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Blood plasma traits associated with genetic merit for feed utilization in Holstein cows

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ABSTRACT

The objective of this study was to evaluate the potential of selection for feed utilization on associated blood plasma metabolite and hormone traits. Dry matter intake (DMI) was recorded in 970 Holsteins from 11 commercial farms in Pennsylvania and used to derive dry matter efficiency (DME; fat-corrected milk yield/DMI), crude protein efficiency (CPE; protein yield/crude protein intake), and residual feed intake (RFI, defined as actual feed intake minus expected feed intake for maintenance and milk production, based on calculation of DMI adjusted for yield, body weight, and body condition score). Estimated breeding values for the 4 feed utilization traits (DMI, DME, CPE, and RFI), yield traits, body traits, and days open were standardized according to their respective genetic standard deviations. Up to 631 blood samples from 393 cows from 0 to 60 d in milk (DIM) were evaluated for blood plasma concentrations of glucose, nonesterified fatty acids (NEFA), β-hydroxybutyrate (BHB), creatinine, urea, growth hormone (GH), 3,5,3′-triiodothyronine (T3), and other parameters. Blood plasma traits were regressed on DIM, lactation number, herd, and standardized genetic merit. Cows with higher genetic merit for yield had significantly higher concentrations of GH, NEFA (milk and protein yield), and BHB (fat yield) from 31 to 60 DIM, but lower concentrations of glucose from 0 to 30 DIM, and T3 (milk yield, 0–60 DIM). The high GH–low glucose–low T3 concentration pattern was further accentuated for cows with genetic merit for enhanced feed efficiency (higher DME and lower RFI). Cows with a genetic tendency to be thin (low body condition score) also had elevated GH concentrations, but lower blood glucose, creatinine, and T3 concentrations. Those characteristics associated with enhanced feed efficiency (higher GH and lower glucose and T3 concentrations) were unfavorably associated with fertility, as indicated by elevated days open. Elevated NEFA and BHB concentrations were also associated with extended days open. Consideration of metabolic profiles when evaluating feed efficiency might be a method of maintaining high levels of health and reproductive fitness when selecting for feed efficiency.
Key words: feed efficiency, residual feed intake, metabolite, hormone

INTRODUCTION

Selection for yield has increased milk production by 3,713 kg in the United States since 1960 (https://www.cdcb.us/eval/summary/trend.cfm). Studies of the genetic relationship of yield with metabolites and hormones in blood and milk have helped researchers more fully appreciate the effects of selection for yield on physiological processes in the cow (for a review, see Veerkamp et al., 2003). In some studies, blood traits were measured in young bulls and heifers with the aim of developing early-life predictors of genetic merit (Hayhurst et al., 2009) or as targets of selection in instances where routine milk recording is not practiced (Peterson et al., 1982); however, such efforts did not materialize and are no longer considered necessary because genomic selection can provide early-life prediction of genetic merit with high accuracy (VanRaden et al., 2009). Recent advances in the evaluation of milk samples (Wittenburg et al., 2013) have also created opportunities to evaluate the potential of selection on metabolites to improve the nutritional composition of milk for humans and to improve cow health and reproductive performance (Koeck et al., 2014).

Selection for milk yield has greatly enhanced the efficiency of feed utilization through dilution of maintenance nutrient requirements (Capper et al., 2009). However, genetic selection programs are increasingly focused on direct selection for feed efficiency by developing predictions for DMI (de Haas et al., 2015) and residual feed intake (**RFI**; Pryce et al., 2015). Insulin signaling and lipid metabolism have been as-

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Table 1. The number of observations (n), mean and standard deviation (SD) for blood metabolites from DIM 0 to 30 and from DIM 31 to 60

	0 to 30 DIM			31 to 60 DIM		
Metabolite[1]	n	Mean	SD	n	Mean	SD
Glucose (mmol/L)	316	3.529	0.504	315	3.694	0.405
NEFA (mmol/L)	301	0.665	0.361	306	0.399	0.229
ln NEFA	301	−0.554	0.560	306	−1.088	0.604
BHB (mmol/L)	316	0.827	0.764	315	0.651	0.783
ln BHB	316	−0.449	0.661	315	−0.715	0.638
Growth hormone (μg/L)	178	8.248	4.440	115	7.370	3.884
T3 (triiodothyronine) (nmol/L)	178	1.227	0.529	116	1.358	0.439
Creatinine (μmol/L)	138	99.732	14.059	199	87.980	9.980
Urea (mmol/L)	316	4.170	1.406	315	4.191	1.313

[1]ln NEFA = natural log of nonesterified fatty acids; ln BHB = natural log of BHB.

sociated with differences in RFI for lactating cattle (Xi et al., 2015). However, relationships of feed efficiency with blood metabolites and hormones have not been defined as clearly as relationships of milk yield with blood metabolites and hormones. The objective of this study was to investigate relationships of feed utilization and related traits with blood metabolite and hormone profiles in early lactating Holsteins.

MATERIALS AND METHODS

Feeding and Feed Intake

Feed intake measures and genetic evaluation of feed utilization have been described previously for this population of lactating Holstein cows (Vallimont et al., 2010, 2011, 2013). Briefly, feed intake was measured over a 24-h period for 970 cows from 11 commercial tiestall herds in Pennsylvania. Herds were visited once a month over a period of 6 mo during the week of monthly milk sampling. The feed intake measures were used to derive 305-d feed intake prediction as well as other feed utilization traits, including DM efficiency (**DME**; FCM yield/DMI); CP efficiency (**CPE**; protein yield/CP intake); and RFI (DMI adjusted for yield, BW, and BCS).

Blood Samples

Blood samples (20 mL) from cows with feed intake measured during their first 2 test dates and that were ≤60 DIM were obtained from the tail vein using evacuated tubes containing EDTA (1.8 g/L of blood) for DNA marker analysis (Dekleva et al., 2012; Dechow and Haagen, 2014) and for evaluation of metabolites, hormones, and aspartate aminotransferase (**AST**). Tubes were immediately cooled on ice and then centrifuged at 1,500 × g for 20 min; the supernatants (plasma) were stored in multiple aliquots at −20°C until analyzed. Concentrations of glucose, nonesterified fatty acids (**NEFA**), triglycerides, cholesterol, creatinine, urea, BHB, growth hormone (**GH**), 3,5,3′-triiodothyronine (**T3**), and activities of AST were determined at the Vetsuisse Faculty at the University of Bern. Hormone concentrations were determined by radioimmunoassay and the other traits were determined using kits as previously described (Aeberhard et al., 2001; Reist et al., 2003). An initial batch of 294 samples was evaluated for glucose, NEFA, BHB, cholesterol, urea, GH, T3, and triglycerides in July 2010, and a second batch of 337 samples was evaluated for glucose, NEFA, BHB, cholesterol, urea, creatinine, and AST in October 2011. There were 238 cows included in both sample periods and 155 cows included in a single sample period. The number of observations, means, and standard deviations for the principal blood traits considered (glucose, NEFA, BHB, cholesterol, urea, GH, T3, creatinine) are reported in Table 1.

Statistical Analysis

Estimated breeding values for selected traits were extracted from the previous genetic evaluations (Vallimont et al., 2010, 2011, 2013) that were conducted with ASREML (Gilmour et al., 2009). The yield traits considered were milk, fat, and protein yields; the feed utilization traits were DMI, DME, CPE, and RFI; and additional traits were BW, BCS, MUN, and days open. To compare results more directly across traits, all EBV were standardized to a mean of 0 and standard deviation of 1. Mean reliabilities for EBV were lowest for days open (35%), BCS (45%), and RFI (50%); all other reliabilities ranged from 61% (DMI) to 79% (MUN).

The relationship of the blood traits with genetic merit was evaluated using a series of regression models in SAS (v 9.3; SAS Institute Inc., Cary, NC). An initial evaluation determined the relationship of herd, DIM, DIM^2, and lactation (1, 2, ≥3) for all blood traits and