U.S. Meat Animal Research Center
Animal Health Research Unit

Scientists in the Animal Health Research Unit are working to provide research for high-impact diseases with molecular and genomic technologies such as:

- *DNA-based disease traceback*
- *Atypical Bovine Spongiform Encephalopathy (BSE)*
- *Bovine respiratory disease*
- *Bovine Gene Atlas*

DNA-Based Traceback of the 2003 Washington State BSE Case

The first recorded BSE case in U.S. history was announced on December 23, 2003 by Secretary of Agriculture, Ann Veneman. On December 27th, scientists from the Animal Health Research Unit were asked to use DNA markers to help trace the origin of the affected animal. AHRU scientists designed DNA experiments, decoded the results, and wrote the report. On January 6, 2004, USDA's Chief Veterinarian Dr. Ron DeHaven of APHIS announced "We now have DNA evidence that allows us to verify with a high degree of certainty, the [Canadian] birthplace of the BSE-infected cow." Canadian officials concurred.

Atypical BSE

Atypical BSE, is a rare type of "mad cow" disease that is not linked to the consumption of contaminated feed. The second (Texas) and third (Alabama) announced cases of U.S. BSE were atypical. Scientists in the AHRU used molecular and high-throughput genomic approaches to identify a genetic risk factor for atypical BSE susceptibility. Additionally, AHRU research has shown that a majority of U.S. cattle do not harbor this genetic risk factor for atypical BSE.

Bovine Respiratory Disease Complex

Bovine respiratory disease complex (BRDC) is the most costly disease affecting beef cattle in U.S. feedlots. Animals infected with BRDC have reduced feedlot performance including lower daily gains and reduced quality grades, and deaths due to BRDC cost the cattle industry over $1 billion annually. AHRU scientists are using a combination of molecular, cellular, and whole animal approaches to identify animals with increased susceptibility or resistance to this multi-factorial disease, as well as to clarify the roles of the heterogeneous pathogen populations involved.
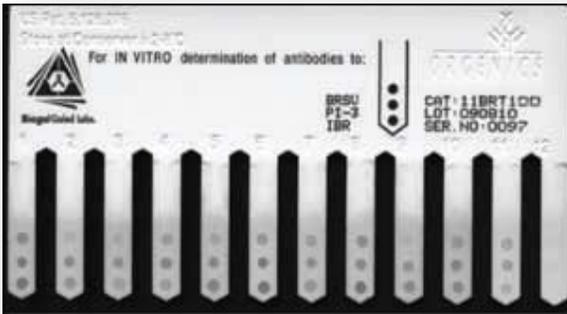
Bovine Gene Atlas

The Bovine Gene Atlas provides gene expression information for 100 tissues from animals used in sequencing the bovine genome. These tissues and gene expression patterns are from animals old and young, and represent important body functions like cardiovascular, digestive, muscular, nervous, reproductive, and respiratory. Scientists world-wide can access and use these gene expression patterns via the internet to answer fundamental molecular genomics questions on their research.