

"Genetics Research Projects Update from UC Davis"

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CCA midyear 6/14/2012





http://animalscience.ucdavis.edu/animalbiotech/

<u>OUTLINE</u>

Overview of CA Commercial Ranch Project

 National Research Initiative Grant no. 2009-55205-05057 from the USDA National Institute of Food and Agriculture

Overview of the BRD CAP project

 National Research Initiative Grant no. 2011-68004-30367 from the USDA National Institute of Food and Agriculture



United States Department of Agriculture National Institute of Food and Agriculture





California Commercial Ranch Project



2400 cows/ K-A K-A K-A

year



Data collection: AAA EPD & pedigree

Sample collection: For genotyping

MBV



Progeny

Ranch and harvest data Collection Genotyping Paternity

Determination

Assessment of DNA-enabled approaches for predicting the genetic merit of herd sires on commercial beef ranches

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Four ranches:

- Cowley (900 cows)
- Kuck (500 cows)
- Mole-Richardson (700 cows) •
- UC Davis (300 cows)

Approximately 120 Angus herd bulls, and 2,400 cows per year on project



USDA Integrated Grant Collaborators "Integrating DNA information into Beef Cattle Production Systems"

Producer Collaborators:

- Jack Cowley, Cowley Ranch, Siskiyou County, CA
- Dale, Greg, and Richard Kuck, Kuck Ranch, Siskiyou County, CA
- Matt Parker, Mole-Richardson Farms, Siskiyou County, CA
 Processor Collaborators:
- Harris Ranch Beef Company, Coalinga, CA
- Los Banos Abattoir, Los Banos, CA

Software Collaborators:

- Jim Lowe, Cow Sense Herd Management Software, NE
- Other Contributors/Collaborators
- Dr. Darrh Bullock, Extension Professor, University of Kentucky, KY
- Dr. Jerry Taylor, University of Missouri, MO
- Dr. Daniel Drake, University of California Cooperative Extension Livestock Advisor, CA
- Dr. Dorian Garrick, Professor, Iowa State University, IA
- Dr. John Pollak, US Meat Animal Research Center, Clay Center, NE
- Dr. Larry Kuehn, US Meat Animal Research Center, Clay Center, NE
- Dr. Mark Thallman, US Meat Animal Research Center, Clay Center, NE
- Dr. Warren Snelling, US Meat Animal Research Center, Clay Center, NE
- Dr. Matt Spangler, University of Nebraska, NE
- Dr. Bob Weaber, Kansas State University, KS

National corado State University-Cornell University-University of Georgia-Iowa State University Beef Cattle Evaluation Consortium

Cowley Ranch

~20 bulls/season



Kuck Ranch

~10 bulls/season

Mole-Richardson Farms

UC Davis – Sierra foothills

S. DAVA









Honest to Goodness Beef

16277 S. McCall Ave.



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BIF 4/20/12



Work flow and collaborators

- DNA on all bulls goes for whole genome scan collaboration with Jerry Taylor (UMC) and John Pollak (MARC)
- Molecular breeding value (MBV) prediction of genetic merit based on MARC training data set – collaboration with Dorian Garrick (IA) and U.S. Meat Animal Research Center
- Ranch data including sire groupings, birth dates and weaning weights on all calves, all EIDed, and "DNAed" for parentage determination – collaboration with Dan Drake and producers
- Steer feedlot in weights, treatments, and carcass traits, weight, grading information and meat sample collected in the processing plant – collaboration with Harris Ranch
- Compile data and compare three sources of genetic estimates: breed EPDs (bEPDs), commercial ranch EPDs (rEPDs), and MBVs – Kristina Weber, Ph.D. student



Frank Baker Award Winners Beef Improvement Federation



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Sample and phenotype collection

Source Tracking And Reporting

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Management Software

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Avenal



Calving Date	Ranches	ww	Feedlot In-Weight	Carcass
Pre-project	2	~550 head	~460 head	~620 head
Spring 2009	2	Fall 2009: ~600 head	Fall 2009/ Winter 2010: ~500 head	Spring/Summer 2010: ~450 head
Fall 2009	4	Winter/Spring 2010: ~1500 head	Late Summer/ Fall 2010: ~900 head	Winter 2011: ~850 head
Spring 2010	2	Fall 2010	Fall 2010/ Winter 2011	Spring/Summer 2011
Fall 2010	4	Winter/Spring 2011	Late Summer/ Fall 2011	Winter 2012
Spring 2011	2	Fall 2011	Fall 2011/ Winter 2012	Spring/Summer 2012
Fall 2011	4	Winter/Spring 2012	Late Summer/ Fall 2012	Winter 2013
Total records	4	7000 records >20 collection trips	4500 records Sent electronically	4500 records >35 collection trips



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Integrated Program for Reducing Bovine Respiratory Disease in Beef and Dairy Cattle Alison Van Eenennaam, Ph.D.

Cooperative Extension Specialist Animal Biotechnology and Genomics Department of Animal Science University of California, Davis <u>alvaneenennaam@ucdavis.edu</u> US Bovine Respiratory Disease Coordinated Agricultural Project <u>http://www.brdcomplex.org</u>



Bovine Respiratory Disease Complex Coordinated Agriculture Project



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.



BRD Coordinated Agricultural Project

Bovine Respiratory Disease Complex Coordinated Agriculture Project

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MISSOURI

$| \operatorname{TEXAS}_{U N U V E R} A \& M$

- Jim Womack, PD
- Alan Dabney
- Scott Dindot
- Noah Cohen
- PD · Chris Seabury
 - Lawrence Falconer
 - Lauren Skow
 - Gary Snowder



- Laurel Gershwin
- Terry Lehenbauer
- Cassandra Tucker
- Alison Van Eenennaam
- Colorado State University • Mark Enns

- MISSOURI
- Jerry Taylor
- United States Department Of Agriculture Agricultural Research Service
 - Mike MacNeil
- Curt Van Tassell

WASHINGTON STATE



- Holly Neibergs
- Shannon Neibergs



- Milt Thomas
- Robert Hagevoort
- Tim Ross
- OTHER COLLABORATORS
- Daniel Pomp (NC)
- Shiela McGuirk (WI)
- Adroaldo Zanella (Norway)



BRD Coordinated Agricultural Project





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

Bovine Respiratory Disease Complex Coordinated Agriculture 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



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.



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



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



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 <u>on several thousands of individuals</u>.

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

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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



BRD CAP: BRD field datasets

Bovine Respiratory Disease Complex Coordinated Agriculture Project

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



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



California Animal Health and Food Safety Laboratory System

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Photo credit: Jessica Davis



Standardization of BRD Diagnosis

Bovine Respiratory Disease Complex Coordinated Agriculture Project

- 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



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

Calf Health Scoring Criteria							
0	1	2	3				
Rectal temperature		5	2				
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		a shu a sha g					
Normal serous discharge	Small amount of unilateral cloudy discharge	Bilateral, cloudy or excessive mucus discharge	Copious bilateral mucopurulent discharge				
Company of the second s							
Eye scores	0	Malantanatat					
Normal	Small amount of	bilatoral discharge	Heavy ocular				
6							
Ear scores							
Normal	Ear flick or head shake	Slight unilateral droop	Head tilt or bilateral droop				



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Blood collection

Nasal swab

Deep pharyngeal swab collection



Sampling location of deep pharyngeal swab



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

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Photo credit: Jessica Davis







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



Year 2: CO Feedlot *Bos taurus beef cattle*

Bovine Respiratory Disease Complex Coordinated Agriculture Project





US cattle numbers (x 106)

Breeder

# US Beef operations	766,350	
Million Cows	31.4	
Average herd size	122	

Seedstock Cows

1.1

Commercial cow/calf producer

35.7

Commercial Cows + replacements

Feedlot

Processing

13.6 (on feed at any one time) 25.6 (cattle fed per year in 2009)

43.2



Other Beef Animals (calves, steers, heifers and bulls)

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The current approach of extracting DNA multiple times for different labs and applications (parentage, genetic defects, genomically-enhanced predictions) makes about as much sense as simultaneously paying to have access to all of the following communication devices



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Ideally cattle would be genotyped ONCE early in life and genotypes shared with downstream production sectors to derive the maximum value from the fixed DNA collection and extraction costs

Cattle industry Sector	Mobile Device// Data Access Plan	Type of DNA product // DNA information access required	Cost? (US\$)
Nucleus seedstock/AI bulls	ipad	Full genome sequence	\$250
Seedstock/bull multiplier	iphone	HD 770 K genotype	\$50
Registered females and stock bulls for commercial sector	Talk and text smart phone	50K genotype + parentage + single gene traits/recessives	\$25
Commercial cattle – Marker- assisted management (MAM), replacement heifer selection	Prepaid cellular phone	Imputation LD chip + parentage + single gene traits/recessives	\$10
Feedlot cattle purchasing, sorting and marker-assisted management (MAM)	Pay as you go contract	Access genotypes from supplier (subset of LD imputation chip).	<\$1
Traceability for voluntary labelling e.g. Angus beef	Friends and family plan	Access genotypes from supplier (subset of LD imputation chip).	<\$1
Traceability for disease outbreak/contaminated meat	Emergency only phone (911 calls)	Access genotypes from supplier (subset of LD imputation chip).	<\$1



CONCLUSIONS

- USDA National Institute of Food and Agriculture is funding several large multi-institution grants on genomic approaches to a variety of important traits to US cattle feed efficiency, BRD, and fertility
- These projects employ high-density genotyping of large numbers of animals
- These traits are valuable to beef cattle industry
- 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 these traits?



United States Department of Agriculture

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