"Assessing the accuracy of genomic predictions: Results from the California commercial ranch project"

Alison Van Eenennaam

Animal Genomics and Biotechnology
Cooperative Extension Specialist
alvaneenennaam@ucdavis.edu

Kristina Weber

Ph.D. graduate student
klweber@ucdavis.edu

Department of Animal Science
University of California, Davis, CA
animalscience.ucdavis.edu/animalbiotech

OUTLINE

- Overview of CA Commercial Ranch Project
- Objectives of the study
- Number of samples collected
- Preliminary analysis of the data

"This project is supported by National Research Initiative Grant no. 2009-55205-05057 to AVE from the USDA National Institute of Food and Agriculture."

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

Research objectives of "Integrating DNA information into beef cattle production systems"

How is DNA information best incorporated into beef cattle production systems?

- Which of several incorporation methods is best?
- Which is feasible for commercial ranches to implement?
- Which provides economic benefit?

- **RESEARCH OBJECTIVE**: Compare the current means of genetic prediction (**bEPDs**) with
  1. whole-genome scan genetic predictions (molecular breeding values, **MBVs**),
  2. "commercial ranch" genetic evaluations (**rEPDs**) based on the actual performance of offspring under field conditions.

Extension objectives of "Integrating DNA information into beef cattle production systems"

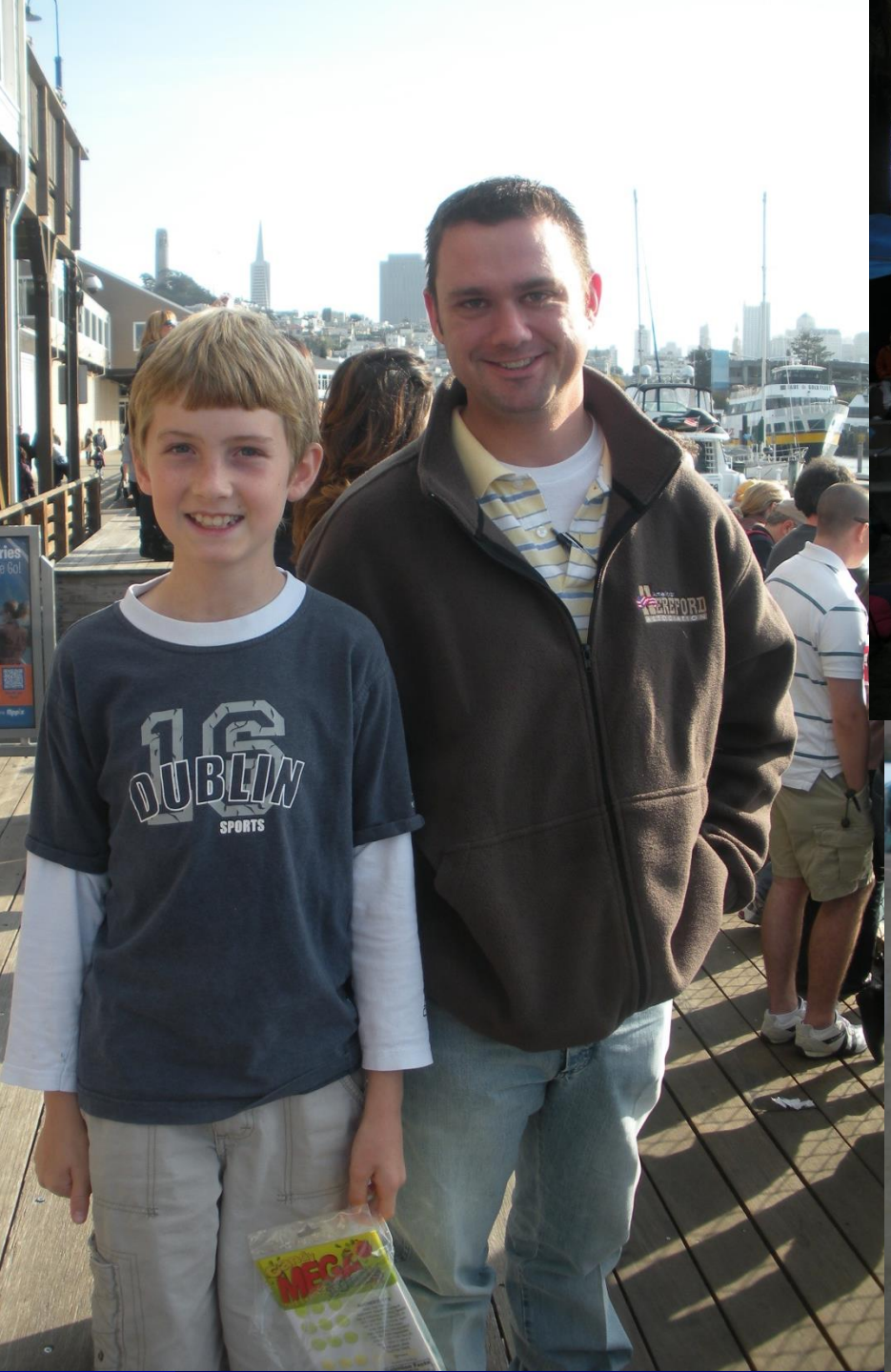
The **extension objective** is to develop and deliver educational materials to a national audience on the integration of DNA information into beef cattle selection programs.

- Includes the development of fact sheets, national educational programs including program at BIF 2009, brown bagger series, popular press articles, and NBCEC workshop entitled "***Integrating DNA information into beef cattle production systems***" – to be held in **Kansas City, MO March 5th 2013**

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

Animal Health
BEEF
USA

Should Consider Every Factor
That Contributes To Efficiency
And Profit.
Thank You
Thank you to
Animal Health

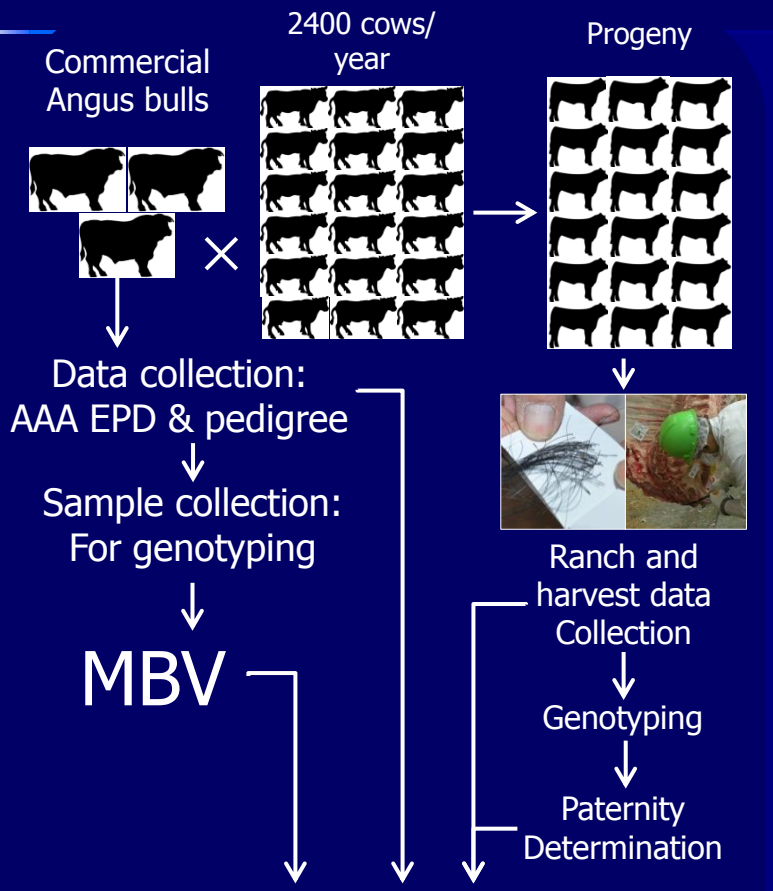

16
DUBLIN
SPORTS

OCCUPYSF = A
LIVING EXAMPLE
OF A BETTER
SYSTEM

OCCUPY
DAVIS!

WE
the
99%
OCCUPY

California Commercial Ranch Project



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 NIFA

United States Department of Agriculture
National Institute of Food and Agriculture

Location of 2011 presentations on data derived from CA commercial ranch project

What does a California Commercial Ranch collaborator look like?

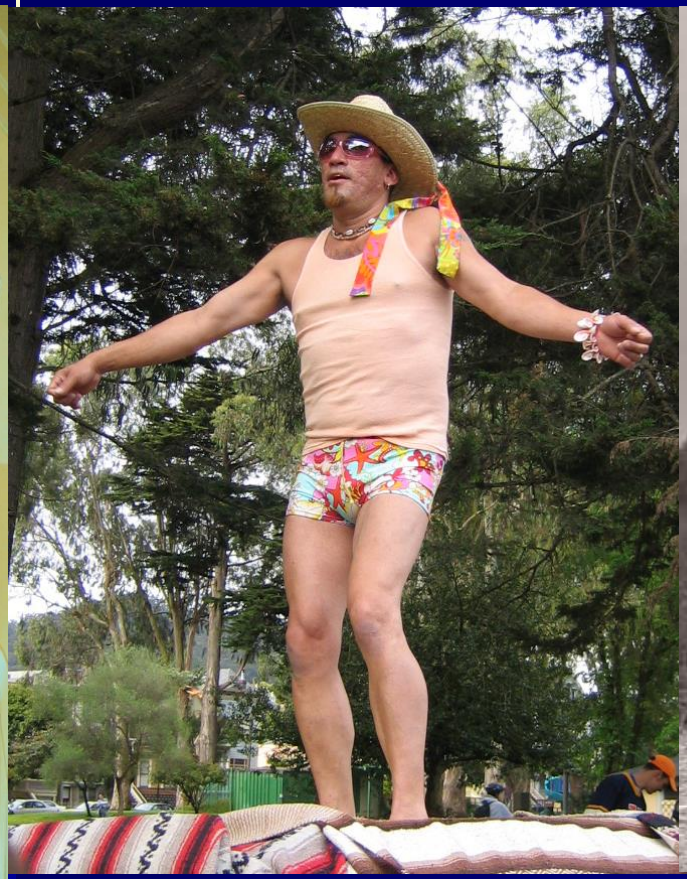
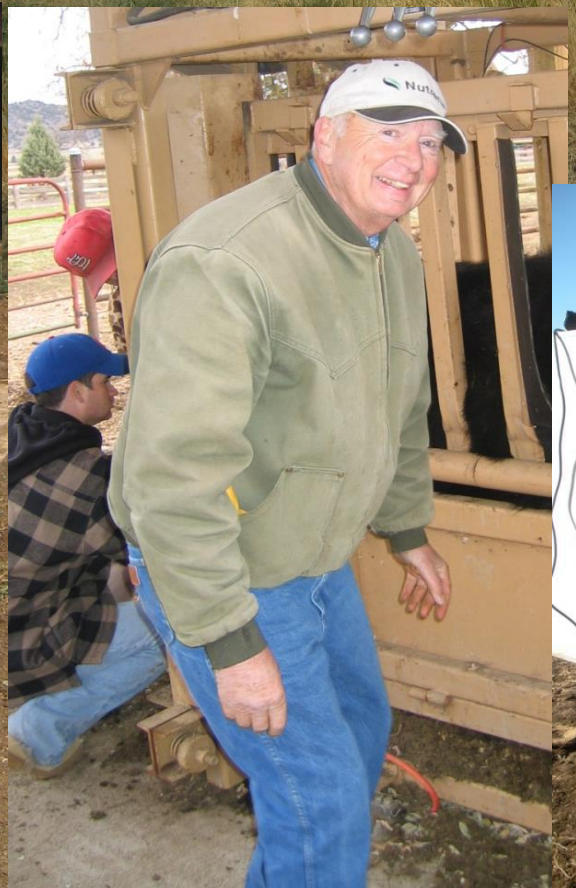


Photo taken in 1949 at Red Bluff Bull Sale, CA Generously provided by Cathy Maas from Crowe Hereford Ranch, Millville, CA.

Cowley Ranch

~20 bulls/season



Jack and Barbara Cowley

Dan Drake

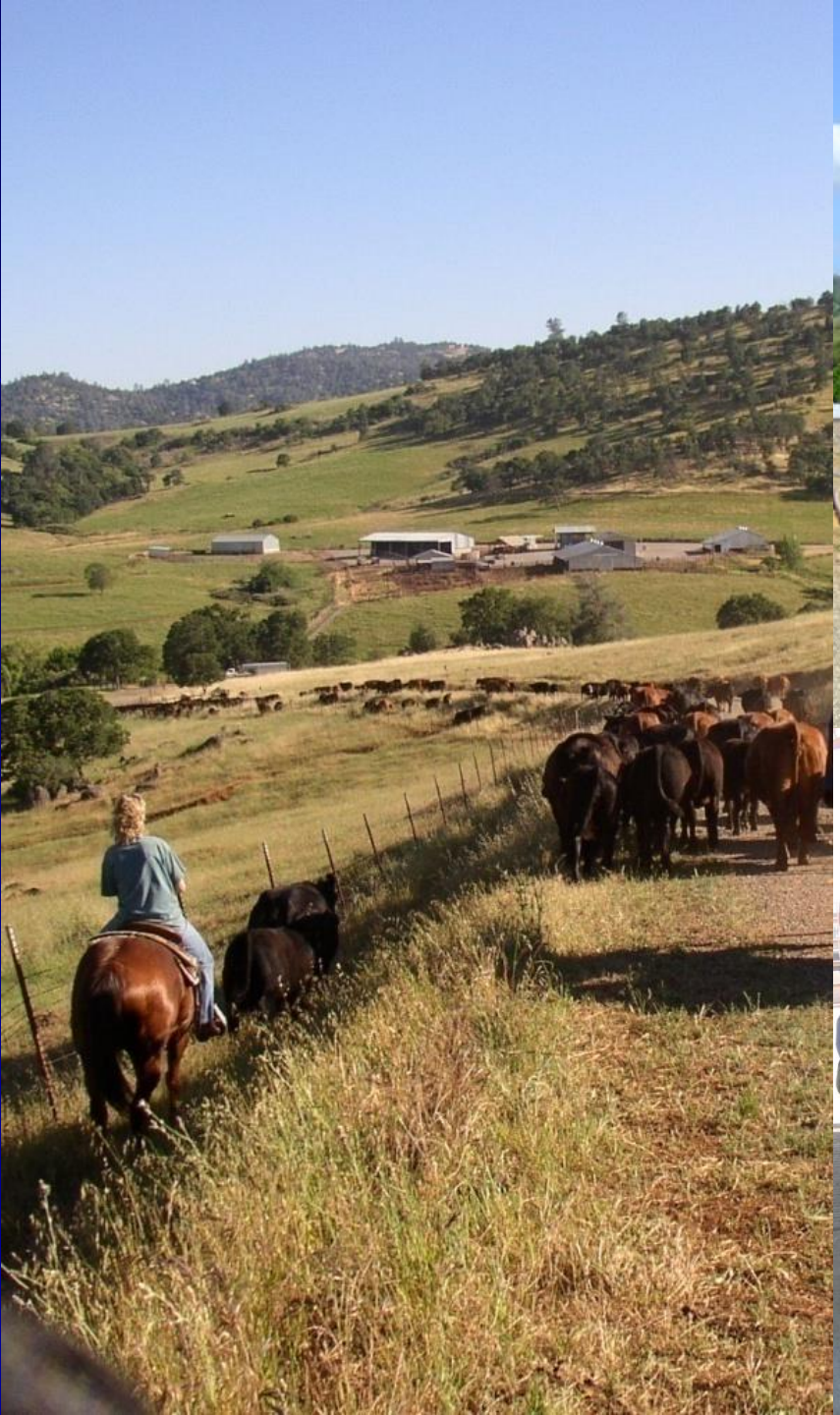
Kuck Ranch

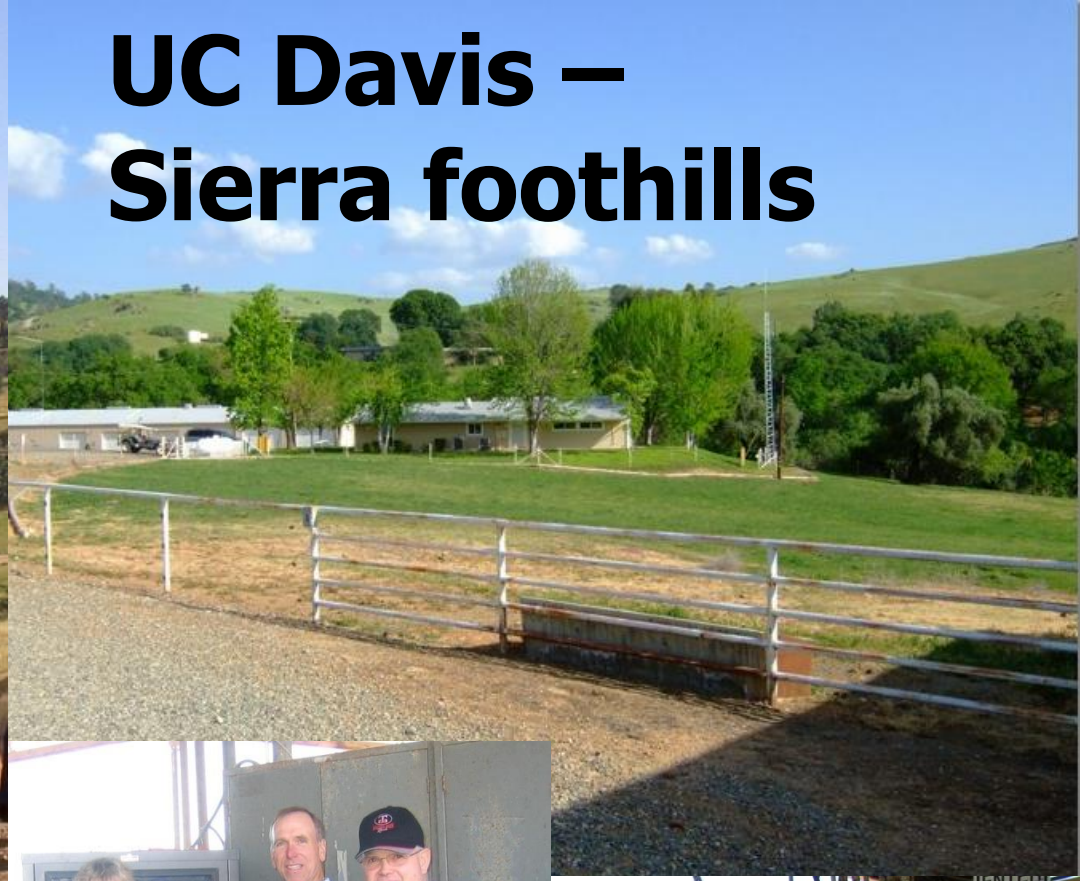
~10 bulls/season

Mole-Richardson Farms

~30 bulls

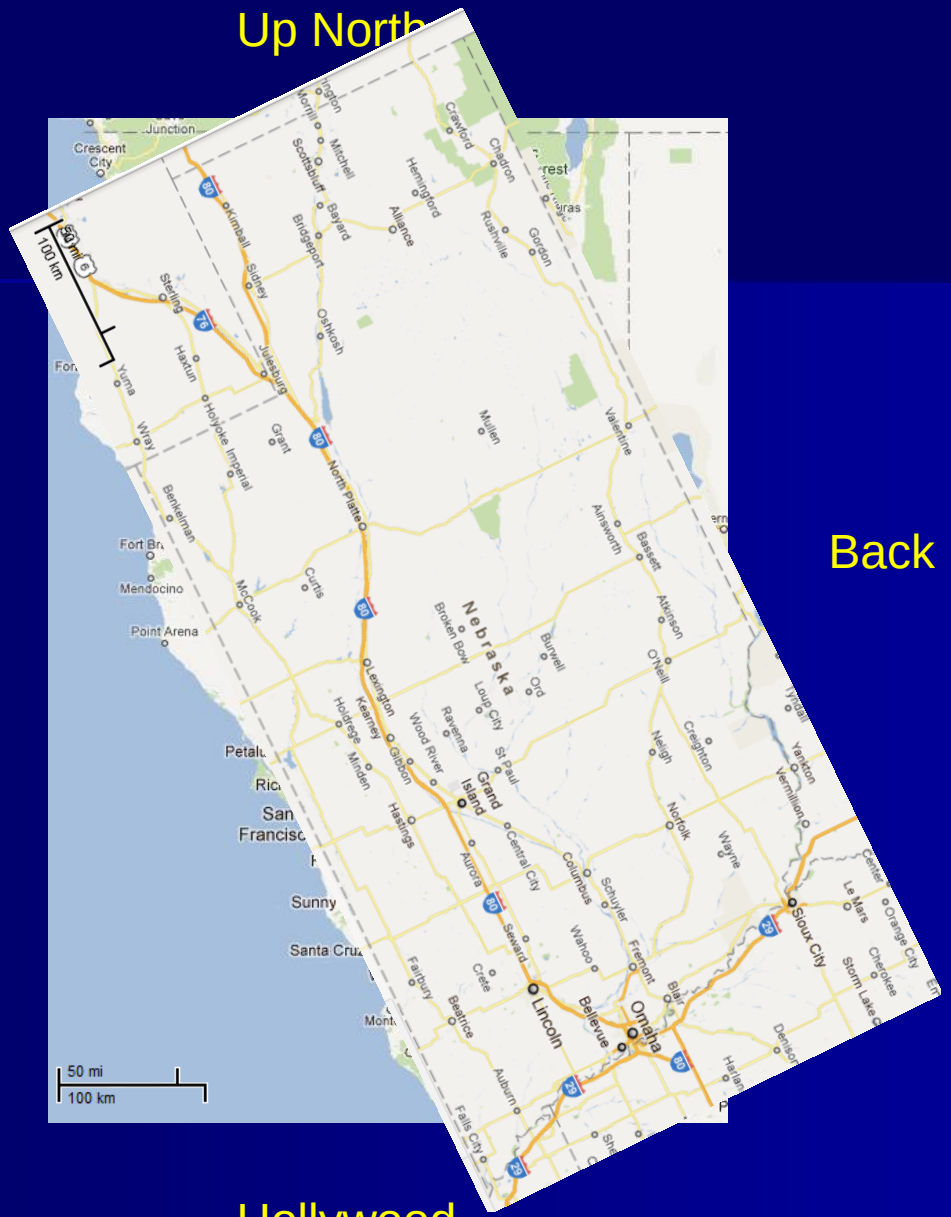
UC Davis – Sierra foothills





Up North

Pacific Ocean



Back East

Hollywood

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

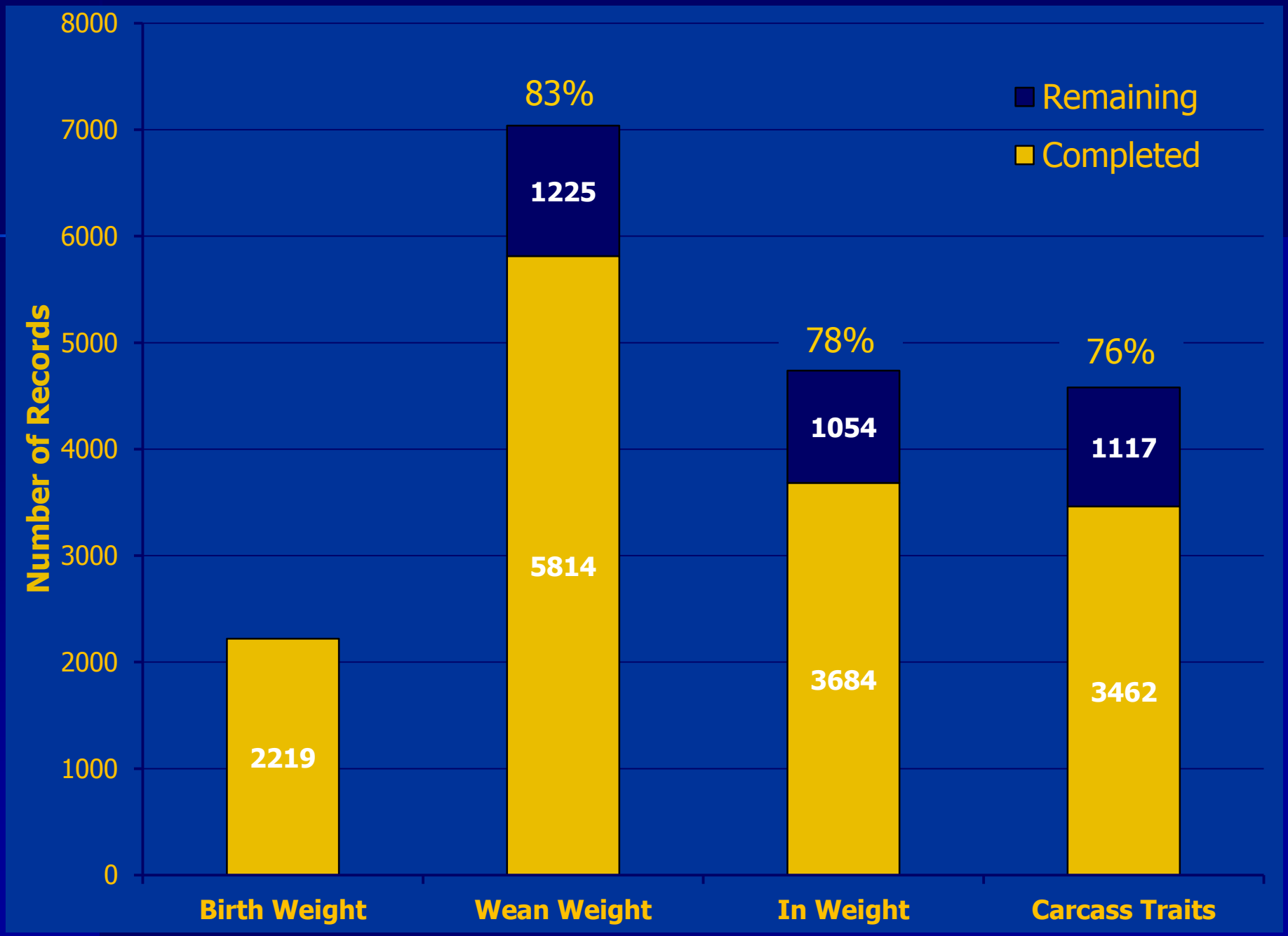
Sample and phenotype collection

Cow Sense® Herd Management Software

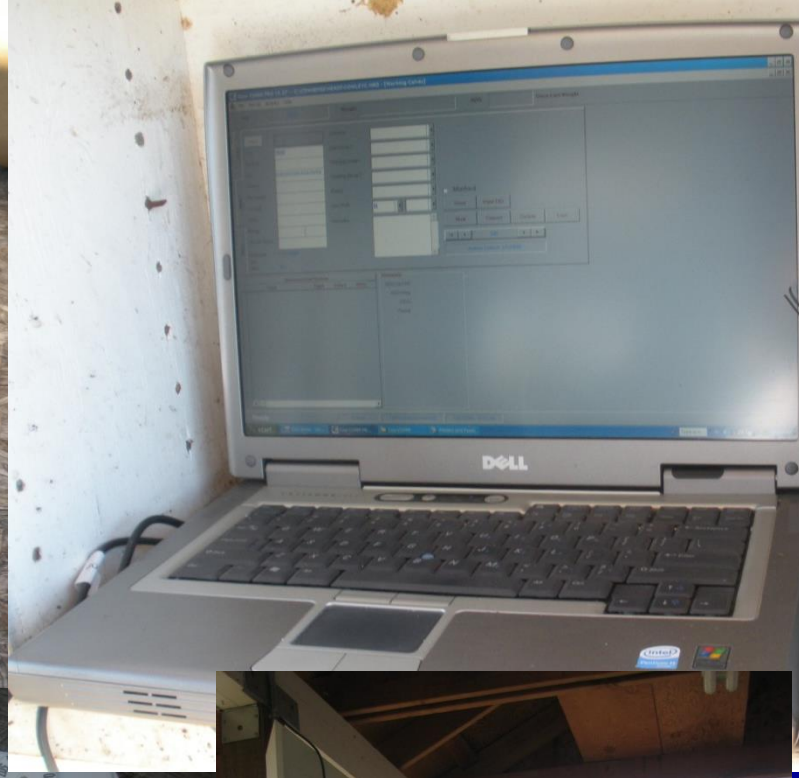
BEEFSTAR™ Source Tracking And Reporting

Cow COMM

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**


8000
7000
6000
5000
4000
3000
2000
1000
0
Number of Records
Remaining
Completed
83%
1225
5814
78%
1054
3684
76%
1117
3462
2219
Birth Weight
Wean Weight
In Weight
Carcass Traits

agrident
TEKLOGIX
WORKABOUT PRO


DELL

DYMO
LabelWriter 400 Turbo

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DELL
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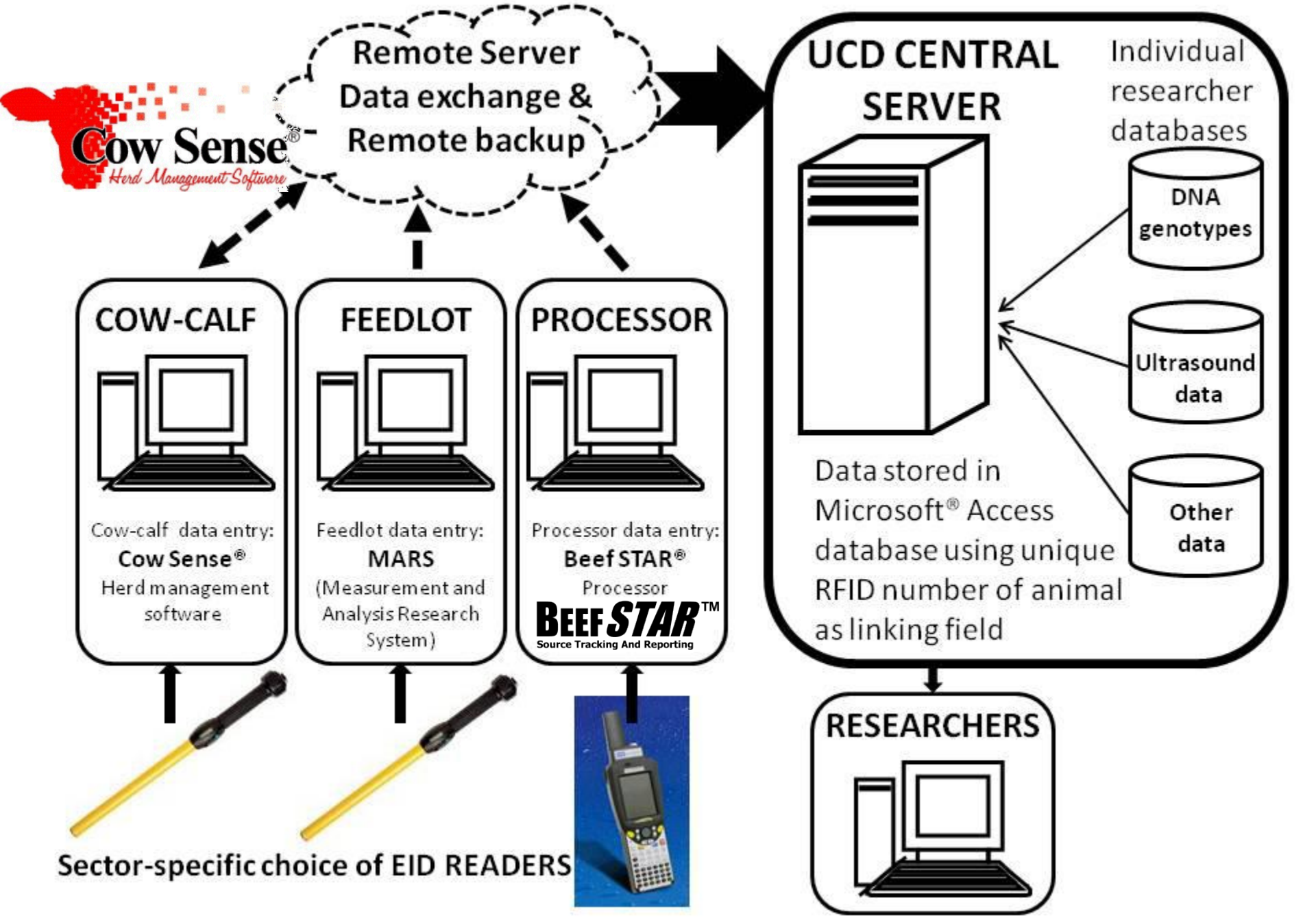
Cow Sense®
Herd Management Software
Remote Server
Data exchange &
Remote backup
UCD CENTRAL SERVER
Individual researcher databases
DNA genotypes
Ultrasound data
Other data
Data stored in Microsoft® Access database using unique RFID number of animal as linking field
COW-CALF
FEEDLOT
PROCESSOR
Cow-calf data entry:
Cow Sense®
Herd management software
Feedlot data entry:
MARS
(Measurement and Analysis Research System)
Processor data entry:
Beef STAR®
Processor
BEEF STAR™
Source Tracking And Reporting
RESEARCHERS
Sector-specific choice of EID READERS

HARRIS
RANCH
Honest
to Goodness Beef
16277 S. McCall Ave.

Assessing the Accuracy of Genomic Predictions: Results from the California Commercial Ranch Project

Kristina Weber, PhD Candidate

PD: Alison Van Eenennaam

UC Davis

Background:

- **Several sets of MBV for quantitative growth and carcass traits have been developed for beef cattle based on 50K SNP genotypes**
  - Commercial tests: IGENITY (MBV_{IG}) and Pfizer Animal Genetics (MVP) → Angus Genetics Inc. → Genomic Enhanced EPDs.
  - Iowa State University and the University of Missouri-Columbia (**ISU/UMC**)
  - U.S. Meat Animal Research Center (**USMARC**; Clay Center, NE).
- **At UCD, we have a population of Angus bulls purchased as yearlings with many progeny records for weaning weight, feedlot in-weight, and carcass traits which we can use to assess the genetic merit of these bulls in a Northern California environment**

Objective:

In this study, the accuracies of 50K-derived MBV were assessed relative to ranch-based breeding values calculated from commercial progeny phenotypes of purebred Angus bulls.

Weber, K.L., D.J. Drake, J.F. Taylor, D.J. Garrick, L.A. Kuehn, R.M. Thallman, R.D. Schnabel, W.M. Snelling, E.J. Pollak, and A.L. Van Eenennaam. 2012. The accuracies of DNA-based estimates of genetic merit derived from Angus- or multi-breed beef cattle training populations. *J. Anim. Sci. (submitted).*

MBV Considered

DNA Test	Number of tested bulls		
	Trait		
	WW	ADG	CW, MS, RE
ISU/UMC	99		99
MBV_{IG} MVP	29	29	29
GPE 2K $2K_{AN}$ $2K_{HH}$	121		121
Total Bulls	121	29	121

- **ISU/UMC:** Iowa State University and University of Missouri-Columbia, Angus, 50K, training: GBLUP with up to 3,570 records
- **MBV_{IG}:** IGENITY, Angus, 384 SNP panel
- **MVP:** Pfizer, Angus, 50K, training: Bayesian model with up to 1,445 records

- 121 natural service bulls from four ranches were 50K genotyped.
- ISU/UMC predictions were available for 99 bulls at the time of publication.
- Due to the cost of purchasing DNA test results, IGENITY and Pfizer predictions were purchased for the 29 bulls with the highest number of progeny records.

MBV Considered

DNA Test	Number of tested bulls		
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GPE 2K $2K_{AN}$ $2K_{HH}$	121		121
Total Bulls	121	29	121

- **GPE:** USMARC, Germplasm Evaluation Program Cycle VII and new GPE crossbred, 50K, training: BayesCπ with up to 3,358 phenotypic records
- **2K:** USMARC, 2000 Bull Project multi-breed, 50K, training: BayesCπ with up to 2,026 records
- **$2K_{AN}$:** USMARC, Angus, 50K, training: BayesCπ with 373 records
- **$2K_{HH}$:** USMARC, Hereford, 50K, training: BayesCπ with 463 records

Weber, K.L., R.M. Thallman, J.W. Keele, W.M. Snelling, G.L. Bennett, T.P.L. Smith, T.G. McDaneld, M.F. Allan, A.L. Van Eenennaam, and L.A. Kuehn. 2012. Accuracy of genomic breeding values in multi-breed beef cattle populations derived from deregressed breeding values and phenotypes. *J. Anim. Sci.* (*submitted*).

Published estimates of MBV Accuracy

DNA Test	Reference	Accuracy(±SE where available)				
		Trait				
		WW	ADG	CW	MS	RE
Angus						
MBV_{IG}	Northcutt, 2011	0.45		0.54	0.65	0.58
MVP	Pfizer Technical Summary 2010	0.53	0.52	0.50	0.49	0.49
	Northcutt, 2011	0.52		0.48	0.57	0.60
$2K_{AN}$	Weber et al., 2012	0.05		0.07	0.24	0.24
Multi-breed						
GPE	Weber et al., 2012	0.12		0.35	0.23	0.25
2K	Weber et al., 2012	0.24		0.12	0.23	0.35
HH						
$2K_{HH}$	Weber et al., 2012	0.24			0.01	0.22

Weber, K.L., R.M. Thallman, J.W. Keele, W.M. Snelling, G.L. Bennett, T.P.L. Smith, T.G. McDaneld, M.F. Allan, A.L. Van Eenennaam, and L.A. Kuehn. 2012. Accuracy of genomic breeding values in multi-breed beef cattle populations derived from deregressed breeding values and phenotypes. *J. Anim. Sci.* (*submitted*).

Population Structure and Relationship to Training Populations

- **Birth year** ranged from 2000-2009

- The UCD bull population included:
  - 3 sets of full siblings
  - 22 sets of paternal half siblings
  - 1 pair of maternal half siblings
- These families ranged in size from 2-9, with siblings present on up to 3 different ranches

Population Structure and Relationship to Training Populations

Relationship to training population

ISU/UMC

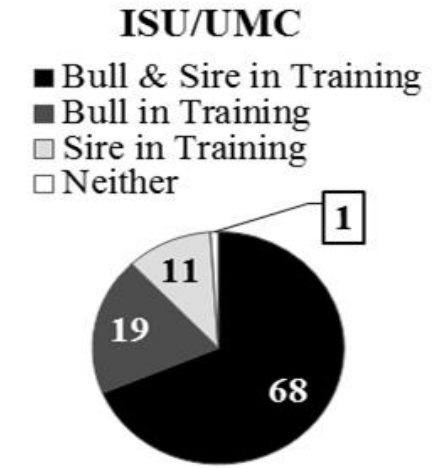
- Data available to AAA by the time of bull sale (i.e. no progeny data) was included in ISU/UMC training set for 87 UCD bulls.
- 79 bulls' sires were present in the ISU/UMC training population
- Of the remaining 20 bulls tested, 15 had grandsires and/or great-grandsires present in the ISU/UMC training population

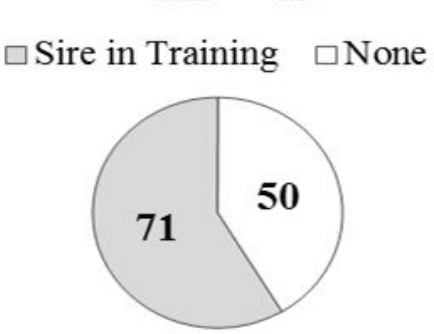
2K

- 71 bulls' sires were present in the 2K training population
- Of the remaining 50 bulls, 44 had grandsires and/or great-grandsires present in the 2K training population

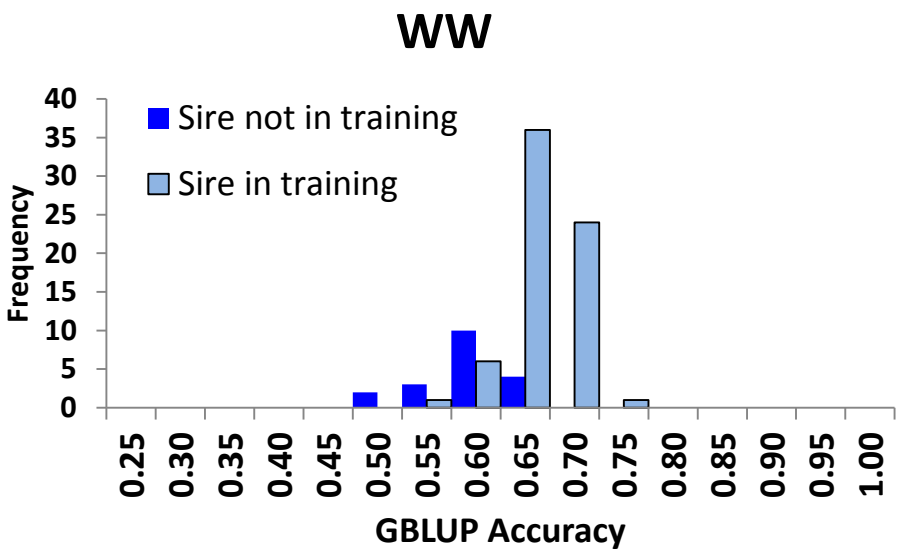
GPE

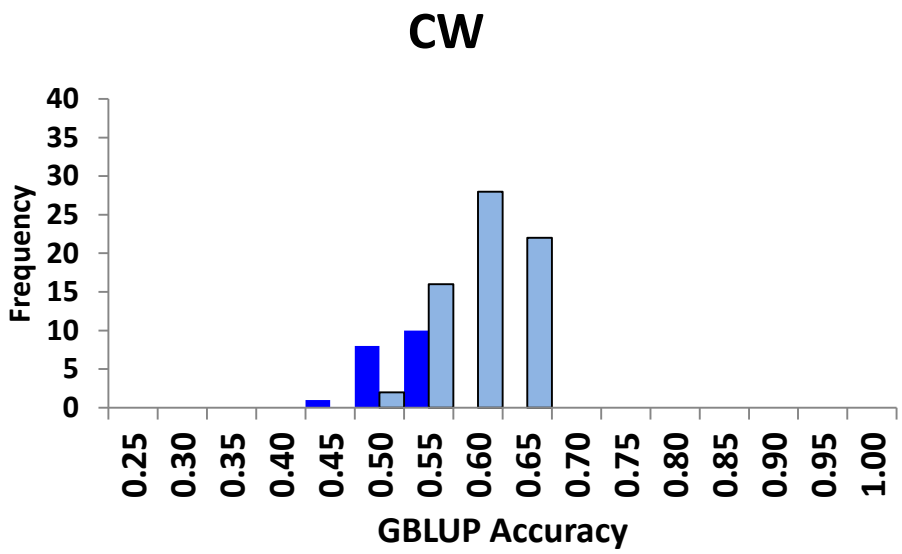
- 10 UCD bulls were related to animals in the GPE training population through sharing a common sire

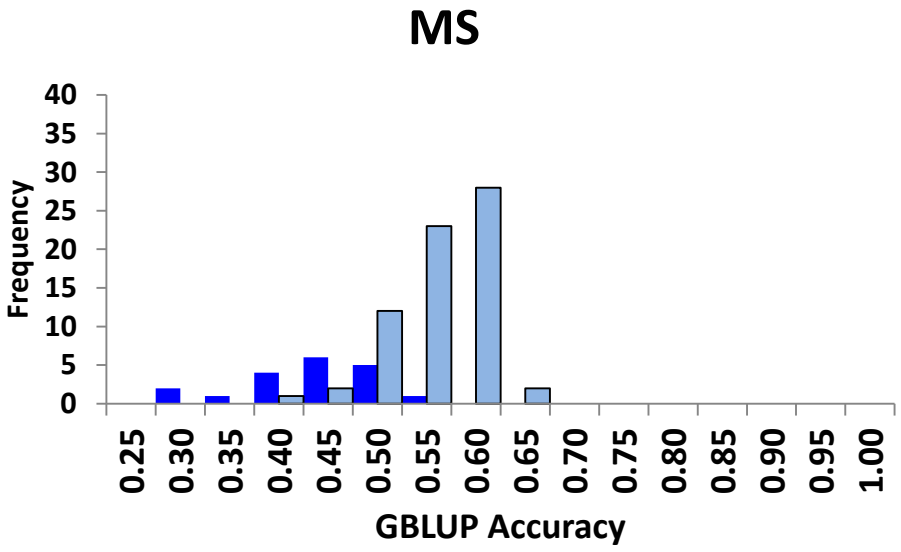


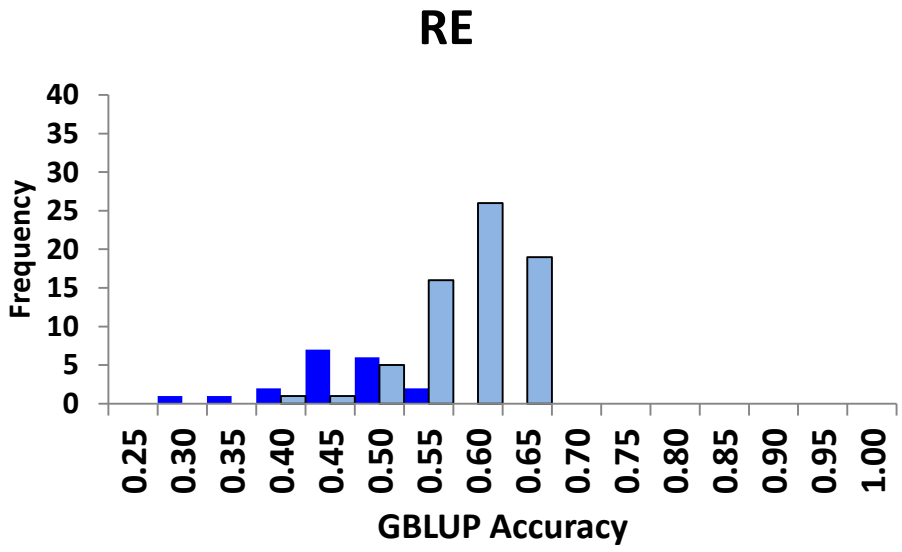


Expected Accuracy of ISU/UMC Predictions









Number of UCD Bulls with Phenotyped Progeny and the Number of Progeny Per Bull

DNA Test	Mean progeny number (range)		
	Trait		
	WW	ADG	CW, MS, RE
ISU/ UMC	44 (1-151)		26 (1-130)
MBV_{IG} MVP	73 (21-151)	44 (15-105)	48 (11-130)
GPE 2K $2K_{AN}$ $2K_{HH}$	42 (1-151)		25 (1-130)

- The bulls for which the IGENITY and Pfizer DNA tests were purchased had 31 more progeny WW records and 23 more carcass records than average for the complete dataset.

Number of UCD Bulls with Phenotyped Progeny and the Number of Progeny Per Bull

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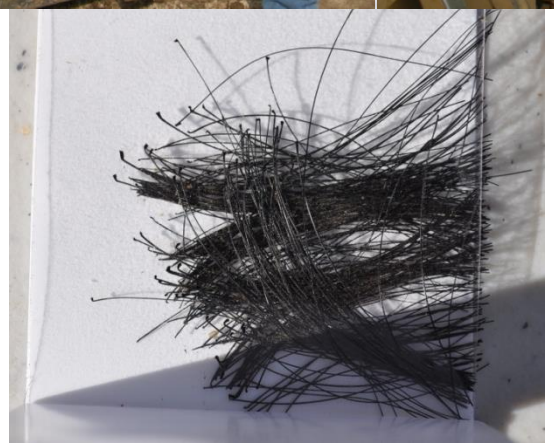
Progeny phenotypes

Trait	Angus sires	**Progeny phenotypes**	Units	Mean	SD	Min	Max
Weaning weight (WW)	129	**4,702**	lb	506.2	76.1	236.5	860.4
Feedlot average daily gain (ADG)	75	**1,902**	lb/day	3.17	0.57	1.17	6.31
Carcass weight (CW)	136	**2,865**	lb	739.2	70.6	497.0	999.0
Marbling score (MS)	136	**2,864**	*	5.83	0.95	3.00	9.33
Ribeye area (RE)	136	**2,864**	in^2	12.6	1.2	4.0	17.2

*3=traces, 4=slight, 5=small, 6=modest, 7=moderate, 8=slightly abundant, 9=moderately abundant

- WW was adjusted for age at weaning and age of dam prior to analysis
- ADG was estimated using rate of gain from feedlot in-weight to estimated feedlot final weight derived from CW, backfat thickness, and RE.
- Fixed effects:
  - Contemporary group: hys for WW, hys+feedlot lot for ADG, and hys+harvest lot for HCW, MS, and RE
  - Age for carcass traits
  - Sex for WW, HCW, and MS.
  - Fixed effects were tested for significance ($p<0.01$) as computed by ASREML from incremental Wald F statistics (Gilmour et al., 2009).

The importance of collecting meat samples and verifying live animal-carcass identification



The importance of collecting meat samples and verifying live animal-carcass identification

Error rates in abattoir reported IDs

- Average error rate of 10.8% across 5 consecutive cohorts from one ranch:
  - 3.5% in 165 head
  - 19.3% in 229 head
  - 6.4% in 167 head
  - 8.1% in 216 head
  - 16.5% in 140 head

- Reasons:
  - Rail outs
  - Inversions
  - Failure to record animals, leading to a sequence of records offset by one or two records from the correct ID

Example

Gang Tag	Carcass ID	Expected live animal ID	Actual live animal ID
Not recorded	127		535
2951	128	535	670
2952	129	670	669
2953	130	669	513
2954	131	513	525
2955	132	525	632
2956	133	799	799

Linear Model for Estimating MBV Accuracy

Accuracy = genetic correlation between the MBV and the ranch-based estimate of the genetic merit of the bulls (Kachman, 2008).

For WW:

$$\begin{bmatrix} y \\ MBV \end{bmatrix} = \begin{bmatrix} X_y & 0 \\ 0 & 1 \end{bmatrix} \begin{bmatrix} b_y \\ \mu_{MBV} \end{bmatrix} + \begin{bmatrix} Z_y & 0 \\ 0 & Z_{MBV} \end{bmatrix} \begin{bmatrix} u_y \\ u_{MBV} \end{bmatrix} + Z_m u_m + \begin{bmatrix} e \\ \varepsilon_{MBV} \end{bmatrix},$$

$$\mathrm{var}\begin{bmatrix} \mathbf{u}_y \\ \mathbf{u}_{MBV} \\ \mathbf{u}_m \\ \mathbf{e} \\ \boldsymbol{\varepsilon}_{MBV} \end{bmatrix} = \begin{bmatrix} \mathbf{A}\sigma^2_{u_y} & \mathbf{A}\sigma_{u_y u_{MBV}} & \mathbf{A}\sigma_{u_y u_m} & \mathbf{0} & \mathbf{0} \\ \mathbf{A}\sigma_{u_y u_{MBV}} & \mathbf{A}\sigma^2_{u_{MBV}} & \mathbf{A}\sigma_{u_{MBV} u_m} & \mathbf{0} & \mathbf{0} \\ \mathbf{A}\sigma_{u_y u_m} & \mathbf{A}\sigma_{u_{MBV} u_m} & \mathbf{A}\sigma^2_{u_m} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma^2_e & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma^2_{\varepsilon_{MBV}} \end{bmatrix}$$

For all other traits, the same model was used, with $\mathbf{Z_m u_m}$ excluded.

Variance components

Parameter	Trait				
	WW	ADG	CW	MS	RE
σ_A^2±SE	663±150	0.07±0.02	1556±286	0.384±0.05	0.42±0.07
σ_{AM}±SE	199±281				
σ_M^2±SE	843±294				
σ_E^2±SE	1994±107	0.18±0.02	2402±230	0.398±0.06	0.77±0.06
h_A^2±SE	0.179±0.04	0.267±0.07	0.393±0.07	0.509±0.07	0.350±0.06

Ranch and AAA EBV Accuracies

Parameter	Trait				
	WW	ADG	CW	MS	RE
Mean BIF Accuracy of Sire EBV±SE (Min-Max)	0.28± 0.01 (0.01-0.55)	0.23± 0.03 (0.00-0.52)	0.27± 0.02 (0.01-0.63)	0.30± 0.02 (0.01-0.66)	0.25± 0.02 (0.01-0.61)
Mean BIF Accuracy of AAA EPD±SE (Min-Max)	0.20± 0.01 (0.05-0.34)		0.16± 0.01 (0.05-0.25)	0.20± 0.01 (0.05-0.28)	0.23± 0.01 (0.05-0.31)

Ranch and AAA EBV Accuracies

Young bulls that have been genotyped but don't have phenotyped progeny yet

Parameter	Trait				
	WW	ADG	CW	MS	RE
Mean BIF Accuracy of Sire EBV±SE (Min-Max)	0.28± 0.01 (0.01-0.55)	0.23± 0.03 (0.00-0.52)	0.27± 0.02 (0.01-0.63)	0.30± 0.02 (0.01-0.66)	0.25± 0.02 (0.01-0.61)
Mean BIF Accuracy of AAA EPD±SE (Min-Max)	0.20± 0.01 (0.05-0.24)		0.16± 0.01 (0.05-0.25)	0.20± 0.01 (0.05-0.28)	0.23± 0.01 (0.05-0.31)

Pedigree only

Ranch and AAA EBV Accuracies

Parameter	Trait				
	WW	ADG	CW	MS	RE
Mean BIF Accuracy of Sire EBV±SE (Min-Max)	0.28± 0.01 (0.01-0.55)	0.23± 0.03 (0.00-0.52)	0.27± 0.02 (0.01-0.63)	0.30± 0.02 (0.01-0.66)	0.25± 0.02 (0.01-0.61)
Mean BIF Accuracy of AAA EPD±SE (Min-Max)	0.20± 0.01 (0.05-0.34)		0.16± 0.01 (0.05-0.25)	0.20± 0.01 (0.05-0.28)	0.23± 0.01 (0.05-0.31)

+Bull's own phenotype

Ranch and AAA EBV Accuracies

+ Many phenotyped progeny

Parameter	Trait				
	WW	ADG	CW	MS	RE
Mean BIF Accuracy of Sire EBV±SE (Min-Max)	0.28± 0.01 (0.01-0.55)	0.23± 0.03 (0.00-0.52)	0.27± 0.02 (0.01-0.63)	0.30± 0.02 (0.01-0.66)	0.25± 0.02 (0.01-0.61)
Mean BIF Accuracy of AAA EPD±SE (Min-Max)	0.20± 0.01 (0.05-0.34)		0.16± 0.01 (0.05-0.25)	0.20± 0.01 (0.05-0.28)	0.23± 0.01 (0.05-0.31)

Genetic correlation with UCD Data

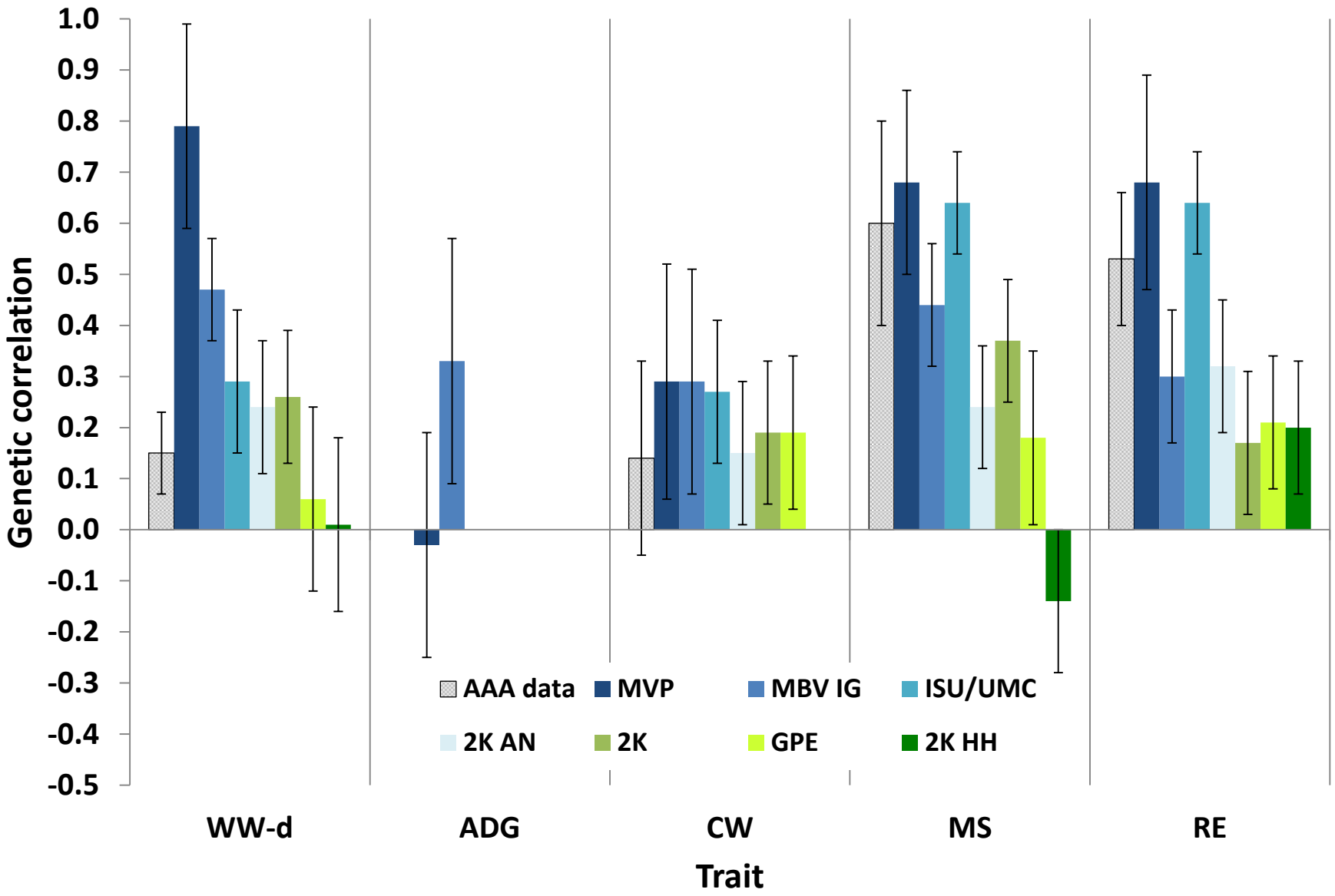
	Number of bulls	Accuracy±SE				
		WW-d	ADG	CW	MS	RE
AAA data	120	0.15±0.08		0.14±0.19	0.60±0.20	0.53±0.13
ISU/UMC	99	0.29±0.14		0.27±0.14	0.64±0.10	0.64±0.10
MBV_{IG}	29	0.47±0.20	0.33±0.22	0.29±0.23	0.44±0.18	0.30±0.21
MVP	29	0.79±0.10	-0.03±0.24	0.29±0.22	0.68±0.12	0.68±0.13
$2K_{AN}$	121	0.24±0.13		0.15±0.14	0.24±0.12	0.32±0.13
GPE	121	0.06±0.18		0.19±0.15	0.18±0.17	0.21±0.13
$2K_{ALL}$	121	0.26±0.13		0.19±0.14	0.37±0.12	0.17±0.14
$2K_{HH}$	121	0.01±0.17			-0.14±0.14	0.20±0.13

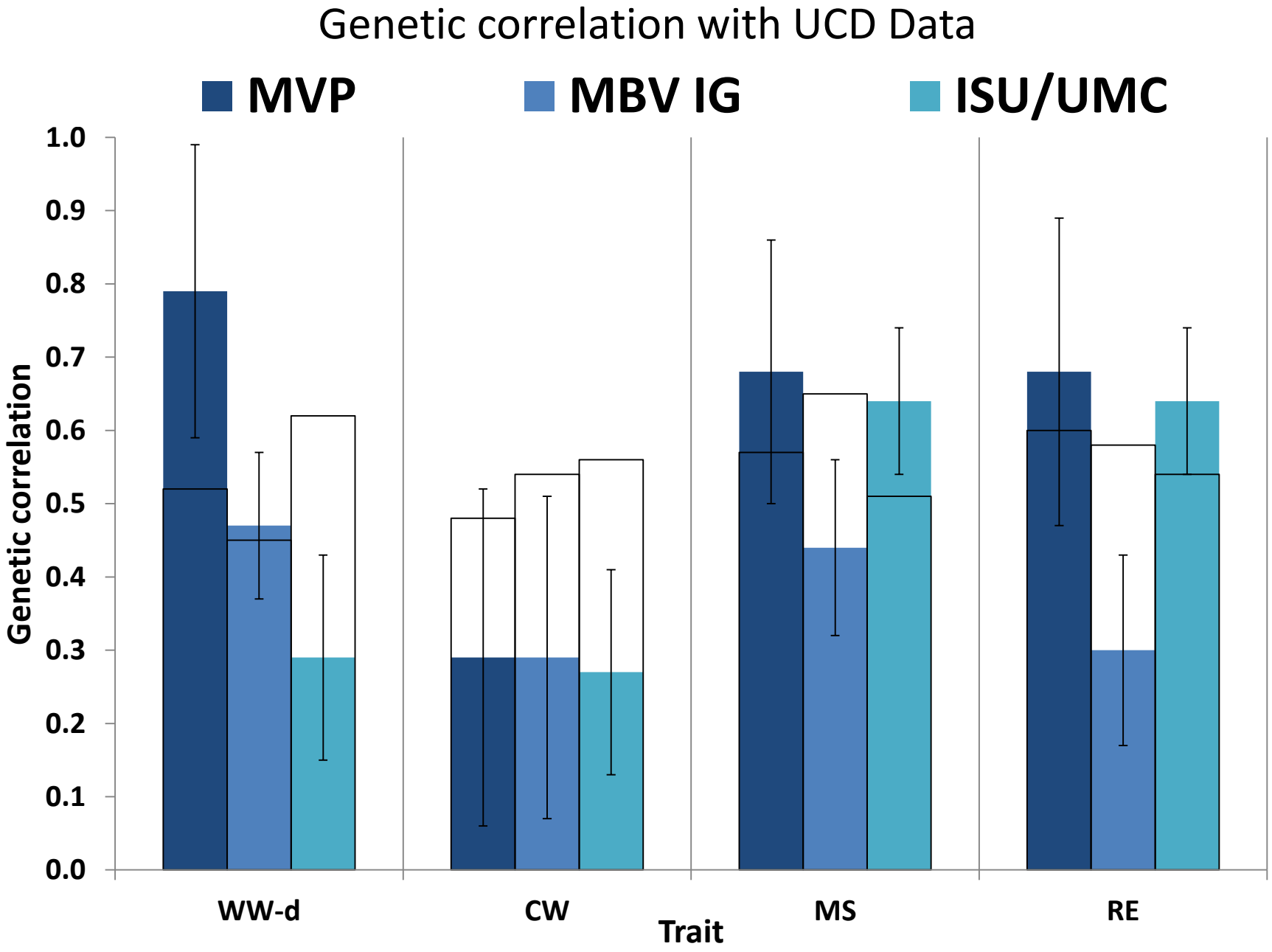
Genetic correlation with UCD Data

	Number of bulls	Accuracy±SE				
		WW-d	ADG	CW	MS	RE
AAA data	120	0.15±0.08		0.14±0.19	0.60±0.20	0.53±0.13
ISU/UMC	99	0.29±0.14		0.27±0.14	0.64±0.10	0.64±0.10
MBV_{IG}	29	0.47±0.20	0.33±0.22	0.29±0.23	0.44±0.18	0.30±0.21
MVP	29	0.79±0.10	-0.03±0.24	0.29±0.22	0.68±0.12	0.68±0.13
$2K_{AN}$	121	0.24±0.13		0.15±0.14	0.24±0.12	0.32±0.13
GPE	121	0.06±0.18		0.19±0.15	0.18±0.17	0.21±0.13
$2K_{ALL}$	121	0.26±0.13		0.19±0.14	0.37±0.12	0.17±0.14
$2K_{HH}$	121	0.01±0.17			-0.14±0.14	0.20±0.13

Genetic correlation with UCD Data

	Number of bulls	Accuracy±SE				
		WW-d	ADG	CW	MS	RE
AAA data	120	0.15±0.08		0.14±0.19	0.60±0.20	0.53±0.13
ISU/UMC	99	0.29±0.14		0.27±0.14	0.64±0.10	0.64±0.10
MBV_{IG}	29	0.47±0.20	0.33±0.22	0.29±0.23	0.44±0.18	0.30±0.21
MVP	29	0.79±0.10	-0.03±0.24	0.29±0.22	0.68±0.12	0.68±0.13
$2K_{AN}$	121	0.24±0.13		0.15±0.14	0.24±0.12	0.32±0.13
GPE	121	0.06±0.18		0.19±0.15	0.18±0.17	0.21±0.13
$2K_{ALL}$	121	0.26±0.13		0.19±0.14	0.37±0.12	0.17±0.14
$2K_{HH}$	121	0.01±0.17			-0.14±0.14	0.20±0.13


Genetic correlation with UCD Data
Genetic correlation
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
-0.1
-0.2
-0.3
-0.4
-0.5
AAA data
MVP
MBV IG
ISU/UMC
2K AN
2K
GPE
2K HH
WW-d
ADG
CW
MS
RE
Trait


Genetic correlation with UCD Data
MVP
MBV IG
ISU/UMC
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
Genetic correlation
WW-d
CW
MS
RE
Trait

Pairwise Genetic Correlations between MBV

	ISU/UMC x MVP	ISU/UMC x MBV_{IG}	MVP x MBV_{IG}
WW	**0.70±0.13**	**0.49±0.14**	**0.31±0.17**
ADG			**0.15±0.18**
CW	**0.64±0.10**	**0.51±0.12**	**0.42±0.16**
MS	**0.77±0.13**	**0.69±0.26**	**0.43±0.15**
RE	**0.64±0.10**	**0.50±0.13**	**0.48±0.15**

High correlations observed between ISU/UMC, MVP and MBV_{IG} for all traits except ADG.

Conclusions

- MBV accuracies for commercially available tests were similar to those reported for the Angus breed but for traits in which ranch EPD were not well correlated with AAA EPD, there was a trend of lower than expected MBV accuracy

- MBV that were not derived from Angus were less accurate than Angus-derived MBV

Future Directions

- Illumina BovineHD genotyping and imputation up to HD from 50K for the training and assessment populations has begun
- Preliminary results suggest that there is some improvement in multi-breed MBV accuracy when training on HD genotype data
- Finish collecting all of the data and graduate!

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 Beef Cattle Evaluation Consortium
Colorado State University-Cornell University-University of Georgia-Iowa State University