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Examining postpartum disease in dairy cows at the molecular level

Helping cows through the transition period by finding alternative diagnostic indicators for metritis at the genetic level is investigated in a new article in *Applied Animal Science*

Champaign, IL, December 7, 2020—Metritis and other postpartum reproductive diseases are familiar challenges in the dairy industry. During the transition period, as a cow moves from pregnancy into lactation, it experiences many physiologic changes, including entering into a negative energy balance, which can impair the innate immune system. As a result, cows are vulnerable during this time and often develop postpartum diseases, such as retained fetal membranes, uterine infection, and sequelae such as displaced abomasums. In an effort to reduce the use of antimicrobials in animal agriculture, emerging research is aiming to reduce disease incidence by studying the relationships among molecular regulatory factors, the immune system, and disease. In a recent [article](#) in *Applied Animal Science*, scientists from Washington State University examined the associations among peripheral leukocyte gene expression, metritis, and associated postpartum disease in dairy cows.

The cows studied had diverse backgrounds, were 14 days in milk or less, and were categorized as having clinical metritis or being healthy. Leukocyte RNA was obtained from the blood of each cow, and the RNA was analyzed for expression of genes related to health. The researchers identified 55 genes that were predictive of health status and focused on 15 genes that were most represented in the diseased cows as compared with the healthy cows.

“These genes are primarily involved in immune cell and receptor function, tissue repair, and cell signaling,” said lead author Craig McConnel, DVM, PhD, Department of Veterinary Clinical Sciences, Washington State University, Pullman, WA, USA. He added, “The top-ranked gene in every rank or error test was *PGLYRP1*, which encodes for peptidoglycan recognition protein 1 (PGLYRP-1). This is an important protein in the innate immune system and has been shown to kill bacteria and have effects on gram-positive and gram-negative bacteria.” Other genes identified by the researchers are responsible for a variety of molecular and biological functions and encode for host-defense antimicrobial peptides and proteins that are key in modulating the immune response. “These proteins provide insight into individual and population-level markers of disease resistance and tolerance that may help guide improvements in host genetic selection,” said David K. Beede, PhD, editor in chief of *Applied Animal Science*.

A more thorough understanding of the immune system’s reaction to postpartum-disease pathogens at the molecular level could not only direct genetic selection but could aid in the prediction and treatment of

disease or help prevent illness altogether. Movement in this direction could provide several alternatives to the use of antibiotics. Once more study in this area has been completed, the researchers plan to connect the findings with therapy and treatment in dairy farms.

The article appears in the December issue of *Applied Animal Science*.

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Notes for Editors

“Transcriptomic analysis of peripheral leukocytes in dairy cows with and without evidence of metritis and associated early postpartum disease” by Craig McConnel, Sierra Crisp, Tyler Biggs, Lindsay Parrish, William Sischo, Amber Adams-Progar, and Stephen Ficklin (DOI: <https://doi.org/10.15232/aas.2020-02092>), *Applied Animal Science*, Volume 36, Issue 6 (December 2020), published by FASS Inc. and Elsevier Inc.

Full text of the article is available to credentialed journalists upon request; contact Brittany Morstatter at +1-217-356-3182 ext. 143 or arpas@assochoq.org to obtain copies. To schedule an interview with the authors, please contact Dr. Craig McConnel at cmcconnel@wsu.edu or 1-509-335-0766.

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