



Cornell University College of Veterinary Medicine

[Home](#) > [News](#) >

Study launched to advance understanding of most important dairy disease

🐾 Tuesday, November 19, 2013 - 12:00am

Mastitis, a highly prevalent dairy cow disease, strikes fear in the hearts of many farmers. The udder infections it entails can ruin cows' health and productivity, wreak economic havoc on farms worldwide, and cost the dairy industry billions of dollars per year.

Faculty at Cornell's College of Veterinary Medicine have embarked on an innovative study to transform the understanding, diagnosis, and treatment of mastitis. Funded by a grant of nearly \$500,000 from the USDA's Cornell National Institute of Food and Agriculture, the three-year study will employ a new technology that is revolutionizing bacteriology to examine mastitis in ways it has never been studied before.



"Mastitis is the most important disease in dairy cows," said principle investigator Dr. Rodrigo Bicalho, assistant professor of dairy production medicine. "Our study will use techniques that were not available until very recently to learn more about mastitis than previously possible. We expect the our results will change perceptions of clinical mastitis, leading to reevaluation of treatment and prevention strategies."

Finding the culprits causing mastitis once required culture techniques that isolated and grew bacterial strains in the lab. But this could only find aerobic bacteria-- those that grow in oxygenated environments. It could not find anaerobic bacteria, which grow in the absence of oxygen. In part because of this limitation, it was long assumed that mastitis was caused by a single bacterial species growing inside the mammary gland and that healthy milk was bacteria-free.

Bicalho's lab was the first to prove that wrong in 2009. Using microbial meta-genomics, which extracts and sequences DNA from all cells in a milk sample, his lab showed a whole new world of anaerobic and aerobic bacteria living inside the mammary gland of both healthy and diseased milk. Bicalho had opened the door to the possibility mastitis can be caused by a combination of several different species of bacteria simultaneously.

In the new study, Bicalho will use meta-genomics to target a fingerprint-like gene called 16s-rRna. Each bacterium has 1-15 copies of these genes, which contain valuable information that can identify species. Bicalho's team will use



Dr. Rodrigo Bicalho

this gene to focus on only bacteria, analyzing their DNA, identifying all bacteria present, and measuring the relative proportion of each species.

This study will use similar techniques to explore the newly discovered bacterial world in milk and how it relates to mastitis. Bicalho and his team will collect samples before, during, and after cows contract mastitis. This will let them map the baseline bacterial ecosystem of normal milk, see the disturbance in that ecosystem when a mastitis-causing pathogen arises, note any other opportunistic pathogens that come in during infection, and observe how bacterial populations return to normal if infection passes.

Major aims of the study include improving the prudent use of appropriate antibiotics and refining meta-genomics techniques into new tools to diagnose mastitis and predict prognoses. To measure how the curative power of various antibiotics relates to the bacteria present, Rodrigo and his team will take milk samples from cows in the field that have contracted mastitis before they treat with antibiotics. They will take follow-up samples from those cows over time to measure the extent and timing of recovery.

“

“This study has huge potential for developing new understanding of how mastitis is caused,” said Bicalho. “We are developing ways to use new meta-genomics technology to better diagnose and treat this devastating disease that will help reduce its health risks and economic burdens.”