

Application of Pooled Sample Metabolic Profiles as a Herd Screening Tool

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Methodologies used in metabolic profiling have ranged from mean analysis of multiple analytes to proportional analysis of single analytes. Periparturient metabolic disease is a result of the cow's inability to maintain coordinated metabolism between lipid, glucose and amino acids. Use of pooled samples was evaluated as a method to collect usable information on herd metabolic status encompassing multiple parameters without the high cost of individual sampling. Aim of this study was to determine if diagnostic interpretation guidelines can be established for pooled metabolic profile samples.

Blood samples were 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 per period) containing between 5 and 12 individuals were randomly composited by blending equal volumes (0.1 to 0.5 ml) of individual serum. Metabolic profiles were performed on individual samples and pooled sample of individuals and included urea nitrogen (SUN), glucose (Glu), albumin (Alb), aspartate aminotransferase (AST), sodium (Na), potassium (K), chloride (Cl), calcium (Ca), magnesium (Mg), total cholesterol (Chol), β -hydroxybutyrate (BHB), and nonesterified fatty acids (NEFA). A population of healthy cows (no disease events; n=49) was used to define reference analyte values (median, standard deviation [SD]). For each analyte measured, arithmetic mean of individuals or pooled sample value were subtracted from a reference median value and divided by the analyte's SD. Laboratory reference criteria were used to determine individual abnormal values. Regression and ANOVA were used to relate number of SD the mean individual and pooled sample values deviated from reference population median to percent of abnormal values within test samples.

Deviation of sample arithmetic mean or pooled value from reference population median was linearly related to percent abnormal values within a pool. Pool size did not seem to influence this relationship. All models within Fresh period were significant ($r^2=.26$ to $.81$, $P<.04$ - $.0001$), except Cl. Close-up period models were significant ($r^2=.36$ to $.79$, $P<.01$ - $.0001$) for Alb, Chol, Cl, Mg, Na, K and NEFA. Across all Fresh analytes, mean or pooled values deviated $.26$ SD from reference population median for every 10% abnormal values within a pooled sample. This relationship was analyte-specific and ranged from $.11$ (Glu) to $.6$ (BHB). Multiples of these regression slopes can be used to generate analyte concentration criteria for interpreting pooled samples. Pooled samples must be interpreted relative to deviation from an expected population mean. The greater a pooled sample deviates from the expected population mean, the greater the abnormal values within the sample.