Diagnostic Use of Pooled Metabolic Profiles in Czech Dairy Herds

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Introduction

Use of blood chemistries in the form of metabolic profiles to determine nutritional status has been advocated, but acceptance has been limited as a result of high cost and interpretation difficulties. A pooled sample approach to metabolic profiling could provide a more comprehensive snapshot of herd metabolic status with minimal economic investment compared to individual sampling. Study objectives were to evaluate diagnostic reference criteria to determine if pooled sample blood analyte concentrations collected at different periods relative to calving can differentiate between herds with and without health problems, and provide diagnostic value in assessment of transition cow problems.

Materials and Methods

In the course of clinical investigations on 37 dairy herds presented for various periparturient diseases or routine monitoring, blood was sampled from three to seven mature cows within defined time periods to run a pooled sample metabolic profile. Time periods were defined as (days relative to calving): Early Dry (>30 d prior), Close-up (<21 d prior) and Fresh (3-50 following). Analytes determined in metabolic profiles included urea nitrogen (UN), glucose (Glu), albumin (Alb), total protein (TP), aspartate aminotransferase (AST), γ-glutamyltransferase (GGT), sodium (Na), potassium (K), chloride (Cl), calcium (Ca), phosphorus (P), magnesium (Mg), total cholesterol (Chol), β-hydroxybutyrate (BHB) and nonesterified fatty acids (NEFA). Based on clinical diagnosis, herds were categorized into health groups (HG) of no problems (NP, n=6), heat stress (HS, n=6), fresh cow diseases (FD, n=16), low production (LP, n=5) and other diseases (OD, n=7). For each analyte measured, the pooled sample value was subtracted from a herd-based healthy population reference value and divided by the analyte's standard deviation (SD) for a given time period. T-test was used to determine if deviation was different from zero. Analyte concentrations and deviations were analyzed by ANOVA with main effects of period, HG and their interaction with herd as a covariate.

Results

Herds ranged in size from 100 to 750 cows with Holstein and Czech Simmental being the predominate breeds. Time period influenced (P<.0001) NEFA, Glu, Chol, BHB, TP, Na, Cl and AST concentrations. Health group influenced NEFA (P=.003), Glu (P<.0001), Chol (P=.01), Alb (P=.0003), TP (P=.04), Ca (P=.0003), K (P<.0001) and UN (P=.01) concentrations. Of interest was the absence of HG effect on BHB concentration, though there was a tendency (P=.06) for a period by HG interaction. No other interactions were found. Collectively, HG influenced deviation of NEFA (.85 SD, P=.002), UN (-.62 SD, P=.001), Alb (-.48 SD, P=.0003), Ca (-.29, P=.007) and AST (1.3 SD, P=.02) with a HG by period effect on BHB (FR, 1.1 SD, P=.02). However, significance, magnitude of analyte deviation and period effects were specific to and differed between HG. Herds experiencing HS showed the most alterations in blood analyte concentrations having higher NEFA (P<.0001) and Cl (P=.005) and lower Gluc (P<.0001), Chol (P=.001), Alb (P=.0005), Ca (P<.0001), P (P=.02) and K (P<.0001) concentrations across periods. Both BHB (P=.03) and AST (P=.04) were higher in HS herds only in the FR period. Herds with FD showed higher NEFA (P=.008), BHB (P=.04) and AST (P=.05) and lower Alb (P=.0001). A period by HG interaction (P=.005) showed higher FR period BHB concentrations in FD herds. Low production herds showed only differences with lower Chol (P=.02) and Urea (P=.0007) in ED and CU periods and higher AST (P=.02) in CU period. Health effects of OD found higher CU and FR NEFA (P=.0001) and ED and CU TP (P=.02) compared to NP herds.

Significance

Results suggest evaluation of pooled samples based on number of SD the sample value deviates from herd-based population reference values have diagnostic potential. Differential patterns of pooled blood analyte changes around the time of calving are associated with specific disease conditions and have herd-based diagnostic potential.