

NEWS RELEASE

For immediate release

Contact: Tonya Femal, Academic Health Center, 612.625.2640
Deane Morrison, University News Service, 612.624.2346

SCIENTISTS CRACK GENOME SEQUENCE OF A MAJOR DAIRY PATHOGEN *Johne's Disease Costs Dairy and Cattle Industry Over \$200 Million a Year*

MINNEAPOLIS / ST. PAUL (November 20, 2002) University of Minnesota researchers, with collaborators at the U. S. Department of Agriculture's National Animal Disease Center in Ames, IA, have completed sequencing the genome of the bacteria that causes Johne's disease, a major chronic wasting disease found in dairy cattle. The bacterium, *Mycobacterium paratuberculosis*, is considered one of the most important threats to the health of dairy cattle worldwide. The gene sequencing will allow researchers to develop new ways of early diagnosis, prevention and treatment of a disease that costs the dairy industry more than \$200 million a year. The results of the sequencing analysis are available on-line at www.pathogenomics.umn.edu, and more about Johne's disease can be found at www.johnes.org.

"This is a horrible, hard to diagnose disease, largely because we lacked an understanding of the basic genetic make-up of the organism and the tools to differentiate the bacterium from other closely related species," said Vivek Kapur, BVSc, Ph.D., principal investigator, faculty of the University of Minnesota Medical School and College of Veterinary Medicine, director of the university's Advanced Genetic Analysis Center, and co-director of the Biomedical Genomics Center. "The genome sequence sheds new light on the genes and biochemical pathways in the bacterium and the research offers a starting point for defining the mechanisms by which the organism causes disease and helping devise new strategies to detect infected animals and ultimately help control the spread of the organism."

M. paratuberculosis is a slow-growing bacterium that causes a chronic gastrointestinal infection in dairy cattle and other small ruminant species (such as sheep, goat, and deer) and has both serious health and economic consequences to dairy farming worldwide. While the bacterium has been recognized to cause Johne's disease for more than 100 years, methods for satisfactory diagnosis, treatment and prevention are lacking. During the sequencing project, scientists discovered several genes that may help differentiate *Mycobacterium paratuberculosis* from other closely related bacterial species. "The genes we've identified will serve as targets for the development of new generations of diagnostic tests that are critically needed for the detection and ultimate

eradication of the disease,” said John Bannantine, Ph.D., co-investigator, USDA, National Animal Disease Center.

The analysis of the *M. paratuberculosis* genome found that its sequence contains nearly 5 million base pairs that are represented on a large circular chromosome with more than 4,500 predicted genes. The researchers also found that the chromosome has a large number of sequences repeated throughout the genome. The identification of all of the genes and key metabolic pathways in this organism may serve to explain some of the unique aspects of the biology of the pathogen, including its slow growth in laboratory culture (it may take up to six months to identify by growth in laboratory culture).

“The slow-growing nature of this bacterium has been an impediment to the diagnosis of infected animals and has also served as a major obstacle for laboratory based research on the pathogen,” said Kapur.

The sequencing project represents part of an ambitious “microbial pathogenomics” research program at the University of Minnesota to sequence the genomes of a wide range of human and animal pathogens and use this information as a basis to understand the mechanisms by which they cause disease.

The genome project supported by the U.S. Department of Agriculture through the Cooperative State, Research, Education & Extension Service's (CSREES) National Research Initiative Competitive Grants Program and the Agricultural Research Service (ARS) is expected to provide a boost for wide-ranging research efforts for the development of the next generation of diagnostic tests and vaccines to protect cattle against infection with the bacterium. Recognizing the importance of the disease and the devastating impact on dairy production, the U.S. House Agriculture Appropriations Subcommittee recently approved \$20,352,000 for a National Johne's Disease Management and Testing Program for the current fiscal year. The appropriation is pending approval in the U. S. Senate.

end

Tonya Femal

Media/Public Relations
University of Minnesota
Academic Health Center
Office of Communications
<mailto://femal001@umn.edu>

(612) 625-2640 office
(612) 899-8799 pager
(612) 625-2129 fax

Mayo Mail Code 735
420 Delaware Street S.E.
Minneapolis, MN 55455
<http://www.ahc.umn.edu>