

"The California commercial ranch project"

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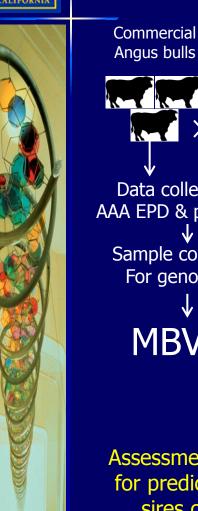


Animal Genomics and Biotechnology Education

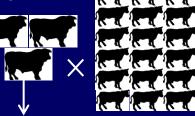




California Commercial Ranch Project



2400 cows/ year R-1 18-1 18-1



Data collection: AAA EPD & pedigree

Sample collection: For genotyping

MBV



Progeny



Ranch and harvest data Collection Genotyping Paternity Determination

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

Siskiyou 8/23/12

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



United States Department of Agriculture National Institute of Food and Agriculture

Animal Biotechnology and Genomics Education

Sample and phenotype collection

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Management Software

Source Tracking And Reporting

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Avenal

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



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







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

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Cowley Ranch

Kuck Ranch

Mole-Richardson Farms

HARDSON









16277 S. McCall Ave.



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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 bulls, and 2,400 cows per year on project



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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

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Commercial ranch sample collection

UNIVERSITY CALIFORNIA





Problems experienced included





Colorado State University-Cornell University-University of Georgia

-National **Beef Cattle Evaluation** _Consortium



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.



Which is better: EPDs or DNA?, and using DNA for parentage assignment

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Selection of bulls

Most genetic progress is made through sire selection.

Decisions have long-term impact: oprofit from sold calves ovalue of replacement heifers



What is an EPD: Expected Progeny Difference

Bull	WW EPD	Progeny Average WW
Α	+30	550
B	+15	535
Difference	15 lb	15 lb



What doesn't an EPD do?

Predict actual performance (EPDs predict average differences)

• Predict how uniform a calf crop will be



Components of Performance

P = Genetics + Environment Weaning weight = Calf's genetics for growth + Dam's genetics for milk and mothering Management Health Weather



How is an EPD calculated

• From a **bull's performance record:**

- Bull's individual weaning weight: 500 lb
- Average of the other bulls on the purebred ranch: 450 lb
- Heritability: 20%

Bull was +50 lb heavier than average.

20% of the difference was the effect of genetics.

\rightarrow +10 lb WW Breeding Value for that bull

Progeny get $\frac{1}{2}$ the bull's genes so you'd expect his progeny to be +5 lb heavier than average. \rightarrow +5 lb WW EPD for that bull

This EPD's accuracy is low because it is based on only 1 record.



How is an EPD calculated

• From progeny records:

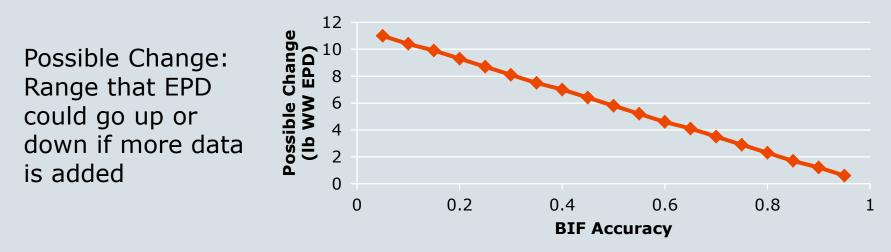
- A bull sires 10 calves with an average weaning weight of +50 lb relative to the rest of the calf crop.
- That +50 lb difference in weaning weight is scaled toward zero based on the number of records and the heritability of the trait.
- Weaning weight EPD ends up being +17.25 lb
- Higher accuracy EPD than from 1 record on bull.





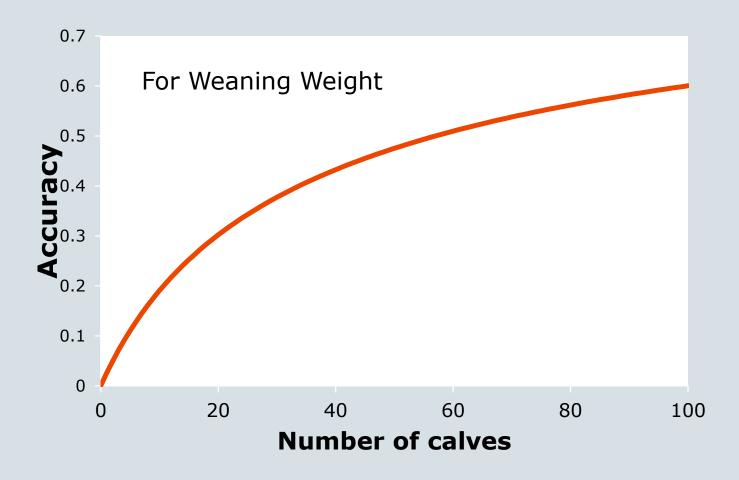
- Indicator of risk or uncertainty
- Increases as more information is used to calculate EPD (performance of bull, his ancestors, his progeny, DNA test information)
- Related to possible change in EPD:

AAA Fall 2012





Effect of Number of Progeny Records on EPD Accuracy

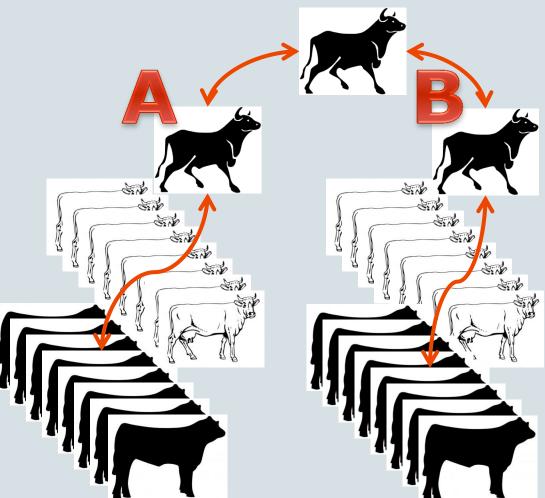




Why Pedigree Improves Accuracy

- With pedigree information:
 - If 2 bulls (A & B) are half-siblings,
 - you would expect their progeny to be more similar than if the bulls were unrelated.

The progeny of A would share 1/16 of their genetics with the progeny of B.



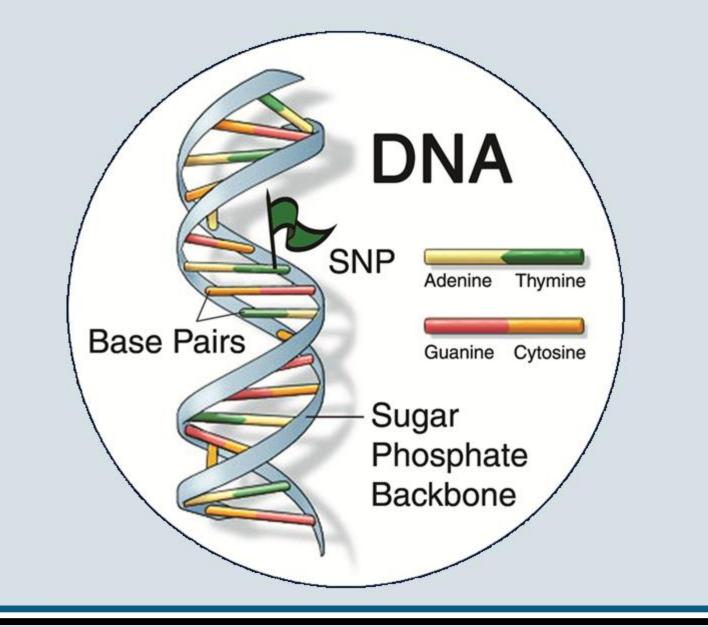


Breed EPD Evaluations

Account for:
All known pedigree
Herd and management differences
Relationships between correlated traits



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Parentage testing: What value does it have?

Prolificacy

- Identify bulls which do not sire calves or sire very few calves
- Identify bulls which sire lots of calves

Quality

- Identify bulls which sire poor quality calves
- Identify bulls which sire high quality calves



Parentage testing: How does it work?









Sample ID Test	Date Banked	BarCode	DQ789028	DQ404151	EF042091	EF034081	AY849381	AY937242	DQ470475	AY851163	DQ995977	DQ500958
1400136 SeekSire_Bv3	4/4/2012	71111038801	C/T	C/C	A/A	A/A	G/G	A/G	A/T	C/T	C/T	A/G
1400137 SeekSire_Bv3	4/4/2012	71111038802	C/T	C/C	A/A	A/T	G/G	A/G	A/T	T/T	T/T	G/G
1400138 SeekSire_Bv3	4/4/2012	71111038803	T/T	C/T	A/A	A/T	A/A	A/G	T/T	C/C	C/C	A/A
1400139 SeekSire_Bv3	4/4/2012	71111038804	c/c	C/T	A/G	A/T	A/G	A/G	A/A	C/T	C/C	A/A
1400140 SeekSire_Bv3	4/4/2012	71111038805	T/T	C/C	A/G	A/T	A/G	A/G	A/A	T/T	C/T	A/G
1400141 SeekSire_Bv3	4/4/2012	71111038806	c/c	C/C	A/A	A/T	A/G	A/G	A/A	C/T	C/T	G/G
1400142 SeekSire_Bv3	4/4/2012	71111038807	C/T	C/C	A/A	T/T	A/A	A/G	A/T	C/T	C/T	A/G
1400143 SeekSire_Bv3	4/4/2012	71111038808	c/c	C/C	G/G	A/T	G/G	A/G	A/T	C/C	c/c	A/A
1400144 SeekSire_Bv3	4/4/2012	71111038810	C/T	C/T	A/G	T/T	A/G	A/A	A/T	C/C	C/T	A/A
1400145 SeekSire_Bv3	4/4/2012	71111038811	T/T	C/C	A/G	A/T	A/G	A/G	A/A	C/T	c/c	A/A
1400146 SeekSire_Bv3	4/4/2012	71111038812	c/c	C/C	A/G	A/A	A/G	A/G	A/A	C/C	C/T	A/G
1400147 SeekSire_Bv3	4/4/2012	71111038813	C/T	C/C	A/A	A/T	A/A	A/A		C/T	c/c	A/A
1400148 SeekSire_Bv3	4/4/2012	71111038814	C/T	C/C	G/G	A/A	G/G	A/G	A/A	C/C	c/c	G/G
1400149 SeekSire_Bv3	4/4/2012	71111038815	c/c	C/T	A/G	A/T	A/G	A/A	A/A	C/T	T/T	A/A
1400150 SeekSire_Bv3	4/4/2012	71111038816	C/C	C/C	G/G	A/A	G/G	A/G	A/T	C/T	C/C	A/A
1400151 SeekSire_Bv3	4/4/2012	71111038817	C/T	C/C	A/A	A/T	A/G	A/G	A/T	C/T	C/C	A/A
1400152 SeekSire_Bv3	4/4/2012	71111038818	C/T	C/T	A/A	A/T	A/G	G/G	A/T	T/T	C/T	G/G
1400153 SeekSire_Bv3	4/4/2012	71111038819	C/T	C/C	A/A	A/A	A/G	A/G	A/A	T/T	C/C	A/G



Parentage Testing: What happens to the genotypes?

• Each bull compared to each calf

• Number of mismatches counted

Examples

• Bull is A/A, Calf is A/G \rightarrow

Calf and bull share A allele; can't exclude bull.

• Bull is A/G, Calf is G/G \rightarrow

Calf and bull share G allele; can't exclude bull.

• Bull is A/A, Calf is G/G \rightarrow

Calf and bull do not share alleles \rightarrow

1 mismatch; this bull cannot be the sire

Siring bull should have zero mismatches with his calves because they should always share alleles.

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al	A	В	С	D	E	F	G	Н	1	J	K	L	M	N	
1	Ciarra 0001	ucd_1 8	lucd_	10ucd_1 10	11 11)!ucd_2 7	ucd_ 13	5 ucd_6	lucd_(13	5!ucd_ 5	7!ucd_7 13	ucd_7	fucd_ 9	8:ucd_ 3	8: uo 1
2	Sierra_0001 Sierra 0002	8	0	10	10	8	8	4	13	5	13	9	9 7	3	7
3	Sierra_0002 Sierra_0003	10	0	4	8	8	9	7	9	2	7	6	5	5	1
5	Sierra_0003	6	0	4	9	6	9	6	12	5	9	6	4	5	1
5		4	0		5	8	6	5	2	4	4	7	7	3	6
	Sierra_0005	7		6	5	8			7				8	2	12
7	Sierra_0006		0	4			11	6		5	8	6			
8	Sierra_0007	9	0	9	8	7	8	6	11	3	8	8	9	3	9
9	Sierra_0008	13	0	11	8	12	7	5	10	8	10	5	6	5	9
10	Sierra_0009	3	0	6	7	7	6	2	9	5	7	3	6	3	10
11	Sierra_0010	8	0	5	6	7	11	3	9	5	11	9	9	2	7
12	Sierra_0011	10	0	9	11	10	12	10	11	6	10	7	9	4	14
13	Sierra_0012	9	0	7	10	6	10	2	13	4	10	8	9	3	10
14	Sierra_0013	3	0	9	4	6	7	3	9	4	7	7	8	3	10
15	Sierra_0014	7	0	7	7	5	8	6	12	5	8	8	6	3	10
16	Sierra_0015	8	0	7	10	8	10	2	15	4	8	7	10	3	7
31	Sierra_0030	7	9	0	11	12	11	11	16	5	9	9	11	3	11
32	Sierra_0031	7	10	0	9	9	7	12	9	5	13	13	6	1	7
33	Sierra_0032	5	8	0	5	5	9	9	10	5	12	7	5	1	7
34	Sierra_0033	9	4	0	10	10	9	9	11	6	7	10	10	3	7
35	Sierra_0034	10	0	8	7	9	9	7	11	5	9	8	8	2	11
36	Sierra_0035	11	0	8	7	10	8	9	6	7	9	7	6	4	11
46	Sierra_0045	9	6	0	9	10	8	8	14	3	7	5	12	2	6
48	Sierra_0047	8	0	9	10	11	9	6	12	9	9	8	11	6	14
49	Sierra_0048	0	16	10	12	11	10	16	11	6	3	6	4	6	14
57	Sierra_0056	10	8	5	8	7	6	5	6	0	5	5	5	3	10
58	Sierra_0057	9	9	10	10	8	0	11	15	6	7	9	9	3	10
59	Sierra_0058	14	7	9	11	8	11	10	0	7	9	9	7	6	15
60	Sierra_0059	8	12	7	8	0	10	10	12	9	8	12	7	4	9
61	Sierra_0060	10	12	11	14	13	0	11	10	8	9	8	7	5	14
62	Sierra_0061	9	8	9	15	6	11	13	0	6	9	6	6	3	12
63	Sierra_0062	7	7	10	9	0	7	6	7	1	9	7	5	1	4
64	Sierra_0063	12	8	10	13	9	15	11	0	7	9	9	6	5	12
65	Sierra_0064	11	11	10	13	9	10	17	13	9	6	9	8	5	13
66	Sierra_0065	5	8	7	8	6	6	9	6	5	3	0	3	5	9
68	Sierra_0067	5	8	10	0	10	13	10	12	8	13	7	10	4	12
69	Sierra_0068	6	8	8	10	11	8	11	12	5	6	0	7	7	14
70	Sierra_0069	6	10	13	11	8	12	11	12	0	8	7	6	1	6
71	Sierra_0070	8	7	13	9	3	7	12	8	6	5	0	4	4	14
72	Sierra_0071	10	12	7	15	10	0	18	16	7	9	9	8	4	1
73	Sierra_0072	12	7	9	9	7	ŏ	7	9	5	10	11	6	3	9
74	Sierra_0072	7	6	4	0	10	11	7	11	6	11	7	7	1	10
75	Sierra_0073	10	13	16	10	9	13	7	13	3	7	12	0	4	8
76	Sierra_0075	13	11	8	10	8	11	9	12	9	13	14	10	0	11
77	Sierra_0075	4	7	5	0	5	6	9	9	5	7	8	7	1	6
78	Sierra_0077	9	3	12	9	6	8	0	10	5	12	12	2	1	3
79	Sierra_0078	10	6	8	12	9	0	10	9	4	8	10	6	3	7
80		5	4	7	9	7	11	0	9 14	3	7	9	5	2	6
81	Sierra_0079	4	10	9	7	5	6	11	8	4	0	7	6	4	10
	Sierra_0080			12	9		8	8	8	7	-	8		4	7
82	Sierra_0081	8	10			0					9		6	5	
83	Sierra_0082	8	15	15	14	12	10	14	10	5	0	10	5	-	11
84	Sierra_0083	5	6	9	15	6	0	11	10	4	5	6	9	5	12
85	Sierra_0084	7	1	6	8	4	8	0	6	1	4	9	3	1	4
86	Sierra_0085	9	10	15	15	6	12	12	8	3	8	6	0	3	9
87	Sierra_0086	11	10	12	10	0	10	11	12	6	9	11	8	6	6
88	Sierra_0087	10	7	11	9	0	9	11	13	9	8	10	9	3	10
89	Sierra_0088	4	7	10	10	5	7	9	11	4	0	6	5	4	11
90	Sierra_0089	8	13	11	12	11	14	13	7	0	7	3	6	4	10
91	Sierra 0090	11	7	11	8	6	10	9	10	7	12	11	10	0	7



DNA Marker Tests for Traits

• How do you get an EPD from DNA marker information?

• Bull EPD

DNA marker "EPD":

Bull	WW EPD	Progeny Average WW	Marker Genotype	EPD	Average WW in a big reference
А	+30	550			population
В	+15	535	A/A	+1	551
Differenc	15 lb	15 lb	T/T	-1	549
e			Difference	2 lb	2 lb



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• How do you get an EPD from DNA marker information?

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DNA marker "EPD":

Bull	WW EPD	Progeny Average WW	Marker Genotype	WW EPD	Average WW in a big reference population
А	+30	550	A/A	+1	551
В	+15	535	T/T	-1	549
Difference	15 lb	15 lb	Difference	2 lb	2 lb

Repeat for lots and lots of DNA markers!!!



How is an EPD calculated when DNA information is available

• Without DNA information

- WW EPD: +5 lb
- WW EPD Accuracy: 0.30
- With DNA information:
 - WW DNA marker test result (as an EPD): +10 lb
 - WW DNA marker test result accuracy: 0.15
 - New EPD = *weighted average* of EPD and DNA marker test result
 - New WW EPD = +7.55 lb WW EPD with accuracy 0.36



DNA Marker Tests and Breeds

- DNA tests can be created for different <u>traits</u> using different <u>markers</u>, with different <u>reference populations</u> from one or more different <u>breeds</u>.
- These affect **DNA test accuracy**!

What is the accuracy of the test in your breed? Is the test for a trait that matters to you?



Important Traits to a Cow-Calf Producer

- Reproductive efficiency
- Calving ease
- Weaning weight
- Post-weaning growth
- Feed efficiency
- Mature size
- Docility
- Carcass traits

S R In Focus 203 Reg: AAA 15579511 Bull

Birth Date: 02/14/2006 Tattoo: 203

Parentage: SNP

EPD Percentiles

As of 08/21/2012

	Production							Maternal						
CED Acc	BW Acc	WW Acc	YW Acc	RADG Acc	YH Acc	SC Acc	Doc Acc	HP Acc	CEM Acc	Milk Acc	MkH MkD	MW Acc	MH Acc	\$EN
+6 .29	+1.2 .37	+52 .28	+84 .28		I+.4 .05	I+1.19 .05			+7 .18	+21 .22				27

	Carcass										
CW Acc	Marb Acc	RE Acc	Fat Acc	Carc Grp Carc Pg	Usnd Grp Usnd Pg						
I+16 .05	I+.55 .05	I04 .05	I+.009 .05								

\$Values										
\$W \$F \$G \$QG \$YG \$B										
+32.79	+23.33	+28.03	+27.22	+.81	+52.58					

EPDs are enhanced by genomic results generated by: () igenity.



Accuracy and Associated Possible Change

The following table lists the possible change values associated with each EPD trait at the various accuracy levels. Possible change is expressed as "+" or "-" pounds of EPD and can be described as a measure of expected change or potential deviation between the EPD and the "true" progeny difference. This confidence range depends on the standard error of prediction for an EPD. For a given accuracy, about two-thirds of the time an animal should have a "true" progeny difference within the range of the EPD plus or minus the possible change value.

For example, a sire with an accuracy of .65 and birth weight EPD of +1.0 is expected to have his "true" progeny value falling within ±.92 pounds for birth weight EPD (ranging between +0.1 and +1.9) about two-thirds of the time.

With the conservative approach taken with respect to heritabilities in the Angus evaluation, actual EPD changes of animals within the population are much less than statistics would indicate.

				Produ	iction					Ι	Maternal				Card	ass	
Accuracy	CED	вw	ww	YW	RADG	YH	sc	Doc	HP	СЕМ	Milk	мw	мн	cw	Marb	RE	Fat
.05	7.8	2.49	11.0	16.2	.082	.41	.70	14.7	6.0	9.3	9.2	38	.62	18	.28	.31	.041
.10	7.2	2.36	10.4	15.3	. <mark>07</mark> 8	.39	.66	13.9	5.7	8.8	8.7	36	.58	17	.26	.29	.039
.15	6.7	2.23	9.9	14.5	.074	.37	.62	13.2	5.4	8.3	8.2	34	.55	16	.25	.27	.037
.20	6.2	2.10	9.3	13.6	.069	.35	.59	12.4	5.0	7.8	7.8	32	.52	15	.24	.26	.035
.25	5.8	1.97	8.7	12.8	.065	.32	.55	11.7	4.7	7.3	7.3	30	.49	14	.22	.24	.033
.30	5.4	1.84	8.1	11.9	.061	.30	.51	10.9	4.4	6.8	6.8	28	.45	13	.21	.23	.030
.35	5.1	1.71	7.5	11.1	.056	.28	.48	10.2	4.1	6.3	6.3	26	.42	12	.19	.21	.028
.40	4.7	1.58	7.0	10.2	.052	.26	.44	9.4	3.7	5.8	5.8	24	.39	12	.18	.19	.026
.45	4.3	1.44	6.4	9.4	.048	.24	.40	8.6	3.4	5.4	5.3	22	.36	11	.16	.18	.024
.50	3.9	1.31	5.8	8.5	.043	.22	.37	7.9	3.1	4.9	4.9	20	.32	10	.15	.16	.022
.55	3.5	1.18	5.2	7.7	.039	.19	.33	7.1	2.8	4.4	4.4	18	.29	9	.13	.15	.020
.60	3.2	1.05	4.6	6.8	.035	.17	.29	6.4	2.5	3.9	3.9	16	.26	8	.12	.13	.017
.65	2.7	. <mark>9</mark> 2	4.1	6.0	.030	.15	.26	5.6	2.2	3.4	3.4	14	.23	7	.10	.11	.015
.70	2.4	.79	3.5	5.1	.026	.13	.22	4.8	1.9	2.9	2.9	12	.19	6	. <mark>0</mark> 9	.10	.013
.75	2.0	.66	2.9	4.3	.022	.11	.18	4.1	1.6	2.4	2.4	10	.16	5	.07	.08	.011
.80	1.6	.53	2.3	3.4	.017	.09	.15	3.3	1.3	2.0	1.9	8	.13	4	.06	.06	.009
.85	1.2	.39	1.7	2.6	.013	.06	.11	2.6	1.0	1.5	1.5	6	.10	3	.04	.05	.007
.90	.8	.26	1.2	1.7	.009	.04	.07	1.8	.7	1.0	1.0	4	.06	2	.03	.03	.004
.95	.4	.13	.6	.9	.004	.02	.04	1.1	.4	.5	.5	2	.03	1	.01	.02	.002

Birth Date: 02/14/2006 Tattoo: 203

Parentage: SNP

💼 EPD Percentiles

As of 08/21/2012

			Pro	duction						I	Naternal			
CED Acc	BW Acc	WW Acc	YW Acc	RADG Acc	YH Acc	SC Acc	Doc Acc	HP Acc	CEM Acc	Milk Acc	MkH MkD	MW Acc	MH Acc	\$EN
+6 .29	+1.2 .37	+52 .28	+84 .28		I+.4 .05	I+1.19 .05			+7 .18	+21 .22				27

	Carcass												
CW Acc	Marb Acc	RE Acc	Fat Acc	Carc Grp Carc Pg	Usnd Grp Usnd Pg								
I+16 .05	I+.55 .05	I04 .05	I+.009 .05										

		\$Value	s		
sw	\$F	\$G	\$QG	\$YG	\$B
+32.79	+23.33	+28.03	+27.22	+.81	+52.58
		•			

EPDs are enhanced by genomic results generated by: 🚫 igenity.



\$Indexes are multi-trait selection indexes, which combine EPDs for several traits into a single economic value, which can be used to make selection decisions.

- Angus \$W is Weaned Calf Value. This is the expected average of future progeny for preweaning performance, within a typical beef cowherd. It accounts for the economic impact of birth weight, weaning weight, maternal milk, and mature cow size.
- Angus \$F is Feedlot Value. This is the expected average of future progeny for postweaning feedlot performance.
- Angus \$QG is Quality Grade. This is the quality grade segment of \$G. The carcass Marbling and ultrasound % Intramuscular Fat EPDs contribute to \$QG.
- Angus \$YG is Yield Grade. This is the yield grade segment of \$G. It combines ribeye, fat thickness, and weight into an economic value for red meat yield.
- Angus \$G is Grid Value. This is the expected average of future progeny for carcass grid merit. It combines \$QG and \$YG, so it focuses on quality and red meat yield simultaneously.
- **Angus \$B is Beef Value.** This is the expected average of future progeny for postweaning performance and carcass value. The \$B value combines information from \$F and \$G.

Birth Date: 02/14/2006 Tattoo: 203

Parentage: SNP



As of 08/21/2012

			Pro	duction						Ν	laternal			
CED Acc	BW Acc	WW Acc	YW Acc	RADG Acc	YH Acc	SC Acc	Doc Acc	HP Acc	CEM Acc	Milk Acc	MkH MkD	MW Acc	MH Acc	\$EN
+6 .29	+1.2 .37	+52 .28	+84 .28		I+.4 .05	I+1.19 .05			+7 .18	+21 .22				27

	Carcass												
CW Acc	Marb Acc	RE Acc	Fat Acc	Carc Grp Carc Pg	Usnd Grp Usnd Pg								
I+16 .05	I+.55 .05	I04 .05	I+.009 .05										

	\$Values												
\$W	\$F	\$G	\$QG	\$YG	\$B								
+32.79	+23.33	+28.03	+27.22	+.81	+52.58								

EPDs are enhanced by genomic results generated by: 🚫 igenity.



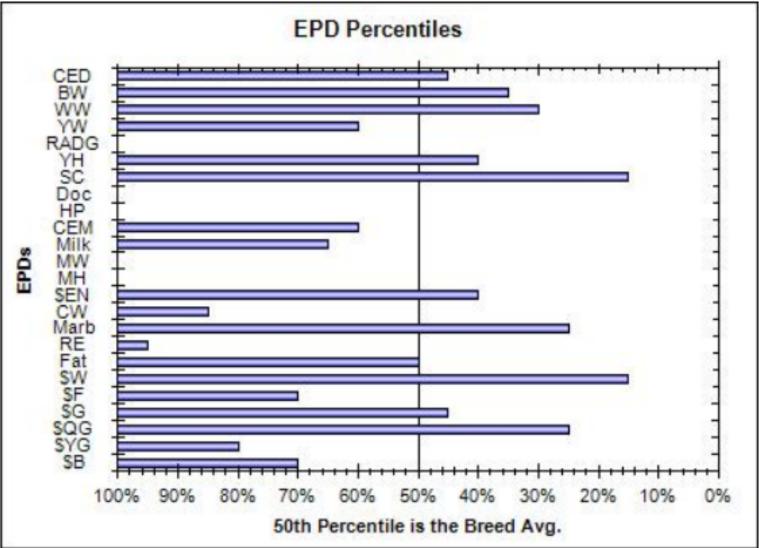
Average breed association EPDs for most traits are not zero.

Birth Date: 02/14/2006 Tattoo: 203

Parentage: SNP

Breeder: 489558 - Joe & Michele Sammis, Dorris CA

Owner(s): 489558 - Joe & Michele Sammis, Dorris CA





Birth Date: 02/14/2006 Tattoo: 203

📠 EPD Percentiles

Parentage: SNP

As of 08/21/2012

			Pro	duction						Ν	A aternal									
CED Acc	BW Acc	WW Acc	YW Acc	RADG Acc	YH Acc	SC Acc	Doc Acc	HP Acc	CEM Acc	Milk Acc	MkH MkD	MW Acc	MH Acc	\$EN						
+6 .29	+1.2 .37	+52 .28	+84 .28		I+.4 .05	I+1.19 .05			+7 .18	+21 .22				27						

	Carcass												
CW Acc	Marb Acc	RE Acc	Fat Acc	Carc Grp Carc Pg	Usnd Grp Usnd Pg								
I+16 .05	I+.55 .05	I04 .05	I+.009 .05										

	\$Values												
\$W	\$F	\$ G	\$QG	\$YG	\$B								
+32.79	+23.33	+28.03	+27.22	+.81	+52.58								

EPDs are enhanced by genomic results generated by: 🔘 igenity.



	Bull
[AMF-CAF-M1F-NHF-RDF] Birth Date: 02/18/2001 Tattoo: 109 Parentage: Blood type, Microsatellite, SNP Genomic: IG1, IG384, PF50 Breeder: 405616 - Mytty Angus Ranch, Florence MT Owner(s): 44424 - Black Pine Farm, Heron MT 405616 - Mytty Angus Ranch, Florence MT 1205261 - Shipwheel Cattle Co, Chinook MT	 AM – arthrogryposis multiplex CA - contractural arachnodactyly M1 - nt821 mutation for double muscling NH - neuropathic hydrocephalus RD - red color gene
	As of 08/21/2012

													A9 UI	00/21/2012
	Production								Maternal					
CED	BW	WW	YW	RADG	YH	SC	Doc	HP	CEM	Milk	MkH	MW	MH	\$EN
Acc	Acc	Acc	Acc	Acc	Acc	Acc	Acc	Acc	Acc	Acc	MkD	Acc	Acc	
+14	-1.3	+54	+98	+.13	+0	+1.84	+22	+6.5	+14	+25	1968	+32	+.3	+2.45
.97	.99	.98	.97	.82	.97	.97	.95	.72	.93	.95	9145	.91	.92	

		Car	cass		
CW	Marb	RE	Fat	Carc Grp	Usnd Grp
Acc	Acc	Acc	Acc	Carc Pg	Usnd Pg
+21	+.71	10	+.021	61	7339
.79	.81	.81	.80	128	22273

		\$Value	s		
\$W	\$F	\$G	\$QG	\$YG	\$B
+45.37	+37.47	+28.51	+31.63	-3.12	+59.06

Mytty In Focus Reg: AAA #13880818 Bull

[AMF-CAF-M1F-NHF-RDF]

Birth Date: 02/18/2001 Tattoo: 109

Parentage: Blood type, Microsatellite, SNP

Genomic: IG1, IG384, PF50

Breeder: 405616 - Mytty Angus Ranch, Florence MT

Owner(s): 44424 - Black Pine Farm, Heron MT 405616 - Mytty Angus Ranch, Florence MT 1205261 - Shipwheel Cattle Co, Chinook MT

EPD Percentiles _____ CED BW ww YW RADG YH Doc CEM Milk EPDs MW MH CW Marb RE Fat SW SF SG SQG SYG SB 100% 90% 80% 60% 50% 40% 30% 20% 10% 0% 70% 50th Percentile is the Breed Avg.

Current Sires Percent Breakdown

Thomas IN Focus 8070 Reg: AAA 16043370 Bull

[AMF]

Birth Date: 01/27/2008 Tattoo: 8070

Parentage: SNP

Breeder: 559318 - Thomas Angus Ranch, Baker City OR

Owner(s): 559318 - Thomas Angus Ranch, Baker City OR

862145 - Jack Cowley, Montague CA

Patntinder + Embryo Transplant

💼 EPD Percentiles

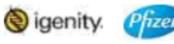
As of 08/21/2012

	Production									Matern	al			
CED Acc	BW Acc	WW Acc	YW Acc	RADG Acc	YH Acc	SC Acc	Doc Acc	HP Acc	CEM Acc	Milk Acc	MkH MkD	MW Acc	MH Acc	\$EN
+10 .32	+.9 .36	+47 .28	+92 .28			+.51 .37			+12 .20	+24 .22		I+31 .05	I+.3 .05	-5.25

Carcass							
CW Acc	Marb Acc	RE Acc	Eat Acc	Carc Grp Carc Pg	Usnd Grp Usnd Pg		
+27	+.94 .26	+.13 .29	+.023 .24				

		\$Values	i		
\$W	\$F	\$G	\$QG	\$YG	\$B
+28.01	+33.86	+35.39	+36.38	99	+70.98

EPDs are enhanced by genomic results generated by:



Thomas IN Focus 8070 Reg: AAA 16043370 Bull

[AMF]

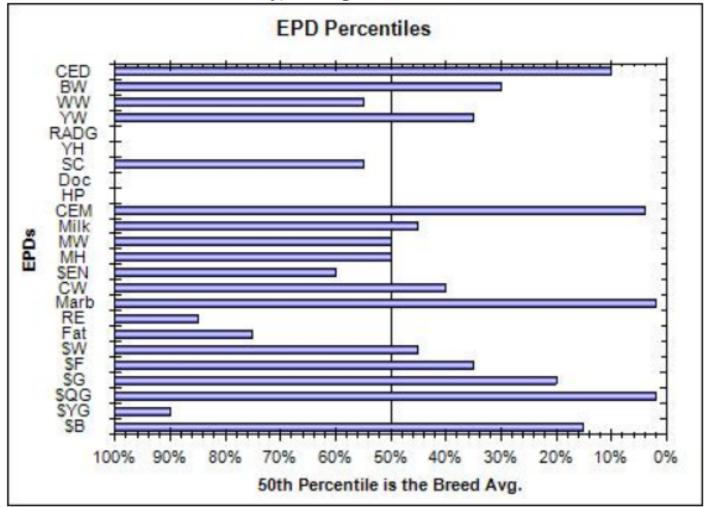
Birth Date: 01/27/2008 Tattoo: 8070

Parentage: SNP

Breeder: 559318 - Thomas Angus Ranch, Baker City OR

Owner(s): 559318 - Thomas Angus Ranch, Baker City OR

862145 - Jack Cowley, Montague CA





Kohl Creek Premium Beef 357M Reg: AAA 15968280 Bull

Birth Date: 04/06/2007 Tattoo: 357M

Parentage: SNP

Breeder: 402790 - Robert F & Carol L Munson, Horse Creek CA

Owner(s):862145 - Jack Cowley, Montague CA

📠 EPD Percentiles

As of 08/22/2012

	Production									Matern	al			
CED Acc	BW Acc	WW Acc	YW Acc	RADG Acc	YH Acc	SC Acc	Doc Acc	HP Acc	CEM Acc	Milk Acc	MkH MkD	MW Acc	MH Acc	\$EN
+6 .29	+1.8 .35	+30 .27	+65 .22						+9 .18	+18 .21				+10.38

		Car	cass		
CW Acc	Marb Acc	RE Acc	Fat Acc	Carc Grp Carc Pg	Usnd Grp Usnd Pg
+28 .19	+.44 .24	+.29 .25	+.021 .21		

		\$Valu	ies		
\$W	\$F	\$G	\$QG	\$YG	\$B
+18.90	+12.83	+25.29	+23.68	+1.61	+60.60

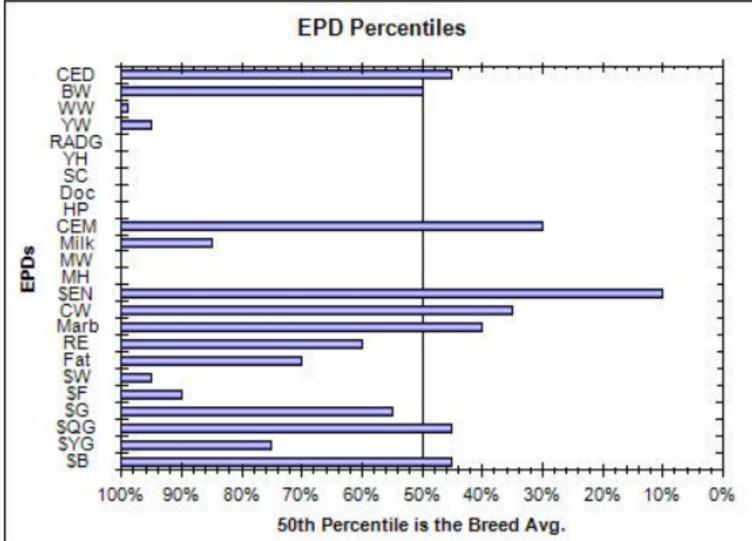
Kohl Creek Premium Beef 357M Reg: AAA 15968280 Bull

Birth Date: 04/06/2007 Tattoo: 357M

Parentage: SNP

Breeder: 402790 - Robert F & Carol L Munson, Horse Creek CA

Owner(s):862145 - Jack Cowley, Montague CA



Cow Energy Value (\$EN), expressed in dollars savings per cow per year, assesses differences in cow energy requirements as an expected dollar savings difference in daughters of sires. A larger value is more favorable when comparing two animals (more dollars saved on feed energy expenses). Components for computing the cow \$EN savings difference include lactation energy requirements and energy costs associated with differences in mature cow size.

Non-Parent Bulls Percent Breakdown

AND TY I		
125		
ISH I		
5		
1		
DAVI		
A A A A A A A A A A A A A A A A A A A	┝┷	

		S R In Focus 203	Thomas IN Focus	
		(20-3)	8070 (8-1)	Difference
	Total Progeny	117	73	44
	Average Progeny/ Season	20 calves	18 calves	+2 calves/season
	WW rEPD (Accuracy)	-0.7 (0.52)	-5.7 (0.46)	+5 lb
ŀ	CW rEPD (Accuracy)	-13.6 (0.53)	-26.0 (0.28)	+12.4 lb
ľ	RE rEPD (Accuracy)	-0.21 (0.51)	-0.29 (0.26)	+0.08 sq in
ŀ	MS rEPD (Accuracy)	0.54 (0.56)	0.33 <mark>(</mark> 0.33)	+0.21
	Average Adj WW (Fall 2011)		559 lb	
	Value of 10 steers at \$1.20/lb	\$6,700	\$6,640	\$60
	Value of 10 steers based on \$W	\$328 \$32.80/head	<mark>\$280</mark> \$28.00/head	\$48
	Value of 10 steers based on \$B	\$526	\$710	-\$184

		S R In Focus 203 (20-3)	Thomas IN Focus 8070 (8-1)	Difference
DAVI	Total Progeny	117	73	44
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	Value of 10 steers based on \$B	\$526	\$710	-\$184





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

US cattle numbers (x 106)

Breeder

# US Beef operations	766,350
Million Cows	31.4
Average herd size	122

Seedstock Cows

Commercial cow/calf producer

35.7

Commercial Cows + replacements

Feedlot

Processing

13.6 (on feed at any one time) 25.6 (cattle fed per year in 2009)

43.2



Other Beef Animals (calves, steers, heifers and bulls)

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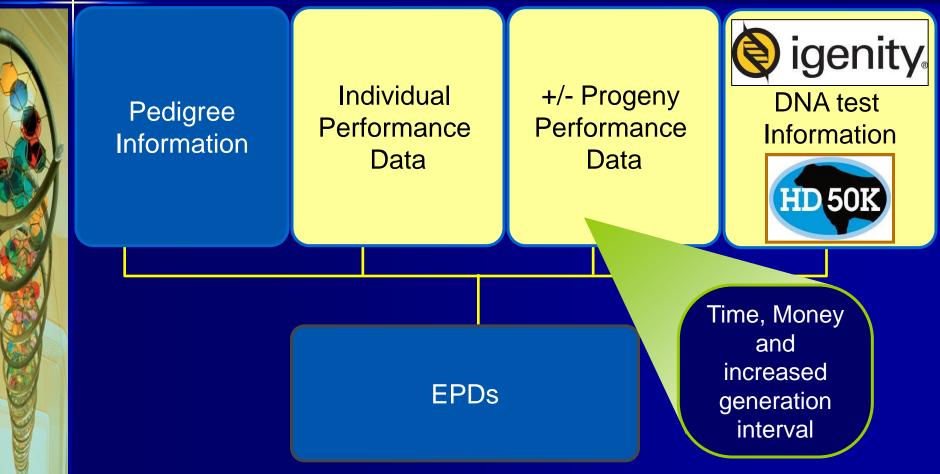


Uses of DNA information for commercial cattle producers

- Improving accuracy of commercial bulls
- Parentage/prolificacy
- Genetic defect testing
- Replacement heifer selection



Information sources for EPDs – DNA tests are another source of information to improve the accuracy of EPDs



Modified from slide from Kent Anderson, Pfizer Animal Genetics, presented at BIF 2011

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Animal Genomics and Biotechnology Education

- Calving ease direct
- Birth weight
- Weaning weight
- Yearling weight
- Yearling height
- Mature weight
- Mature height
- Dry matter intake
- Residual feed intake
- Scrotal circumference
- Docility
- Calving ease maternal
- Milking ability
- Carcass weight
- Fat thickness
- Ribeye area
- Marbling score
- Tenderness







Pfizer Animal Health Animal Genetics 50K SNP chip assays 50,000 SNPs spread throughout genome



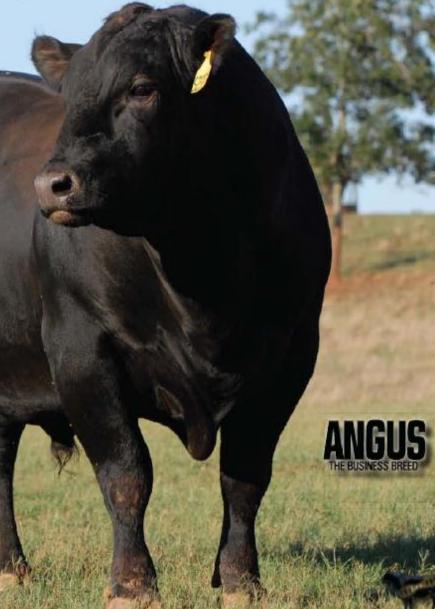
The Power of the IGENITY[®] profile for Angus

The American Angus Association® through its subsidiary, Angus Genetics Inc.® (AGI), has a vision to provide Angus breeders with the most advanced solutions to their genetic selection and management needs.

Genomic-enhanced Expected Progeny Differences (EPDs) can now be calculated for your animals using the highly predictable American Angus Association database along with IGENITY* profile results to provide a more thorough characterization of economically important traits and improved accuracy on young animals.

Using the IGENITY profile for Angus, breeders receive comprehensive genomic results for multiple, economically important traits.

- 1. Dry Matter Intake
- 2. Birth Weight
- 3. Mature Height
- 4. Mature Weight
- 5. Milk
- 6. Scrotal Circumference
- 7. Weaning Weight
- 8. Yearling Weight
- 9. Marbling
- **10. Ribeye Area**
- 11. Fat Thickness
- 12. Carcass Weight
- 13. Tenderness
- 14. Percent Choice (quality grade)
- **15. Heifer Pregnancy**
- **16. Maternal Calving Ease**
- **17. Direct Calving Ease**
- **18. Docility**
- 19. Average Daily Gain
- **20. Feed Efficiency**
- 21. Yearling Height





American Angus Association performs weekly evaluations with genomic data – recently updated to include new traits

	Igenity	Pfizer
Calving ease (CED)	\checkmark	\checkmark
Growth (BW WW YW Milk)	\checkmark	\checkmark
Residual Average Daily Gain (RADG)	\checkmark	\checkmark
Docility (DOC)	\checkmark	\checkmark
Yearling Scrotal/Height (SC,YH)	\checkmark	\checkmark
Mature Weight (MW)	\checkmark	\checkmark
Carcass (CWT MARB RIB FAT)	\checkmark	\checkmark

http://www.angus.org/AGI/GenomicChoice11102011.pdf (updated 11/18/2011)



How much do DNA tests help increase accuracy of EPDs?

	AGI Heritability	AGI HD 50K Correlation	Avg. 50k Change in ACC - from .05 ¹	Approximate Progeny Equivalents
BW	0.42	0.51	0.25	8
ww	0.20	0.52	0.23	16
YW ²	0.20	0.64	0.27	20
RADG ³	0.31	0.65	0.27	13
Milk	0.14	0.32	0.15	12
CW	0.31	0.48	0.17	7
Marb ⁴	0.26	0.57	0.24	12
RE ⁴	0.32	0.60	0.23	9
FAT ⁴	0.26	0.56	0.23	11

¹These changes are less for higher initial accuracy values

²Post-weaning ADG

³Dry matter intake

⁴Carcass progeny, not scanned progeny

Data from Kent Anderson, Pfizer Animal Genetics, presented at BIF 2011

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Animal Genomics and Biotechnology Education



What about the other breeds?



The following breed associations are working with Dorian Garrick (IA State) to develop their own 50K-based prediction equations

Breed	Breed code	# Training Records
Hereford	HER	1,725
Red Angus	RAN	296
Simmental	SIM	2,853
Brangus	BRG	896
Limousin	LIM	2,319
Gelbvieh	GVH	847
Maine Anjou	RDP	115

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Predictions in Some Beef Breeds (Data provided by Dorian Garrick)

	Angus	Hereford	Simmental	Gelbvieh	Gelbvieh
# Records in training	(3,500)	(800)	(2,800)	(847)	including Angus (1,181)
BirthWt	0.64	0.43	0.65	0.38	0.41
WeanWt	0.67	0.32	0.52	0.31	0.34
YearlingWt	0.75	0.30	0.45	0.21	NC
Milk	0.51	0.22	0.34	0.36	0.34
Fat	0.70	0.40	0.29	NA	NA
REA	0.75	0.36	0.59	0.38	0.48
Marbling	0.80	0.27	0.63	0.54	0.56
CED	0.69	0.43	0.45	NC	0.48
CEM	0.73	0.18	0.32	NC	NC
SC	0.71	0.28	NA	0.50	0.50

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Uses of DNA information for commercial cattle producers

- Improving accuracy of commercial bulls
- Parentage/prolificacy
- Genetic defect testing
- Replacement heifer selection



Benefits of DNA-based parentage identification

- Correct pedigree errors so improve the rate of genetic gain
- Enables the use of multi-sire breeding pasture
 - Higher fertility
 - Elimination of sire failure
 - Tighter calving season
- Reduces the need for different breeding pastures
 - Allows for better pasture management
 - Less sorting and working of animals into different groups
- Identify sires that have few/many progeny
- Enables the development of commercial-ranch genetic evaluations
 - Can determine which bull is causing calving problems



Uses of DNA information for commercial cattle producers

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Value of genomic information for recessive genetic defects



- Arthrogryposis multiplex (AM) is a lethal recessive deletion for which a DNA test was developed in 2008
- In the 11 months following the release of the test, the American Angus Association posted the results of tests for AM on about 96,247 cattle.
- @\$25/test this amounts to \$2.4 million in tests
- Of these, 20% (19,529) were carriers of AM. That leaves 23,638 bulls and more than 53,000 heifers which tested as free of AM.

At \$4K/bull and \$2K/heifer ~\$200 million

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Estimates of US and Australia genetic testing costs (Angus)

	US	AUSTRALIA
AMF (Arthrogryposis multiplex)	113,526	12,021
NHF (Neuropathic Hydrocephalus)	77,067	9,936
CAF (Congenital Contractural Arachnodactyly)	28,837	2,532
TOTAL NUMBER	294,054	34,991
COST (@ \$25/test)	\$7,351,350	\$874,775

Numbers kindly shared by Bryce Schumann, American Angus Association; and Carel Teseling, Angus Australia; current as of 5/2011

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Uses of DNA information for commercial cattle producers

- - Improving accuracy of commercial bulls
 - Parentage/prolificacy
 - Genetic defect testing
 - Replacement heifer selection



Value of DNA tests for heifer selection

The value of using DNA information in making replacement heifer selection decisions will depend upon

- the information available at the time of selection
- Whether the DNA test predicts economically-important traits
- what proportion of available heifers are selected.
- In practice, selection for replacement heifers is frequently driven by size as heifers that are born later in the calving season are too immature to be cycling in time for the first potential breeding season. This tends to put indirect selection on fertility traits of the dam (e.g. days to calving). Commercial producers typically select on at least a visual estimate of a heifer's 400d weight.



What is the value of genetic improvement in commercial females?

The value of increasing the accuracy of commercial replacement heifer genetic evaluations is much less than that for bulls because bulls produce more descendants from which to derive returns for accelerated genetic improvement.

Also many of the economically important traits with regard to replacement females (fertility, stayability) are not well predicted by the genetic tests that are currently on the market

Animal Genomics and Biotechnology Education



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Table 2. Genetic correlation between genomic results and phenotypic trait of interest (AAA data) by genomics company

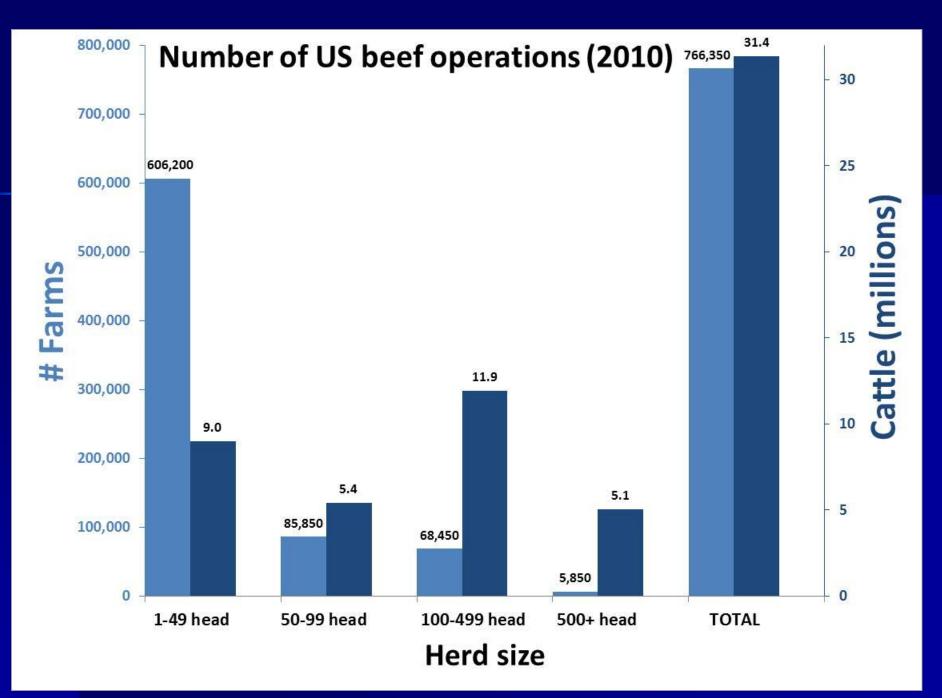
	Igenity	Pfizer
Calving Ease Direct	.47	.33
Birth Weight	.57	.51
Weaning Weight	.45	.52
Yearling Weight	.34	.64
Dry Matter Intake (component of RADG)	.45	.65
Yearling Height	.38	.63
Yearling Scrotal	.35	.65
Docility	.29	.60
Milk	.24	.32
Mature Weight	.53	.58
Mature Height	.56	.56
Carcass Weight	.54	.48
Carcass Marbling	.65	.57
Carcass Rib	.58	.60
Carcass Fat	.50	.56

Which of these traits are important for replacement heifer selection?



Ninety percent of US cattle operations have fewer than 100 head, and most sell their cattle at auction prior to feedlot entry

- In reality most producers' financial returns are tied very closely to the number of calves, a function of reproduction, and less if at all to feedlot performance and carcass traits, and even less to feedlot health and mortalities.



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Ninety percent of US cattle operations have fewer than 100 head, and most sell their cattle at auction prior to feedlot entry

- In reality most producers' financial returns are tied very closely to the number of calves, a function of reproduction, and less if at all to feedlot performance and carcass traits, and even less to feedlot health and mortalities.
- To incentivize the inclusion of traits that provide value in downstream sectors in selection decisions, a mechanism to equitably share some of the value derived from improved feedlot performance and carcass quality is needed to compensate breeders and producers for including those considerations in their selection and management decisions.

Questions?