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Proteomic characterization of dairy cattle plasma: establishment of biomarkers for endometritis

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Early diagnosis of endometritis following calving in dairy cattle is difficult because subclinical endometritis is poorly described. The goal of this study is to utilize a gel-free mass-spectrometry based proteomics approach to compare plasma proteome of dairy cattle with endometritis to those without. Blood plasma was collected from a commercial herd seven days postpartum (N=20, 10 with endometritis, 10 without). The plasma was then subjected to an acetone protein extraction. The protein pellet was analysed using mass spectrometry to identify and quantify all proteins present. Differential abundance of proteins between treatment groups was determined using both fold change ($\geq$1.5 increase OR $\leq$.75 decrease) and a statistical ANOVA test (P<0.05). 181 non-redundant proteins were quantified with a total of 33 differentially abundant proteins identified between one or more comparisons. The tool ReviGO was used to summarize gene ontology terms associated with differentially abundant proteins. Proteins that met the statistical requirements for differential abundance are extensively involved in immune function. Gene ontology for differentially abundant proteins includes associations with innate immune recognition processes, acute phase responses and immune regulation. These differentially abundant proteins provide physiological information on endometritis. The most promising single potential marker identified here is the "uncharacterized protein G5E513," a protein only previously defined by RNA-transcripts. This poorly described protein is abundant in cows with endometritis, and maybe a potential biomarker of the disease.

Biography

Blake A. Miller is completing his PhD from Ross University School of Veterinary Medicine in St. Kitts. His background is on postgenomics technologies and their applications in diagnostics and selection indices.

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Page 62