Integrated Program for Reducing Bovine Respiratory Disease in Beef and Dairy Cattle

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US Bovine Respiratory Disease Coordinated Agricultural Project
http://www.brdcomplex.org

Bovine Respiratory Disease Complex Coordinated Agriculture Project

USDA United States Department of Agriculture National Institute of Food and Agriculture

The "Integrated Program for Reducing Bovine Respiratory Disease Complex (BRDC) in Beef and Dairy Cattle" Coordinated Agricultural Project is supported by Agriculture and Food Research Initiative Competitive Grant no. 2011-68004-30367 from the USDA National Institute of Food and Agriculture.

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Overview

- Need for novel approaches for BRD
- What is the BRD Coordinated Agricultural Project
- What is needed to develop accurate genomic/DNA tests
- Work of BRD CAP to address these needs
- Description of field populations being collected
- Implications to beef cattle breeders
- Beef cattle industry structure implications

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Background and Rationale

"Year in and year out, diseases of the respiratory system are a major cause of illness and death in cattle from 6 weeks to two years of age. Sadly, this is as true today as it was 30 years ago despite development of new and improved vaccines, new broad spectrum antibiotics, and increased fundamental knowledge as to the cause of disease"

- Bovine Respiratory Disease (BRD) has been extensively studied since the 1800s, and yet it remains prevalent
- More effective vaccines have not decreased the morbidity or mortality of BRD
- Mortality has increased as vaccine efficiency has increased
- 1.4% of all US feedlot cattle perish before reaching harvest weight
- **Need to develop new approaches to tackle BRD**

Montgomery, D. 2009. Bovine Respiratory Disease & Diagnostic Veterinary Medicine. Proceedings, The Range Beef Cow Symposium XXI. December 1, 2 and 3 2009, Casper, WY. Pages 1-6.

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BRD Coordinated Agricultural Project

Long-term goal is to reduce the incidence of BRD in beef and dairy cattle by capitalizing on recent advances in genomics to enable novel genetic approaches to select for cattle that are less susceptible to disease

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Potential benefits of genomics are greatest for economically-important traits that:

- Are difficult or expensive to measure
- Cannot be measured until late in life or after the animal is dead
- Are not currently selected for because they are not routinely measured
- Have low heritability

Yep, looks like all of ‘em were susceptible

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Disease resistance is a very attractive target trait for genetic improvement

- The presence of genetic variation in resistance to disease, coupled with the increased consumer pressure against the use of drugs, is making genetic solutions to animal health problems increasingly attractive.
- The non-permanent effectiveness of chemical agent (due to development of resistance by the pathogen) further contributes to this interest.

Newman, S. and Ponzoni, R.W. 1994. Experience with economic weights. Proc. 5th World Congress on Genetics Applied to Livestock Production. 18:217-223.

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Other animal industries have successfully targeted selection for disease resistance

- In dairy cattle, selection programs have been developed to take advantage of genetic variability in mastitis resistance, despite the fact that the heritability of clinical mastitis is low and mastitis resistance has an adverse correlation with production traits
- Likewise chicken breeders have long used breeding to improve resistance to avian lymphoid leucosis complex and Marek's disease

Stear, M. J., S. C. Bishop, B. A. Mallard, and H. Raadsma. 2001. The sustainability, feasibility and desirability of breeding livestock for disease resistance. Res Vet Sci 71: 1-7

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What is needed to develop DNA-tests for BRD susceptibility?

Large training/discovery populations with BRD observations and SNP genotypes = used to estimate the value of every chromosome fragment contributing variation BRD susceptibility. This allows for prediction of which chromosome segments regions are important for the trait.

Prediction equation = the results of training can then be used to predict the genetic merit of new animals, not contained in the training data set

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Need for large discovery populations

- The ready availability of dense single nucleotide polymorphism arrays (i.e. 700 K SNP chips) has given rise to hitherto unforeseen opportunities to dissect host variation and identify possible genes contributing to this variation using genome wide association studies

- To have the power to meaningfully quantify genetic variation or perform a genome scan using a dense SNP chip it is necessary to have datasets comprising observations **on several thousands of individuals**.

Bishop, S. C., and J. A. Woolliams. 2010. On the genetic interpretation of disease data. Plos One 5: e8940.

Lead Today with 50K

1. Birth weight
2. Weaning weight
3. Weaning maternal (milk)
4. Calving ease direct
5. Calving ease maternal
6. Marbling
7. Backfat thickness
8. Ribeye area
9. Carcass weight
10. Tenderness
11. Postweaning average daily gain
12. Daily feed intake
13. Feed efficiency (net feed intake)

Pfizer Animal Health
Animal Genetics

50K SNP chip assays
50,000 SNPs spread
throughout genome ($139)

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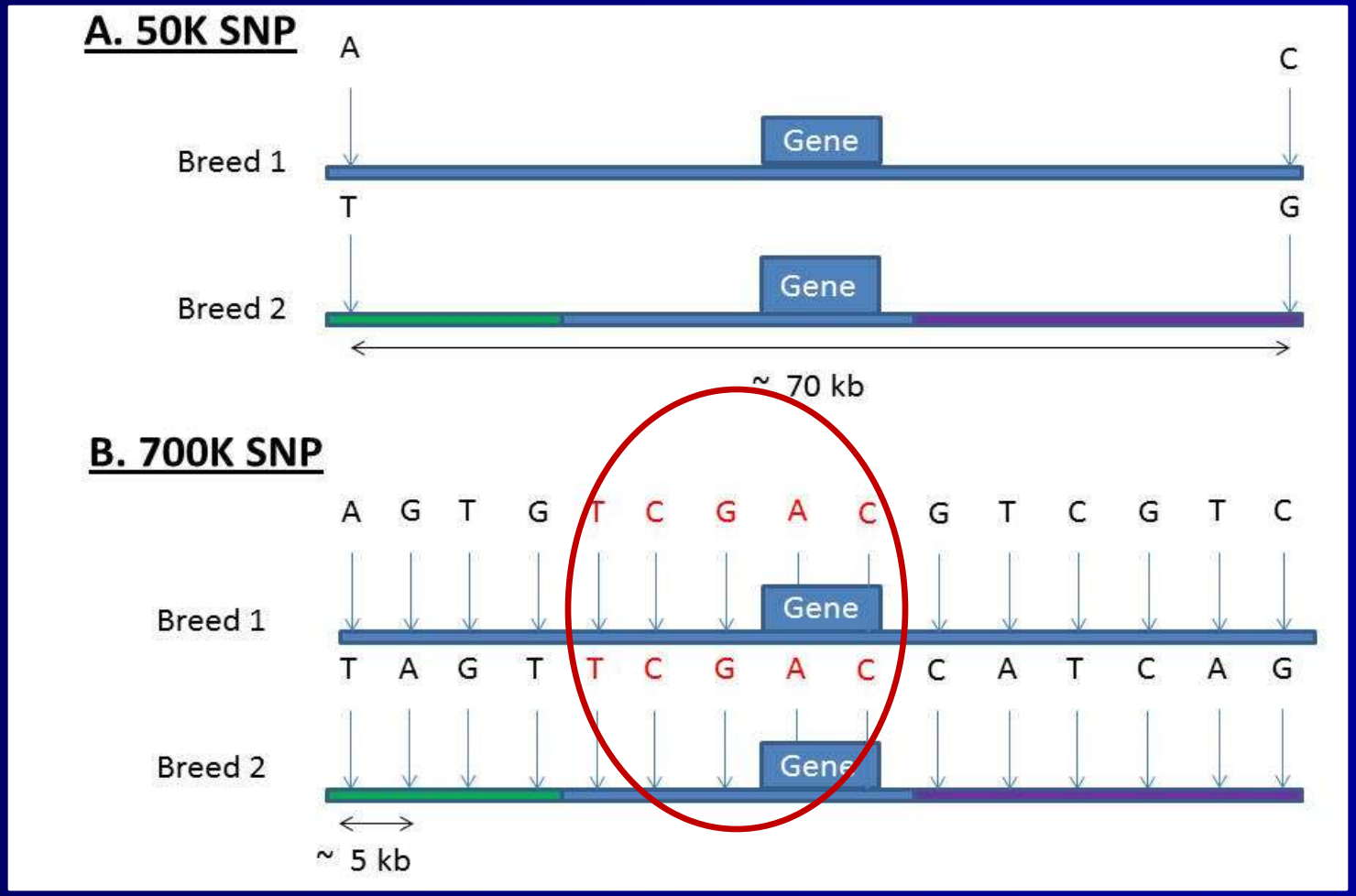
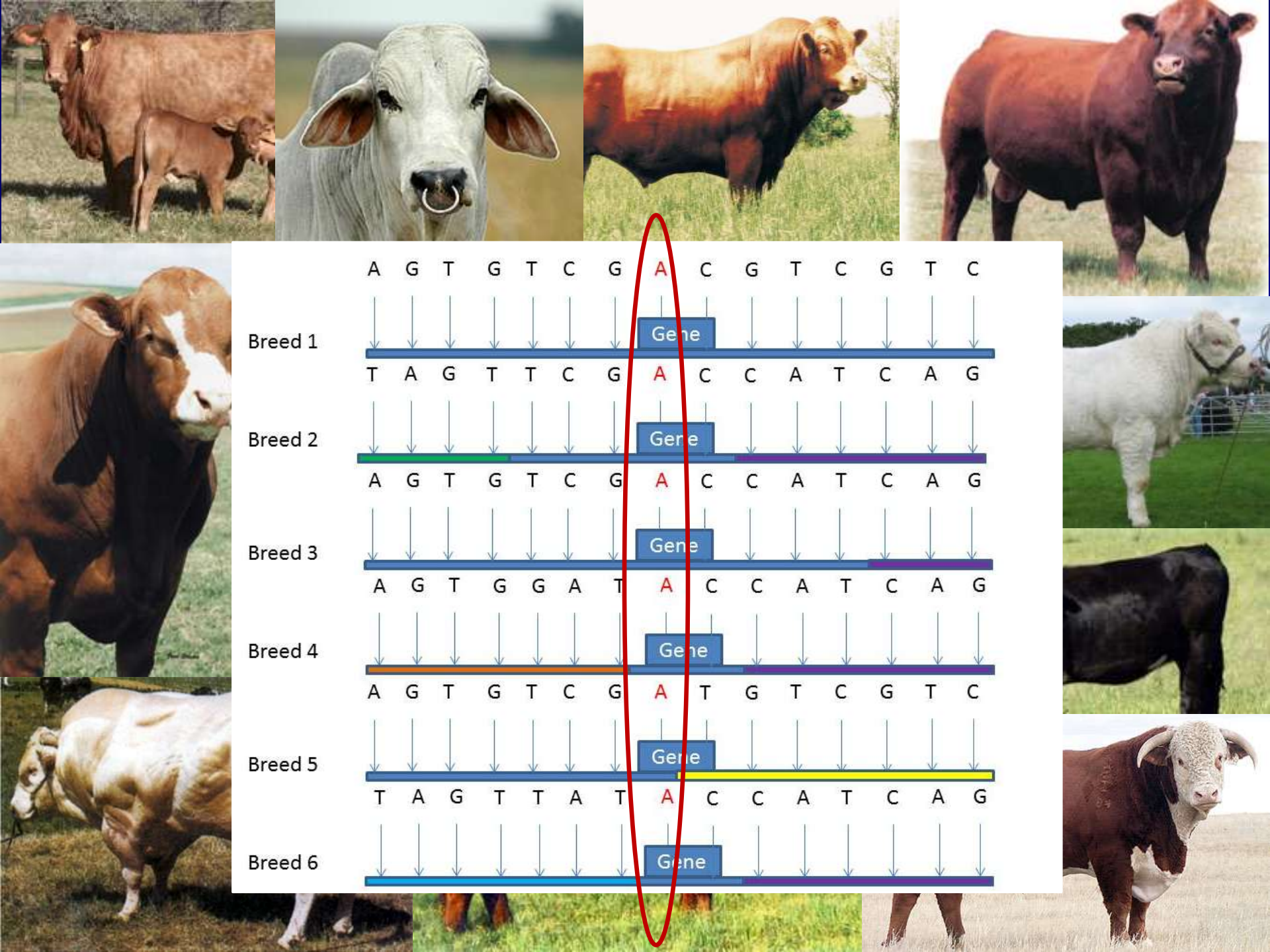
Hopeful that high density SNP chips will enable tests to work across breeds




A G T G T C G A C G T C G T C
Breed 1
Gene
T A G T T C G A C C A T C A G
Breed 2
Gene
A G T G T C G A C C A T C A G
Breed 3
Gene
A G T G G A T A C C A T C A G
Breed 4
Gene
A G T G T C G A T G T C G T C
Breed 5
Gene
T A G T T A T A C C A T C A G
Breed 6
Gene

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Need for careful "case" definition

- For studies of infectious diseases this usually necessitates utilizing field data because challenge experiments of a sufficient scale will not be possible.
- However, such field data is very 'noisy'
  - diagnosis of infection or disease may be imprecise; it can be difficult to determine when infection of an individual occurred
  - it is often unclear whether or not apparently healthy individuals have been exposed to the infection
- These factors add environmental noise to the epidemiological data.

Bishop, S. C., and J. A. Woolliams. 2010. On the genetic interpretation of disease data. Plos One 5: e8940.

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Accurate diagnosis (i.e. case definition) of BRD is critical for success of studies

- Traditional methods for detecting morbid cattle include visual appraisal once or twice daily.
- Animals displaying nose or eye discharge, depression, lethargy, emaciated body condition, labored breathing or a combination of these, should be further examined
- Symptomatic animals with a rectal temperature ≥ 103°F are usually considered morbid and given treatment.
- All of these diagnostic systems are **subjective in nature**.
- Confounding factors include the diligence and astuteness of those checking the animals, the variability and severity of the symptoms the animals experience with chronic and acute BRD, and the disposition of the animals

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Accurate diagnosis (i.e. case definition) of BRD is critical for success of studies

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Accurate diagnosis (i.e. case definition) of BRD is critical for success of studies

- Animals with docile temperaments are more likely to be diagnosed than aggressive or flighty animals
- In one study pulmonary lesions were examined at slaughter in an attempt to confirm the live BRD diagnosis
  - 35% of feedlot steers received treatment for BRD between birth and slaughter, whereas 72% had pulmonary lesions at slaughter.
  - For steers treated for BRD, 78% had pulmonary lesions, whereas 68% of untreated steers also had pulmonary lesions.
- Another study also found that many (29.7%) apparently healthy animals had subclinical disease.
- These studies suggests that the morbidity estimates derived from clinical observations of pen riders likely underestimate the incidence of BRD in feedlot cattle

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BRD CAP: BRD field datasets

Case:control field datasets are being developed for bovine respiratory disease

- 6000 animals – case:control design
  - 2000 dairy calves diagnosed on a collaborating dairy calf rearing ranch (CA)
  - 2000 feedlot cattle diagnosed on a collaborating feedlot (TX)
  - 1000 dairy (NM) and 1000 beef (NV) case:control animals will be used to validate loci associated with BRD in the discovery populations
- All will be genotyped on 700K high density SNP chip

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Year 1: CA Dairy Calf Ranch: 70,000 head capacity

Jessica Davis, DVM
Intern at Veterinary Medicine Teaching and Research Center, University of California, Davis; Tulare
Terry Lehenbauer, DVM
Sharif Aly, DVM
Pat Blanchard, DVM
California Animal Health and Food Safety Laboratory System

Photo credit: Jessica Davis

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Standardization of BRD Diagnosis

- 1000 case and 1000 control 30-60 day old calves
- Use Dr. Sheila McGuirk's calf respiratory scoring chart
  - Temperature, eyes, ears, nose, +/- cough
  - Additional clinical signs: tachypnea, dyspnea, position of head, appetite
  - Give score and either enroll or not (5 or greater to enroll as case)
- Sample collection
  - Blood for DNA extraction and high density SNP genotyping
  - Nasal swab and deep pharyngeal swab to identify viruses (PCR: IBR, BVD, BRSV, and Corona) and bacteria (*Manheimia haemolytica, Pasteurella multocida*, and *Histophilus somni*, and Mycoplasma spp.) present in the nasopharyngeal and pharyngeal recesses

SCHOOL OF VETERINARY MEDICINE
University of Wisconsin-Madison

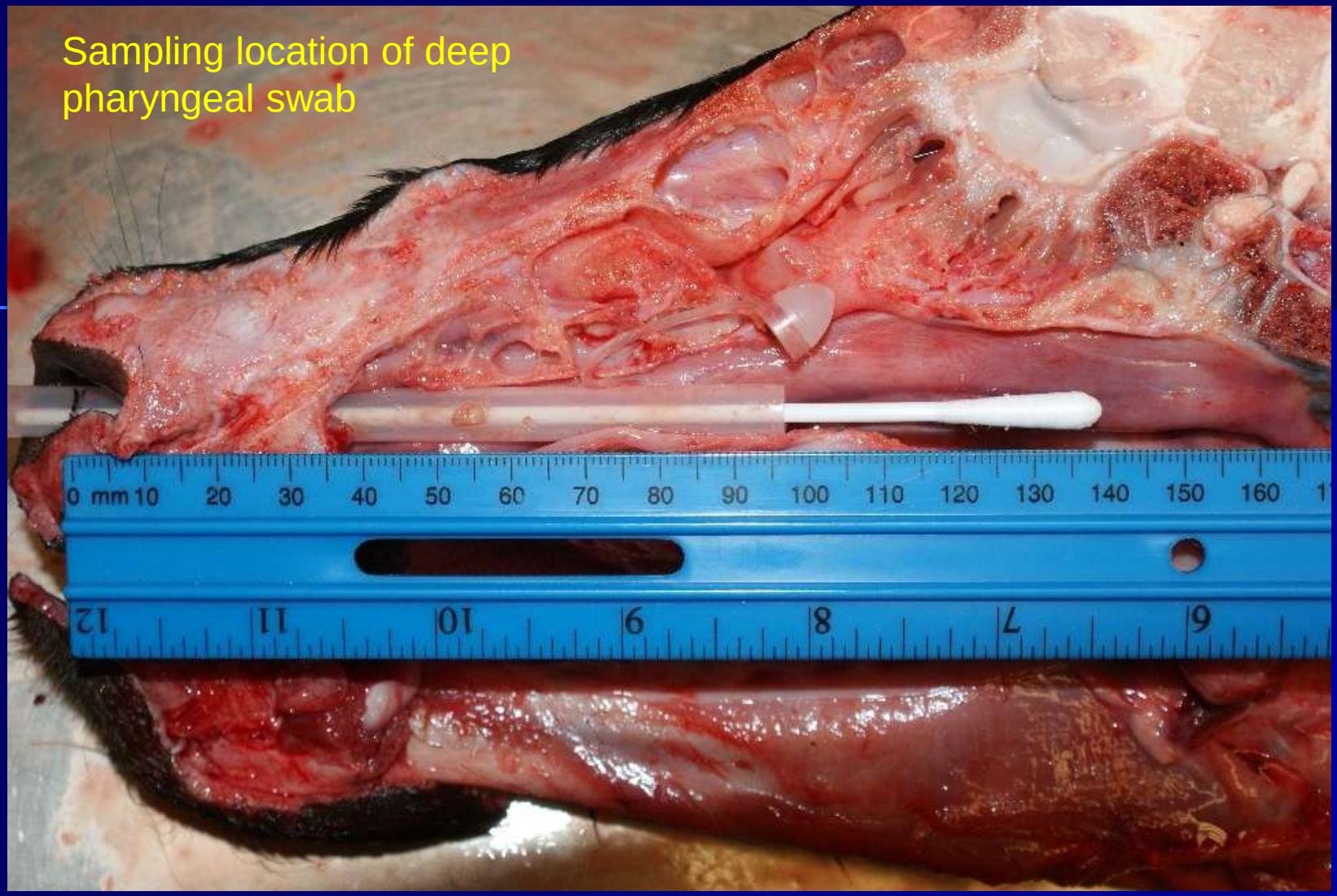
http://www.vetmed.wisc.edu/dms/fapm/fapmtools/8calf/calf_health_scoring_chart.pdf

Calf Health Scoring Criteria			
0	1	2	3
Rectal temperature			
100-100.9	101-101.9	102-102.9	≥103
Cough			
None	Induce single cough	Induced repeated coughs or occasional spontaneous cough	Repeated spontaneous coughs
Nasal discharge			
Normal serous discharge	Small amount of unilateral cloudy discharge	Bilateral, cloudy or excessive mucus discharge	Copious bilateral mucopurulent discharge

Eye scores			
Normal	Small amount of ocular discharge	Moderate amount of bilateral discharge	Heavy ocular discharge

Ear scores			
Normal	Ear flick or head shake	Slight unilateral droop	Head tilt or bilateral droop

Photo credit: Jessica Davis



To culture organisms associated with BRD, pharyngeal swabs offer a less invasive, less stressful and more rapid alternative to broncheoalveolor lavage.

Photo credit: Jessica Davis

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Controls

- Score control in same way as cases (score of 4 or less)
- Try to select animals in the adjacent hutch, same dairy of origin, and same sex
- Collect samples for control animals in same was as case

Objective: Try to identify cases and controls in a relatively constant environment, subjected to the same exposure and stresses, to decrease the environmental "noise" of these field BRD datasets

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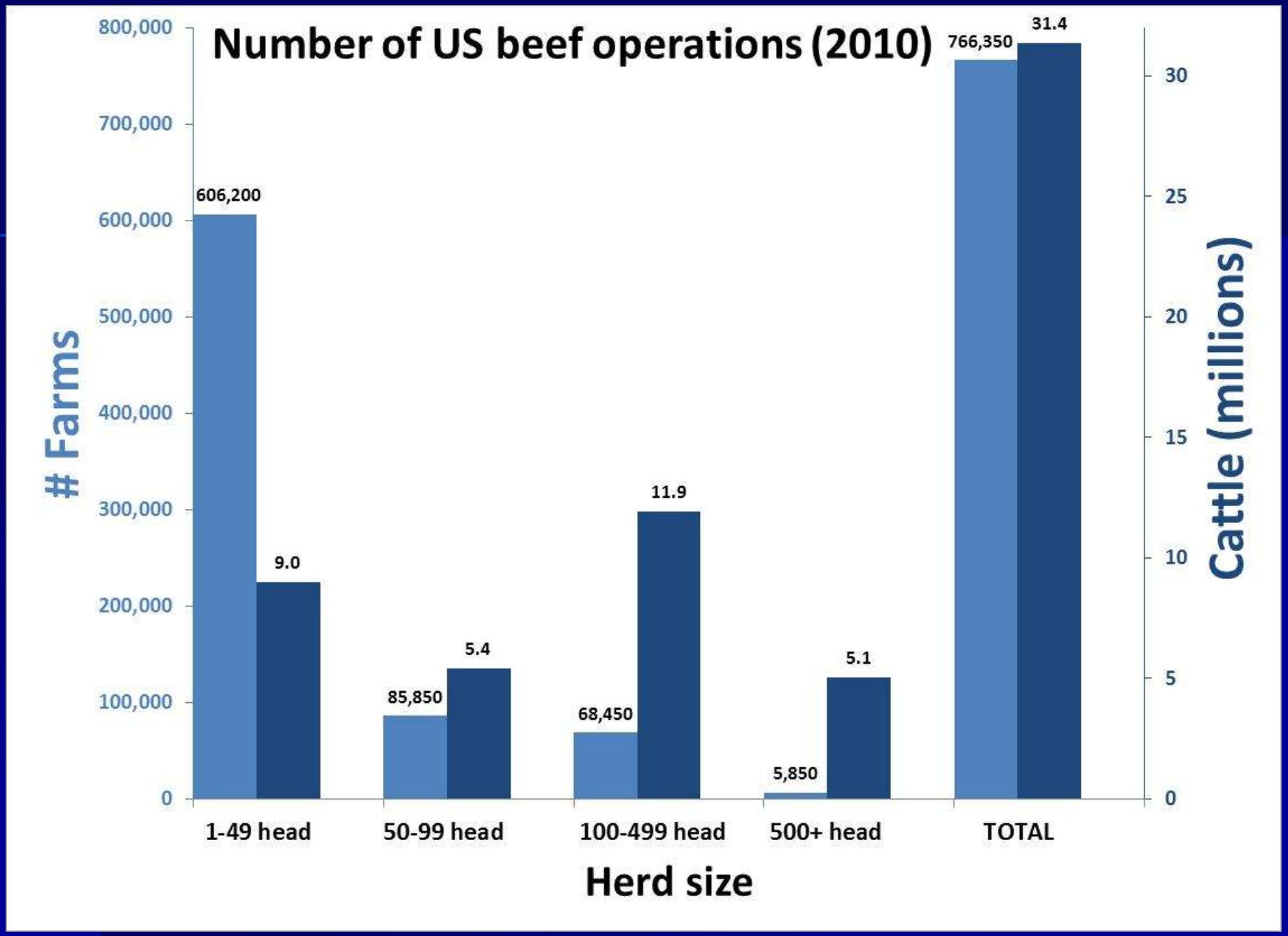
Year 2: TX Feedlot Gonzalez, Texas

Sample collection (1000 case and 1000 controls) scheduled to be completed by 3/2013 and analysis of genotype data completed by 12/31/2014

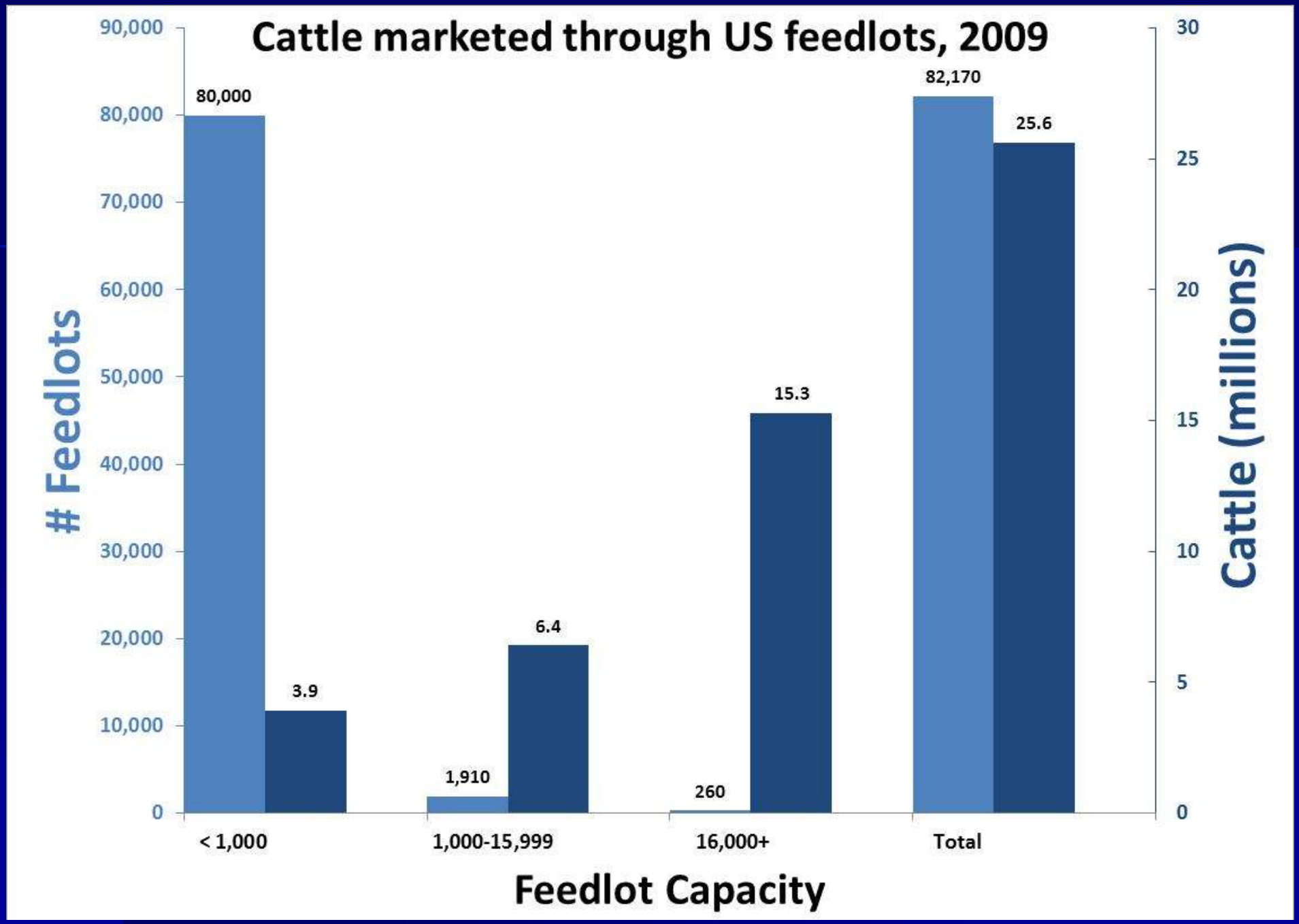
Cole McQueen, Masters student
Dr. Noah Cohen
Dr. Scott Dindot
Texas A&M University

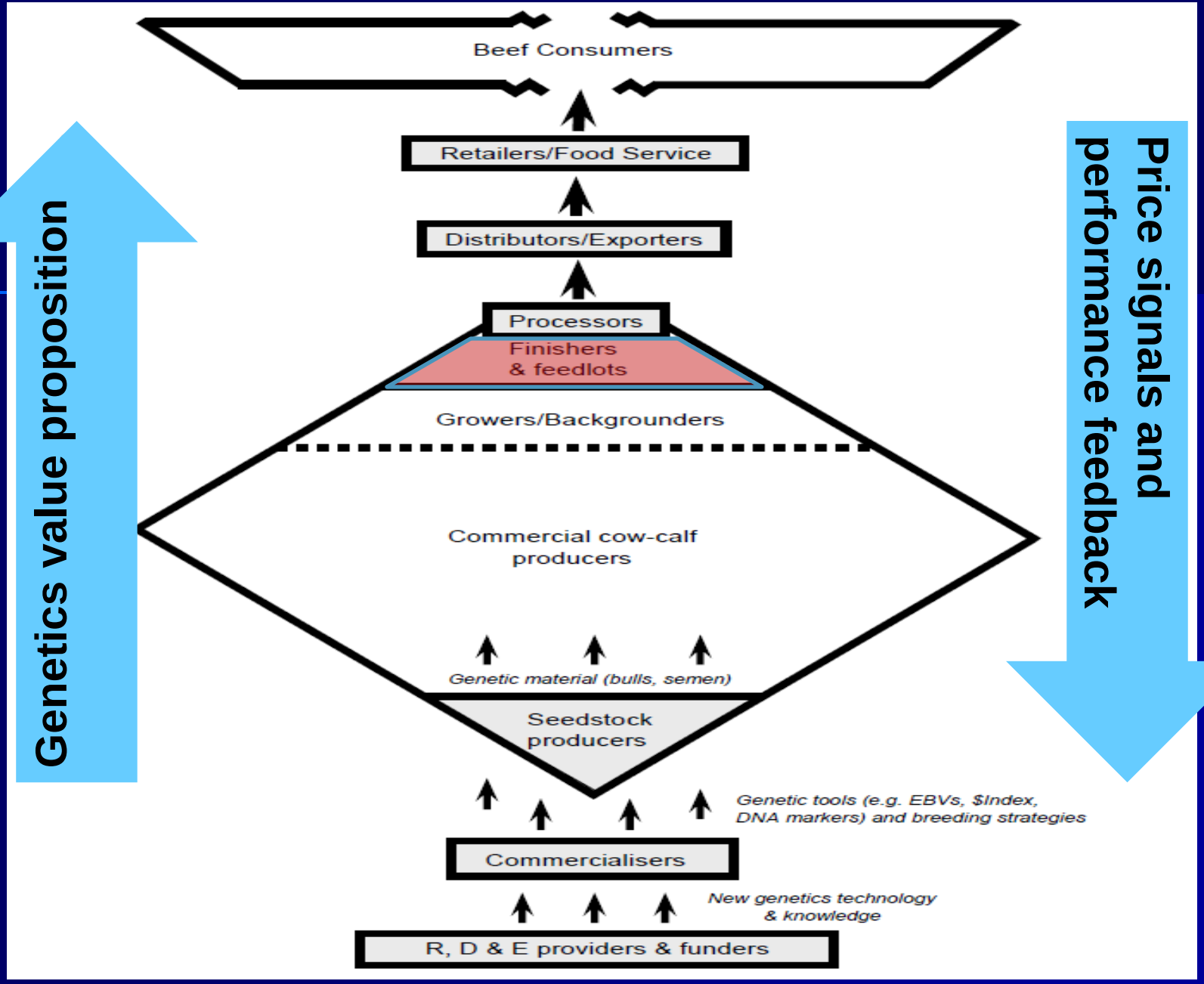

The Future
NEXT EXIT


Number of US beef operations (2010)
Farms
Cattle (millions)
800,000
700,000
600,000
500,000
400,000
300,000
200,000
100,000
0
30
25
20
15
10
5
0
606,200
9.0
85,850
5.4
68,450
11.9
5,850
5.1
766,350
31.4
1-49 head
50-99 head
100-499 head
500+ head
TOTAL
Herd size

Ninety percent of US cattle operations have fewer than 100 head, and most sell their cattle at auction prior to feedlot entry

- In reality most producers' financial returns are tied very closely to the number of calves, a function of reproduction, and less to feedlot performance and carcass traits, and even less to bovine respiratory disease incidence.
- To incentivize the inclusion of BRD resistance in selection decisions, a mechanism analogous to a calf preconditioning bonus would be needed to equitably share some of the value derived from reduced feedlot disease incidence and to compensate breeders and producers for reducing selection emphasis on other economically-relevant traits.


Cattle marketed through US feedlots, 2009
Feedlots
Cattle (millions)
90,000
80,000
70,000
60,000
50,000
40,000
30,000
20,000
10,000
0
30
25
20
15
10
5
0
80,000
3.9
1,910
6.4
260
15.3
82,170
25.6
< 1,000
1,000-15,999
16,000+
Total
Feedlot Capacity



Parnell, P.F. 2007. *Effective value chain partnerships are essential for rapid adoption of beef genetics technology.* Association for the Advancement of Animal Breeding and Genetics. 18. 167-174 .

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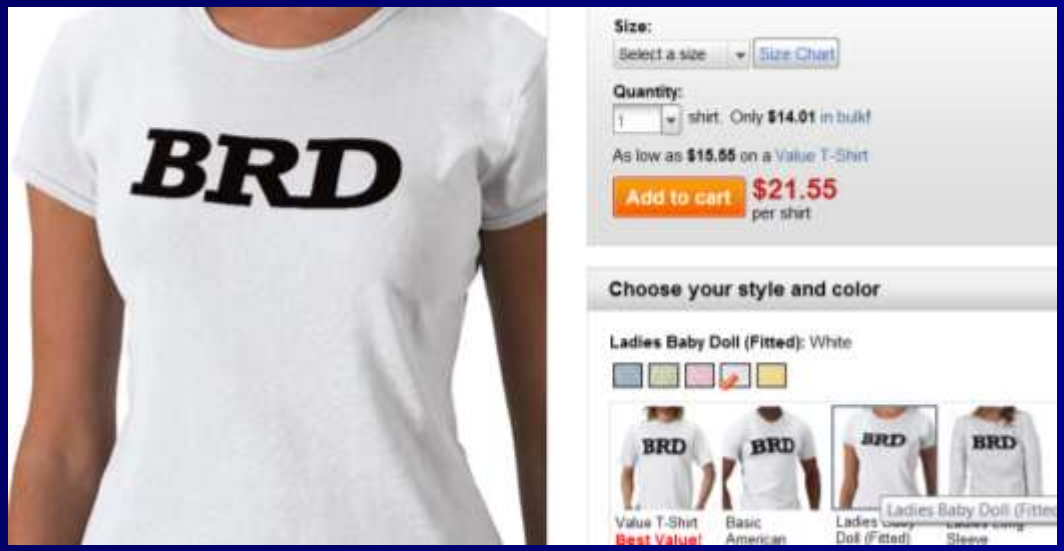
Integrated Program for Reducing Bovine Respiratory Disease Complex in Beef and Dairy Cattle Coordinated Agricultural Project (BRD CAP)

The search for a logo……



What is BRD?

Black Rifle Disease- An obsession with the AR-16/M16 family of firearms. The sufferer feels the need to accessorize/buy more black rifles.

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CONCLUSIONS

- USDA National Institute of Food and Agriculture has recently funded two large 5-year, multi-institution grants on genomic approaches to feed efficiency and BRD
- Both projects employ high-density genotyping of large numbers of animals
- Both traits are valuable – especially to the feedlot sector
- Need to derive relative economic value of these traits and include them in breeding objectives
- Will beef industry organize increased sharing of feedlot performance data and value to drive investment in using genomics to make genetic improvement in feedlot traits?

www.brdcomplex.org

The “Integrated Program for Reducing Bovine Respiratory Disease Complex (BRDC) in Beef and Dairy Cattle” Coordinated Agricultural Project is supported by Agriculture and Food Research Initiative Competitive Grant no. 2011-68004-30367 and the DNA value determination project was supported by National Research Initiative competitive grant no. 2009-55205-05057 (“Integrating DNA information into beef cattle production systems”) from the USDA National Institute of Food and Agriculture.

http://www.brdcomplex.org/

www.brdcomplex.org

About

Bovine Respiratory Disease Complex
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BRD Complex — Facts | Prevention — What you can do | Education — Teaching Materials | Links — Resources | About — Our Research

We are a collaborative group of researchers whose goal is to reduce the prevalence of bovine respiratory disease complex in beef and dairy cattle for the improvement of animal welfare and profitability. The "Integrated Program for Reducing Bovine Respiratory Disease Complex (BRDC) in Beef and Dairy Cattle" Coordinated Agricultural Project is supported by Agriculture and Food Research Initiative Competitive Grant no. 2011-68004-30367 from the USDA National Institute of Food and Agriculture. Our project is led by Dr. James Womack of Texas A&M University and includes scientists and educators from the University of California-Davis, Colorado State University, the University of Missouri, New Mexico State University, Washington State University and USDA's Agricultural Research Service.

USDA NIFA

United States Department of Agriculture
National Institute of Food and Agriculture

Research Plan (PDF 6MB)

Our Researchers

Our Advisory Board

Calendar of Events (PST)

Grant Announcements

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