

# "Update: Integrating DNA Information into Beef Cattle Production Systems"

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# Ranch resources/collaborators on “Integrating DNA information into beef cattle production systems”

Four ranches on this project (UC Davis and  
3 commercial cooperators in Siskiyou Co.)

- Cowley 900 (550 Spring; 350 Fall) 45
- Kuck 500 (200 Spring; 300 Fall) 16
- Mole-Richardson 700 (Fall) 40
- UC Davis 300 (Fall) 26

*Approximately 125 Angus bulls, and 2,400  
cows per year on project*



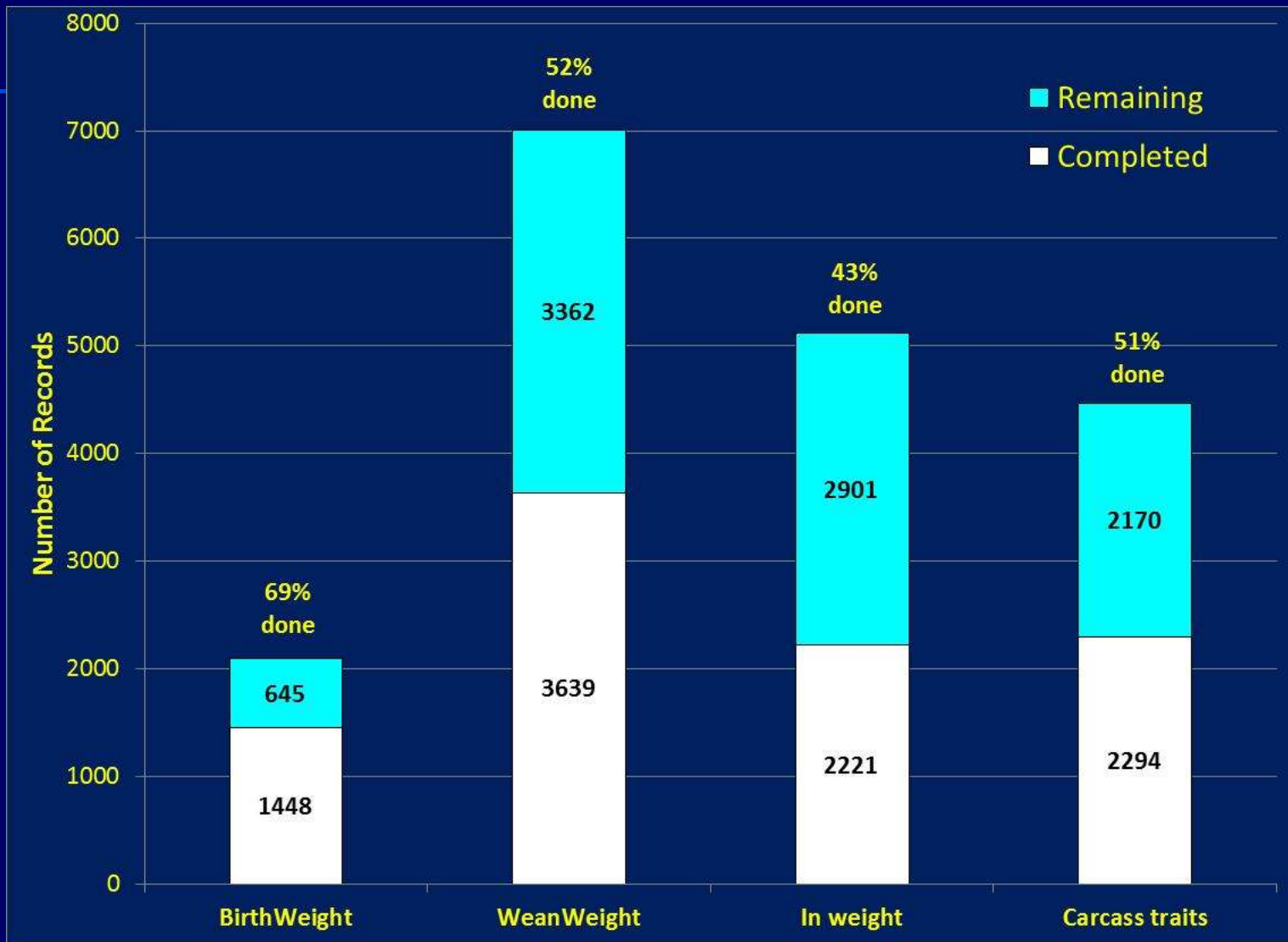
# Work flow and collaborators



- DNA on all bulls goes for 50K whole genome scan – collaboration with **Jerry Taylor (MO)** and **John Pollak (Meat Animal Research Center (NE))**
- Molecular breeding value (MBV) prediction of genetic merit based on MARC training data set – collaboration with **Dorian Garrick (IA)** and **Mark Thallman, 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 (CA)**
- Steer feedlot in weights, treatments, and carcass traits (Hot 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, UC Davis, PhD student**



# Sampling Summary : Total Number of Records to date







# Description of the data



- Progeny records of Angus bulls from calf cohorts beginning in 2006 (bulls bred 2005). Though the dataset included over 3500 progeny records, only 1852 were direct progeny of the 29 analyzed bulls, though all were progeny of Angus bulls produced on those ranches and related by pedigree. Not all progeny had records for every trait.
- Of progeny of these particular sires, the most records were available for weaning weight (1734), then ADG (defined as rate of gain between weaning weight and entry weight into the feedlot (1356); then carcass traits HCWT, MRB, and REA (455).
- The pedigree included at least 4-generations on all registered Angus bulls.



# Methods



- Genetic correlations were estimated between IGENITY and Pfizer MBV and the genetic merit of 29 Angus bulls as estimated from performance of progeny produced on 3 commercial ranches since 2005.
- Definition of a correlation (a and b being the genetic components of the two correlated traits):
- Each estimated correlation is reported with its standard error, defined as the square root of the variance of the estimate. This is defined as:

$$r = \sigma_{ab} / \sqrt{\sigma_a^2 \sigma_b^2}$$

$$\begin{aligned} \text{var}(r) = r^2 & \left[ \frac{\text{var}(\sigma_a^2)}{4\sigma_a^2} + \frac{\text{var}(\sigma_b^2)}{4\sigma_b^2} + \frac{\text{var}(\sigma_{ab})}{\sigma_{ab}^2} \right. \\ & \left. + \frac{2\text{cov}(\sigma_a^2, \sigma_b^2)}{4\sigma_a^2 \sigma_b^2} - \frac{2\text{cov}(\sigma_a^2, \sigma_{ab})}{2\sigma_a^2 \sigma_{ab}} - \frac{2\text{cov}(\sigma_{ab}, \sigma_b^2)}{2\sigma_{ab} \sigma_b^2} \right] \end{aligned}$$



# Model



The model used to estimate the genetic correlations and EBV for bulls was a standard bivariate animal model. MBV were treated as a second trait correlated with ranch performance.

- The mean and contemporary group {herd, season, sex, age of dam (binary classification as 1<sup>st</sup> calf heifer or cow), and feedlot or harvest cohorts} were fit.
- Breed was not included in the model, but all progeny were at least 50% Angus based on their sire, and likely predominantly Angus on their maternal side in most cases.
- Weaning weight was adjusted to 205 days based on known age and birth weight (Kuck) or known age and assumed birth weight based on BIF guidelines by sex (Cowley & Mole-Richardson) on ranches where birth weight was not recorded.
- Random maternal effects were included in the weaning weight model but random permanent environmental effects were not included in the model due to the scarcity of information available on the dams.

# Results: Genetic correlations

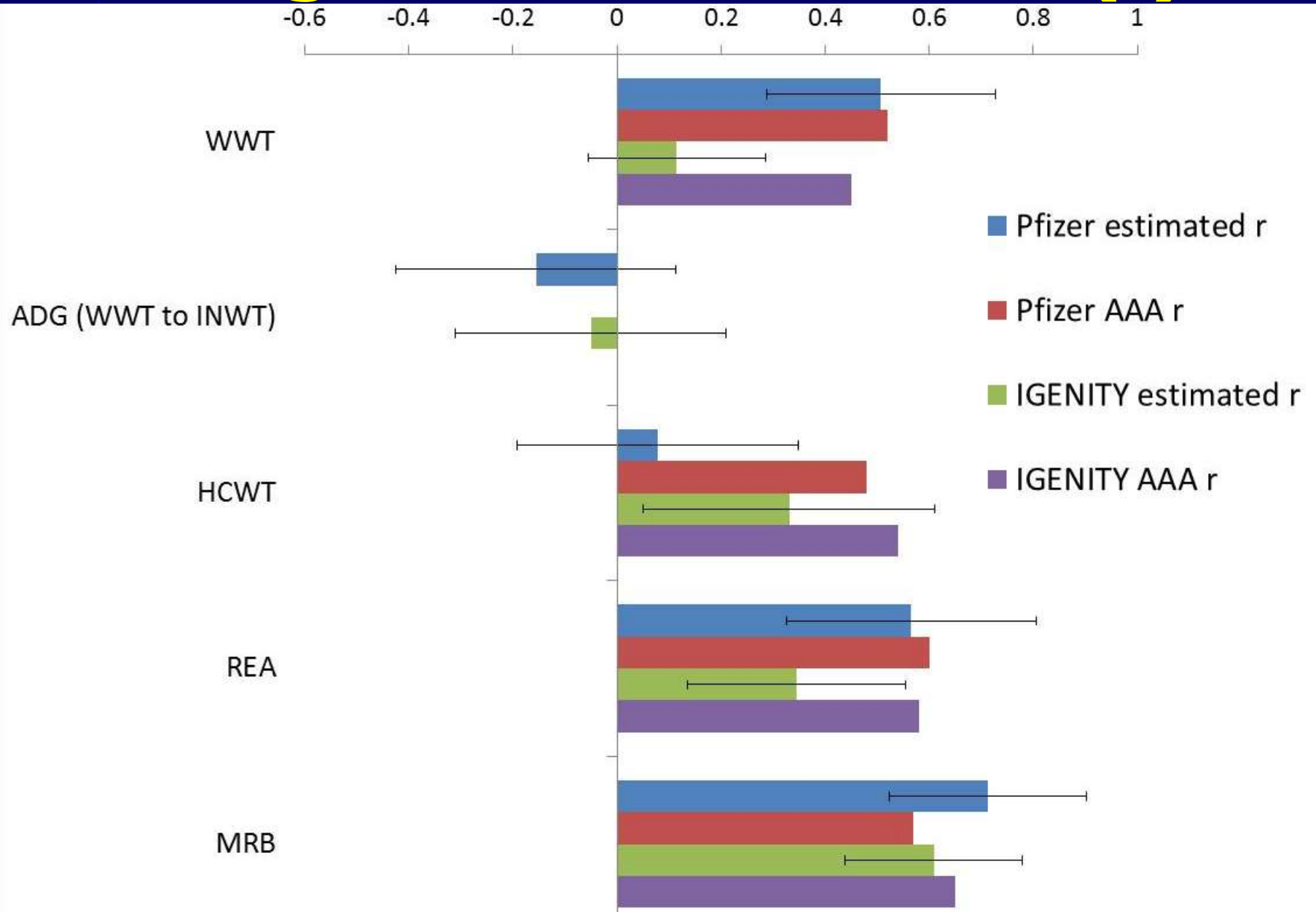


	<b>Bulls with ranch BIF acc &gt; 0.05</b>	<b># direct progeny in dataset</b>	<b>Pfizer estimated r</b>	<b>IGENITY estimated r</b>
WWT	29	1734	0.507 (0.17)	0.115 (0.22)
ADG (WWT to INWT)	28	1356	-0.156 (0.26)	-0.050 (0.27)
HCWT	20	455	0.078 (0.28)	0.331 (0.27)
REA	23	455	0.565 (0.21)	0.345 (0.24)
MRB	23	455	0.713 (0.17)	0.609 (0.19)

- MBVs had heritabilities near or equal to 1.



# Est. genetic correlations (r)





# Results: Regression analyses

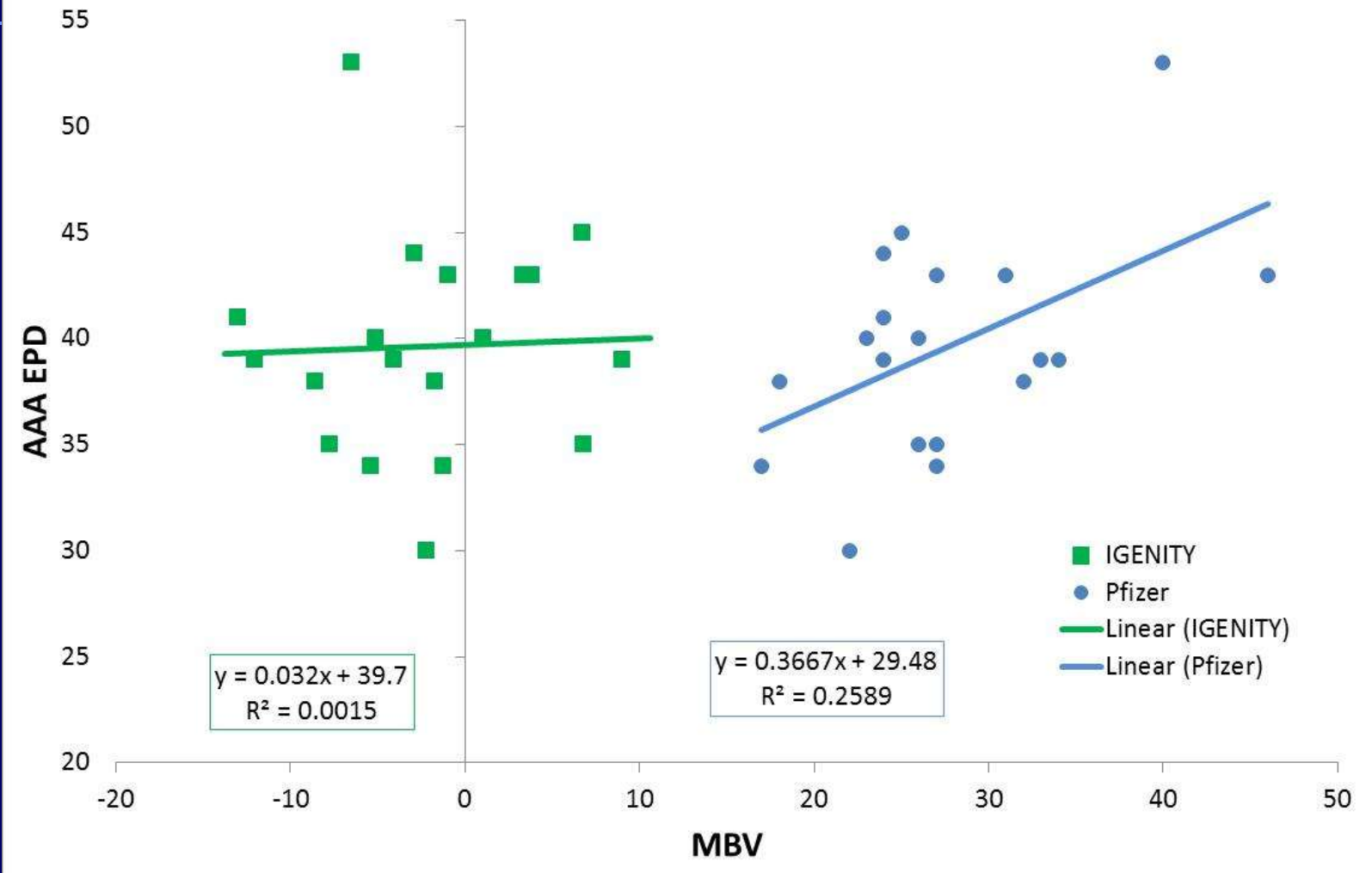


<u>Trait</u>	<u>Source of EPD</u>	<u>Test</u>	<u>Slope</u>	<u>Sterr</u>	<u>Prob</u>	<u>Significance</u>
WW	AAA	IGENITY	0.03	0.20	0.87	
WW	Ranch	IGENITY	0.13	0.74	0.86	
<b>REA</b>	<b>AAA</b>	<b>IGENITY</b>	<b>0.79</b>	<b>0.17</b>	<b>0.0001</b>	<b>***</b>
REA	Ranch	IGENITY	1.69	0.83	0.06	
<b>MRB</b>	<b>AAA</b>	<b>IGENITY</b>	<b>0.87</b>	<b>0.20</b>	<b>0.0002</b>	<b>***</b>
<b>MRB</b>	<b>Ranch</b>	<b>IGENITY</b>	<b>2.07</b>	<b>0.58</b>	<b>0.0023</b>	<b>**</b>
<b>CW</b>	<b>AAA</b>	<b>IGENITY</b>	<b>0.95</b>	<b>0.22</b>	<b>0.0002</b>	<b>***</b>
CW	Ranch	IGENITY	1.09	0.75	0.17	
ADG	AAA	IGENITY	--	--	--	
ADG	Ranch (PostWG)	IGENITY	-1.08	1.23	0.39	
<b>WW</b>	<b>AAA</b>	<b>Pfizer</b>	<b>0.37</b>	<b>0.15</b>	<b>0.03</b>	<b>*</b>
<b>WW</b>	<b>Ranch</b>	<b>Pfizer</b>	<b>1.78</b>	<b>0.65</b>	<b>0.01</b>	<b>*</b>
<b>REA</b>	<b>AAA</b>	<b>Pfizer</b>	<b>0.54</b>	<b>0.10</b>	<b>0.00002</b>	<b>***</b>
<b>REA</b>	<b>Ranch</b>	<b>Pfizer</b>	<b>1.60</b>	<b>0.48</b>	<b>0.004</b>	<b>**</b>
<b>MRB</b>	<b>AAA</b>	<b>Pfizer</b>	<b>0.55</b>	<b>0.09</b>	<b>0.000001</b>	<b>***</b>
<b>MRB</b>	<b>Ranch</b>	<b>Pfizer</b>	<b>1.22</b>	<b>0.33</b>	<b>0.002</b>	<b>**</b>
<b>CW</b>	<b>AAA</b>	<b>Pfizer</b>	<b>0.57</b>	<b>0.11</b>	<b>0.00002</b>	<b>***</b>
CW	Ranch	Pfizer	-0.04	0.47	0.94	
ADG	AAA	Pfizer	--	--	--	
ADG	Ranch (PostWG)	Pfizer	-0.39	0.45	0.39	



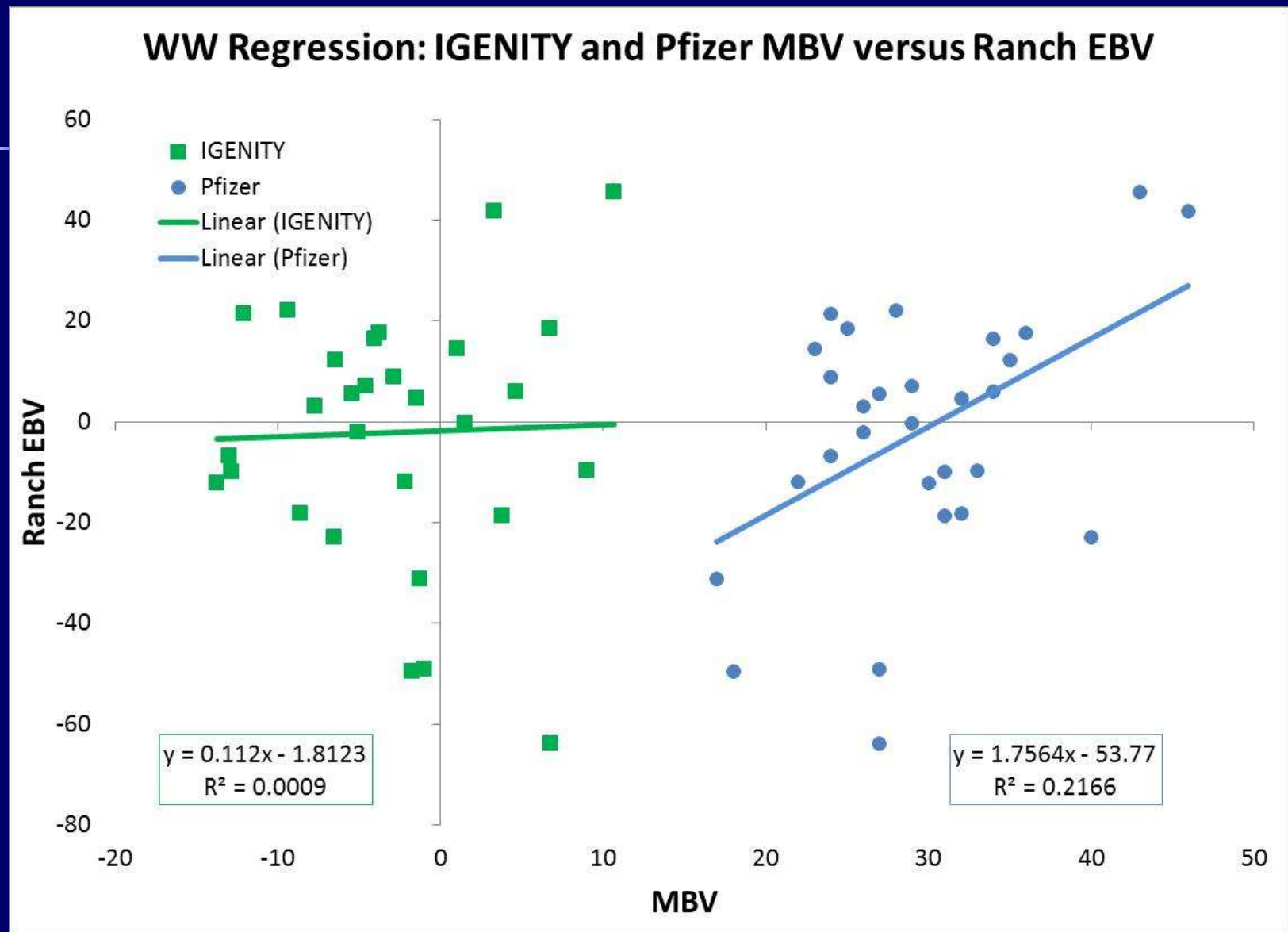
# Results: AAA Weaning weight

### WW Regression: IGENITY and Pfizer MBV versus AAA EPD





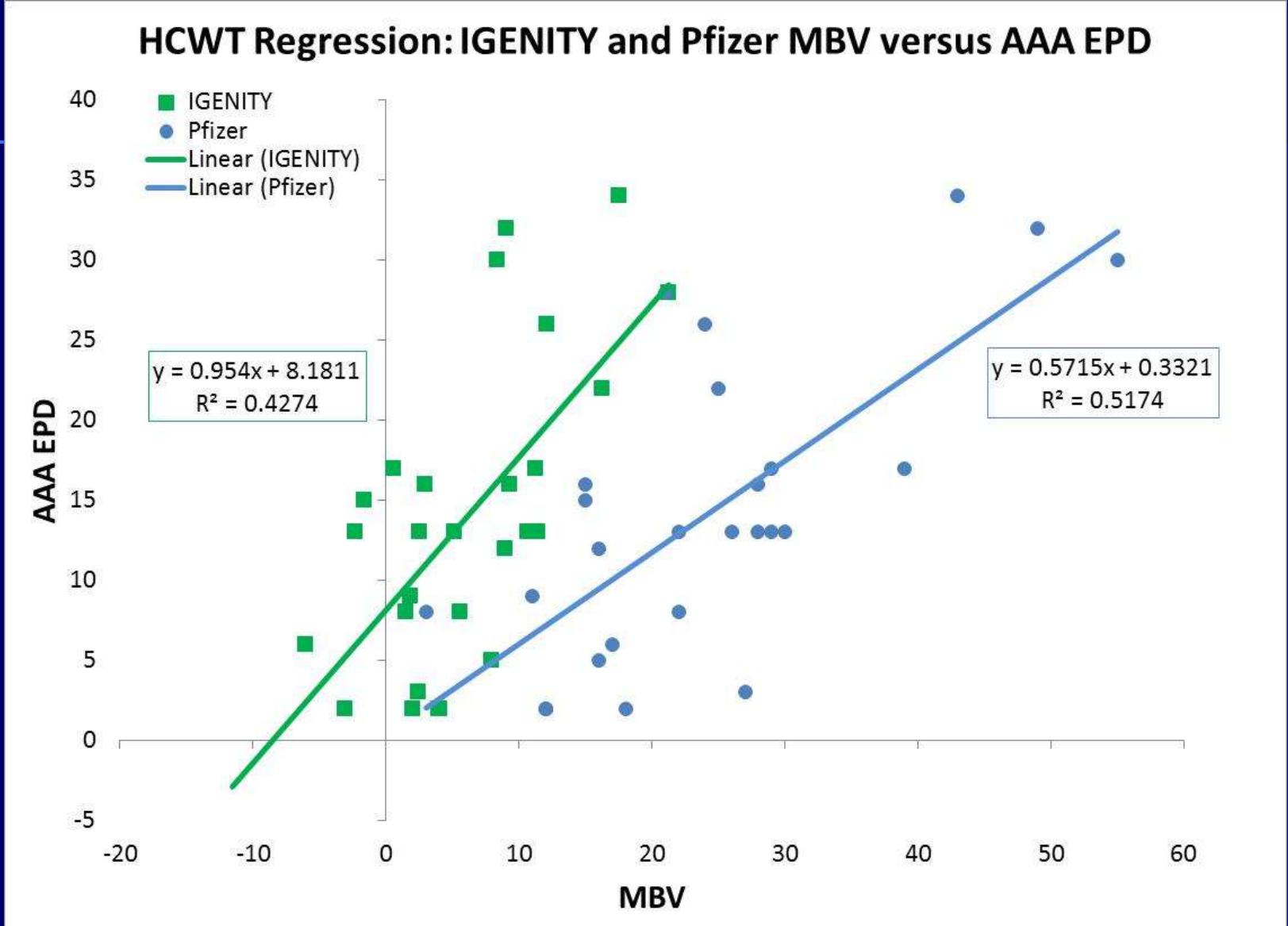
# Results: Ranch Weaning weight





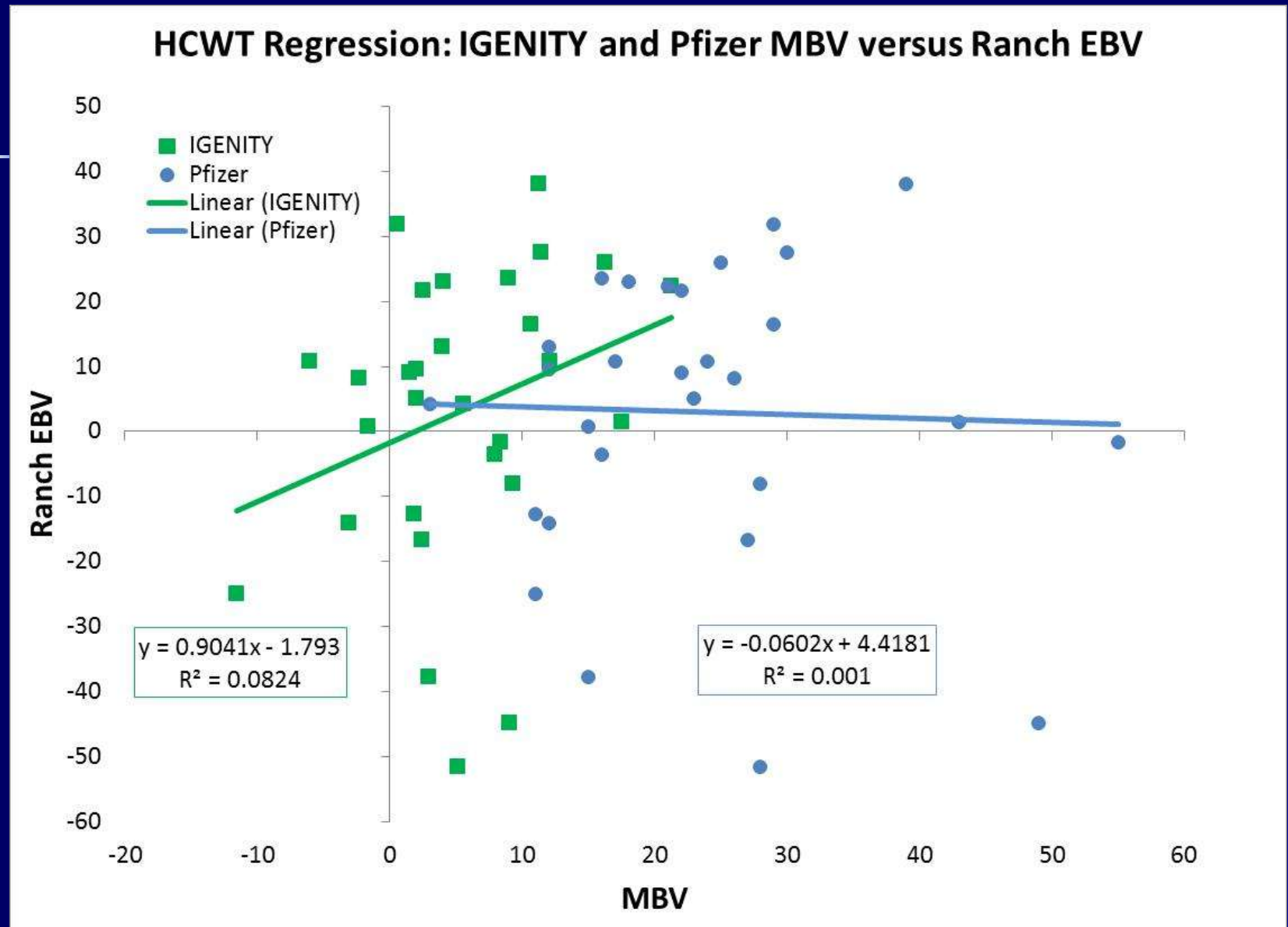


# Results: AAA Hot Carcass Weight





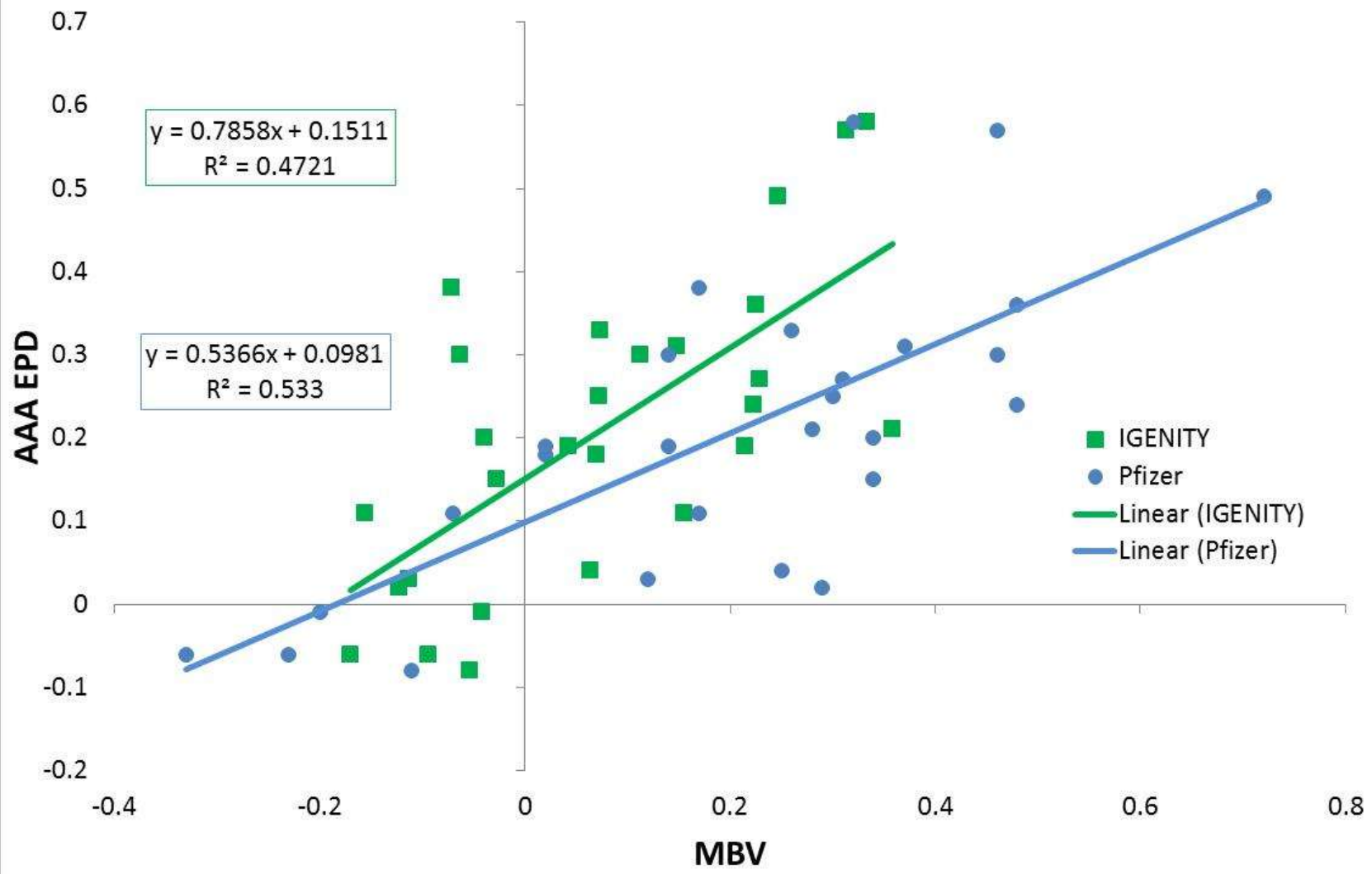
# Results: Ranch Hot Carcass Weight





# Results: AAA Ribeye Area

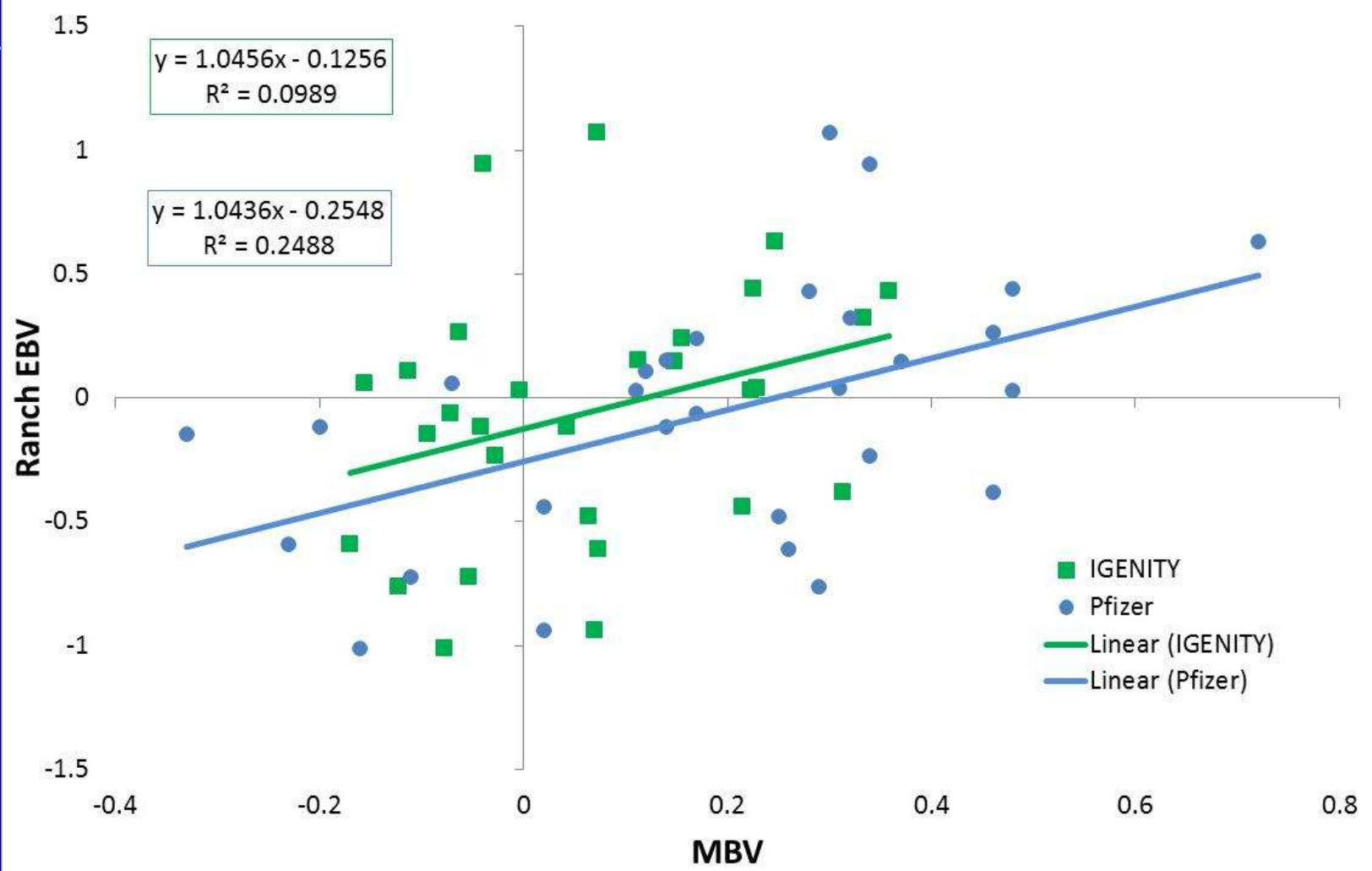
## REA Regression: IGENITY and Pfizer MBV versus AAA EPD





# Results: Ranch Ribeye Area

## REA Regression: IGENITY and Pfizer MBV versus Ranch EBV

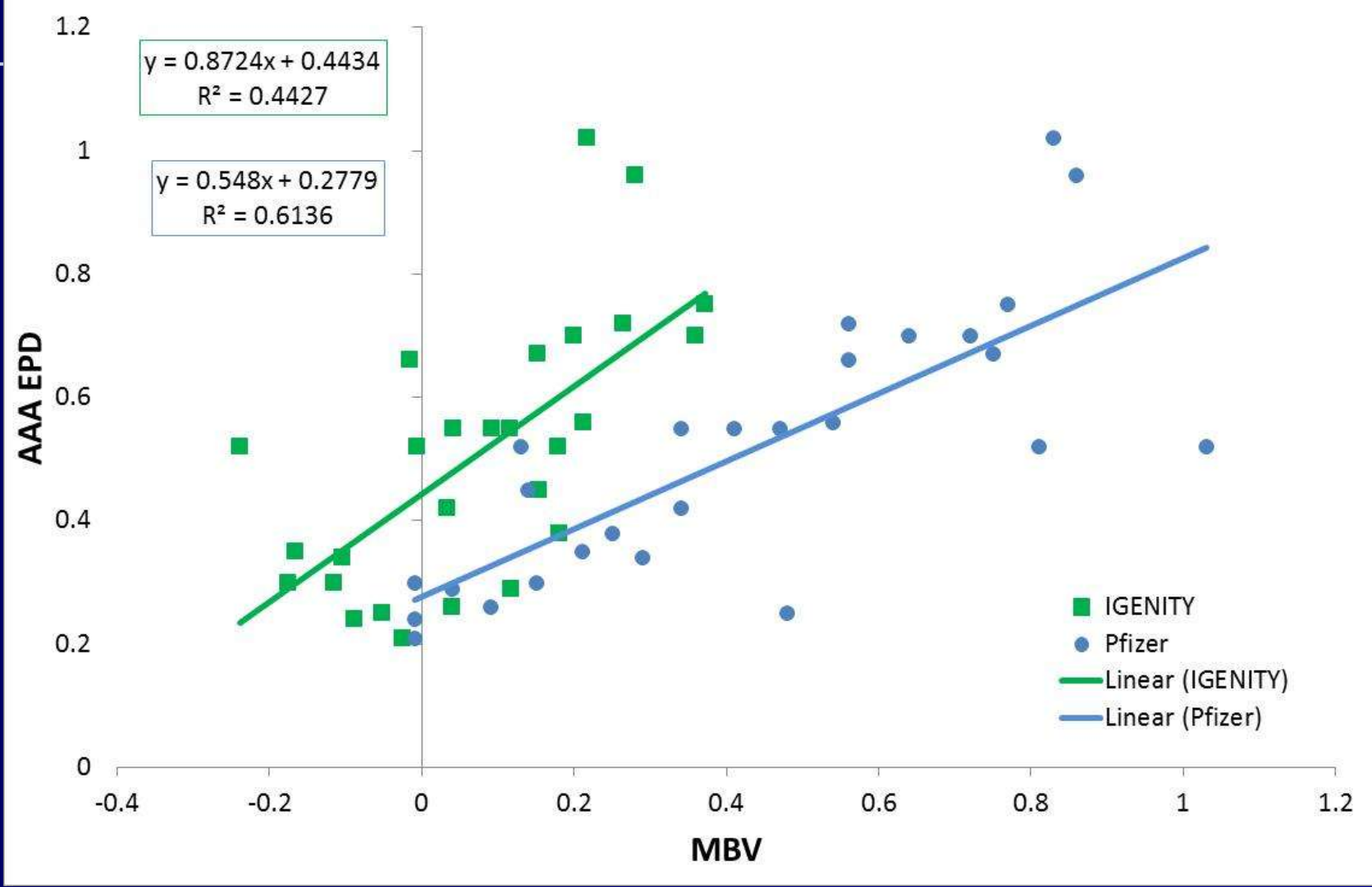






# Results: AAA Marbling

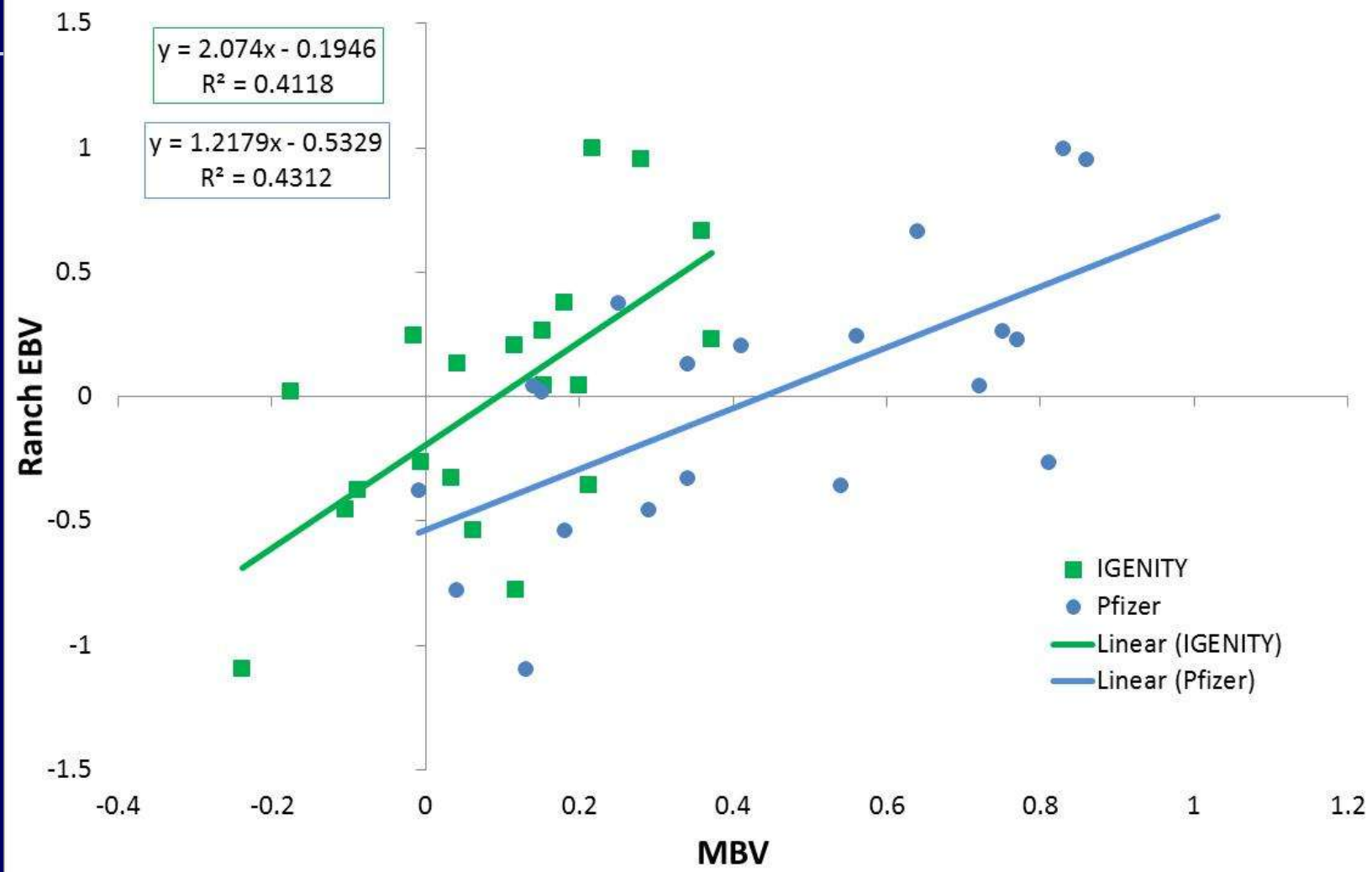
## MARB Regression: IGENITY and Pfizer MBV versus AAA EPD






# Results: Ranch Marbling

## MARB Regression: IGENITY and Pfizer MBV versus Ranch EBV





# Correlation between ranch EBV when incorporating Pfizer or Merial MBVs as a correlated trait



- Variance components were not fixed except for the residual covariance between ranch performance and MBV, which was assumed zero. For weaning weight, covariance between maternal effects and MBV were assumed zero.
- Variance components were completely fixed when estimating EBV for bulls in which the correlation between MBV and genetic merit for ranch performance was assumed fixed (to AAA standard). In this case, estimates of residual and genetic variances were derived from the un-fixed case and the appropriate genetic covariance was used to obtain the necessary genetic correlation.



# Correlation between Ranch EBVs and MBV-adjusted Ranch EBVs using different r values



	<b>Bulls with ranch bif acc &gt; 0.05</b>	<b># direct progeny in dataset</b>	<b>Pfizer-Estimated r</b>	<b>Pfizer-AAA r</b>	<b>IGENITY-Estimated r</b>	<b>IGENITY-AAA r</b>
<b>WWT</b>	<b>29</b>	<b>1734</b>	<b>0.9870</b>	<b>0.9861</b>	<b>0.9992</b>	<b>0.9828</b>
<b>ADG</b>	<b>28</b>	<b>1356</b>	<b>0.9921</b>		<b>0.9993</b>	
<b>HCWT</b>	<b>20</b>	<b>455</b>	<b>0.9985</b>	<b>0.9311</b>	<b>0.9727</b>	<b>0.7991</b>
<b>REA</b>	<b>23</b>	<b>455</b>	<b>0.9311</b>	<b>0.9206</b>	<b>0.9809</b>	<b>0.9389</b>
<b>MRB</b>	<b>23</b>	<b>455</b>	<b>0.9442</b>	<b>0.9715</b>	<b>0.9591</b>	<b>0.9512</b>





# Correlation between Pfizer and IGENITY MBVs



<b>Trait</b>	<b>Bulls with ranch BIF acc &gt; 0.05</b>	<b>Raw correlation between Pfizer and IGENITY MBV</b>
WWT	29	0.22
ADG (WWT to INWT)	29	0.14
HCWT	20	0.45
REA	23	0.59
MRB	23	0.56



# 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.

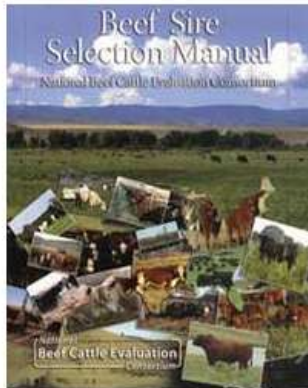
- Includes the development of fact sheets, national educational programs including program at BIF 2009, brown bagger series, popular press articles, and in year 4 a stakeholder workshop entitled “*Integrating DNA information into beef cattle production systems*”

## Animal Biotechnology

Marker-Assisted Selection and Breeding



Alison L Van Eenennaam



[NBCEC Beef Sire Selection Manual](#) - National Beef Cattle Evaluation Consortium (2010)  
**UPDATED 2010**

[Commercially-available DNA Tests for Beef Cattle](#) (06/10)



[Value of DNA Information for beef bull selection](#) (6/10)



[Are DNA tests for you?](#) *Beef Magazine* (3/10)



[DNA markers... Revolution or Evolution?](#) *ABS Breeders Journal* (Fall/Winter 2009)

[Do DNA tests work?](#) *Beef Magazine* (10/09)

[Basics of DNA Markers and Genotyping](#) (6/09)

[DNA-Based Progeny Testing](#) (6/09)

[Fundamentals of Expected Progeny Differences](#) (6/09)

[Marker-Assisted Selection in Beef Cattle Handout](#) (6/09)

[The Value of Improving Accuracy of Yearling Bulls](#) (6/09)

[Validation of Marker Tests](#) (6/09)

[Whole Genome Selection](#) (6/09)

[2009 Beef Improvement Federation Conference Proceedings](#)

[Curly Calf Syndrome \(Arthrogyrosis Multiplex \(AM\)\) Update](#) (2/09)

Cattlemen to Cattlemen streaming [video](#) (5/08)

["No Bull" Discussion on Genetic Markers](#) (5/08)



# 2010 Deliverables

Presentation of preliminary data at World Congress of Genetics  
NBCEC brownbagger series

"The value of accuracy"

Two outreach presentations at regional or national meeting

9 outreach presentations were given to beef cattle audiences regionally, nationally and internationally

Publication of two popular press articles in breed association and/or trade magazines

Are DNA tests for you? **Beef Magazine**. March. 18-23.

Value of DNA marker information for beef bull selection. Pages 98-102 in Proceedings of the Beef Improvement Federation 42<sup>nd</sup> Annual Research Symposium and Annual Meeting. Columbia, MO.

DNA-based biotechnologies. Pages 68-78 in Beef Sire Selection Manual. Second Ed.

Utilizing molecular information in beef cattle selection. Pages 79-84 in Beef Sire Selection Manual. Second Edition. National Beef Cattle Evaluation Consortium.

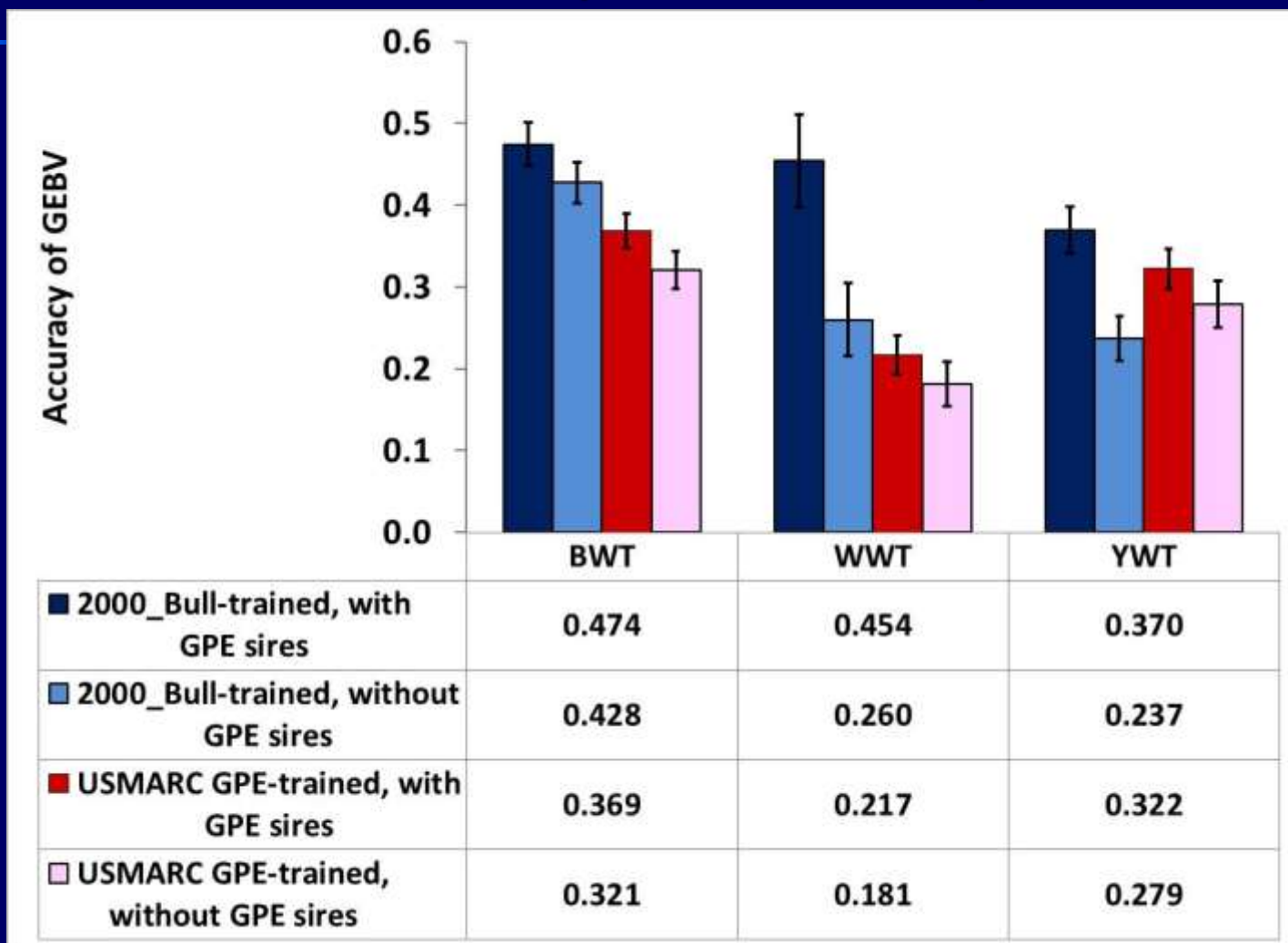
## Publications

Van Eenennaam, A. L., K. L. Weber, K. Coopriider, and D. J. Drake. 2010. **Development and implementation of a vertically-integrated beef cattle data collection system**. California Agriculture. 64: 94-100.

Van Eenennaam, A. L., J.H. van der Werf, and M.E. Goddard. 2011. **The economics of using DNA markers for beef bull selection in the seedstock sector**. Journal of Animal Science. 89:307-320

# Genomic Selection In Beef Cattle: Training And Validation In Multibreed Populations

Kristina Weber , Ph.D. student, UC Davis







# Planning for 2011 onwards

- Weber K. L., G. Bennett, J. Keele, W. Snelling, R. M. Thallman, A.L. Van Eenennaam, L. Kuehn. 2011. **Genomic Selection in Beef Cattle: Training and Validation In Multibreed Populations.** Plant and Animal Genome Conference
- PAG presentation “**Translational genomics**” January 2011.
- Beef magazine. 2011. (February issue) **Improving the accuracy of EPDs with DNA information**
- Comparison of different prediction equations (2000 bull, MARC trained, any one else that wants to be involved) versus Angus EPDs versus integrated ranch data (Years 1 and 2) – also have Pfizer MVPs and Igenity MBVs on bulls with at least 10 carcass trait records
- BIF paper: Economic analysis of value of emerging MBV for ERT for which no bEPD exist (Collaboration with Mike MacNeil and Shannon Neibergs)



# Australian PAG 50K HD Calibration Results

Pfizer Animal Genetics Trait	h <sup>2</sup>	% Genetic variation explained		BIF accuracy if EPD derived from DNA information alone
		Pfizer 50K (2010)*	Australian Calibration (11/2010)	
Average Daily Gain	0.28	30%	1-10%	.01-0.05
Net Feed Intake	0.39	12%	0%	0
Dry matter intake	0.39	11%	4-5%	.02-.03
Tenderness	0.37	26%	Not evaluated	
Calving Ease (Direct)	0.1	22%	6%	.03
Birth weight	0.31	28%	12-16%	.06-.08
Weaning Weight	0.25	32%	12-19%	.06-.10
Calving ease (maternal)	0.1	40%	4%	.02
Milking Ability	0.25	27%	10-14%	.05-.07
Carcass weight	0.39	29%	6-13%	.03-.07
Backfat thickness	0.36	40%	14-19%	.07-.10
Ribeye area	0.4	29%	10-20%	.05-.11
Marbling score	0.37	34%	4-11%	.02-.06

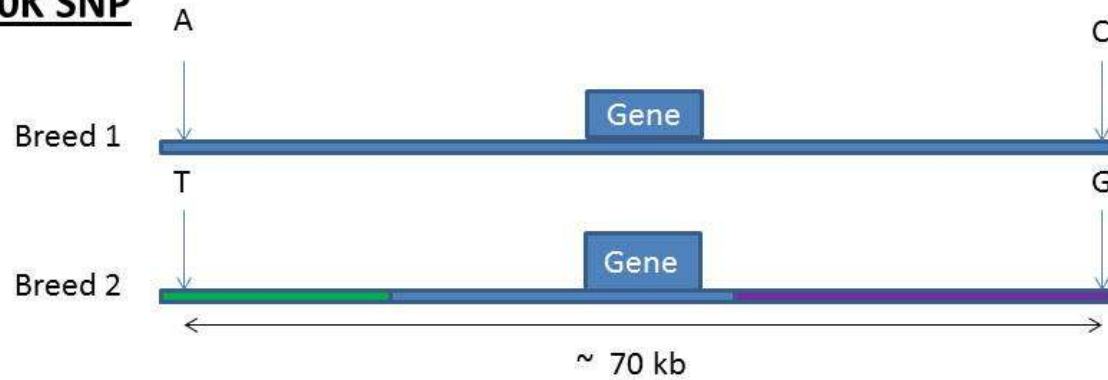
\* <http://www.pfizeranimalgenetics.com/sites/PAG/Documents/50K%20Tech%20Summary.pdf>



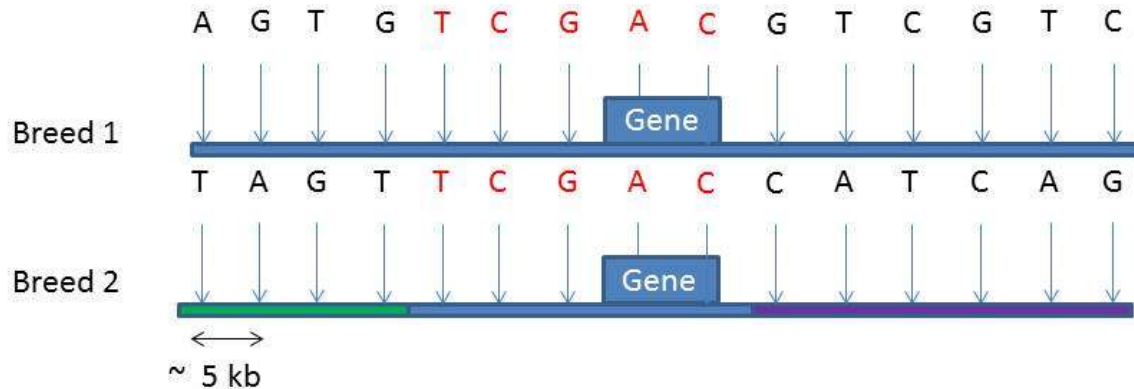
# Marker location relative to the gene of interest in two breeds when using the (A) 50K SNP chip assay (markers spaced at ~ 70 kb intervals), or (B) the high density 700 K SNP chip assay (markers spaced at ~ 5 kb intervals)



## A. 50K SNP

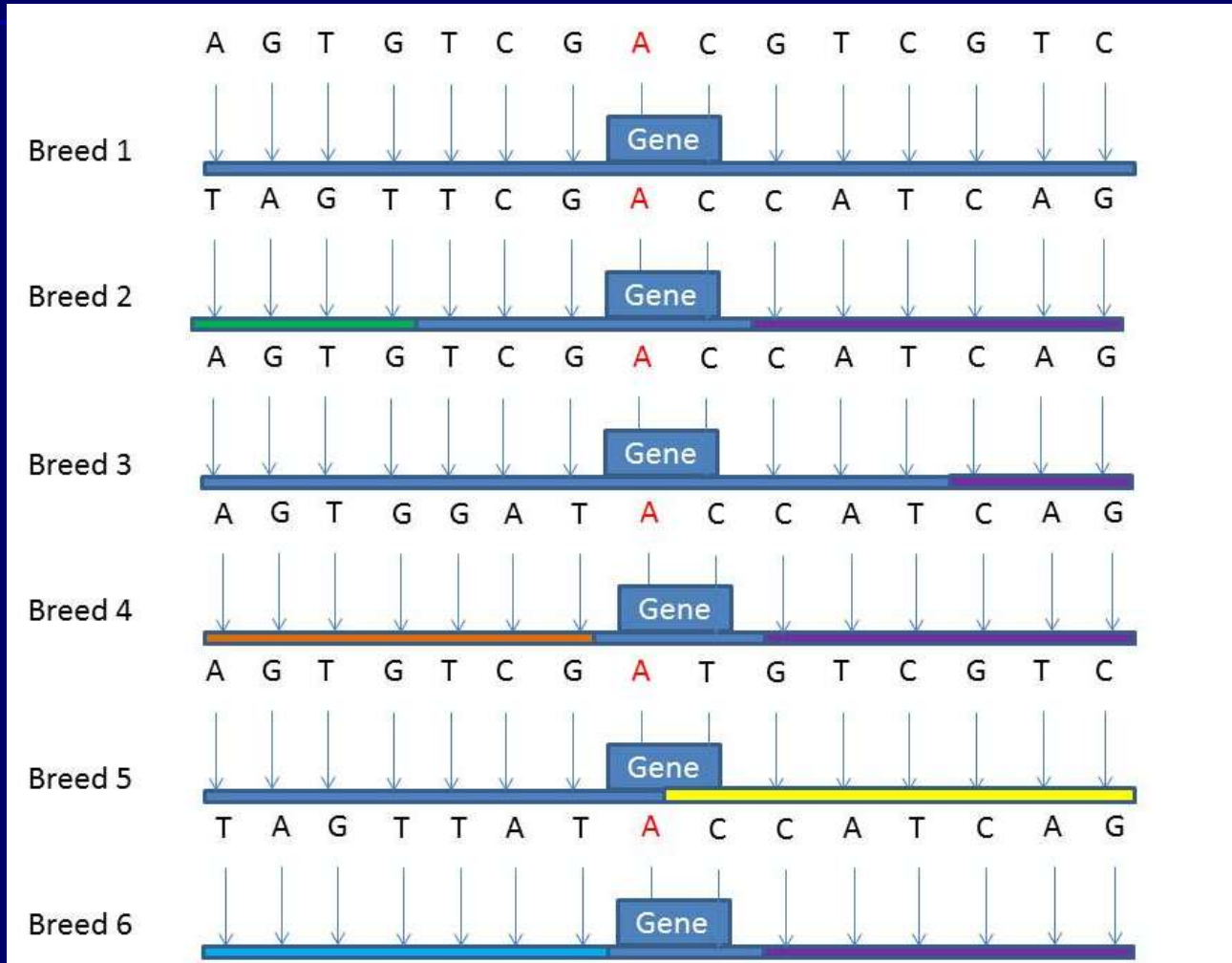




## B. 700K SNP





# High density panels offer the opportunity to accelerate discovery of the causal mutations underlying genetic variation – especially if combined with full sequence data on key ancestors





# **“Integrating DNA information into Beef Cattle Production Systems”**

## **USDA Integrated Grant Collaborators**

- Dr. Darrh Bullock, Extension Professor, University of Kentucky, KY
- Dr. Leslie “Bees” Butler, Extension Marketing Specialist, UC Davis, CA
- Dr. Daniel Drake, University of California Cooperative Extension Livestock Advisor, CA
- Dr. Dorian Garrick, Professor, Iowa State University, IA
- Dr. John Pollak, Professor, Cornell University, NY
- Dr. Mark Thallman, US Meat Animal Research Center, Clay Center, NE

### **Graduate Students**

- Kristina Weber, Ph.D. Candidate, UC Davis, CA and Krista Coopriker, MS Candidate, UC Davis, CA

### **Producer Collaborators:**

- Jack Cowley, Cowley Rancher, Siskiyou County, CA
- Dale, Greg, and Richard Kuck, Kuck Ranch, Siskiyou County, CA
- Matt Parker, Mole-Richardson Ranch, 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. Jerry Taylor, University of Missouri, MO
- Dr. Mike Goddard, University of Melbourne and Victorian DPI, Australia





United States  
Department of  
Agriculture

National Institute  
of Food and  
Agriculture

This project is supported by National Research Initiative Competitive Grant No. 2009-55205-05057 Integrating DNA information into beef cattle production systems" from the USDA National Institute of Food and Agriculture.



**Questions?**