Moving Forward with Genomics
Brown Bagger NBCEC

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Utilizing Genomic Information

- Training and Validation
- Change from Microsatellites to SNP
- Implementation
- Future

Training and Validation

- Nearly 1200 US Hereford bulls have 50K genotypes and these have been used to train and validate a Hereford Specific genomics panel.
- These bulls were done through various projects including US-MARC 2000 bull project, Weight-Trait Project, Genetic Abnormality research and American Hereford Association (AHA) genotyping of high accuracy bulls and young sire candidates.

American **HEREFORD** ASSOCIATION

THE EFFICIENCY EXPERTS

Training and Validation

AHA Trait	EPD Acc.	Correlation	New Acc.	Progeny
CE	.12	.40	.18	7.4
BW	.12	.45	.20	2.1
WW	.12	.32	.16	2.2
YW	.12	.32	.16	1.2
Milk	.12	.26	.14	2.8
MCE	.12	.18	.13	1.3
Fat	.12	.45	.20	3.1
REA	.12	.42	.18	3.1
MARB	.12	.33	.15	1.8

- June 2012 Saatchi, Garrick

How Good can it Be?

EPD Acc.	MBV Correlation	Trait Heritability	Enhanced EPD Acc.	Effective Progeny
.12	.10	.30	.12	.1
.12	.20	.30	.13	.5
.12	.30	.30	.15	1.2
.12	.40	.30	.18	2.3
.12	.50	.30	.22	4.1
.12	.60	.30	.27	6.9
.12	.70	.30	.33	11.8
.12	.80	.30	.43	21.9
.12	.90	.30	.58	52.6

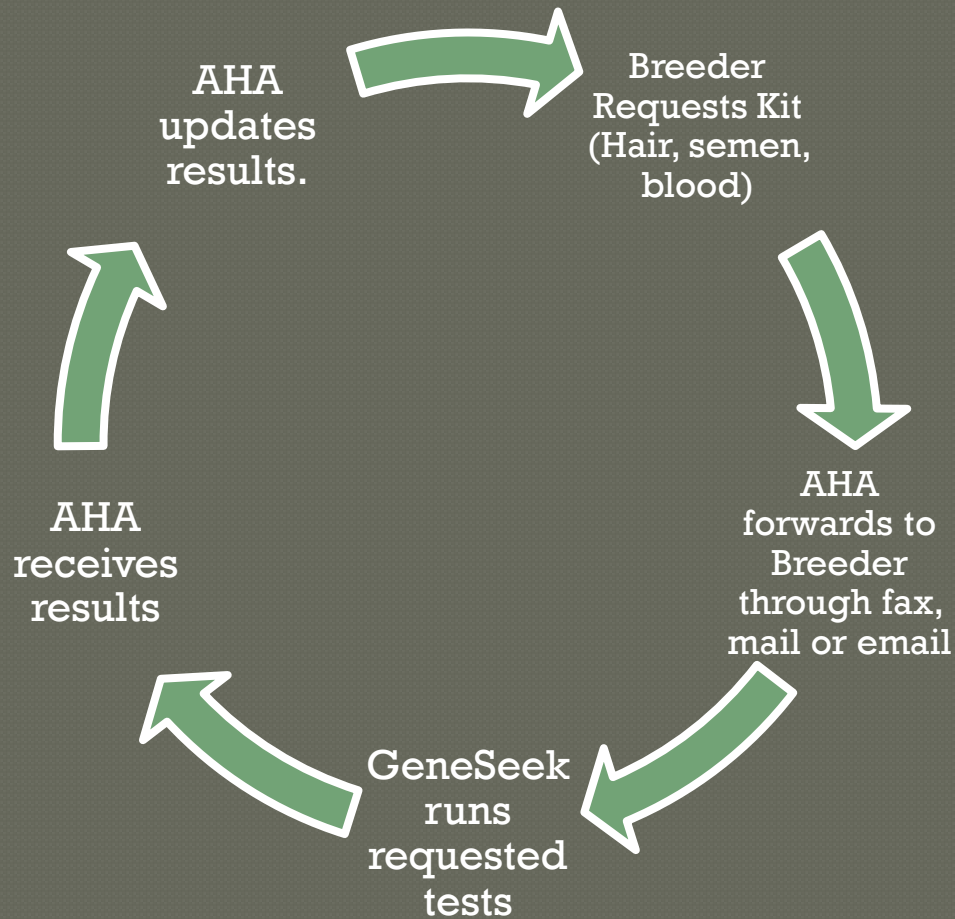# International Hereford Comparisons
(Pan American Evaluation)

Trait	US Prediction	Raw Corre. 99 UR Bulls	Raw Corre. 75 CA Bulls	Raw Corre. 59 Unrelated Arg Bulls	Raw Corre. 41 US Like Arg Bulls
BW	.43	.22	.40	.15	.24
WW	.32	.13	.07	-.35	.23
YW	.30	.03	.12	-.27	.32
Milk	.22	.23	.09	.15	-.03
Fat	.40	.22	.39	.02	.10
REA	.36	.01	-.01	-.11	.18
Marbling	.27	.25	.29	.17	.35

Next Step for the AHA

- Changed labs and technology from Maxxam Analytics to GeneSeek. The platform changed from Microsatellites to SNP's.
- There are four options to AHA membership
  -Parentage and abnormality testing-$30
  -H/P test- $48
  -50K Genotype for GE-EPD- $85
  -Parentage, Abnormality test, GE-EPD-$100

Implementation

Breeder Requests Kit (Hair, semen, blood)

AHA forwards to Breeder through fax, mail or email

GeneSeek runs requested tests

AHA receives results

AHA updates results.

Utilizing Genomic Information

- Produce only an EPD and using MBV as correlated trait.
- Only compliant Performance Breeders will get update GE-EPD
- Pedigree + MBV + Phenotype
- Currently, does not go up and down pedigree. Generated outside the genetic analysis
- Because the AHA has access to the Pedigree, Genotypes and Phenotypes, we can recalculate MBV's at anytime.

Breeder results sheet

Results for Case No. AHA43180206-03   Date Sent: 08/30/12   **Date Tested**

Parentage Request Type: Not Tested   Panel Type: SNP Panel   09/18/12

Name	Registration Number	Result
Sire: CL 1 DOMINO 862U	42897556	Not Tested
Dam: 4V MS H LG 8J DOMINO U33	42898189	Not Tested

COLOR DILUTOR   **IDIOPATHIC EPILEPSY**   **HYPOTRICHOSIS**

Not Tested   Not Tested   Not Tested

GE-EPD   09/18/12

Tested

	CE EPD Acc	BW EPD Acc	WW EPD Acc	YW EPD Acc	Milk EPD Acc	M&G EPD Acc	MCE EPD Acc	MCW EPD Acc	Scrotal EPD Acc	FAT EPD Acc	REA EPD Acc	MARB EPD Acc	BMI $	CEZ $	BII $	CHB $
AHA GE-EPD	4.5 .06	1.1 .39	38 .31	66 .32	21 .10	40	2.6 .05	64 .20	0.7 .27	-0.029 .23	0.23 .24	0.28 .20	21	19	18	25
EPDs Pre-GE Data:	4.5 .06	0.4 .38	41 .29	63 .31	20 .09	41	2.6 .05	63 .20	0.6 .26	-0.007 .20	0.24 .20	0.32 .18	21	19	18	26

How to identify Hereford animals with GE-EPD

- These animals are identified on the web at www.Hereford.org and under the EPD Search site. You can "Sort by" and find all animals with GE-EPD. Or if you do a search and on an animals detail screen under the EPD you will find ![AHA GE-EPD] logo which means the EPD are enhanced.

Future of Genomics at AHA

- Continue to Collaborate with Scientists, other countries and all research entities.
- Continue to build populations of **50K** genotypes. Additional 1000 sires by year end.
- Continue to collect phenotypes on Economically Relevant Traits (ERT's) that are hard to measure like Feed Intake and Fertility (Whole Herd Reporting) and Health.
- Begin to Sequence Legacy Sires. (8 bulls in 2012) and imputation

Summary

- Genomic predictions do work (US Dairy, poultry, swine industries and Angus, Hereford, Simmental, Red Angus)
- It is in its infancy
- Predictions work well within populations that are closely related.
- Phenotypes will still be important to the evolution of Genomics.
- It is exciting.