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## Vision of New Selection Tools, DNA into Performance




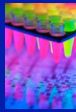
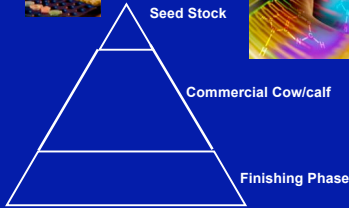
Mark Allan, PhD  
Beef Cattle Geneticist  
ARS, U.S. Meat Animal Research Center  
Clay Center, NE






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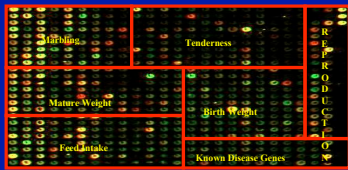

## Young and Changing Technology








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## Over Sold?


- Through the years
  - yes
  - WHY
    - Genome is highly complex
    - Difficult to understand, manipulate
    - Historically, oversold to producers
- Need patience, research support, partnerships, education





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## Information Recorded on Individual Animal

- Family pedigree
- Birth date
- Birth weight
- Individual calving difficulty score
- Weaning weight
- Yearling weight
- Ultrasound - yearling
- Hip height
- Mature wt body condition scores
- Udder and teat - Ames
- Breeding records
- Carcass data
- Scrotal
- Docility









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## Traditional Selection Works Well

**Selection Practices**


- Visual
- Performance Data \*\*\*
- EPDs\*\*\*\*
- Pedigree
- DNA Marker Information
- Modelling
- Economic Indexes

Production										Maternal				
CEM	BW	WW	YW	YH	SC	CEM	Mk	MkH	MV	MV	Mk	SEN		
Acc	Acc	Acc	Acc	Acc	Acc	Acc	Acc	Acc	Acc	Acc	Acc	Acc		
+11	+1.8	+48	+12	-5	-76	44	+13	2					+18.31	
85	85	85	78	53	66	22	48	5						

Carcass					Ultrasound				
Dwt	Mb	RE	Fat	Grp	SRF	RE	Fat	Grp	Prog
Acc	Acc	Acc	Acc	Prog	Acc	Acc	Acc	Acc	Prog
+1	+0.99	+29	-0.09	1	-0.55	+0.9	+0.23	34	
10	11	10	09	1	74	75	75	117	

Values				
BE	EE	SG	BYG	SE
+27.94	+22.58	+4.25	+3.19	+2.02
				+26.07




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## Selection Index

**\$VALUE INDEXES**

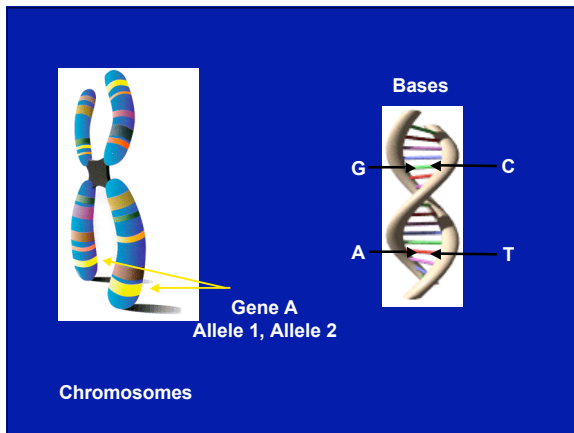
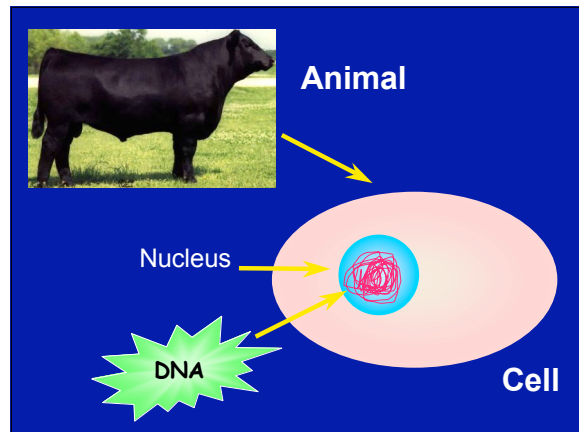
- Weaned Calf Value (\$W)
- Grid Value (\$G)
- Quality Grade (\$QG)
- Yield Grade (\$YG)
- Beef Value (\$B)

Different indexes for different phases of production!

### How Do We Collect DNA?

- Blood
- Hair Roots
- Saliva
- Skin
- Semen
- Fecal Samples
- Other Tissues

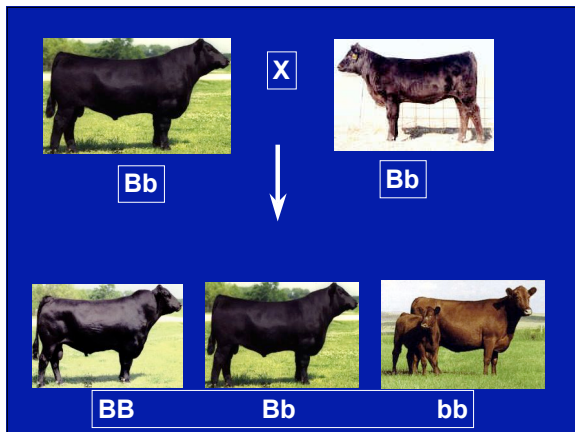


### Coat Color Testing

Gene tested homozygous black

Black Dominant BB

Red Recessive bb



### Using DNA Technology

- Increase the accuracy of selection
- Hard (expensive) traits to measure
- Sex-limited traits
- Lowly heritable traits
- Speed selection decisions

**Selection Practices**

- Visual
- Performance Data \*\*\*
- EPDs\*\*\*\* NCE
- Pedigree
- DNA Marker Information**
- Modeling
- Economic Indexes

### Marker-Assisted Selection (MAS)

- Inherited Diseases
- Coat Color
- Embryo Sexing
- Horned/Polled
- Quantitative Traits
- Feed Efficiency, Growth, Reproduction, Carcass Traits

### Marker-Assisted Management (MAM)

### Carcass Traits – Minor Success

Traits*	QTL <sup>b</sup>	Chromosomes <sup>c</sup>
TEND	8	2 4 5 7 8 9 10 11 15 18 19 20 29
MAR	24	2 3 4 5 6 7 8 9 10 12 13 14 16 17 18 20 21 23 26 27 29
PCHOICE	7	1 2 5 11 14 19 26
FATD	24	1 2 3 5 6 7 8 14 16 19 21 23
BFAT EBV	12	5 6 14 19 21 23
AFAT	2	1 19
EEFAT	1	19
FATTYD	3	1 18 26
RIBFAT	5	5 13 18 26
KPH	7	2 3 11 15 16 17
FA*	5	19
LMA	7	2 4 6 12 14 26
REA	6	2 12 14 19 21
RIBB	1	5
SWT	10	1 2 3 12 14 16 17 24
RPYD	13	1 2 3 5 9 12 13 18 19 26 29
CW	27	1 2 4 5 6 7 10 12 13 14 16 18 22 23 24 29
DP	8	1 5 10 13 16 24 29
YG	10	1 2 5 11 12 14 16 19 21 26

### CAPN1 Story – Small Success

- QTL found on BTA29 for shear force in the Piedmontese/Angus sired population
- CAPN1 mapped to region

### Parentage Verification

**Animal Identification Youth Livestock Shows**

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**Tracing Products**

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**Marker-Assisted Selection (MAS)**

- At the seed stock/multiplier level

**Marker-Assisted Management (MAM)**

- At the commercial level

The pyramid is divided into three horizontal sections:

- Top section: Seed Stock MAS
- Middle section: Commercial Cow/calf MAM & MAS
- Bottom section: Finishing Phase MAM

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**Tools for Selection**

- Growth
- Feed efficiency
- Carcass composition - quality
- Reproduction
- Disease susceptibility
- Production traits (udder and teat scores)

Will markers replace "traditional" selection?

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**Sequencing the Bovine Genome**

**PHASE 1 - \$53 million**

- NHGRI - \$25 million
- New Zealand - \$1 million
- Texas - \$5 to 10 million
- National Cattlemen's Beef Association, Texas and South Dakota cattle producers - \$820,000

Hereford Cow from Miles City

Baylor College of Medicine-Human Genome Sequencing Center

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**SNP Genotyping**

**SNP- Single Nucleotide Polymorphism**

- Occur much more frequently throughout the genome
- 2 alleles possible

ATGCAATTGCACGTTGCAAT  
 ATGCAATTGCTACGTTGCAAT  
 ATGCAATTGCC/TACGTTGCAAT

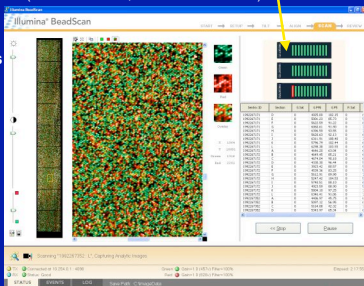
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**USDA** **Q2S**

### Illumina Infinium Bovine BeadChip

- ~ 54,008 SNP markers across the bovine genome
- On average SNP every <67,000 base pair
- Discovery SNP includes many breeds

(Van Tassell et al., 2008 Nature Methods)



BARC  
USMARC  
University of Missouri  
University of Alberta

### WGS – Whole-Genome Selection

- “There is no doubt that whole genome-enabled selection has the potential for being the most revolutionary technology since artificial insemination and performance-based index selection to change the nature of livestock improvement in the foreseeable future”

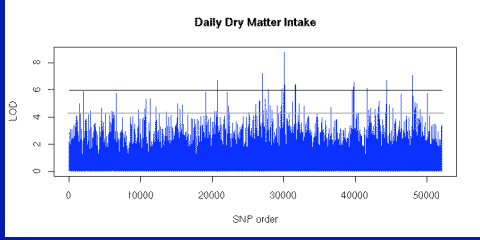
*Dorrian Garrick, Iowa State University*

### WGS?

- Using a large panel of markers to estimate genetic merit (MBV) marker breeding value.
- Using the marker information from across the whole-genome to estimate the sum of effects.
- How - Uses foundation information for the estimation process derived from training data sets (Equations).
- Animals are genotyped that may or may not have phenotypic information and genetic merit is estimated.

**USDA** **Q2S**


### WGA vs. WGS



**USDA** **Q2S**


### Release the Data- Breed Association

- The results of the DNA tests will be critical in the National Sire Evaluations in the future.
- To estimate genetic effects for a trait, all the data needs to be used (“good and bad alleles”).
- Selective reporting is a long-term disadvantage.

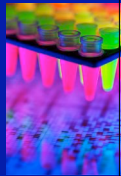


**USDA** **Q2S**

### Players Changing



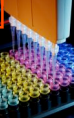



- Genetic Visions (WI)
- Infigen (WI)
- Celera AgGen (California, Maryland)
- Frontier Beef Systems
- Genaisance
- Genmark
- Pyxis
- ImmGen
- Geneseek
- Viagen
- Identigen
- Pfizer (Bovigen- Catapult)
- Igenity
- SCR
- MMI
- Genmark
- Maxxam
- Genetic Solutions





**Using DNA in Selection Programs**

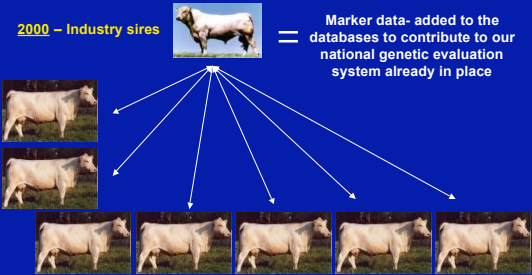
- Just because the animal is not carrying the favorable allele for a specific test does not mean the animal is not genetically superior for the trait.
- Increase the accuracy of EPDs
- Hard (expensive) traits to measure
- Sex-limited traits
- Lowly heritable traits
- Speed selection decisions
- Merchandising genetics

**Implementation to the Industry**

2000 – Industry sires


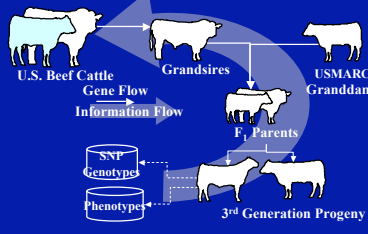
Marker data- added to the databases to contribute to our national genetic evaluation system already in place



Feed efficiency EBV through WGS

Additional tool to be used in making genetic progress


**Future Genetic Improvement of Beef Cattle?**

Accurate Multi-trait Selection

**Present/Future**

- Will DNA testing play a role in the future of beef cattle- **yes**  
Parental ID, Quantitative tests (panels), Simple genetic inheritance, WGS
- Will implementation be tough- Maybe; **Yes** (implementation of EPDs 80s, acceptance of crossbreeding programs, ultrasound)
- Collect tissues for DNA analysis  
Populations with phenotypes
- Breed Association responsibilities  
database, education
- Build database structure and become proactive in the implementation of the new technology




Marbling	Known Disease
Mature Wt	B Wt
Feed Intake	Y Wt
Udder/teat	Tenderness
Feet/legs	

But... another valuable tool for the breeder's tool box

**Vision**

- Larger panels of markers that explain greater portions of the genetic variation for traits. **MAS MAM**
- WGS - ?  
Example - BW EPD 1.2 acc .75 on yearling bull  
- Validation, implementation
- Change in costs?  
- Technology driven



Questions

