“Cattle Genomics Research at UC Davis”

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Animal breeders have used the resemblance between relatives to select parents of the next generation and make genetic change.
Breeding Objective

“*A breeding objective need not be economic. For example, in many companion animal species it is tempting to believe that the breeding objective must be the maintenance of a ridiculous appearance and congenital abnormalities!*”

(John Gibson, UNE)
Rate of change is accelerated when breeders can accurately identify those individuals that have the best genetics at a young age.

\[
\Delta G = \text{intensity of selection} \times \text{accuracy of selection} \times \left( \frac{\sqrt{\text{genetic variance in population}}}{\text{generation interval}} \right)
\]
The genome age

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GENES CONTAIN INSTRUCTIONS FOR MAKING PROTEINS

PROTEINS ARE THE BUILDING BLOCKS OF LIFE AND COLLECTIVELY ACT TO DETERMINE PHENOTYPE
What is a Genetic Marker?

A DNA sequence variation that has been associated with a given trait in one or more populations.
We want to use DNA markers (SNPs) in addition to pedigree and performance information to help select the best animals.
High-throughput genotyping technology enabled a new approach

- The sequencing of the bovine genome allowed for the development of a 50,000 marker chip!
- Can simultaneously test 50,000 markers
With high density (50K) SNP chips it is possible to:

- Divide genome into 50,000 chromosome segments based on marker intervals
- Marker density must be sufficiently high to ensure that all of the genes affecting a traits are “linked” (close to) a marker
- Idea is to capture all genetic variance with evenly spread markers and assign an “EPD” value to each segment
What is needed for “genomic” selection?

**THEORY**
- Population
- Phenotypes
- Genotypes

**Training** = estimate the value of every chromosome fragment contributing variation in a population with phenotypic observations

**Prediction** = the results of training can then be used to predict the merit of new animals, not contained in the training data set
Implementation of Genomic Selection

**Training 1:**
Old Progeny Tested Bulls

**Retraining each generation:**
Old Bulls & New Progeny of Tested Bulls

**Calibration (Validation)** (Estimation of $r_g$):
New Progeny of Tested Bulls

**Application:**
New Sire Candidates

Degree of genetic relationship between populations (ideally similar)

Slide modified from Marc Thallman, US MARC

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Breeding value prediction in Dairy Sires

Young sire
Parent Average

Young sire
Progeny Test

Young sire
Genomic Selection

Birth

5 years; $50,000 cost

Birth; << $50,000 cost

Reliability 0.20
Reliability 0.80
Reliability 0.65

Mendelian Sampling

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Dairy industry suited to WGS

- High use of AI
- Mostly one breed
- Clear selection goal (total net merit)
- Large number of high accuracy A.I. sires for training
- Extensive, uniform collection of data on traits
- Central evaluation (AIPL) receiving genotypes
- Obvious way to increase rate of genetic gain
- AI companies funding the genotyping because they get a clear cost savings in terms of young sire program

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Little use of AI
- Relatively few high accuracy sires for training
- Multiple competing selection goals – cow/calf, feedlot, processor – little data sharing between sectors
- Few/no records on many economically-relevant traits
- Many breeds, some small with limited resources
- Crossbreeding is important
- No centralized “national” cattle evaluation
- Not clear who should pay for testing
Historically not all beef cattle breeding objectives have been economic.

Photo taken in 1949 at Red Bluff Bull Sale, CA. Kindly provided by Cathy Maas from Crowe Hereford Ranch, Millville, CA.

1986. "Coblepond New Yorker" weighed 2529 lbs and measured 65 inches tall at 35 mos. (Frame 10) when he was Denver Champion.

1988 Grand Champion Bull, National Polled Hereford Show (frame 10).


Images from Harlan Ritchie’s historical review of type https://www.msu.edu/~ritchieh/historical/cattletype.html
We can make genetic changes in our cattle (and our dogs) - the question is are we making profitable change?

Killed same day at IBP in Iowa:
The small female weighed 835 lbs and was extremely fat. The large male weighed 1900 lbs and was very lean.

Images from Harlan Ritchie’s historical review of type https://www.msu.edu/~ritchieh/historical/cattletype.html
“Integrating DNA information into beef cattle production systems. ”

Alison Van Eenennaam, Animal Science, UC Davis (PD)
Dan Drake, UCCE Siskiyou County, CA
Kristina Weber, PhD student, Animal Science, UC Davis

Siskiyou County Producer Collaborators:
Jack Cowley, Cowley Rancher, CA
Dale, Greg, & Richard Kuck, Kuck Ranch, CA
Matt Parker, Mole-Richardson Ranch, CA

Processor Collaborators:
Harris Ranch Beef Company, Coalinga, CA
Los Banos Abattoir, Los Banos, CA

Software Collaborators:
- Jim Lowe, MidWest Microsystems, NE

Other Contributors/Collaborators
Dr. Jerry Taylor, University of Missouri, MO
Dr. Mike Goddard, University of Melbourne, Australia
Dr. Darrh Bullock, University of Kentucky, KY
Dr. Leslie “Bees” Butler, UC Davis, CA
Dr. Dorian Garrick, Professor, Iowa State University, IA
Dr. John Pollak, US Meat Animal Research Center, NE

This work is funded by grant 2009-55205-05057 from the USDA National Institute of Food and Agriculture. 1/1/09-12/31/13
The overall objective of this project is to develop a genotyped, phenotyped population to enable the evaluation and/or assessment of different DNA-enabled approaches for predicting the genetic merit of herd sires on commercial beef ranches.

The research objective is to compare the current means of genetic prediction of herd sires (i.e. breed-based expected progeny differences) with DNA-assisted genetic predictions, and "commercial ranch" genetic evaluations based on the performance of their offspring under field conditions.

An additional objective is to determine the costs and benefits associated with the application of DNA-based technologies on commercial beef operations.
aka “California Commercial Ranch Project”

Data collection:
AAA EPD & pedigree

Sample collection:
For genotyping

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

Four collaborating 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

Kristina Weber
Animal Biology
Ph.D. student
### Sample and phenotype collection

#### Calving Date

<table>
<thead>
<tr>
<th>Calving Date</th>
<th>Ranches</th>
<th>WW</th>
<th>Feedlot In-Weight</th>
<th>Carcass</th>
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<tbody>
<tr>
<td>Pre-project</td>
<td>2</td>
<td>~550 head</td>
<td>~460 head</td>
<td>~620 head</td>
</tr>
<tr>
<td>Fall 2009</td>
<td>4</td>
<td>Winter/Spring 2010:~1500 head</td>
<td>Late Summer/Fall 2010:~900 head</td>
<td>Winter 2011:~850 head</td>
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<tr>
<td>Spring 2010</td>
<td>2</td>
<td>Fall 2010</td>
<td>Fall 2010/Winter 2011</td>
<td>Spring/Summer 2011</td>
</tr>
<tr>
<td>Fall 2010</td>
<td>4</td>
<td>Winter/Spring 2011</td>
<td>Late Summer/Fall 2011</td>
<td>Winter 2012</td>
</tr>
<tr>
<td>Spring 2011</td>
<td>2</td>
<td>Fall 2011</td>
<td>Fall 2011/Winter 2012</td>
<td>Spring/Summer 2012</td>
</tr>
<tr>
<td>Fall 2011</td>
<td>4</td>
<td>Winter/Spring 2012</td>
<td>Late Summer/Fall 2012</td>
<td>Winter 2013</td>
</tr>
<tr>
<td>Total records</td>
<td>4</td>
<td>7000 records &gt;20 collection trips</td>
<td>4500 records Sent electronically</td>
<td>4500 records &gt;35 collection trips</td>
</tr>
</tbody>
</table>

**Note:** Ranches are indicated by red pins on the map. The map shows Siskiyou Ranches, SFREC, and UCD locations.
“Identification of gene targets for improved efficiency and sustainability of beef production using exome capture, RNA-seq and high density SNP genotyping technologies.”

Objectives: Using next generation sequencing technologies to find gene targets associated with residual feed intake (RFI) and correlated or component traits such as dry matter intake (DMI), methane production, mitochondrial respiration, composition of gain, and carcass traits in beef steers.

Through the identification of genes that regulate beef production efficiency at several physiological levels, gene targets for more efficient and sustainable beef production may be identified.

Kristina Weber
Animal Biology
Ph.D. student

This work is being funded by a Zoetis Cattle Call 2012 initiative Grant Project #201224918. 10/1/2012-10/1/2014
“Genomic Interrogation of the Putative Etiological Agent of Epizootic Bovine Abortion (EBA)”

EBA is leading cause of beef cattle abortion in CA
45,000-90,000 calves lost annually
Vector *Ornithodoros coriaceus* (Pajaroello tick)

- Assemble a reference genome for the novel deltaproteobacterium which is the etiologic agent of epizootic bovine abortion (EBA)
- Identify highly transcribed bacterial genes as possible candidates for a recombinant vaccine

Funded by the Rustici endowment 1/1/2013-12/31/2013

UC Davis Collaborators:
Dr. Jeff Stott
Myra Blanchard
Dr. Juan Medrano

Bryan Welly,
Animal Biology
MS student
“Identification and management of alleles impairing heifer fertility while optimizing genetic gain in Angus cattle”

David Patterson, University of Missouri, MO
Jerry Taylor, University of Missouri, MO
Michael Smith, University of Missouri, MO
Scott Brown, University of Missouri, MO
Alison Van Eenennaam, UC Davis, CA
Mike MacNeil, DeltaG consulting, MT
Brian Kinghorn, Armidale, Australia

This work is funded by Grant 2013-68004-20364 from the USDA National Institute of Food and Agriculture.” 1/1/13-12/31/17
The overall objective of this project is to improve reproductive rates in cattle by identifying genes which cause embryonic or early developmental mortality.

- Identify and characterize the impact of genes associated with reproductive failure in cattle;
- Develop a fertility EPD (Expected Progeny Difference) based on genotype information for these specific genes that will provide estimates of the genetic value of an animal;
- Develop economic selection indexes for beef producers that will support selection and breeding decisions, inclusive of fertility;
- Develop economic estimates that are based on improvements in reproductive rates for the beef industry;
- Develop decision support software for beef producers that will improve breeding schemes using selection indexes and new mating selection strategies based on sire and dam genotypes;

The long-term goal of this project is to improve reproductive rates of US beef cattle based on improvements in selection to improve overall profitability to the herd enterprise.
Genotype-Driven Screens for Embryonic Lethals

- Sequence bulls and identify SNPs that are predicted to have a disruptive effect on protein structure (also called causative DNA sequence variants **DSV**)
- Develop chip of DSVs and sequence large number of healthy individuals to identify embryonic lethals
- True embryonic lethals should never be observed in the homozygous state among healthy animals and the resulting departure from Hardy-Weinberg equilibrium should be statistically significant
- Carrier status of the sire and dam should have a negative effect on fertility traits
If allele frequency of SNP is 50% A: 50% T then expect 25% AA; 50% AT, 25% TT

If see 33% AA and 66% AT then have a case of missing homozygotes (i.e. TT is likely lethal)
The exact genes and their underlying biological roles in fertilization and embryo development are unknown, but it is assumed that the outcome of inheriting the same haplotype from both parents is failed conception or early embryonic loss.

The reactive approach of attempting to eradicate every animal with an undesirable haplotype is not recommended in light of their economic impact, and is not practical given the likelihood that many more undesirable haplotypes will be found.

Producers should neither avoid using bulls with these haplotypes nor cull cows, heifers, and calves that are carriers, because this will lead to significant economic losses in other important traits.

Computerized mating programs offer a simple, inexpensive solution for avoiding affected matings, so producers should use these programs and follow through on the mating recommendations.
“Integrated program for reducing bovine respiratory disease complex in beef and dairy cattle” (aka BRD CAP)

“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”

Funded by Agriculture and Food Research Initiative Competitive Grant no. 2011-68004-30367 from the USDA National Institute of Food and Agriculture. 4/15/2011–4/15/2016.

Jim Womack, PD
Texas A&M
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• Curt Van Tassell

• Holly Neibergs
• Shannon Neibergs

• Robert Hagevoort
• Tim Ross

• Daniel Pomp (NC)
• Shiela McGuirk (WI)
• Adroaldo Zanella (Norway)
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
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
# Calf Health Scoring Criteria

<table>
<thead>
<tr>
<th>Rectal temperature</th>
<th>0</th>
<th>1</th>
<th>2</th>
<th>≥103</th>
</tr>
</thead>
<tbody>
<tr>
<td>100-100.9</td>
<td></td>
<td>101-101.9</td>
<td>102-102.9</td>
<td>≥103</td>
</tr>
</tbody>
</table>

**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 |

[Download Calf Health Scoring Chart](http://www.vetmed.wisc.edu/dms/fapm/fapmtools/8calf/calf_health_scoring_chart.pdf)
Nasal swab

Blood collection

Deep pharyngeal swab collection

Photo credit: Jessica Davis
To culture organisms associated with BRD, pharyngeal swabs offer a less invasive, less stressful and more rapid alternative to bronchoalveolar lavage.

Photo credit: Jessica Davis
“Risk Assessment, welfare analysis, and extension education for dairy calf respiratory disease management in California.”

Sharif Aly, VMTRC, Tulare, CA
Terry Lehenbauer, VMTRC, Tulare, CA
Betsy Karle, UCCE Glenn County, CA
Alison Van Eenennaam, UC Davis, CA

Lindsey Hulbert, Kansas State University, KS

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Mission statement of the Animal Genomics and Biotechnology Cooperative Extension Program

"The mission of the Animal Genomics and Biotechnology Program is to provide research and education on the use of animal genomics and biotechnology in livestock production systems."

Make a gift here!