

321 Use of big data to monitor herd health. H. White\*, *University of Wisconsin Madison, Madison, WI.*

The ability of early detection and treatment to ameliorate negative outcomes associated with health indices have emphasized the value of early detection and treatment. Although this is recognized, the labor-intensiveness and costs associated with monitoring herd health are cumbersome for many farms. Increasing data streams available to farms presents opportunities to use data to better monitor cow and herd health. Within the transition to lactation period, data are presented in the form of milk production and composition, fourier-transform infrared spectroscopy (FTIR) analysis, cow management records, and genomics: all components are employed to monitor postpartum onset of hyperketonemia (HYK). First attempts to predict postpartum HYK from test-day milk and performance variables incorporated into multiple linear regression models had sufficient accuracy to monitor monthly herd prevalence; however, the sensitivity (SEN) and specificity (SPC) lacked for individual cow diagnostics. Subsequent artificial neural network prediction models employing FTIR data and milk composition variables achieved 83 and 81% SEN and SPC. While this fails to reach the diagnostic goals of 90%, it is achieved without individual cow blood samples, which may justify acceptance of lower performance.

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The caveat is that these models depend on milk analysis which is traditionally done every 4 weeks, only catching half of the fresh cows once. Benefits to farms are greatly improved if postpartum cows are tested weekly. This also allows for close monitoring of SCC and may open the door for other herd health monitoring tools to be employed. Future improvements in these models may be achievable by tailoring models to reflect risk factors for each farm or by maximizing SEN at the expense of SPC, especially in HYK and other disorders when the cost of treatment is less than mistreating. Incorporation of genome-wide association studies identifying SNPs associated with risk for metabolic disorders may allow for at-risk cows to be identified and flagged with lower thresholds on prediction models. Alignment of data sources, and integration of existing models, may provide valuable real-time management tools to producers.

**Key Words:** ketosis, hyperketonemia, transition cow