

# Genome Sequencing Completed For Major Dairy Cattle Microbe

AMES, Iowa—U.S. Department of Agriculture and University of Minnesota scientists have sequenced the genome of the bacterium that causes Johne's disease, a devastating ailment that primarily afflicts dairy cattle.

The bacterium, *Mycobacterium paratuberculosis*, is among the biggest threats worldwide to the health of dairy cattle and other ruminant species such as deer and goats.

"This represents a major research breakthrough that could speed the development of new ways to detect and ultimately eliminate Johne's disease," said Undersecretary for Research, Education and Economics Joseph Jen. He chairs the U.S. Interagency Working Group on Domestic Animal Genomics.

Johne's is a chronic and potentially fatal intestinal disorder that brings about severe diarrhea and weight loss in infected cattle. It is found in eight percent of beef herds and 22 percent of dairy herds in the United States.

The sequencing was achieved at two locations: the Agricultural Research Service (ARS) National Animal Disease Center in Ames, Iowa, under microbiologist John P. Bannantine; and the University of Minnesota's Advanced Genetics Analysis Center

under the leadership of its director, Vivek Kapur, a faculty member of the university's medical school and College of Veterinary Medicine.

Kapur received a National Research Initiative (NRI) Competitive Grant for the research. NRI grants are administered by USDA's Cooperative State Research, Education and Extension Service (CSREES).

While CSREES is the extramural research arm of USDA, ARS conducts the department's intramural scientific research.

Kapur said several genes discovered during the sequencing may help differentiate *M. paratuberculosis* from other closely related bacterial species. "I believe the genomes sequence's availability will provide a much-needed boost to research toward the detection of the disease, the development of vaccines and the ultimate eradication of the disease," he said.

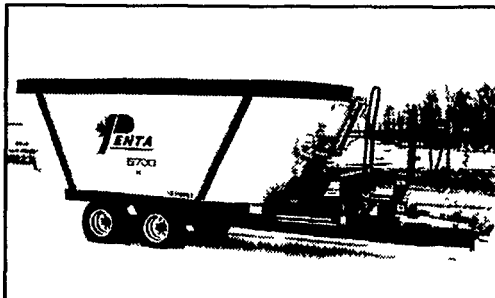
*M. paratuberculosis*' slow growth—it takes up to six months to identify in laboratory culture—impedes both the diagnosis of infected animals and lab-based research on the microbe. "The genome sequence may enable us to not only to understand why this pathogen grows so slowly, but to identify it more rapidly," said Bannantine.

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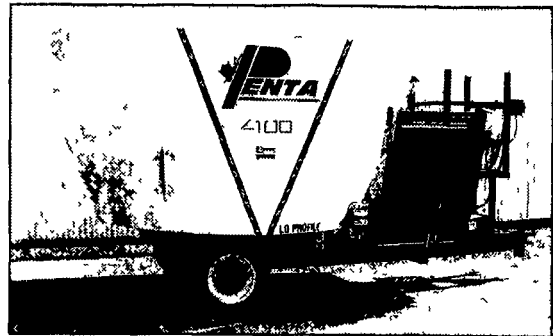
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