



Computer-driven BRD Research

Genome mapping yields clues about cattle disease.

by Patti Drapala

Mississippi State University (MSU) researchers are developing a biological map of how three tiny pathogens cause big losses for cattle producers each year.

Faculty members Mark Lawrence, Shane Burgess and Bindu Nanduri of the College of Veterinary Medicine, and Susan Bridges of the Department of Computer Science and Engineering are studying the genes and proteins of *Mannheimia haemolytica*, *Histophilus somni* and *Pasteurella multocida*. The research team is using state-of-the-art genome science and computer modeling to detect, confirm and locate harmful genes that cause bovine respiratory disease (BRD).

"This disease is known in the cattle industry as shipping fever, because it commonly occurs when cattle are stressed from being shipped hundreds of miles to feedlots," says Burgess, a veterinarian, genome biology researcher and co-director of MSU's Institute for Digital Biology. "Many animals that develop this syndrome stop eating, suffer and die."

The cost of the disease to the cattle industry is more than \$1 billion each year, he says.

The research is funded through a competitive grant from the U.S. Department of Agriculture's (USDA's) Cooperative State Research, Education and Extension Service (CSREES).

Using a newly developed technique called proteogenomic mapping, MSU researchers

have overcome the limitations inherent in computer modeling. They are using mass spectrometers at the MSU Life Sciences and Biotechnology Institute to identify protein amino acid sequences and map them back onto the genome DNA sequences.

Genome sequencing is the process of determining the exact order of the chemical building blocks that make up the genetic instructions, or DNA, used by all living organisms. The speed at which researchers can sequence DNA and identify proteins is made possible by biotechnologies and the development of computational technology to perform these tasks.

"Computers have advanced the process of genome sequencing," says Bridges, a computer scientist, computational biologist and co-director of the Institute of Digital Biology. "The modeling programs that have been developed allow us to chop DNA into manageable pieces of information that we can examine and manipulate."

Accurate identification of all genes in the genomes of the three pathogens will advance the research needed to render the pathogens nonvirulent and develop more effective vaccines to protect against BRD, she adds.

Once the MSU investigators sequenced

the genomes, they used computer algorithms to predict where genes are located. But there are precautions to address in using computer

modeling to map DNA.

"We get false-negative and false-positive predictions," says Lawrence, a veterinarian and microbiologist directing the research.

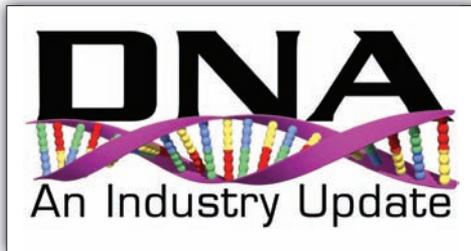
"Additionally, there is no experimental evidence that the predicted genes are real in most cases. Computer programs don't always identify all the genes in a genome."

Genome sequencing will be even more important to agriculture in the future as it becomes useful for unlocking the mysteries of disease. The ultimate goal of the MSU research team is to accelerate disease research by enhancing the genomic tools used to explore how bacteria cause disease.

"The techniques we have developed in this project could be used to confirm gene predictions in other bacterial species as well," Lawrence says. "Our project illustrates how multidisciplinary teams are critical in today's biology and how they can be successful."



Editor's Note: Patti Drapala is with MSU Ag Communications.



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