

INTEGRATING MOLECULAR DATA INTO NCE: EXPECTATIONS, BENEFITS, AND NEEDS

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Paradigm—Disjoined Information

EPD

- Sum of the additive effect of all genes that influence a given trait divided by two
- Genes are unknown
- Time delay in collecting phenotypes



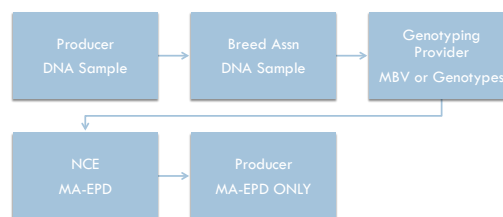
MBV (MVP, etc.)

- Sum of the additive effect of SNP alleles (multiplied by copy number) that influence a trait
- These are not genes, but associated with genetic variance
- Can be collected at birth (In Theory)

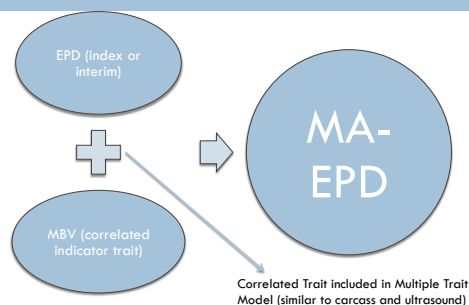
Two General Approaches

- Molecular information can be included in NCE in two ways:
- The first requires access to genotypes
 - ▣ Allows genomic relationships to be calculated
- The second is what AAA uses and the context we are currently in
 - ▣ Maybe not for long?

Flow of Information



Integrated Information



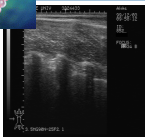
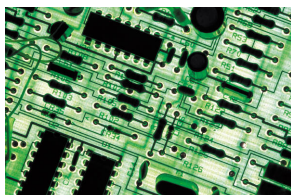
MENDELIAN SAMPLING

How many possible genetically different full sibs from a mating?

1,152,921,504,606,850,000

Every one has the same Pedigree Index EPD

Mendelian Sampling



Increased Accuracy-Benefits

- Mitigation of risk
- Faster genetic progress

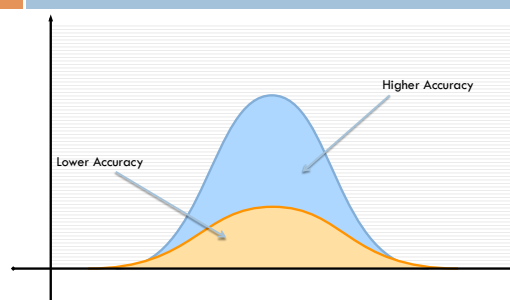
$$\Delta_{BV} / t = \frac{r_{BV,EBV} i \sigma_{BV}}{L}$$

- Increased accuracy does not mean higher or lower EPDs!
- Increased information can make EPDs go up or down

Example-CED

- Bull A Bull B
- +5 +5
- Add molecular scores as additional information
- Bull A Bull B
- -1 +11
- In this extreme case risk was 12% more calving difficulties
- Average is still +5*

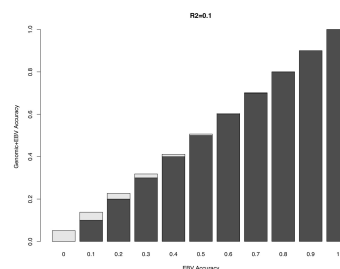
Distribution Change-Mitigating Risk



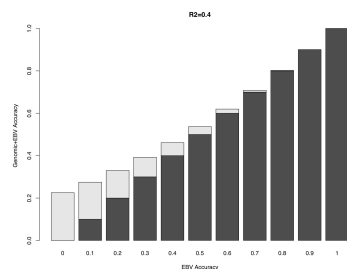
MBV BIF Accuracy

Genetic Correlation	% GV	BIF Accuracy
0.1	1	0.005
0.2	4	0.020
0.3	9	0.046
0.4	16	0.083
0.5	25	0.132
0.6	36	0.2
0.7	49	0.286

Impact on Accuracy--%GV=10%

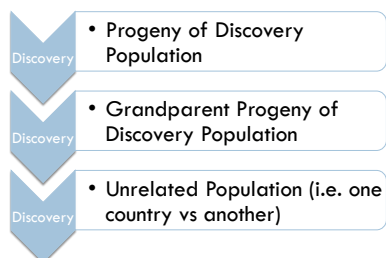


Impact on Accuracy--%GV=40%



Trait	PAG	AUS PAG
ADG	30	1-10
NFI	12	0
DMI	11	4-5
Tenderness	26	--
CED	22	6
BW	28	12-26
WW	32	12-19
CEM	40	4
Milk	27	10-14
CWT	29	6-13
FT	40	14-19
REA	29	10-20
MARB	34	4-11

Robustness Over Time



Issues to Address

Robustness

- Angus
- Charolais
- Bos indicus

“New Traits” in the Genomic Era

- Healthfulness of beef
- Disease susceptibility
- Tenderness
- Adaptation
- Feed Efficiency
- The list will continue to grow
- INFORMATION OVERLOAD!

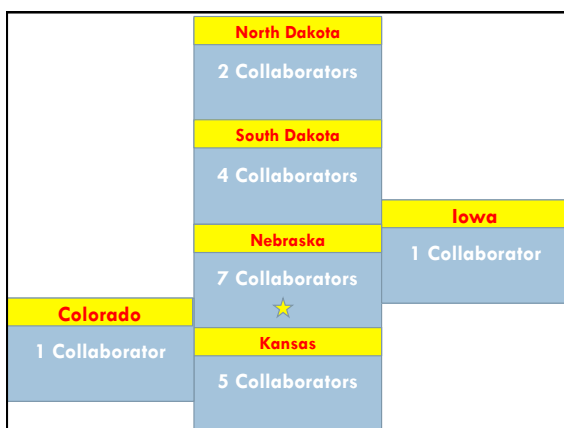
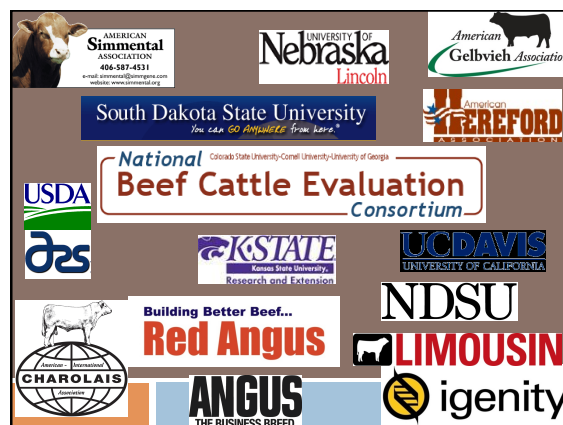
Which is More Profitable?

Bull	WW	YW	MARB	REA
1	21	53	0.62	0.08
2	33	73	0.63	-0.19

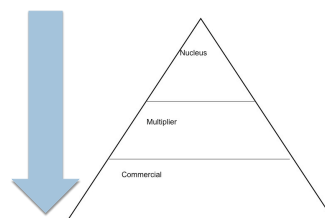
Depends...

- What is your breeding/marketing objective?
- How to weigh the differences?
- ICLs?
 - ▣ WW>20, YW>50, MARB>0.5, REA>0.05

BULL	WW	YW	MARB	REA	TI
1	21	53	0.62	0.08	70
2	33	73	0.63	-0.19	76



Technology Adoption



Simmental Example

Whitacre and Spangler (2011)

	10%	25%	50%	75%	100%
SS	3	9	29	102	3,466
SD	5	19	81	369	8,168
DS	5	22	100	419	7,179
DD	16	81	361	1,360	15,291

WTP panel

- Derived from USMARC 50K chip data
- Used an iterative method
 - ▣ Individual regions
 - ▣ Reduced to set of SNP that accounted for the most genetic variation (192 SNP from USMARC)

WTP-Panel

- 384 SNP for Weaning weight
- Training on MARC Cycle VII
 - 3,328 calves
 - 192 SNP discovered here
 - 192 from Igenity
 - After QC 255 (diagnostic=159)
 - Some of the most valuable SNP excluded

Breed Contribution to Training

Breed	Average Contribution
Angus	26
Hereford	19
Red Angus	6.5
Simmental	6.5
Charolais	6.5
Gelbvieh	6.5
Limousin	6.5

WTP-Population

- Seven major U.S. beef breeds
 - Angus, Hereford, Red Angus, Simmental, Limousin, Charolais, Gelbvieh
- Total of 3,500 2009 born bulls calves genotyped
- Over 19,000 DNA samples collected

Process

- Tail hair
- Samples genotyped at GeneSeek
- MBV calculated using US MARC derived predictions
- Herd data garnered from breed associations

Data

- 4-gen pedigree
- Adjusted weaning weights (148, 897)
- Pedigree index values

Analysis

- MBV fit as a correlated trait
- 2 and 3-trait animal model
- WW (direct and maternal component)
- MBV direct effect only
- CG-herd and sex

Missing Genotypes

- Average call rate-85.2%
- Range 11.3-100%

Results

Breed	WW h ²	MBV h ² (Before)	MBV h ² (After)	rg (Before)	rg (After)
Angus	0.23 (0.02)	0.87 (0.16)	0.75 (0.12)	0.00 (0.10)	0.15 (0.11)
Charolais	0.12 (0.03)	0.33 (0.16)	0.47 (0.18)	0.28 (0.15)	0.38 (0.16)
Gelbvieh	0.22 (0.02)	0.64 (0.18)	0.62 (0.16)	0.25 (0.13)	0.26 (0.14)
Hereford	0.14 (0.04)	0.83 (0.15)	0.96 (0.14)	0.20 (0.20)	0.25 (0.21)
Limousin	0.27 (0.02)	0.60 (0.19)		0.24 (0.12)	
Red Angus	0.24 (0.03)	0.67 (0.16)	0.89 (0.14)	0.10 (0.10)	0.14 (0.11)
Simmental	0.75 (0.03)	0.61 (0.16)	0.73 (0.16)	-0.05 (0.08)	-0.03 (0.09)

Outreach Meeting

Day 1

- Open Extension
- Use of Marker Information
- Results from previous grant activity

Day 2

- Producer collaborators
- Review of previous year results
- Plans for coming year
- WTP focus in 2011

Educational Benefits

Survey-Fall of 2010 (85% response rate)

Knowledge Gained (1-4)	
EPD	1.5
Parentage verification	2.0
MAS	3.4
Across Breed Predictions	2.7
Validation	2.8
Accuracy Improvement	2.9
Genomic Terminology	2.8
Behavior Change (1-5)	
Making informed decisions	3.9
Educating Clientele	3.8
Comfort with terminology	4.3
Quest for continued education	4.6

Team

- Mark Thallman
- Garry Bennett
- Larry Kuehn
- Warren Snelling
- Steve Kachman
- Kathy Hanford
- John Pollak

Looking Forward

FE

- Progeny test of producer owned bulls
- Develops a validation population
- Relationship of female reproduction and male FE

GxE

- Fescue environments

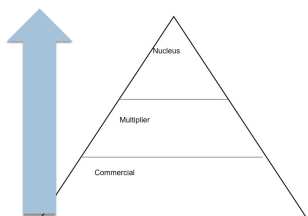
Good News

- Education has occurred, and documented
- Capstone of extension
- Vast resource population built, and growing
 - ▣ Leveraged into larger projects

Summary

- Genomic information has the potential to increase accuracy
 - ▣ Proportional to %GV
 - ▣ Impacts inversely related to EPD accuracy
- Multiple trait selection is critical and could become more cumbersome
 - ▣ Economic indexes help alleviate this
 - ▣ Use index values that meet your breeding objective

Market Signal



Action Points

- Collect phenotypes and DNA samples
- Maintain Flexibility—Have genotypes
- Across Breed Predictions
- Knowledge of GxE
- Inclusion of input traits
 - ▣ Genomics will be used as an indicator
- Focus on EPD
 - ▣ Not components even molecular scores
- Index Selection
- Reduced Rank Models
- Genotyping strategy
 - ▣ Resources used effectively

Checks for Reasonableness



Environmental Changes

