SUSCEPTIBILITY TO BRDC: THE ONGOING SEARCH FOR GENETIC MARKERS

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Bovine respiratory disease complex

- Most costly disease to the cattle industry
  - Over 90% of feedlots vaccinate
  - 13.4% of cattle are treated for symptoms
  - Accounts for over 50% of feedlot deat
  - Cattle treated for BRDC expected to return at least $40 less than untreated calves (NAHMS 2011)

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Bovine respiratory disease complex

- BRDC one of the most studied livestock diseases (Fulton, 2009)
- Despite decades of research, effective immunization or antimicrobial therapies have not been developed that substantially reduce the prevalence or severity of BRDC.

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Bovine respiratory disease complex

- Selection for reduced BRDC incidence has many complications
  - Multiple bacterial and viral causes
  - Subclinical animals
  - Accuracy of diagnosis

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Causes of BRDC

- BRDC is a complex multi-factor disease
- At least five primary viral agents
  - Parainfluenza-3 (PI$_3$)
  - Bovine coronavirus (BCV)
  - Bovine Viral Diarrhea (BVD; 2 strains)
  - Bovine herpesvirus-1 (BHV-1)
  - Bovine Respiratory Syncytial Virus (BRSV)
- Four primary bacterial causes
  - *Mannheimia haemolytica*
  - *Pasteurella multocida*
  - *Mycoplasma bovis*
  - *Histophilus somni*

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BRDC Grant

- Collaborative grant between USMARC (Keele, Kuehn, McDaneld, Smith) and CSU (Enns)
- The long-term goal of the research is to provide genetic tools to decrease susceptibility of beef cattle herds to BRDC and reduce the impact of this costly disease in beef production.

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Objectives

1. Identify QTL associated with incidence of BRDC in commercial feedlot cattle using a large-scale case/control strategy in conjunction with genotyping of pooled DNA samples genotyped on high density bovine genotyping arrays.

2. Use QTL position information to develop SNP markers with consistent predictive merit for resistance/susceptibility, using targeted resequencing of the exome regions near QTL.

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• Can we identify cattle with a propensity to succumb to bovine respiratory disease complex (BRDC)?

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Data Collection

• Health status (treatment records):
  • Healthy/sick
• Collection of samples:
  • Collaboration with multiple feedlots in Nebraska and Colorado
  • Animals selected based on health records
  • 7,500 affected and 7,500 unaffected animals
    • 10,000 used for initial discovery
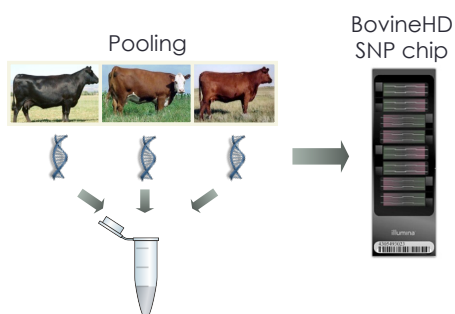   • 5,000 used to identify additional variations in the genome
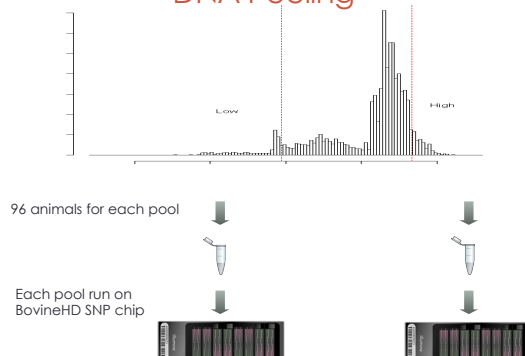
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Data Collection

• Collection of samples:
  • Collect ear samples for DNA extraction at harvest facilities
• Processing of samples:
  • Pool DNA samples
• Genotyping:
  • 770K Bovine Chip

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DNA Pooling

Pooling

BovineHD SNP chip

DNA Pooling

96 animals for each pool

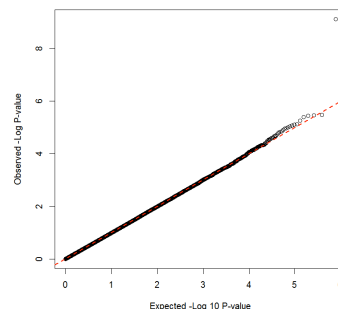Each pool run on BovineHD SNP chip

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Results

- 70 DNA pools (approximately 96 animals in each pool) have been genotyped
  - 35 case and 35 control pools

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Results

Results

- 1 SNP achieved a FDR of 5% or less
- Located on chromosome 16
- This SNP occurs within non-coding region of gene USH2A
  - These gene associated with cilia an microvilli

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Moving Forward

- Continue sampling for DNA pools and genotyping
- Evaluation of additional genomic regions
- Identification of informative SNP in genomic regions

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Thank You!

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