Genetic Relationships among Metabolic Profile Components, Body Condition Score, Persistency of Lactation and Milk Yield in Holstein Cattle

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Introduction

Health problems for dairy cows are serious concerns for farmers because of their economic loss including reduced milk, increased culling rates and cost for treatment. Several indicators are considered to assess cow condition. Body condition score (BCS) is widely accepted to measure the energy reserves of a cow. Extremely high or low BCS associates with the potential risk of metabolic disorders and the loss of productivity and fertility (Roche et al. (2009)). Persistency of lactation is an ability to maintain peak yield and easily calculated from the individual lactation curve (Gengler (1996)). Persistent animals are more resistant to desease and show increased conception rate and probability of pregnancy (Bar-Anan and Ron (1985); De Vries (2006)). However, recent study shows undesirable genetic relationships among persistency and metabolic diseases (Harder et al. (2006); Appuhamy et al. (2009)). Metabolic profile test (MPT) was established in order to diagnose the dairy herd health (Payne et al. (1970)). MPT is also useful to monitor the metabolic status for individual cows but it is not known how relate with other condition traits and milk yield. The objective of this study was to estimate genetic correlations between MPT traits, body condition score, lactation persistency and 305-d milk yield.

Materials and Methods

Metabolic Profiles. Blood samples of 21,879 Holstein cows were collected from 789 commercial herds in Japan since 2003 to 2004 by veterinarian belonging to National Agricultural Insurance Association (NOSAI). Cows considered were up to 11-th lactation and they were in different stage of lactation or dry period. Earlier record was extracted for few cows sampled twice so that all animals had only one observation. The twelve metabolic indicators were analyzed: hematocrit (Ht), albumin (Alb), blood urea nitrogen (BUN) and serum total protein (TP) for evaluation of protein metabolism; glucose (Glc), total cholesterol (T-Cho) and nonesterified fatty acid (NEFA) for protein metabolism; aspartate transaminase (AST) and γ-glutamyl transpeptidase (GGT) for liver function; calcium (Ca), inorganic phosphorus (iP) and magnesium (Mg) for mineral metabolism. Some records had been missing due to technical problems. Transformation was carried out by taking the natural logarithm for NEFA,

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AST and GGT or square root for T-Cho. Body condition score was also recorded by the same veterinarian.

Milk Yields. Test-day milk records were provided by Hokkaido Dairy Cattle Milk Recording and Testing Association. 305-d milk yield (MILK) and lactation persistency (PERS) were either calculated from lactation curve. Individual curves were estimated using test day records by multiple-trait prediction (Schaeffer and Jamrozik (1996)). Lactation persistency (PERS) was defined the difference of the height of the curve between 240 and 60 so that more persistent cow had larger value. Lactation number of cow dried was assigned to last one.

Final Data. Two data files were merged and only cows with known sire were selected. Pedigree information was provided by Holstein Cattle Association Japan, Hokkaido Branch. Final dataset contained 4,145 cows in 92 herds. Total 31,015 animals were found in the pedigree file.

Parameter Estimation. Fifteen-trait animal model was considered. Following mixed linear model was fitted to metabolic indicators and BCS:

$$y_{ijkl} = HY_i + A_j + PS_k + u_l + e_{ijkl}$$

where y_{ijkl} = observation; HY_i = herd-year of sampling (fixed); A_j = age of calving (fixed); PS_k = parity-stage of lactation (fixed); u_l = additive genetic effect (random); e_{ijkl} = residual error (random). For MILK and PERS, we consider a slightly different model:

$$y_{ijkl} = HY_i + A_j + M_k + u_l + e_{ijkl}$$

where HY_i = herd-year of calving (fixed); M_k = month of calving (fixed) and others are common to above.

(Co)variance components were estimated via Gibbs Sampling by GIBBS2F90 program (Misztal et al. (2002)). The first 100,000 samples were discarded as burn-in. Posterior mean was calculated using 100,000 samples after burn-in. The 95% highest posterior density interval (HPD95) was also calculated for each genetic and phenotypic correlations.

Results and Discussion

Estimates of genetic parameters are shown in Table 1. Heritabilities of metabolic profiles were 0.2 or larger except Glc (0.08), NEFA (0.13) and BUN (0.15). A few genetic correlations excluded zero from their HPD95. Although almost phenotypic correlations did not contain zero there, their absolute values are totally low. The largest genetic (and phenotypic) correlation was found between Alb and Ca. This reflects the fact that half of Alb in blood is combined to Ca in dairy cattle (Capen and Rosol (1989)).

MILK had negative genetic correlation with NEFA (-0.46) and positive with T-Cho (0.32). It indicates that cows with genetically high yielding achieve high level of milk production without serious mobilization of body fat or with desirable liver function. A negative genetic correlation (-0.35) was found between PERS and T-Cho. Cows with greater persistency have lower activity in their livers. Therefore, selection for persistency itself would cause metabolic disorders due to impairment of liver function. This unfavorable genetic relationship was also

Table 1: Genetic (upper) and phenotypic (lower) correlations among traits and heritabilities (diagonal) for each traits.[a]

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	Glc	**8**	12	3	5	−27	8	−22	−24	−1	23	23	27	38 *	−21	−15
2	NEFA	−2	**13**	−32*	4	−29	−12	−21	−33*	29	−2	−1	−24	−6	−9	−46*
3	T-Cho	−4*	−5*	**29**	16	14	31*	8	8	15	24	−17	31*	2	−35*	32*
4	Ht	3*	10*	4	**30**	26	45*	−11	2	−3	23	11	27*	39 *	−9	1
5	BUN	0	−4*	13*	8*	**15**	36*	19	35*	1	23	−1	33*	5	1	−14
6	Alb	−8*	3	32*	31*	14*	**25**	−4	8	19	62*	−2	47*	21	−16	16
7	TP	8*	−7*	5*	−6*	−6*	−9*	**28**	8	−6	−2	−5	−24	8	−10	9
8	AST	−12*	8*	10*	6*	8*	3	0	**23**	4	−15	9	19	8	−25	4
9	GGT	−3	2	13*	1	3	5*	4*	16*	**33**	2	−11	12	16	−8	1
10	Ca	−7*	0	26*	13*	0	41*	4*	1	0	**24**	−28*	31*	0	−21	17
11	iP	−1	−3	−2	5*	10*	1	−7*	0	−1	3	**28**	−4	10	18	−10
12	Mg	3	−5*	22*	15*	19*	33*	−7*	1	5*	10*	−2	**29**	20	0	13
13	BCS	5*	0	−3	9*	−2	9	−3	−3	−4*	5*	4*	4	**17**	−19	−17
14	PERS	−4*	−3	−4	−3	0	−7	−5*	−3	0	−4*	2	−3	−5 *	**19**	24
15	MILK	−14*	−1	24*	−5*	7*	13	0	8*	3	7*	−1	7*	−14 *	−8*	**31**

[a] All values are multiplied by 100.
* Not contained zero within their HPD95.

reported by Harder et al. (2006). BCS was genetically correlated with Glc (0.38) and Ht (0.39). These are common physiological characteristics for obese animals. No significant genetic correlations with other MTP components. This result agrees with previous other studies e.g. Oikonomou et al. (2008).

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