

## Machine learning-based mobile application simplifies the interpretation of on-farm culture results of clinical mastitis milk samples

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On-farm culture (OFC) enables rapid identification of mastitis-causing pathogens, which is a key feature of protocols for selective therapy of clinical mastitis (CM). Nevertheless, the accurate interpretation of OFC results demands personnel with specialized training and experience, presenting a potential challenge for dairy farms. We hypothesized that a machine learning-based automated plate reading mobile application (specifically, Rumi; OnFarm, Brazil) could achieve OFC results interpretation with a level of accuracy comparable to that of a specialist. To test that, we designed 2 trials. First, we compared OFC reading results from a trained specialist and Rumi using mass spectrometry results as reference. We utilized 476 CM milk samples from 11 farms, which were inoculated in chromogenic media plates (Smartcolor 2), and digital images were captured and read by Rumi and the specialist 24h after incubation in the laboratory. Thereafter, we designed a second trial to compare Rumi with farm personnel users after training. We used 208 images of OFC results carried out in 150 herds enrolled in an OFC program. The images were read by Rumi and farm users, and Bayesian Latent Class Models were used to compare results of the two approaches. In Trial 1, Rumi performed as well as the specialist for most CM pathogens. In Trial 2, Rumi presented similar Se and Sp as the FPU for all major groups of pathogens causing CM, which supports its use either in the training of farm users or as a diagnostic tool on farms.

**Take home message:** Rumi excels in reading culture plates on farms, performing on par with a trained specialist. This positions it as a crucial tool for herds seeking to implement protocols for selective therapy of CM.

## The utility of serum biochemical analytes to enhance the resilience of dairy cattle through genetic selection

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Early lactation in dairy cows is characterized by negative energy balance and compromised immune function that could lead to metabolic and inflammatory diseases. Circulating biochemical serum analytes are used as indicators of metabolic and inflammatory diseases. This study aimed to estimate the genetic parameters of serum acute phase proteins (haptoglobin, C-reactive protein (CRP), serum amyloid A (SAA)), liver enzymes (gamma-glutamyl transferase (GGT), aspartate-amino-transferase (AST), glutamate dehydrogenase (GLDH)) and 6 other serum analytes including cholesterol. Blood samples were collected from 885 lactating dairy cows on 11 commercial farms in Alberta, between 2 and 14 days in milk. Serum concentrations of acute phase proteins were determined using enzyme-linked immunosorbent assay and the other analytes were assayed using an automated biochemistry analyzer. Genotype data were collected using Illumina 100K Bovine BeadChip with 78,146 SNPs after quality control. Heritability estimates and standard errors for haptoglobin, CRP and SAA, were  $0.11 \pm 0.08$ ,  $0.35 \pm 0.09$ , and  $0.17 \pm 0.07$ , respectively, and the heritability of other serum analytes ranged from 0.05 to 0.39. GGT was the most heritable and AST the least. The genetic correlations between haptoglobin, CRP, SAA and other analytes varied from -0.95 to 0.91, -0.35 to 0.76 and -0.77 to 0.68, respectively. Genome-wide association studies identified QTL regions on chromosomes BTA24 and 29 for SAA, on BTA12 and 17 for GGT and on BTA11 for cholesterol. Candidate genes were then identified within 100 kb distance of significant SNPs in these regions.

**Take home message:** These results showed low-to-moderate heritability of serum analytes and identified genomic variants associated with serum SAA, GGT and cholesterol. This indicates the potential utility of these analytes to enhance resilience of dairy cows through genetic selection.