



Update on animal genomics and biotechnology research projects and activities

Alison Van Eenennaam

Animal Genomics and Biotechnology

Cooperative Extension Specialist

Department of Animal Science

University of California, Davis, CA

Ph: (530) 752-7942

alvaneennaam@ucdavis.edu

UC DAVIS
ANIMAL SCIENCE





"Integrating DNA information into beef cattle production systems."

Alison Van Eenennaam
Dan Drake
Kristina Weber



Kristina Weber
Animal Biology
Ph.D. graduate

Siskiyou County Producer Collaborators:

Jack and Barbara 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

This work is funded by an integrated grant 2009-55205-05057 from the USDA National Institute of Food and Agriculture.

Other Contributors/Collaborators

Dr. Darrh Bullock, University of Kentucky, KY
Dr. Scott Brown, University of Missouri, MO
Dr. Dorian Garrick, Professor, Iowa State University, IA
Dr. Mike Goddard, University of Melbourne, Australia
Dr. John Pollak, US Meat Animal Research Center, NE
Dr. Jerry Taylor, University of Missouri, MO



United States
Department of
Agriculture

National Institute
of Food and
Agriculture



Objectives:

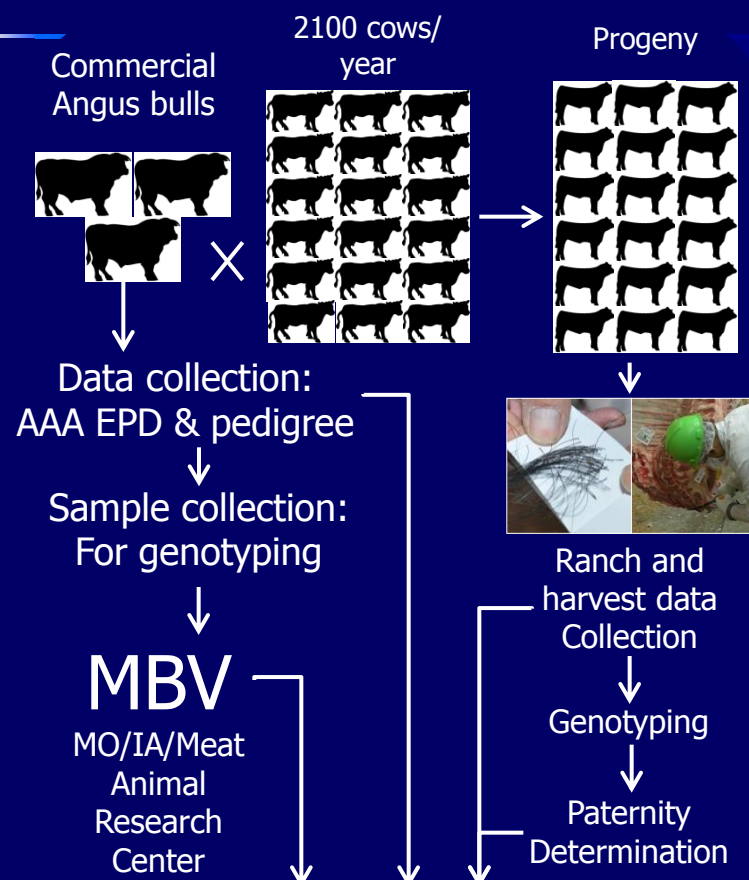
“Integrating DNA information into beef cattle production systems”



- 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



California Commercial Ranch Project



Three ranches:

- Cowley (900 cows)
- Kuck (500 cows)
- Mole-Richardson (700 cows)

Approximately 150 Angus bulls, and 6000 calves on project

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

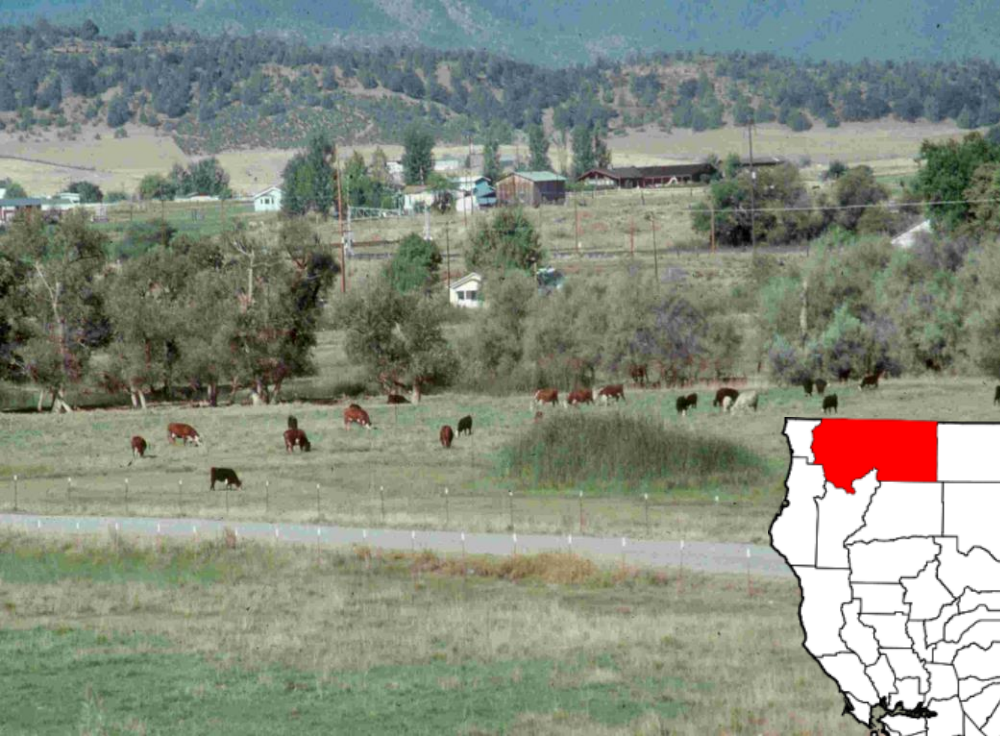




Work flow and collaborators



- DNA on all bulls goes for whole genome scan – collaboration with **Jerry Taylor (MO)** and **John Pollak (MARC)**
- Molecular breeding value (MBV) prediction of genetic merit based on various training data sets – collaboration with **Dorian Garrick (IA)**, **Taylor (MO)**, and **U.S. Meat Animal Research Center (NE)**
- 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 (CA)**
- Compile data and compare three sources of genetic estimates: breed EPDs (bEPDs), commercial ranch EPDs (rEPDs), and MBVs
Kristina Weber, PhD student with occasional guidance from PI



Cowley Ranch



~20 bulls/season





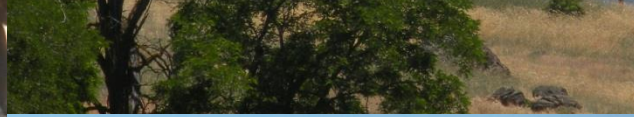
Kuck Ranch

~10 bulls/season



Mole-Richardson Farms

~30 bulls





HARRIS
RANCH

*Honest
to Goodness Beef*

16277 S. McCall Ave.

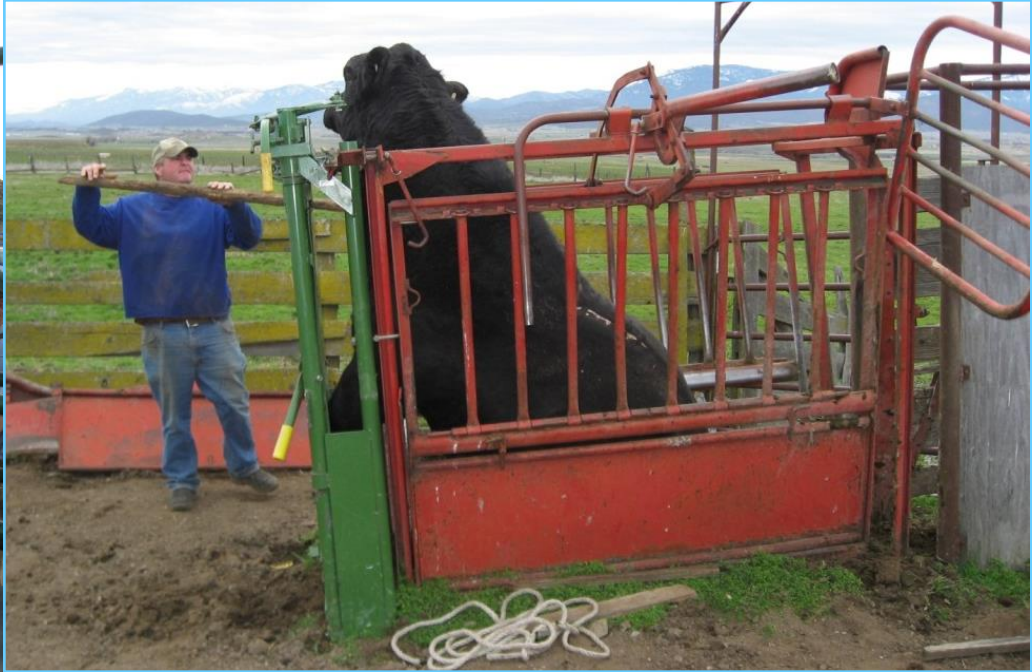




Cooperating ranchers were key to success of this project



- Need to test new technologies to see how they work under practical conditions
- Inadequate research on field application of new technologies
- Cooperating ranches make a substantial contribution of time, labor and expenses





Technology Tools Learnings

EIDs, electronic scales, computers, handhelds, DNA sampling, genotyping

- **Technology problems were constant but declined as we obtained experience**
- **Each additional piece of equipment exponentially increased problems**
- **Background knowledge and expertise in computing level for troubleshooting was very high**
- **Electronics were remarkably durable**
- **Record keeping was an important attribute to make this project work**





Number of calves per bull

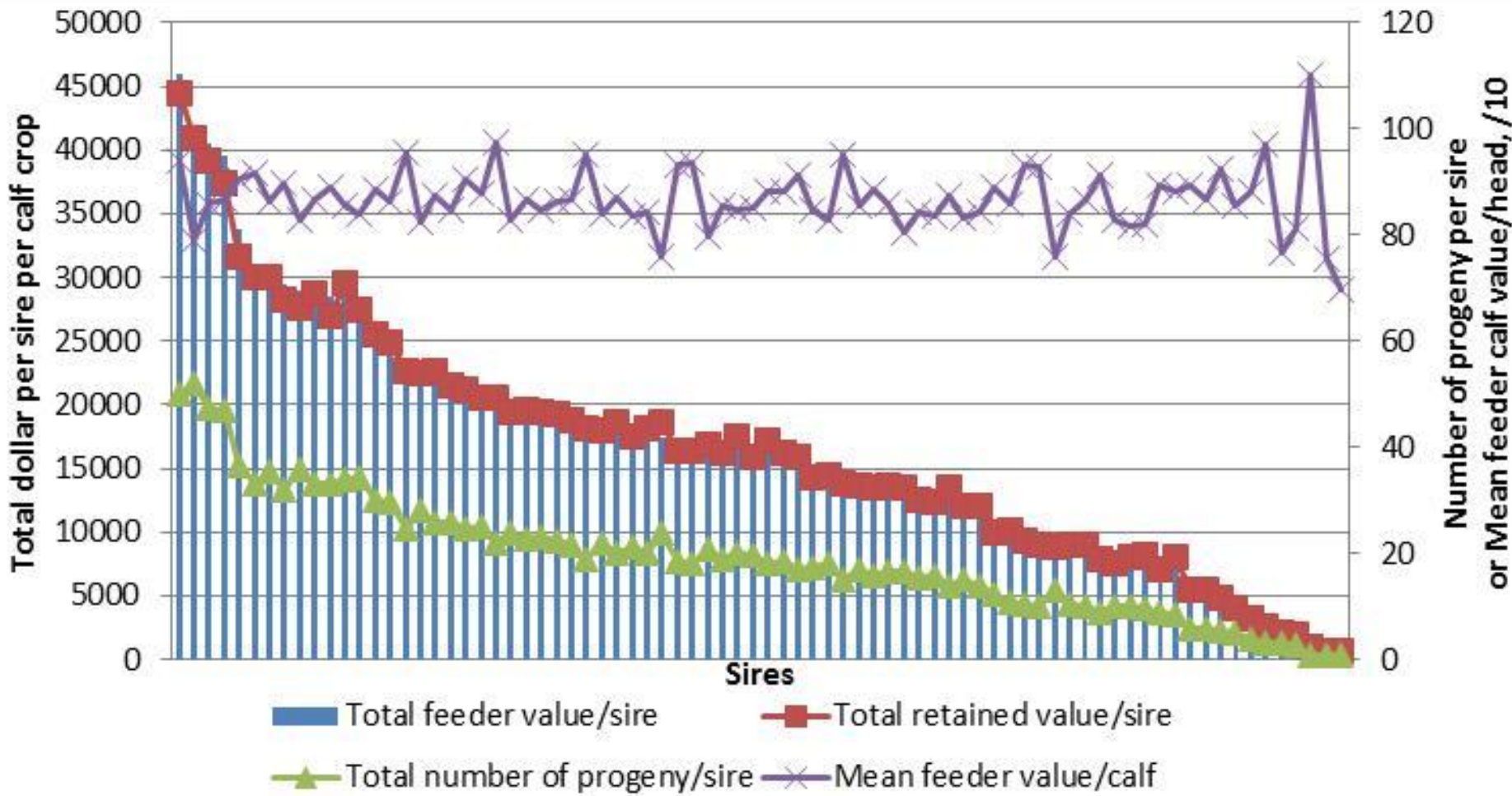
Ranch	Year	Season	# Bulls/season	Mean bull age (± SD)	Total # calves	Per bull		
						Min # calves	Max # calves	Mean # calves (± SD)
A	2009	Spring	18	3.8 ± 1.2	353	3	47	19.6 ± 13.4
A		Fall	19	4.7 ± 0.8	113	1	29	16.1 ± 10.0
A	2010	Spring	22	3.6 ± 0.9	346	1	47	18.2 ± 14.2
A		Fall	19	4.5 ± 1.0	328	1	48	17.3 ± 12.6
A	2011	Spring	17	3.9 ± 1.1	402	4	53	23.6 ± 13.6
A		Fall	19	5.4 ± 0.7	286	1	33	15.0 ± 9.2
B	2009	Spring	8	4.6 ± 3	141	1	45	17.6 ± 17.0
B		Fall	10	5.1 ± 2.5	214	10	50	21.4 ± 11.4
B	2010	Spring	8	3.4 ± 1.4	142	3	30	17.8 ± 8.4
B		Fall	12	5.1 ± 2.7	247	4	44	20.5 ± 11.4
B	2011	Spring	4	4.6 ± 1.7	110	18	42	27.5 ± 11.0
B		Fall	12	5.3 ± 2.9	266	3	51	22.2 ± 15.2
C	2009	Fall	30	4.2 ± 1.1	642	2	54	21.4 ± 13.8
C	2010	Fall	27	4.6 ± 1.3	567	1	52	21.0 ± 13.0
C	2011	Fall	38	5.4 ± 1.8	573	1	64	15.1 ± 16.1
A	2009-11	All	114	4.0 ± .2	2150	1	53	18.8 ± 1.2
B	2009-11	All	54	4.8 ± .2	1120	1	51	20.8 ± 1.8
C	2009-11	All	95	4.8 ± .2	1782	1	64	18.7 ± 1.4
A,B,C	2009-11	All	263	4.4 ± 1.7	5052	1	64	19.2 ± 13.3

Additionally, 7.3% sires failed completely (i.e. no calves sired) in any given breeding season.



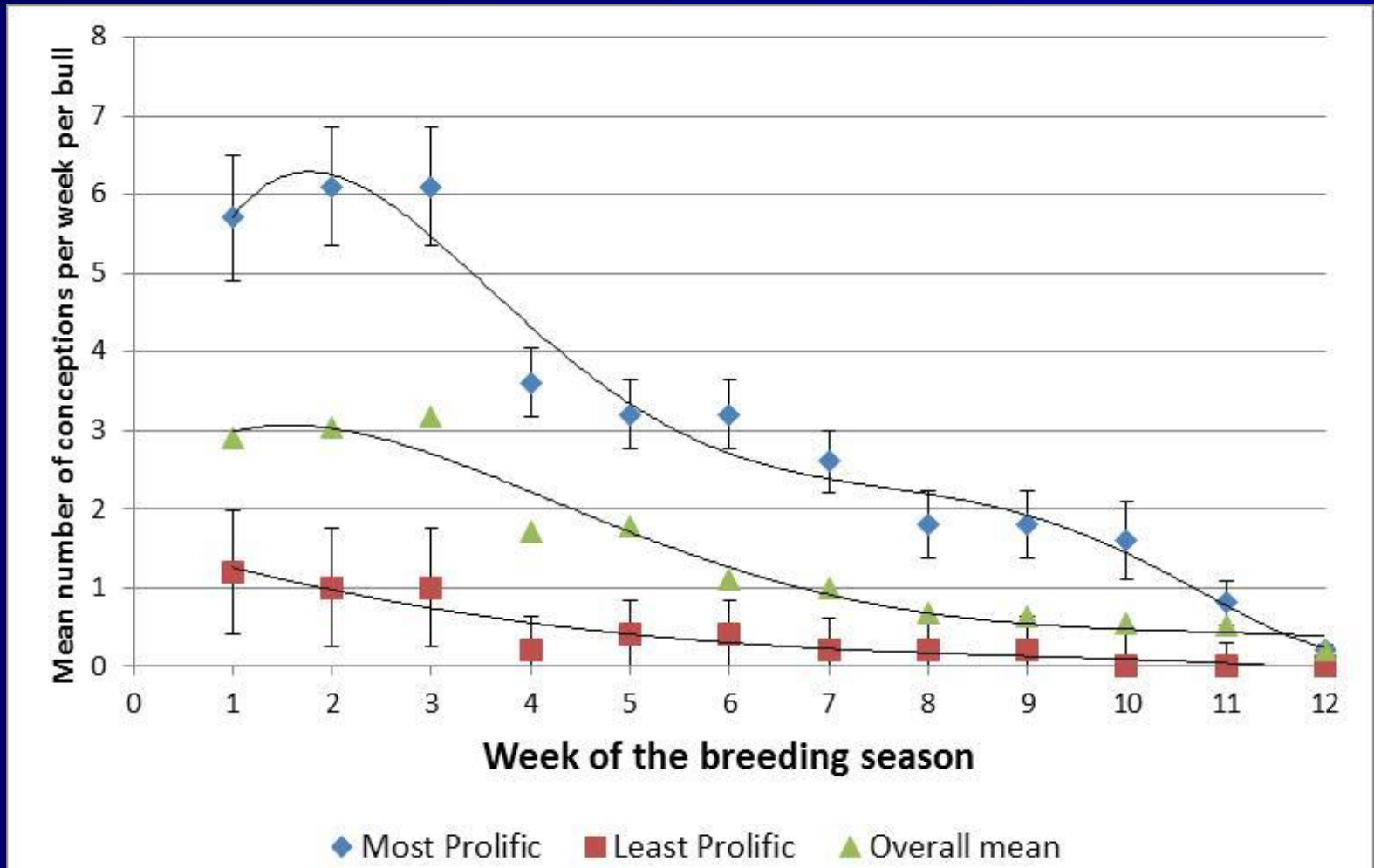


Total income as feeder calves per sire or total retained ownership (selling "on the rail") varied by sire (Total dollar per sire per calf crop, left axis), and the number of progeny per sire (right axis) and the mean individual feeder value/calf (right axis, \$/10)





The most prolific bulls (top 1/3) sired a disproportionately high number of early calves





EPDs, prolificacy and total income.



- Repeatability of prolificacy for full season bulls with data for more than one breeding season was 0.43 (± 0.08).
- Scrotal circumference (SC) EPD was positively related to prolificacy ($P < 0.01$).
- Approximately 5% of the total variation in sire prolificacy was explained by SC EPD.
- The calves that were sired by South Devon ($n=217$) and Hereford ($n=145$) bulls were on average 20.4 kg and 16.4 kg heavier than Angus-sired calves at weaning
- Irrespective of hybrid vigor (heterosis), prolificacy was the main driver of total calf weight weaned per sire.



Summary and practical implications

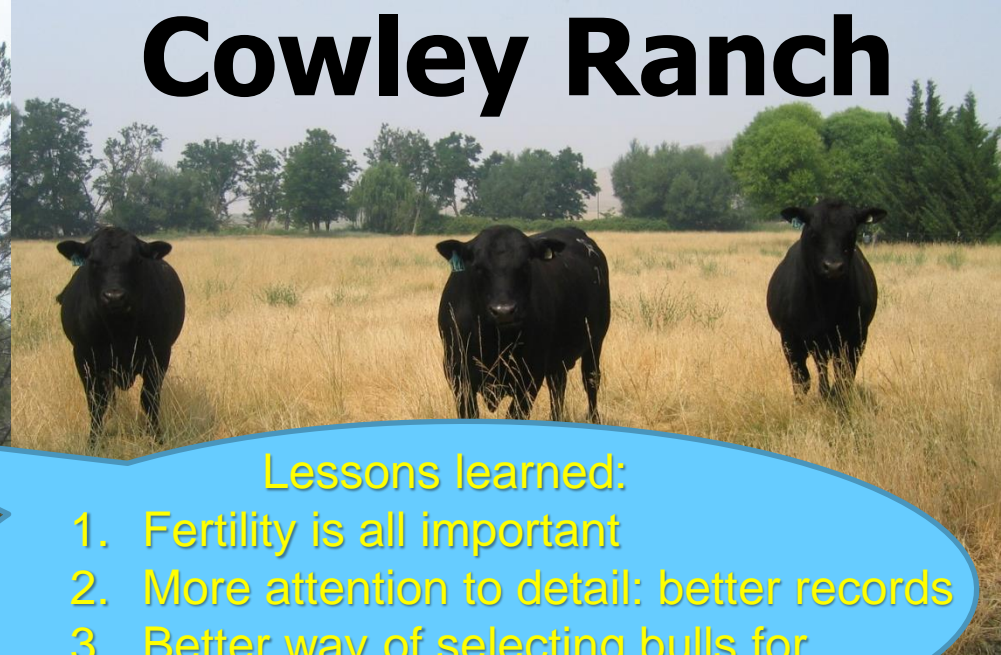


- The number of calves born per sire per calf crop varied from 0 to 64.
- Prolificacy was by far the main driver of total weight weaned per sire. The total adjusted 205d weight per bull per calf crop was related ($P < .01$) to the number of calves (220 ± 1.8 kg increase for each calf) explaining 98 percent of the variation in sire weight weaned per calf crop, and showed little correlation with mean adjusted progeny weaning weight per sire.
- Scrotal circumference (SC) was positively correlated with herd sire prolificacy (# of calves), and both total feeder calf & retained ownership value per sire.
- These data suggest inclusion of SC EPDs might be useful as selection criteria in commercial herd sire selection, & emphasize the importance of management approaches to increase the proportion of calves born in the first 21 or at most 42 days of the calving season
- Commercial ranch evaluations using natural service sires frequently have too few offspring due to variations in prolificacy to give an accurate evaluation

CHANGES IN BEHAVIOR?



Cowley Ranch



Lessons learned:

1. Fertility is all important
2. More attention to detail: better records
3. Better way of selecting bulls for servicing cows

~20 bulls/season



FARMER UPTAKE?



Thanks again for the project. I truly think it was very beneficial and of course in areas not expected. I recently read somewhere that you are working on a DNA project regarding BRD. Just curious, would you be able to take the DNA panels taken from our set of calves and use that in your study? Just thought I would ask

“Identification and management of alleles impairing heifer fertility while optimizing genetic gain in beef cattle”



David Patterson, MO
Jerry Taylor, MO
Scott Brown, MO
Mike Smith, MO
Alison Van Eenennaam, CA



Looking for a good UCD graduate student here...



This work is funded by an integrated grant 2013-68004-20364 from the USDA National Institute of Food and Agriculture.



United States Department of Agriculture

National Institute of Food and Agriculture



Objectives:

"Identification and management of alleles impairing heifer fertility while optimizing genetic gain in beef cattle"

- Sequence ~ 150 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





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



Missing homozygotes....

[Display Settings:](#) Abstract

[Send to:](#)

[J Dairy Sci.](#) 2011 Dec;94(12):6153-61.

Harmful recessive effects on fertility detected by absence of homozygous haplotypes.

[VanRaden PM](#), [Olson KM](#), [Null DJ](#), [Hutchison JL](#).

Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD 20705-2350, USA. paul.vanraden@ars.usda.gov

Abstract

Five new recessive defects were discovered in Holsteins, Jerseys, and Brown Swiss by examining haplotypes that had a high population frequency but were never homozygous. The method required genotypes only from apparently normal individuals and not from affected embryos. Genotypes from the BovineSNP50 BeadChip (Illumina, San Diego, CA) were examined for 58,453 Holsteins, 5,288 Jerseys, and 1,991 Brown Swiss with genotypes in the North American database. Haplotypes with a length of ≤ 75 markers were obtained. Eleven candidate haplotypes were identified, with the earliest carrier born before 1980; 7 to 90 homozygous haplotypes were expected, but none were observed in the genomic data. Expected numbers were calculated using either the actual mating pattern or assuming random mating. Probability of observing no homozygotes ranged from 0.0002 for 7 to 10^{-4} for 90 expected homozygotes. Phenotypic effects were confirmed for 5 of the 11 candidate haplotypes using 14,911,387 Holstein, 830,391 Jersey, and 68,443 Brown Swiss records for conception rate. Estimated effect for

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)





Haplotypes Affecting Fertility and their Impact on Dairy Cattle Breeding Programs

Dr. Kent A. Weigel, University of Wisconsin

<http://documents.crinet.com/Genex-Cooperative-Inc/Dairy/KWeigel-Haplotypes-Affecting-Fertility.pdf>



- 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.



Translational questions that remain assuming success

- All animals carry recessive genetic conditions – how should “embryonic lethals” be managed
- What is the appropriate penalty to put on embryonic lethals when making mating decisions – how to incorporate into mate selection
- What is the frequency of the embryonic lethals in the target population – if small then less important
- Are appropriate decision support tools available for producers???





Classic "decision" systems



Targets

Data

Parameters

Breeding Objective

Sets of Rules

Sire use

Dams per sire

Avoid inbreeding

Trait distributions

Avoid genetic defects

Reproductive technologies

...etc.



ACTION

Not always arriving at optimal solution to complex problem

Modified from slide kindly provided by Dr. Brian Kinghorn, UNE, Australia

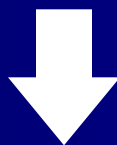
Livestock UCCE 11/14/2013

Animal Genomics and Biotechnology Education



Finding the right balance

- The formal breeding objective
- Inbreeding
- Additional constraints e.g. use no animal with a genetic defect in pedigree



Mate selection tool shows you the 'opportunity cost' of imposing non-optimal constraints on mate selection





Genetic implications of recessive genetic factors



"Carrier animals...their overall breeding value worth may outweigh the economic value of carrier status"

Chalier C. et al. (2008) Highly effective SNP-based association mapping and management of recessive defects in livestock. *Nature Genetics* 40:449-454

Need to penalize carrier animals appropriately (*not prohibit their use entirely*) and let mate selection software optimize their use in the breeding programs





MateSel

Optimised Mating Allocation

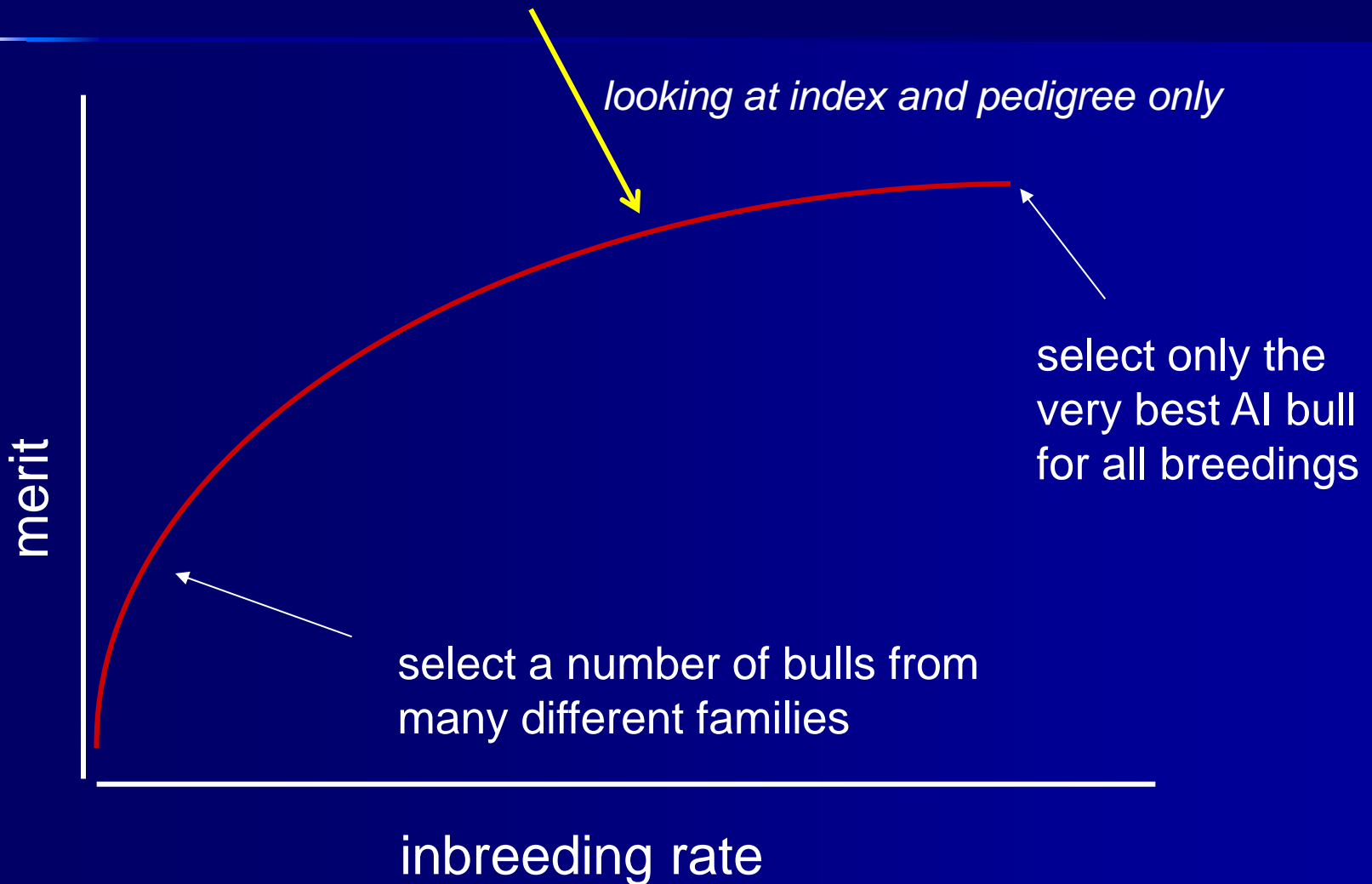


MateSel integrates complex breeding issues into a single, easy to use, decision making framework. Technical, logistical and economic issues compete for attention in a system that can be guided by the breeder, with the resulting mating list covering decisions on items like semen purchase, bulls used, animal selection/culling, forming mating groups and mate allocation, genetic gain (Indexes), genetic diversity, inbreeding, trait distributions, genetic defect management, logistical constraints and costs. The resulting mating lists optimize the matings for the candidate animals while allowing for all of these variables and constraints.





Mate Sel: Balancing inbreeding and genetic merit – the frontier gives the unconstrained solution





Develop software to handle the mutations discovered in this project, and deliver selection and mating recommendations to US beef breeders that exploit this information optimally in competition with other factors of importance (e.g. trait merit, genetic diversity (inbreeding), genetic defects and recessive lethals, logistical constraints, semen costs, etc.)



Dr. Brian Kinghorn

"Adapt mate selection methodology and develop software that can be used to optimize the rate of genetic gain (using the selection indexes developed by Mike MacNeil) and mate allocation with a key objective being to reduce both the phenotypic expression and allele frequency of the lethals identified in the project. Equally important, this will be carried out in concert with other important issues such as the management of trait merit, genetic diversity, other genetic defects, genome-wide inbreeding, logistical constraints and costs."



“Genomic Interrogation of the Putative Etiological Agent of Epizootic Bovine Abortion (EBA)”



Alison Van Eenennaam
Juan Medrano, ANS
Jeff Stott, SVM
Myra Blanchard, SVM
Mike Miller, ANS



Bryan Welly
Animal Biology
Masters student

This work is funded by a 2013 Rustici endowment grant.



Other Projects



- **Integrated program for reducing bovine respiratory disease complex in beef and dairy cattle.** USDA National Institute of Food and Agriculture Competitive Grant no. 2011-68004-30367. 4/15/2011–4/15/2016. Jim Womack (PD). A. L. Van Eenennaam (Co-PD).
- **Risk Assessment, welfare analysis, and extension education for dairy calf respiratory disease management in California.** UC ANR Grant Program. 9/1/2012-8/31/2016 Sarif Aly (PD), Terry Lehenbauer (Co-PD), A. L. Van Eenennaam (Co-PD)
- **New Approaches to Bovine Respiratory Disease Prevention, Management, and Diagnosis Conference Grant.** USDA National Institute of Food and Agriculture Competitive Grant no. 2013--01236. 9/30/2013–12/31/2014. A. L. Van Eenennaam (PD).
- **A metagenomic analysis of the effect of transportation stress and pathogen infection on the nasal bacterial microbiota of cattle** UC Davis Academic Federation Innovative Development Award Program. 7/1/2012-6/30/2014. A. L. Van Eenennaam (PD)
- **Characterizing the nasal microflora of diseased and healthy cattle.** UC Davis Genome Center Core Facility Pilot Projects. 10/1/2012-10/1/2014. A. L. Van Eenennaam (PD)
- **Identification of gene targets for improved efficiency and sustainability of beef production using exome capture, RNA-seq and high density SNP genotyping technologies.** Pfizer cattle call. 10/1/2012-10/1/2014. A. L. Van Eenennaam (PD), actually written by Kristina Weber, currently Post-Doc



Other subjects



- Genetically engineered salmon (AquAdvantage salmon)
- Safety of genetically engineered feed for livestock
- Labeling of genetically engineered food (GMOs)
- Animal biotechnology website
 - Outreach
 - Marker-Assisted selection
 - Presentations
 - Videos
 - Peer-reviewed publications
 - Producer-level proceedings
 - Fact sheets



Kasey DeAtley
Post-Doc

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



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



[Home](#)

[My Lab](#)

[Genomics](#)

[Biotechnology](#)

[Outreach](#)

[Marker Assisted Selection](#)

[Presentations](#)

Animal Biotechnology
UC Cooperative Extension

Alison L Van Eenennaam



"Gene Shop"

2013 winner of the ASAS Video Competition

[Home](#)

[My Lab](#)

[Genomics](#)

[Biotechnology](#)

[Outreach](#)

[Marker Assisted
Selection](#)



Mission statement of the Animal Genomics and Biotechnology
Cooperative Extension Program

2013 ASAS video competition winner