows were more than 0.2, respectively. König *et al.* (2008) reported that the genetic correlation between average MUN of the earlier two test-days and DFS were 0.29, and which was similar to the results of this study. However, the results of Mitchell *et al.* (2005) were different from this study. As reported by König *et al.* (2008), these results might come from the difference in the definition of MUN as traits. The genetic correlation values between the MUN increases between DIMs and reproduction traits for the second lactation cows tended to be lower than the first lactation. However, the genetic relationship between MUN_{96-125} and DFS was slightly negative (-0.28) in the second lactation. Since these was no relationship to the first lactation, the genetic relationships between the MUN increases and DFS should be investigated separately for each lactation.

Table 1: Descriptive statistics of the MUN increases by DIM intervals and reproduction traits for the first and second lactation cows

	First lactation		Second lactation	
Trait	mean	SD	mean	SD
MUN_{6-35} (mg/dl)	2.0	6.4	1.3	6.1
MUN_{36-65} (mg/dl)	0.5	1.4	0.4	1.5
MUN_{66-95} (mg/dl)	0.2	0.4	0.1	0.5
MUN_{96-125} (mg/dl)	0.1	0.4	0.1	0.5
Days open (days)	133.2	73.0	138.4	73.5
Days from calving to first service (days)	82.6	30.8	83.2	30.9

Table 2: Estimates of genetic parameters of the MUN increases by DIM intervals and reproduction traits for the first and second lactation cows

	First lactation			Second lactation		
Trait	σ_a^2	σ_e^2	h^2	σ_a^2	σ_e^2	h^2
MUN_{6-35} [a]	0.06	2.60	0.01	0.04	3.17	0.02
MUN_{36-65}	0.04	1.43	0.02	0.03	1.67	0.03
MUN_{66-95} [a]	0.07	1.10	0.06	0.07	1.30	0.05
MUN_{96-125} [a]	0.06	1.10	0.05	0.06	1.30	0.04
Days open [b]	0.03	0.47	0.06	0.03	0.48	0.06
Days from caiving to first service [b]	0.05	0.73	0.06	0.04	0.76	0.05

[a] σ_a^2 and σ_e^2 has been divided by 10^{-1}

[b] σ_a^2 and σ_e^2 has been divided by 10^{3}

Table 3: Genetic and phenotypic correlations between the MUN increases by DIM intervals and reproduction traits for the first and second lactation cows

	First lactation				Second lactation			
	Days open		DFS[a]		Days open		DFS[a]	
Trait	r_g	r_p	r_g	r_p	r_g	r_p	r_g	r_p
MUN_{6-35}	0.25	0.03	0.26	0.02	0.14	0.02	0.13	0.01
MUN_{36-65}	0.20	0.02	0.23	0.02	0.10	0.01	0.05	0.01
MUN_{66-95}	0.10	0.02	0.13	0.00	-0.04	-0.01	-0.16	-0.01
MUN_{96-125}	0.03	-0.05	0.00	-0.02	-0.09	-0.03	-0.28	-0.03

[a] DFS = days from calving to first service

Conclusion

Genetic correlations between MUN increases in early intervals and reproduction traits were small found for the first lactation, however their heritabilities were very low. The levels of MUN for each cow were not considered in this analysis. Therefore, the investigation of the relationships between MUN increases and the levels of MUN will be necessary in further studies, because information on MUN increases may be helpful in clarifying the genetic relationship between MUN and fertility if the levels of MUN for each individual are also used.

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