



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

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OUTLINE


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



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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.

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

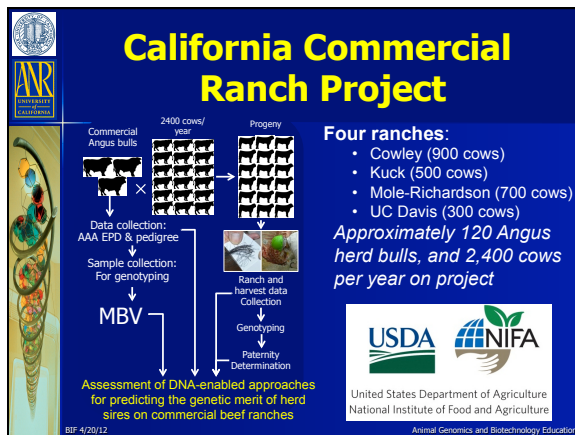
The **extension objective** is to develop and deliver educational materials to a national audience on the integration of DNA information into beef cattle selection programs.

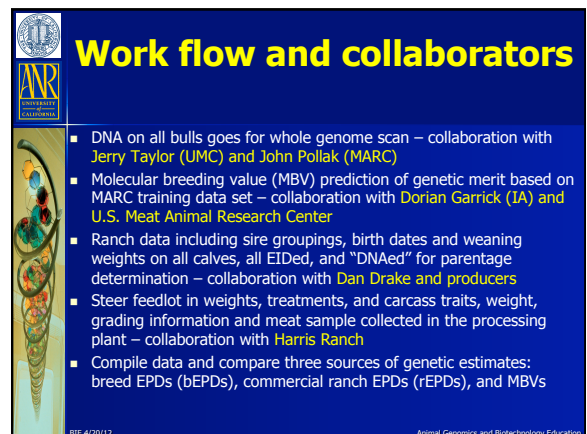
- Includes the development of fact sheets, national educational programs including program at BIF 2009, brown bagger series, popular press articles, and NBCEC workshop entitled "**Integrating DNA information into beef cattle production systems**" – to be held in **Kansas City, MO March 5th 2013**

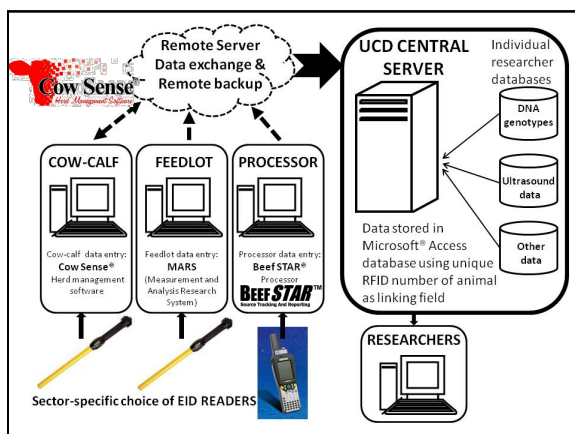
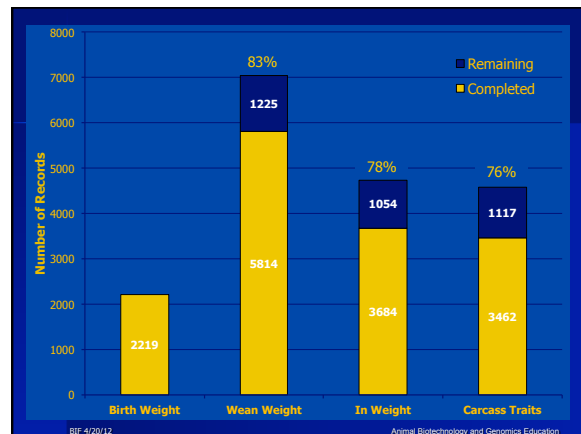
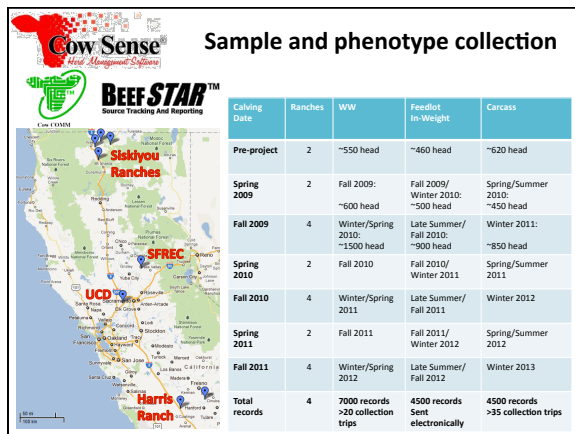
National Beef Cattle Evaluation Consortium

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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}	29	29	29	
MVP				
GPE				
2K	121		121	
2K _{AN}				
2K _{HH}				
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.

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

Weber, K.L., R.M. Thallman, J.W. Keele, W.M. Snelling, G.L. Bennett, T.P.L. Smith, T.G. McDanel, 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. McDanel, 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

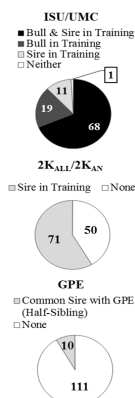
- Data available to AAA by the time of bull sale (i.e. no progeny data) was included in ISU/UMC training set for 87 UCD bulls.
- 79 bulls' sires were present in the ISU/UMC training population
- Of the remaining 20 bulls tested, 15 had grandsires and/or great-grandsires present in the ISU/UMC training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

2K

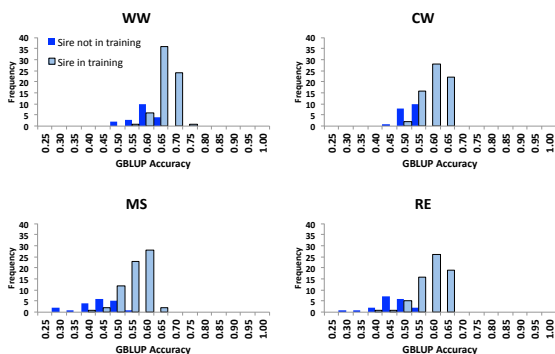
- 71 bulls' sires were present in the 2K training population
- Of the remaining 50 bulls, 44 had grandsires and/or great-grandsires present in the 2K training population

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}	73 (21-151)	44 (15-105)	48 (11-130)
MVP			
GPE			
2K	42 (1-151)		25 (1-130)
2K _{AN}			
2K _{HH}			

- 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.

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2K _{AN}			
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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

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:

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

$$\text{var} \begin{bmatrix} u_y \\ u_{MBV} \\ u_m \\ e \\ e_{MBV} \end{bmatrix} = \begin{bmatrix} \Lambda \sigma_{u_y}^2 & \Lambda \sigma_{u_y u_{MBV}} & \Lambda \sigma_{u_y u_m} & 0 & 0 \\ \Lambda \sigma_{u_y u_{MBV}} & \Lambda \sigma_{u_{MBV}}^2 & \Lambda \sigma_{u_{MBV} u_m} & 0 & 0 \\ \Lambda \sigma_{u_y u_m} & \Lambda \sigma_{u_{MBV} u_m} & \Lambda \sigma_{u_m}^2 & 0 & 0 \\ 0 & 0 & 0 & \Lambda \sigma_e^2 & 0 \\ 0 & 0 & 0 & 0 & \Lambda \sigma_{e_{MBV}}^2 \end{bmatrix}$$

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

Variance components

Parameter	Trait	WW	ADG	CW	MS	RE
$\sigma_{u_y}^2 \pm SE$		663±150	0.07±0.02	1556±286	0.384±0.05	0.42±0.07
$\sigma_{u_{MBV}}^2 \pm SE$		199±281				
$\sigma_{u_y u_{MBV}} \pm SE$		843±294				
$\sigma_e^2 \pm SE$		1994±107	0.18±0.02	2402±230	0.398±0.06	0.77±0.06
$\sigma_{e_{MBV}}^2 \pm SE$		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		0.28±	0.23±	0.27±	0.30±	0.25±
Accuracy of		0.01	0.03	0.02	0.02	0.02
Sire EBV±SE		(0.01-0.5	(0.00-0.5	(0.01-0.6	(0.01-0.6	(0.01-0.6
(Min-Max)		5)	2)	3)	6)	1)
Mean BIF		0.20±		0.16±	0.20±	0.23±
Accuracy of		0.01		0.01	0.01	0.01
AAA EPD±SE		(0.05-0.3		(0.05-0.2	(0.05-0.2	(0.05-0.3
(Min-Max)		4)		5)	8)	1)

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		0.28±	0.23±	0.27±	0.30±	0.25±
Accuracy of		0.01	0.03	0.02	0.02	0.02
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(Min-Max)		5)	2)	3)	6)	1)
Mean BIF		0.20±		0.16±	0.20±	0.23±
Accuracy of		0.01		0.01	0.01	0.01
AAA EPD±SE		(0.05-0.3		(0.05-0.2	(0.05-0.2	(0.05-0.3
(Min-Max)		4)		5)	8)	1)

Pedigree only

Ranch and AAA EBV Accuracies

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Mean BIF		0.20±		0.16±	0.20±	0.23±
Accuracy of		0.01		0.01	0.01	0.01
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(Min-Max)		4)		5)	8)	1)

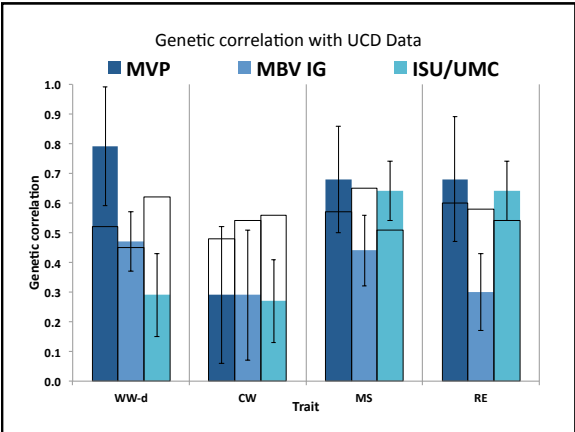
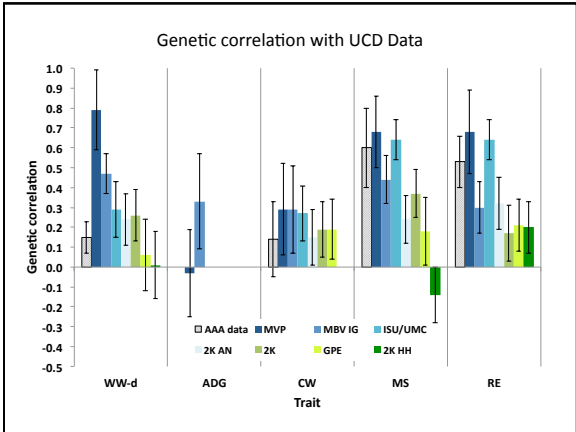
+Bull's own phenotype

Ranch and AAA EBV Accuracies						
+ Many phenotyped progeny						
Parameter	Trait	WW	ADG	CW	MS	RE
Mean BIF		0.28±	0.23±	0.27±	0.30±	0.25±
Accuracy of		0.01	0.03	0.02	0.02	0.02
Sire EBV±SE		(0.00-0.5)	(0.00-0.5)	(0.01-0.6)	(0.01-0.6)	(0.01-0.6)
(Min-Max)		(5)	(2)	(3)	(6)	(1)
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(Min-Max)		4)		5)	8)	1)

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

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2K _{HH}	121	0.01±0.17			-0.14±0.14	0.20±0.13



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:

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- Los Banos Abattoir, Los Banos, CA

Software Collaborators:

- Jim Lowe, Cow Sense Herd Management Software, NE

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