Jersey Johnes Research

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AJCC Research Foundation

- Managed by a Research Advisory Committee appointed by the American Jersey Cattle Association
- Established in 1988
- Funded $850,000 in Jersey-specific research
- Projects selected on:
  - Merit
  - Competence
  - Relevance
Foundation Priorities

- Nutrition of high-producing Jerseys, particularly practical feeding methods to maximize production of valuable milk components
- Factors affecting management of Jersey calves
- Factors affecting yield and/or quality of products manufactured from Jersey milk
- Factors affecting economic impact of Jerseys: efficiencies, net income, longevity, and lifetime profit
- Optimizing the genetic basis for improving animal health and/or enhancing product quality
- Enhancing environmental impact associated with Jerseys
- New technologies for safe and sustainable food production from Jersey cattle
- Feasibility of adding value and increasing consumer acceptance of Jersey-derived products through enhanced product quality and branding.
Projects funded in 2009 & 2010

- Two distinctly different Johnes projects
- Represented one-third of the financial awards made by the Research Foundation in 2009 & 2010
- $10,378 for UW-Madison project
- $6,000 for WA State/USDA-ARS
Genetic Markers Associated with Susceptibility to Paratuberculosis in Jersey Cattle

Sponsored by
AJCA Research Foundation
at
University of Wisconsin-Madison
College of Agricultural and Life Sciences
School of Veterinary Medicine
Project Team

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Dairy cattle genetics
Health traits

Brian Kirkpatrick
Molecular genetics &
DNA analysis

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Veterinary microbiology
Johne’s diagnosis and control
Jersey Project

• **OBJECTIVE:** Examine in Jerseys the 40 most significant DNA markers in Holsteins

• **EXPECTED RESULTS:** Many, but not all, Holstein markers will be significant in Jerseys
  - Some unique susceptibility mutations in each breed
  - Breeds may differ in linkage of DNA markers with genes that cause susceptibility
Jersey Data

• **Current AJCA project**
  - Two herds, 1100 cows, sampling in 2009
  - Expect about 90 infected; 180 matching negative cows

• **“Healthy Cows for a Healthy Industry” project**
  - Two herds, 360 cows, sampled in 2007-08
  - 50 disease positive; 100 matching negative cows

• **Total:** Genotype 140 infected and 280 matching negative Jerseys
Sampling and Testing

• Blood samples for DNA extraction and JD antibody test (ELISA)
• Fecal samples for culture of JD pathogen
• Susceptible group:
  - Cows positive to both JD tests
• Non-susceptible group:
  - Cows negative to both tests
  - Two cows matched to each positive cow by herd, sire & birth date
Jersey Genotyping

- Genotype 40 DNA markers that were most significant in Holsteins
- Calculate genotype frequencies for each marker in each JD group
- For a given marker, different genotype frequency between JD groups indicates linkage of that marker with a gene that causes susceptibility
Benefits to Jersey Breeders

• Which Holstein DNA markers can be used in Jerseys?

• Select Jersey cows and bulls with genotypes that have lower susceptibility to JD
Identification of Gene Mutations Responsible for Susceptibility to Tissue Infection of *Mycobacterium avium* spp *paratuberculosis* in Jersey Cattle

Holly Neibergs, PhD (Washington State University)
Curt Van Tassell, PhD (USDA, ARS, Beltsville, MD)
Long-Term Goal

- Our long-term goal is to reduce the prevalence or severity of Johne’s disease in cattle through genetic selection.

Objective

- The objective of this proposal is to identify if mutations in *HIVEP3* or *EDN2* genes are associated with susceptibility to *Mycobacterium avium subsp. paratuberculosis* (*Map*) tissue infection in Jersey cattle thus gaining critical information to select for animals that are less susceptible to Johne’s disease.
Hypothesis

- Our hypothesis is that mutations in *EDN2* or *HIVEP3* genes are responsible for the association of bovine chromosome 3 with susceptibility to tissue infection of *Map* (the bacteria that leads to Johne’s disease).
The proposed research seeks to determine if a chromosomal region identified in Holsteins is equally important in susceptibility to *Map* tissue infection in Jerseys. This information will be very important to determine if the same genetic mutations are resulting in disease susceptibility in both breeds. The identification of this region as associated with *Map* tissue infection in Jerseys and the identification of the mutation(s) responsible will provide much needed knowledge on the initiation of Johne’s disease through *Map* tissue infection and provide tools to select animals that are less susceptible to Johne’s disease.
Research Design

- The DNA variants in and around these genes on chromosome 3 have been further evaluated in Jerseys and Holsteins by DNA sequencing.

- The DNA variants will be screened for in Jersey cattle with known exposure to Map.
  - DNA differences in animals that became infected will be compared with animals that were resistant to identify if EDN2 or HIVEP3 are the genes associated with susceptibility to Map tissue infection, the first step towards Johne’s disease.
Identify if *HIVEP3* or *EDN2* genes are associated with susceptibility to Johne’s disease.
Value to Jersey Milk Producers

- Identifying gene mutations responsible for susceptibility to *Map* tissue infection in Jersey Cattle will:
  - Provide tools for selection for animals resistant to Johne’s disease
- Reducing the prevalence of Johne’s disease through genetic selection will:
  - Reduce morbidity
  - Reduce mortality
  - Improve animal welfare
  - Improve production
  - Improve profitability
Jersey Marketing Service

• Subsidiary of the American Jersey Cattle Association
• Public auctions and private treaty sales
• Leader in animal health testing
  - Negative Johnes test required for all animals over 24 months old at national sales
Summary

• We view Johnes disease as an important area of research
• We expect the results of these projects will have an impact on the profitability of Jersey dairy businesses