

Use and Interpretation of Pooled Metabolic Profiles for Evaluating Transition Cow Health Status

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Introduction

Use of metabolic profiles for evaluating herd nutritional or health status has not been widely accepted in the United States. Costs associated with metabolic profiling have been a primary deterrent, as well as interpretation. In a traditional profile protocol eight to 12 individuals are sampled within a herd or animal group for evaluation. Profile results are then interpreted as a mean value or percent of individuals deviating from some defined values. Use of pooled samples was evaluated as a method to collect usable information on herd metabolic status without the high cost of individual sampling. Objectives of this study were to determine if blood metabolite concentrations from pooled serum samples were different from arithmetic mean results of individual samples, and to develop preliminary guidelines for interpretation of pooled samples.

Materials and Methods

Metabolic profiles were performed on serum samples collected from 113 cows on 15 different farms for three defined time periods relative to calving (early dry, close-up dry, fresh). Pooled samples (n=48, 16 in each time period) containing between five and 12 individuals were randomly composited by blending equal volumes of individual serum. Metabolic profile analyses included 22 different analytes, but only data on urea nitrogen (SUN), albumin (Alb), aspartate aminotransferase (AST), calcium (Ca), total cholesterol (Chol), beta-hydroxybutyrate (BHB) and nonesterified fatty acids (NEFA) were used to develop pooled sample guidelines. Individual pooled sample results were compared to arithmetic means of individuals by a one sample T-test. Difference between mean and pooled value, percent mean difference and difference as a proportion of the sample population standard deviation were tested by T-test. Effect of period and herd were tested by ANOVA. Using data from only healthy cows, 0.5, 1 and 2 sigma deviation ranges around the population mean at each time period were calculated. Significance was defined as $P \leq 0.05$.

Results

For the selected analytes, no significant differences were found in comparing arithmetic mean to pooled

sample values. Arithmetic mean minus pooled value difference as a proportion to sample population standard deviation was less than 0.1 standard deviations for all analytes, except Ca (ratio = 0.3). Number of pooled values that were significantly different from sample arithmetic mean for SUN, Chol, Alb, AST, Ca, BHB and NEFA were 1 (2.1%), 3 (6.3%), 8 (16.7%), 2 (4.2%), 14 (29.2%), 4 (8.3%) and 1 (2.1%), respectively. There was no effect of time period on mean-pooled value differences. Of the individual mean-pool comparisons, herd of origin accounted for 73% ($P < .003$) of the variation attributed with significantly different values. Pooled samples from three herds accounted for 39.6% (76 of 192) of the significantly different comparisons. Sample size had minimal effect on pooled sample differences. Pooled or arithmetic sample means for BHB or NEFA exceeding the 2 sigma range indicated more than 33% of individual values were outside of expected normals. Values outside the 1 sigma range indicated between 25 and 33% of individuals had abnormal analyte concentrations. Pooled or mean values within 0.5 sigma range generally had one or no individuals with abnormal analyte concentrations.

Significance

These data suggest pooled samples may be used to assess metabolic status of a group of cows. Most important measures of metabolic status showed minimal differences between pooled and individual samples. Effect of herd on sample differences may suggest poor sample handling practices. Interpretation of pooled values requires different population mean-based criteria rather than traditional individual reference ranges. Preliminary evidence suggests pooled values exceeding 1 or 2 standard deviations around an analyte's population mean indicates moderate or high risk, respectively, for abnormal analyte concentrations within individual animals sampled. Use of a statistical process control monitoring process approach may allow use of pooled metabolic profiles samples as a herd monitoring tool. Further work to determine how best to interpret pooled samples should be explored.

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