PATERNITY ANALYSIS IN LARGE COMMERCIAL CATTLE RANCH SETTING USING SNPs - UC DAVIS EXPERIENCES

Alison Van Eenennaam
Cooperative Extension Specialist
Animal Biotechnology & Genomics
alvaneenennaam@ucdavis.edu

Daniel J. Drake
M. Cecilia T. Penedo
University of California, Davis

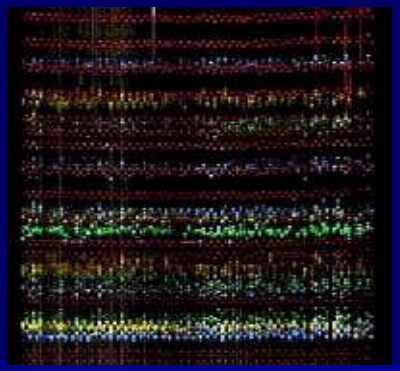
http://animalscience.ucdavis.edu/animalbiotech/

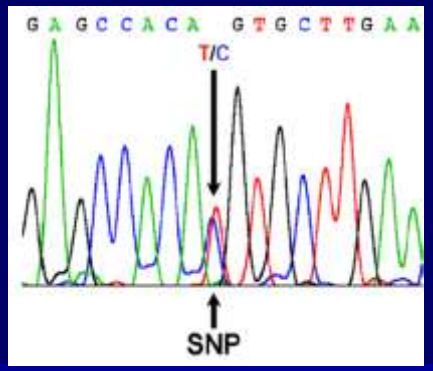
Prather Ranch – Macdoel Northern California

DNA Sample Collection

- Blood collected on FTA cards from **27** herd sires and **624** calves derived from a multiple-sire pasture
- DNA also collected from semen straws from **8** AI sires
- After AI, entire herd was run as one group with the 27 herd sires

Genotyping





- **Genotyping and paternity assignments based on microsatellites (STRs) were done by the UC Davis Veterinary Genetics Laboratory using a panel of 23 cattle markers (P_E=99.9%)**
- **Genotyping based on SNPs were done by a commercial genotyping company using a panel of 28 loci (PE=95.5%)**

A. L. Van Eenennaam, R. L. Weaber, D. J. Drake, M. C. T. Penedo, R. L. Quaas , D. J. Garrick, E. J. Pollak. 2007. DNA-based paternity analysis and genetic evaluation in a large commercial cattle ranch setting. Journal of Animal Science. 85:3159–3169

Results of the paternity analysis

(PE=99.9%)

	23 Microsatellite (STR) panel	
One possible sire	533*	85.4%
More than one sire	4	0.6%
All excluded	76	12.2%
Resubmits	11	1.8%
TOTAL	624	

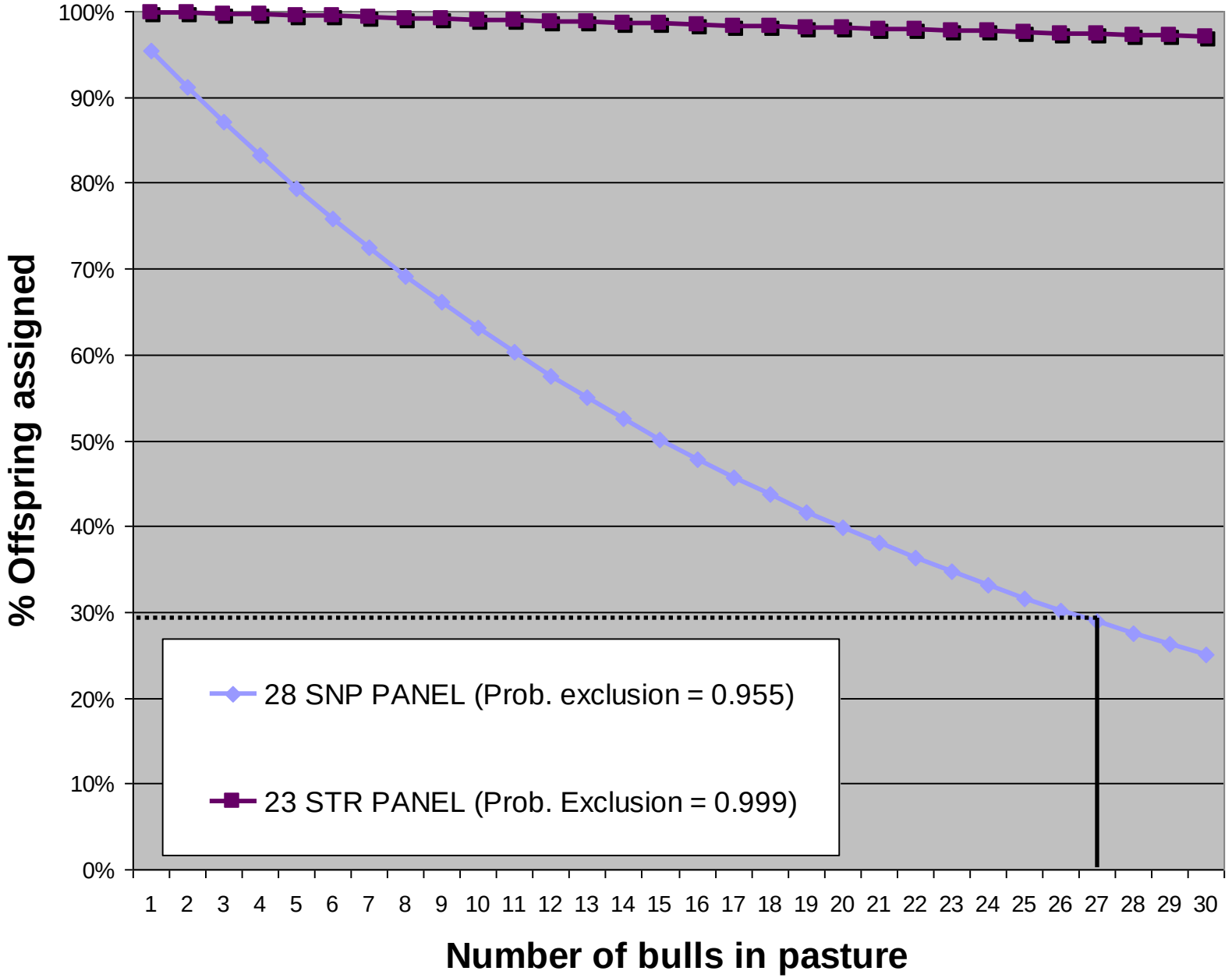
DNA from more than one animal

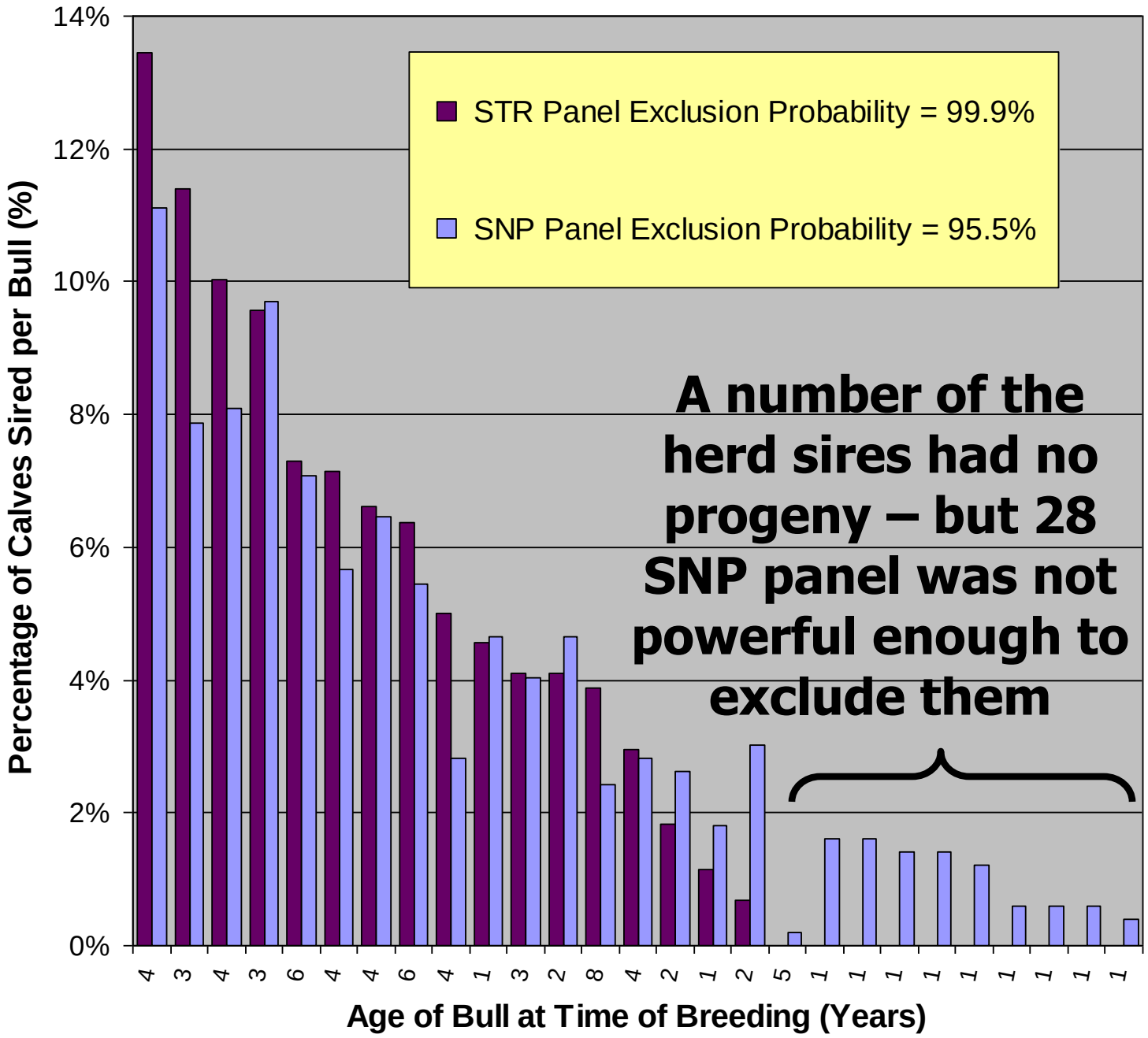
* 10 assignments allowed a one locus mismatch

	23 Microsatellite (STR) panel (PE=99.9%)		28 SNP panel (PE=95.5%)	
One possible sire	533*	85.4%	**175**	**23.3%**
More than one sire	4	0.6%	**420**	**67.3%**
All excluded	76	12.2%	**29**	**4.6%**
Resubmits	11	1.8%	**0**	**0%**
TOTAL	624		**624**	

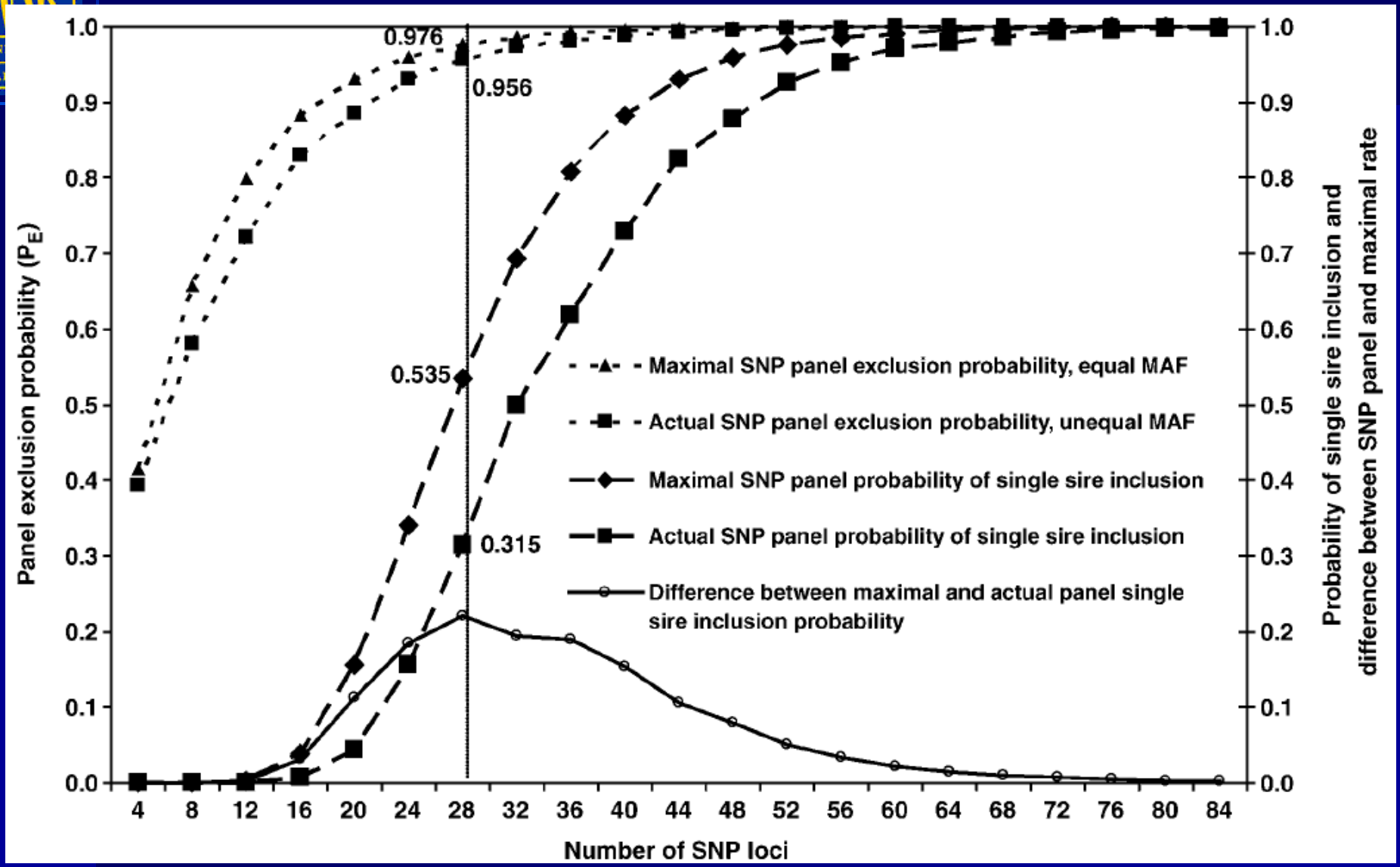
* 10 assignments allowed a one locus mismatch

Unambiguous Assigment of Calves to a Single Sire Using a 28 SNP Panel versus a 23 STR Panel




14%
12%
10%
8%
6%
4%
2%
0%
Percentage of Calves Sired per Bull (%)
STR Panel Exclusion Probability = 99.9%
SNP Panel Exclusion Probability = 95.5%
A number of the herd sires had no progeny – but 28 SNP panel was not powerful enough to exclude them
4 3 4 3 6 4 4 6 4 1 3 2 8 4 2 1 2 5 1 1 1 1 1 1 1 1 1
Age of Bull at Time of Breeding (Years)

Theoretical maximal and actual SNP marker panel exclusion probabilities (PE) with increasing numbers of SNP based on equal minor allele frequencies (MAF) and observed (unequal) MAF, respectively, and probability of single sire inclusion for a multiple-sire breeding pasture containing 27 sires. The number of loci (28) included in the SNP panel used to analyze the field data set is indicated with a vertical line



2006 UCD Sample Collection

- Blood collected on Typifix tags cards from **23** herd sires and **298** calves derived from multiple-sire pastures
- Compared 62 "MARC" parentage loci – average number of loci compared was 53.86 with a range from 6-62; allowed ≤ 1 mismatch
- P_E (assuming equal minor allele frequency) = 0.999746

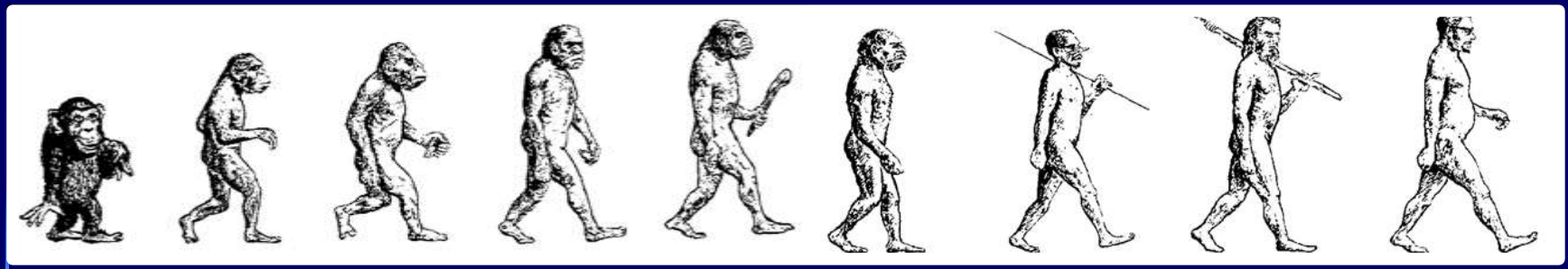
2007 UCD Sample Collection

- Blood collected on Typifix tags cards from **28** herd sires and **303** calves derived from multiple-sire pastures
- Compared 99 "MARC" parentage loci – average number of loci compared was 87.04 with a range from 14-99; allowed ≤ 1 mismatch
- P_E (assuming equal minor allele frequency) = 0.999998185

Results of paternity determinations – 2006, 2007 SNP panels

2006 (62 potential loci. PE=0.99975, number of sires 23)

Sires assigned per calf	Predicted % of calves	Observed % of calves	Observed #
0	0.0	8.00%	24
1	99.4	86.67%	260 (20)
2	0.6	4.67%	14
3	0.0	0.003%	1
4	0.0	0.003%	1
5	0.0	0.00%	0
6+	0.0	0.00%	0
Total:	100	100.00%	300



	28 SNP Panel – 27 sires 2005 (PE=95.5%)		62 SNP Panel – 23 sires 2006 (PE=99.975%)		99 SNP Panel – 28 sires 2007 (PE=99.999%)	
One sire assigned	175	23.3%	260	86.7%	294	97.0%
More than one sire	420	67.3%	16	5.3%	1	0.33%
All excluded	29	4.6%	24	8.0%	8	2.6%
TOTAL	624		300		303	

SNPs and parentage using the 50K chip

"The low rate of genotyping errors meant that less than five inconsistencies were usually found when parent-progeny assignment was correct. However, several thousand inconsistencies were usually found when the parent-progeny assignment was incorrect"

Wiggans et al. Genomic Evaluations in the United States and Canada: A collaboration. ICAR 2008

Problems we ran into along the way

- Changing SNP panels from year to year without regenotyping all bulls
- Poor call rate – especially problematic when it was a sire (from a panel of 99 SNP loci, the call rate was as low as 5% on occasion)
- Discrepancies between genotypes of bulls genotyped multiple years
- Sample integrity problems – genotypes or ID swapped, genotyped processed incorrectly or in wrong order

Implications and considerations regarding SNPs for parentage

It is likely that SNP markers will replace alternatives (i.e. microsatellites) over the next 5 years

- Which SNP panel should be used and how many SNP markers should be included in the panel?
- What should be the number of compared loci cutoff in the case of incomplete genotyping?
- How many exclusions (as a function of number of compared loci) should be allowed to account for genotyping errors – platform dependent?

Development of an Integrated Animal Identification and Tracking System for Research and Extension Education

The animal identification does not go with the animal – lost at processing

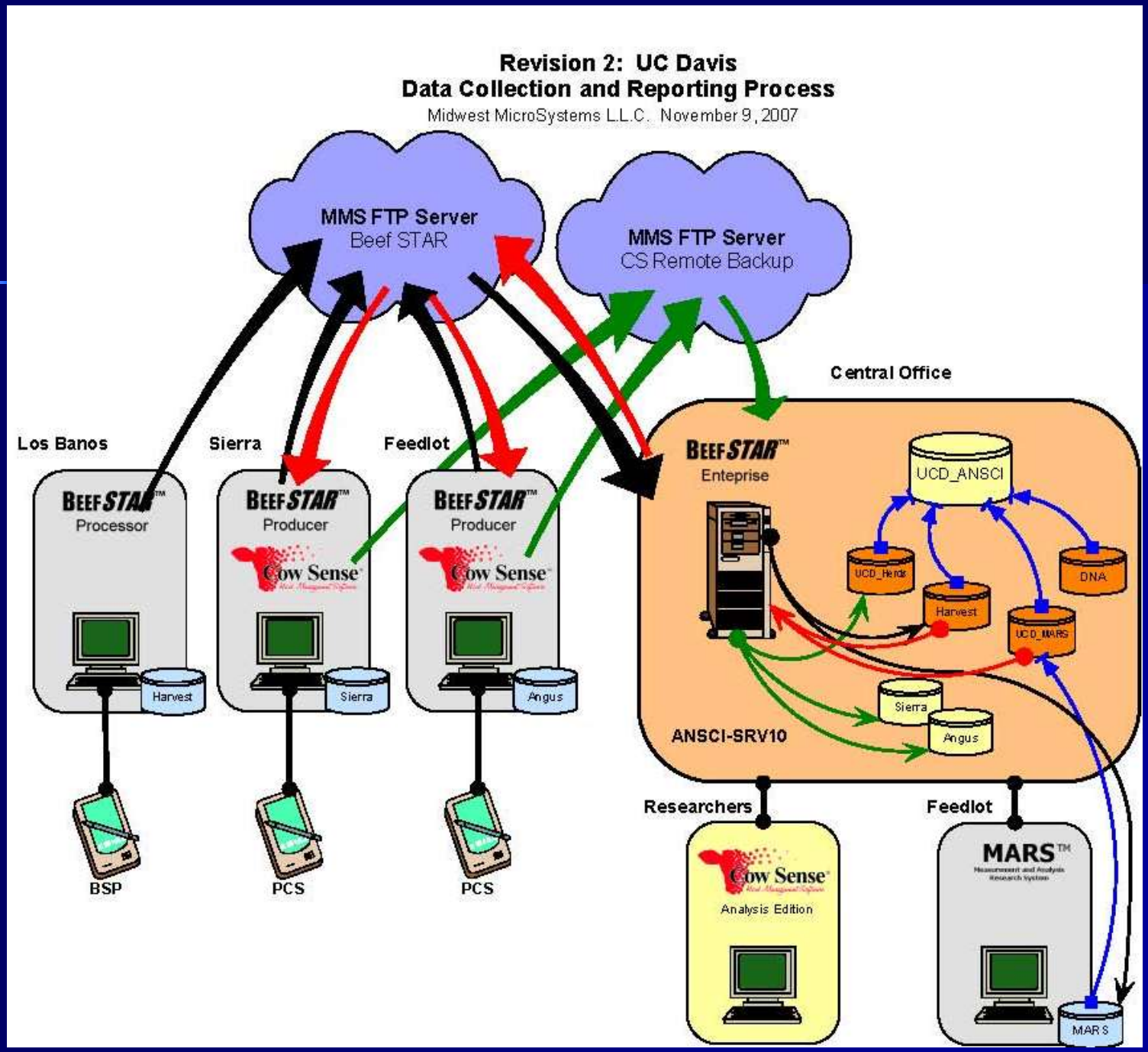
Sierra Cow-Calf Operation

UC Davis Feedlot Operation

UC Davis Research Data

Los Banos Processing Plant Carcass Data

Psion reader scans EID and carcass data is entered


Revision 2: UC Davis
Data Collection and Reporting Process
Midwest MicroSystems L.L.C. November 9, 2007
MMS FTP Server
Beef STAR
MMS FTP Server
CS Remote Backup
Central Office
Los Banos
Sierra
Feedlot
BEEFSTAR™
Processor
Harvest
BEEFSTAR™
Producer
Cow Sense
Sierra
BEEFSTAR™
Producer
Cow Sense
Angus
BSP
PCS
PCS
BEEFSTAR™
Enteprise
UCD_ANSCI
UCD_Herds
DNA
Harvest
UCD_MARS
Sierra
Angus
ANSCI-SRV10
Researchers
Feedlot
Cow Sense
Analysis Edition
MARS™
MARS

Results: calving to carcass

Calf ID	Sex	EID	Bull Breed	Bull ID	Cow ID	Cow Breed
9	B	982000089711796	Angus	208	3009	XB
10	B	982000089711990	Angus	1AN1000	2097	XB
34	B	982000036041361	Angus	205	1096	XB
44	B	982000089712184	Angus	1AN1000	8147	XB
52	B	982000089712028	Gelbvieh	579	8762	XB
55	B	982000036018645	Angus	241	2119	XB
75	B	982000035362898	Hereford (Horned)	115	1053	XB
89	B	982000035361265	Angus	359	9466	XB
104	B	982000035363236	Angus	241	2016	XB

Calf ID	Location	Birth Date	Birth Weight	Adj Birth Wt	Wean Wt Date	Wean Weight	Adj Wean Wt	ADG Calf
9	UC Davis	9/18/2006	64	69	5/8/2007	532	518	2
10	UC Davis	9/23/2006	68	70	5/8/2007	546	520	2.1
34	UC Davis	10/12/2006	72	72	5/8/2007	508	502	2.1
44	UC Davis	10/9/2006	80	80	5/8/2007	568	554	2.3
52	UC Davis	10/17/2006	84	84	5/8/2007	598	603	2.5
55	UC Davis	10/18/2006	68	70	5/8/2007	512	539	2.2
75	UC Davis	10/23/2006	84	84	5/8/2007	558	577	2.4
89	UC Davis	10/24/2006	76	76	5/8/2007	566	589	2.5
104	UC Davis	10/27/2006	82	84	5/8/2007	506	552	2.2

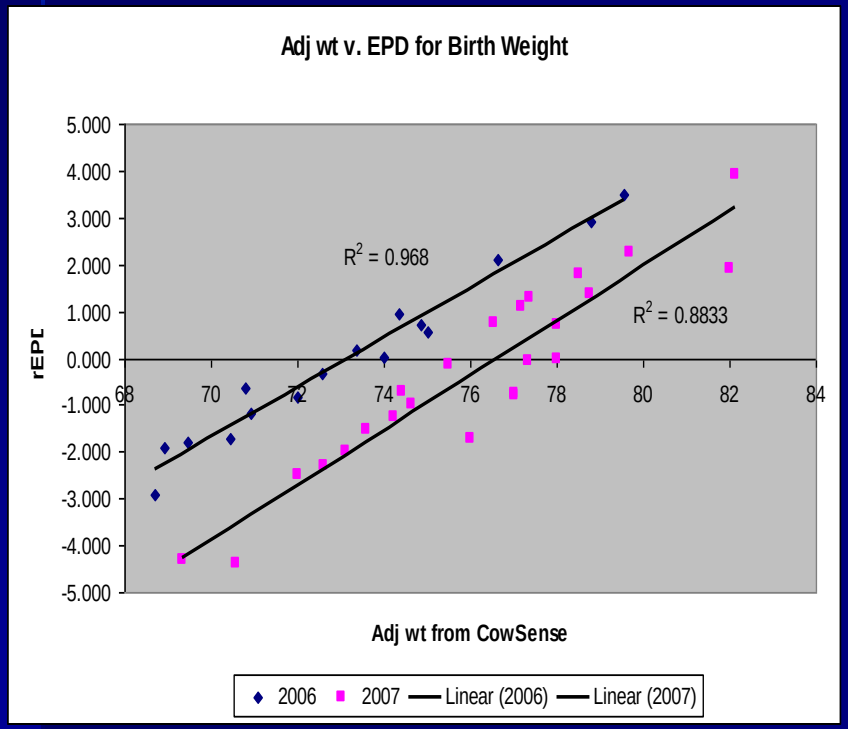
Calf ID	Location Date	DNA Case	Feeding In Date	Feeding Feeder	Feeding In Weight	Feeding Days	Feeding Final Weight	Feeding ADG
9	9/15/2007	840000000167575	12/13/2007	UCD Feedlot	1025	47	1150	2.7
10	9/15/2007	840000000167577	12/13/2007	UCD Feedlot	1155	47	1270	2.4
34	9/15/2007	840000000196545	12/13/2007	UCD Feedlot	1095	47	1180	1.8
44	9/15/2007	840000000196535	12/13/2007	UCD Feedlot	1145	47	1250	2.2
52	9/15/2007	840000000196568	12/13/2007	UCD Feedlot	1130	47	1225	2
55	9/15/2007	840000000196578	12/13/2007	UCD Feedlot	1135	47	1300	3.5
75	9/15/2007	840000000196820	12/13/2007	UCD Feedlot	1070	47	1190	2.6
89	9/15/2007	840000000196841	12/13/2007	UCD Feedlot	1115	47	1240	2.7
104	9/15/2007	840000000196871	12/13/2007	UCD Feedlot	1070	47	1220	3.2

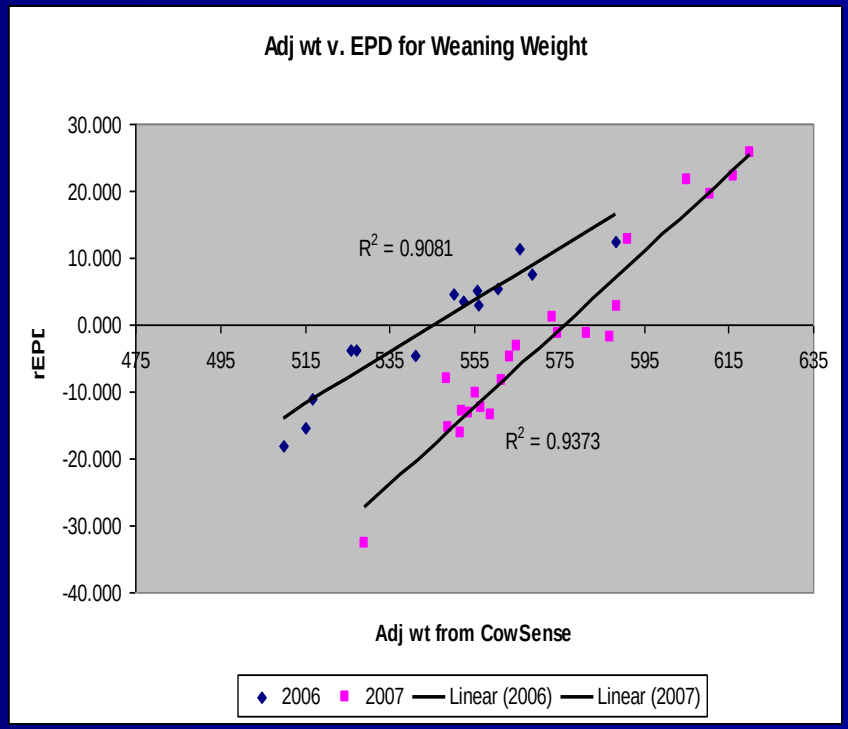
Calf ID	Carcass Kill Date	Carcass Hot Weight	Carcass Backfat	Carcass Final YG	Carcass KPH	Carcass REA	Carcass Marbling Score	Carcass Quality Grade	Carcass ID
9	2/1/2008	714	0.8	3.3	2	13.5	MT30	Ch	333
10	2/1/2008	782	0.45	3	3	13.2	SM80	Ch-	332
34	2/1/2008	723	0.6	3.4	3	12.2	SM20	Ch-	337
44	2/1/2008	756	0.45	3.6	3.5	11.1	MT30	Ch	338
52	2/1/2008	737	0.4	2.7	3	13.2	SL40	Sel-	341
55	2/1/2008	783	0.65	3.8	2.5	11.9	SM30	Ch-	330
75	2/1/2008	699	0.45	3.3	3	11.2	SM60	Ch-	339
89	2/1/2008	733	0.5	2.9	2.5	13	SM50	Ch-	340
104	2/1/2008	743	0.5	2.8	2.5	13.5	SM-	Ch-	335

rEPDs

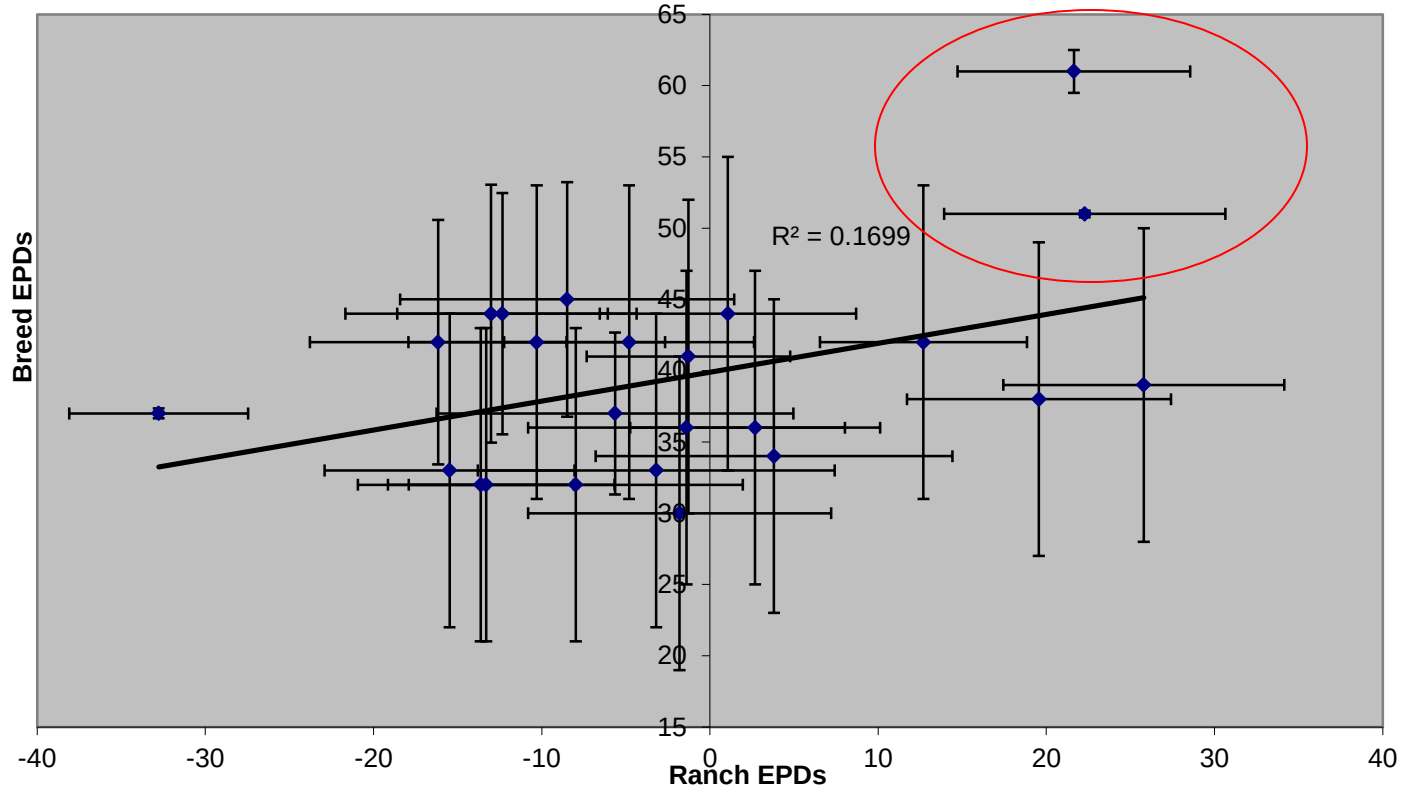
- For Angus calves only
- Used MTDFREML to calculate ranch EPDs from 2006 and 2007 calf crops using adjusted birth and weaning weight records.
- Fixed effects included sex of calf and contemporary group information

Correlation between average adjusted weight of progeny and ranch EPDs calculated for each sire

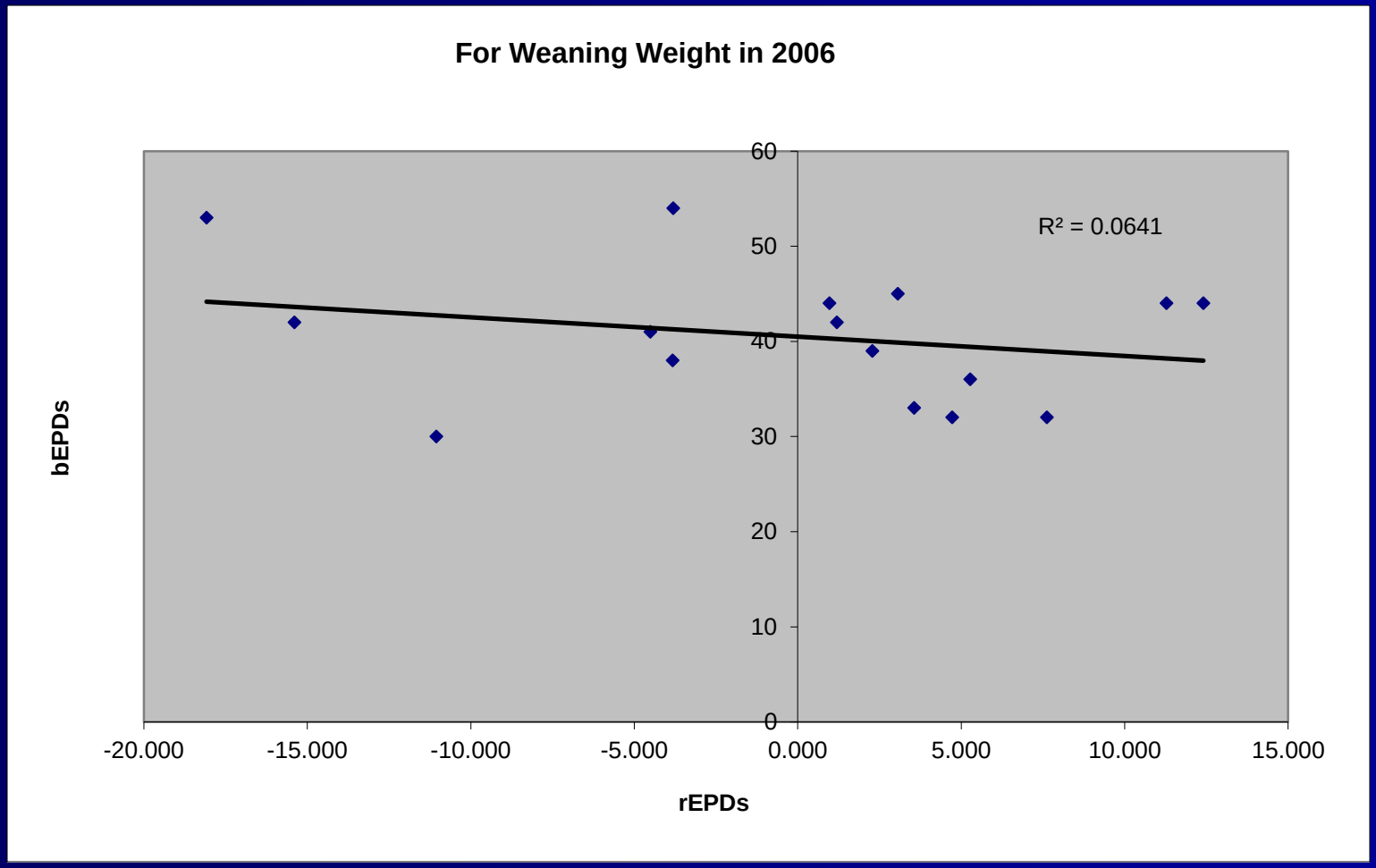




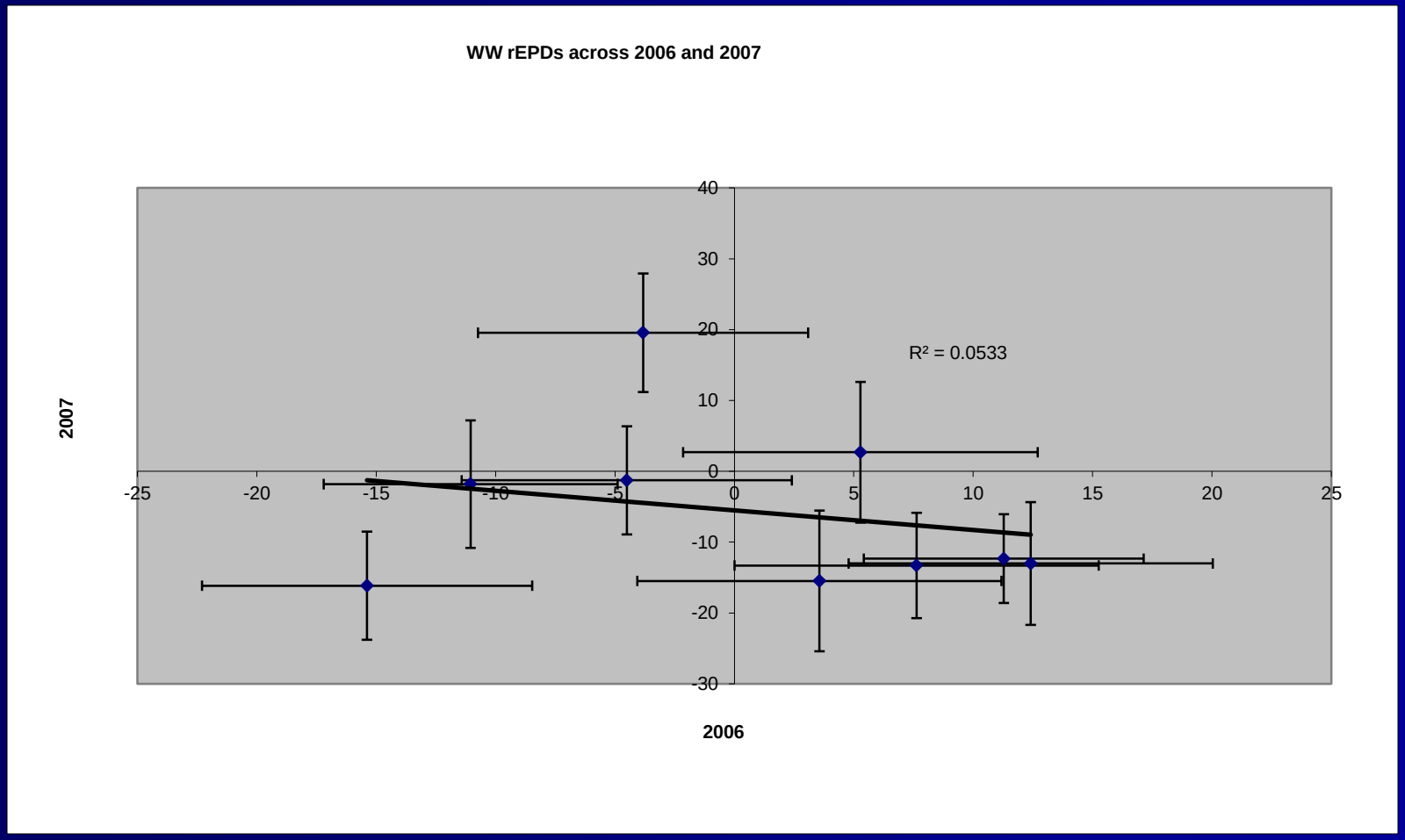
Correlation of Angus bEPDs to rEPDs for Weaning Weight in 2007



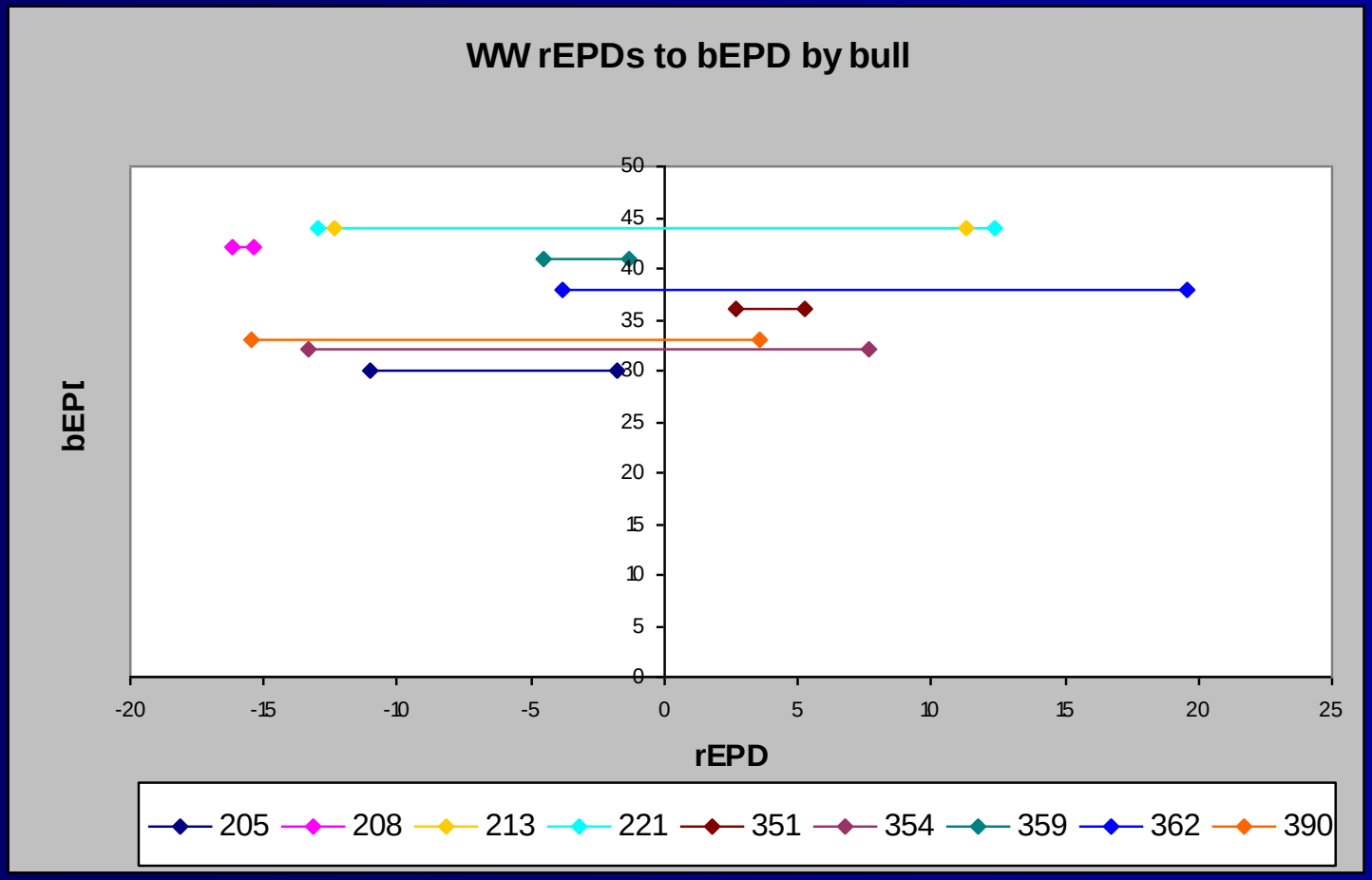
Correlation of Angus bEPDs to rEPDs for Weaning Weight in 2006



Comparison of WW rEPDs calculated in 2006 and 2007 for sires that had a least 3 progeny in each year



Comparison of rEPDs to bEPDs for bulls with 3 or more progeny



Weaning Weight

ID	bEPD WW	Rank	
221	44	1	
213	44	1	
208	*42*	*3*	
359	41	4	
362	38	5	4.03
351	36	6	
390	33	7	
354	32	8	
205	30	9	-5.02

ID	2006 WW	Rank		2007 WW	Rank	
221	12.409	1		-13.013	6	
213	11.283	2		-12.339	5	
208	*-15.388*	*9*		*-16.161*	*9*	
359	-4.504	7		-1.281	3	
362	-3.823	6	-0.004468172	19.560	1	-4.647053452
351	5.280	4		2.685	2	
390	3.564	5		-15.481	8	
354	7.628	3		-13.306	7	
205	-11.052	8	1.355124036	-1.809	4	-6.97761928

USDA Integrated Grant

UNIVERSITY OF CALIFORNIA, DAVIS

BERKELEY • DAVIS • IRVINE • LOS ANGELES • MERCED • RIVERSIDE • SAN DIEGO • SAN FRANCISCO SANTA BARBARA • SANTA CRUZ

DEPARTMENT OF ANIMAL SCIENCE
TELEPHONE: (530) 752.1250
FAX: (530) 752-0175

ONE SHIELDS AVENUE
DAVIS, CALIFORNIA 95616.8521

Friday March 14, 2008

Letter of Intent for an integrated research proposal

Integrating DNA information into beef cattle production systems

Lead Project Director: Dr. Alison Van Eenennaam
Animal Genomics and Biotechnology Cooperative Extension Specialist
Department of Animal Science
University of California
Davis, CA 95616

Collaborating Investigators:
Dr. Darrh Bullock, Extension Professor, University of Kentucky
Dr. Leslie "Bees" Butler, Extension Marketing Specialist, University of California, Davis
Dr. Daniel Drake, University of California Cooperative Extension Livestock Advisor
Dr. Dorian Garrick, Professor, Iowa State University
Dr. John Pollak, Professor, Cornell University

Logic Model: Integrating DNA Information into Beef Cattle Production Systems

Situation

- Need to move animal genome science from the laboratory to the field
- A number of DNA-based selection tools are, or soon will be, available to beef producers
- There are few outreach programs or educational materials explaining the basics of DNA technologies and their various applications for commercial beef producers
- The lack of independent information documenting the costs and benefits associated with the use of different DNA-technologies in the commercial beef sector is hindering industry adoption

Priorities

- Determine how to make best use of DNA data in commercial animal production
- Compare and evaluate different sources of DNA-enabled genetic evaluations for commercial ranch bulls
- Determine the costs and benefits associated with the use of DNA–based technologies on commercial ranches
- Develop extension materials to explain DNA technologies and place them in the context of commercial beef operations

INPUTS

What we invest

- Expertise of a unique team of quantitative geneticists and extension researchers
- Genetic resources, time, and labor of industry collaborators/ stakeholders
- Computing resources to collect, store, and analyze data
- Creative energy to develop innovative extension programming
- Time and money to conduct and evaluate educational programs

OUTPUTS

Activities | Participation

What we do

- Work collaboratively to collect DNA information, production, carcass and financial data from cow-calf cooperators
- Evaluate different DNA-enabled genetic improvement approaches
- Work with stakeholders to develop educational materials to address identified knowledge gaps
- Deliver educational materials for eXtension, workshops, and seminars.

Who we reach

- Scientific community at meetings and via journal articles
- Industry partners and cooperators through meetings
- Extension educators through "train the trainer" workshops and the eXtension initiative
- Allied industry and producers through industry workshops
- Other interested parties through popular press articles

OUTCOMES – IMPACT

Short Term | Medium Term | Long Term

What the short term results are

Learning

- Commercial ranch field evaluation of DNA-based approaches to genetic improvement
- Identification of cost-effective applications of DNA data in commercial beef cattle production systems
- Increased awareness of the uses of DNA-based technologies in the beef industry
- Wide distribution of project results and outreach materials

What the medium term results are

Action

- Documented changes in management of herd genetics on cooperator ranches and continued use upon project completion based on realized benefits
- Successful transfer of findings to industry and adoption of DNA-based technologies by other producers
- Utilization of DNA data and information by feedlots and processors to add value

What the ultimate impacts are

Conditions

- Adoption of cost-effective DNA-based technologies by beef producers resulting in increased profitability
- Enhanced genetic progress on difficult to measure traits resulting in improved animal health, product quality and food safety.
- Integration of DNA-based technologies resulting in synergistic benefits for all sectors of the beef industry

Evaluation

Collect Data-Analysis and Interpretation-Report-Feedback-Deliver