Slide 1

Genetic Technology in Beef Cattle

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Slide 2

Selection

Phenotype/pedigree

Since (or before) domestication

Statistical Predictions

Really 40ish years ago
Think EPD and indices
Utilizes pedigree and phenotype

Genomic-enabled predictions

~ 10 years ago
Utilizes framework for EPD

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Fundamentals

- P=G+E
- Phenotype = Mean + BV + Environment

- 600= 550 + 10 +40
- 600=550 + (-5) + 55

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Progeny Inform Us About Parents

+30 lb

+15 lb

-10 lb

+ 5 lb

+10 lb

Sire

(EPD is "shrunk")

Sire EPD +8 lb ← Progeny +10 lb

Slide Adapted from Garrick

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Phenotypes
(n=Millions)

Pedigree
(n=Millions)

Genotypes
(n=10K-450K individuals with 10K-250K genotypes

Genetic Prediction

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Breeding Value Estimation

- Progeny receive half of their genetic material from each parent (PA)

$$BV = \frac{1}{2}BV_{(sire)} + \frac{1}{2}BV_{(dam)} + \Phi$$

- Estimated Breeding Value (EBV)=genetic merit of an individual; EPD=genetic merit of an individual as a parent (1/2 EBV)
- Φ=Mendelian sampling term
- Genomic data
  - Account for part of the Mendelian sampling term

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Relationships

- Pedigree information was the primary method to incorporate relationship information into genetic prediction and is still the backbone.
  - Usually deep
  - Prone to errors
    - ~10%
- Genomic data now augments pedigree, allowing for deviations from expected degrees of relationships
  - Cleans up pedigree errors

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Pedigree Relatedness

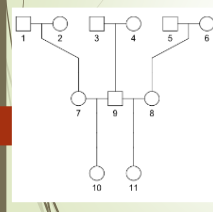- The **expected** (averaged across loci) relationship between individuals.

	1	2	3	4	5	6	7	8	9	10	11
1	1	0	0	0	0	0	0.5	0	0	0.25	0
2		1	0	0	0	0	0.5	0	0	0.25	0
3			1	0	0	0	0	0	0.5	0.25	0.25
4				1	0	0	0	0	0.5	0.25	0.25
5					1	0	0	0.5	0	0	0.25
6						1	0	0.5	0	0	0.25
7							1	0	0	0.5	0
8								1	0	0	0.5
9									1	0.5	0.5
10										1	0.25
11											1

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Genomic Relatedness

- The **realized** (averaged across loci) relationship between individuals.

	1	2	3	4	5	6	7	8	9	10	11
1	0.99	0.01	0.01	-0.13	0.12	-0.04	0.49	0.01	-0.09	0.2	-0.04
2		0.81	0.00	-0.18	0.09	0.08	0.41	0.1	-0.03	0.11	0.06
3			0.8	0.16	-0.03	-0.01	-0.09	-0.06	0.46	0.14	0.24
4				1.03	-0.09	0.13	-0.12	0.05	0.57	0.25	0.27
5					0.95	-0.04	0.09	0.5	-0.1	-0.05	0.41
6						0.85	0.00	0.43	0.11	0.16	0.09
7							0.95	0.09	-0.08	0.44	0.04
8								1.11	0.06	0.13	0.58
9									1.04	0.52	0.51
10										0.99	0.23
11											1.03

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Grandparent Relationships
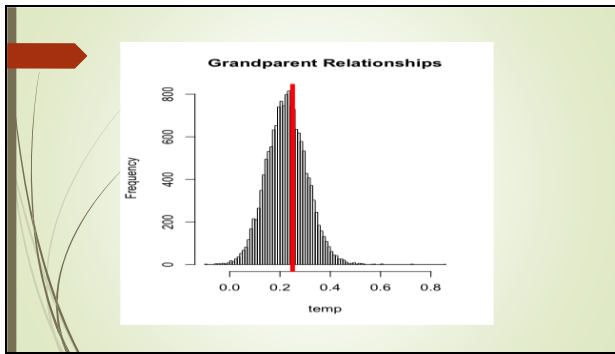
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Methods Used to Incorporate Genomic Information into EPD

- In all cases shown to be more accurate compared to historical methods
- AGI and American Breeds (via John Genho)
  - ssGBLUP via UGA software
  - Uses approximately 50,000 markers to infer relationships
  - Blend pedigree and genomic relationships
- AHA and IGS
  - sHybrid via BOLT software (Theta Solutions)
  - Identifies subset of markers that are actually used

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Progeny Equivalents

TRAIT	AAA	AHA	IGS
CED	28	17	25+
BWT	21	8	22
WWT	26	12	25+
YWT	21	9	25+
MCE	18	4	4
Milk	33	15	19
STAY	No EPD	----	15
Marbling	9	3	8

Accuracy, h^2 and Progeny Counts

Approximate number of progeny needed to reach accuracy levels (true (r) and the BIF standard) for three heritabilities (h^2)

Accuracy		Heritability Levels		
r	BIF	h^2 (0.1)	h^2 (0.3)	h^2 (0.5)
0.1	0.01	1	1	1
0.2	0.02	2	1	1
0.3	0.05	4	2	1
0.4	0.08	8	3	2
0.5	0.13	13	5	3
0.6	0.2	22	7	4
0.7	0.29	38	12	7
0.8	0.4	70	22	13
0.9	0.56	167	53	30
0.999	0.99	3800	1225	700

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 EPD!
  - Increased information can make EPDs go up or down

Purchase bulls with GE-EPD

- Genetic change is driven by sire selection in commercial herds
  - ~80% is due to the bulls used the last 4 years in self replacing herds,

- Increased accuracy enables more informed bull selection decisions.
  - Think possible change.

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Possible change example

CED EPD = 9.0
ACC. = 0.20

- Possible change +/- 6.2
- 68% confident his true EPD is between 2.8 and 15.2

- What if ACC increases to 0.4?
- 68% confident his true EPD is between 4.3 and 13.7

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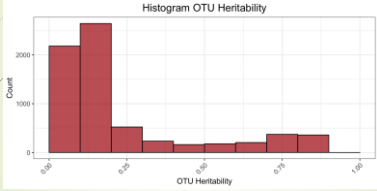
Use genotypes to the fullest

- Improvement in accuracy of EPD
- Parentage determination
- Tracking inbreeding
- Identification and management of lethal and sub-lethal haplotypes
- Breed identification
- Estimating retained heterozygosity (heterosis)
- New trait development
- Identification of putative causal variants from sequence

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Heritability Across OTUs

Histogram OTU Heritability

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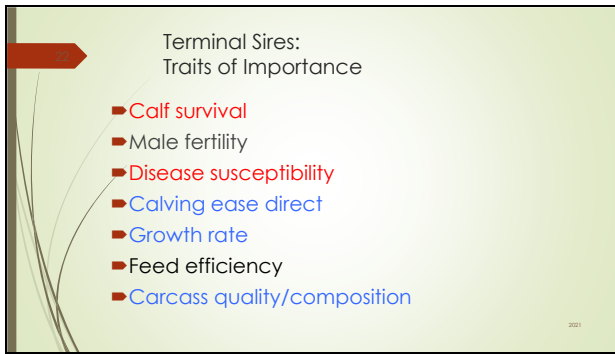
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Slide 21
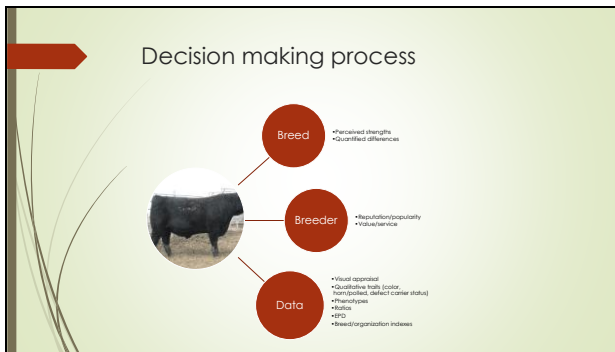
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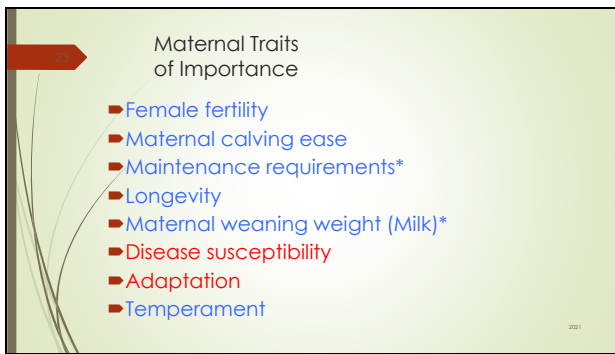
Terminal Sires:
Traits of Importance

- Calf survival
- Male fertility
- Disease susceptibility
- Calving ease direct
- Growth rate
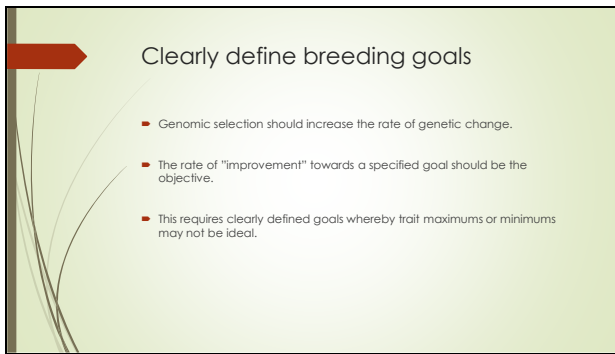- Feed efficiency
- Carcass quality/composition

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Maternal Traits
of Importance

- Female fertility
- Maternal calving ease
- Maintenance requirements*
- Longevity
- Maternal weaning weight (Milk)*
- Disease susceptibility
- Adaptation
- Temperament

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Clearly define breeding goals

- Genomic selection should increase the rate of genetic change.
- The rate of "improvement" towards a specified goal should be the objective.
- This requires clearly defined goals whereby trait maximums or minimums may not be ideal.

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Independent Culling Levels

CED = 20 WW = 60 STAY = 15 MARB = 0.50

	CED	WW	STAY	Marb	Index
1	22	62	18	0.8	20.50
2	21	60	16	0.5	20.55
3	20	60	15	0.6	19.35
4	18	70	20	1.0	21.64

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Use selection indices

- As the list of EPD grows, multiple-trait selection becomes more complex.

- Use indices that best fit your breeding objective
  - Do you retain replacement heifers?
  - What is the sale point of your animals?

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Selection index in a nutshell

- Tool to enable informed multiple-trait selection
- Based on:
  - Breeding objectives
  - Economic parameters
  - Relationships among traits
  - Population (herd) means
- Designed to improve commercial level profitability
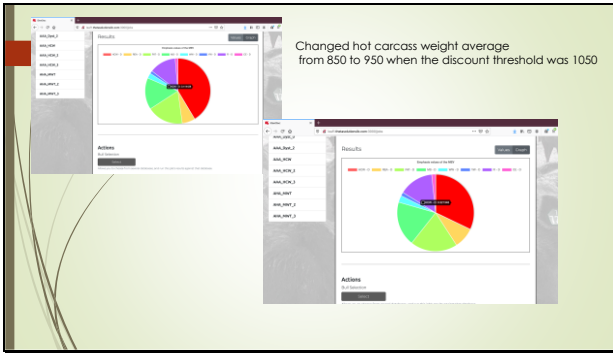- New (~ 10 years) to the beef industry but "old hat" to other industries

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User Interface

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Breeding Objective

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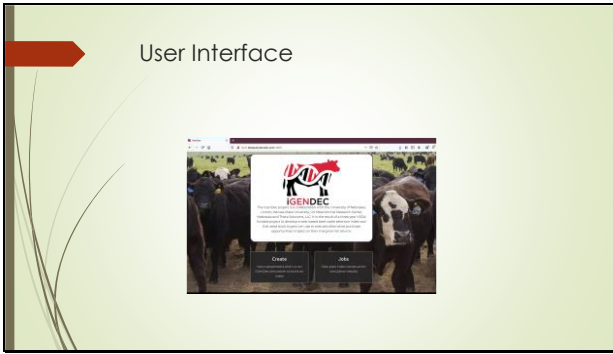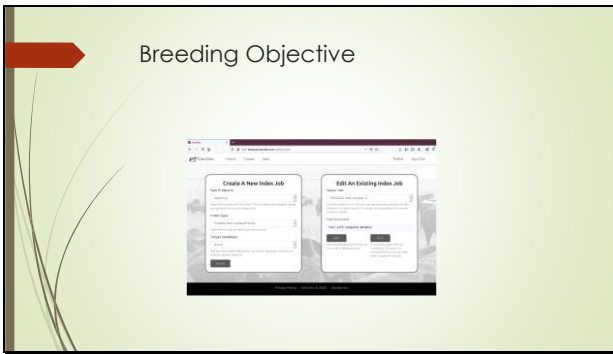
Changed hot carcass weight average
from 850 to 950 when the discount threshold was 1050
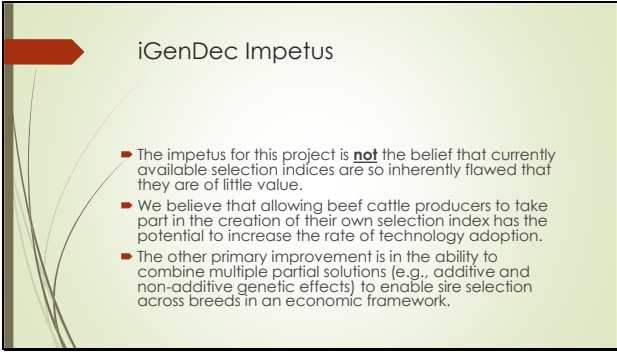
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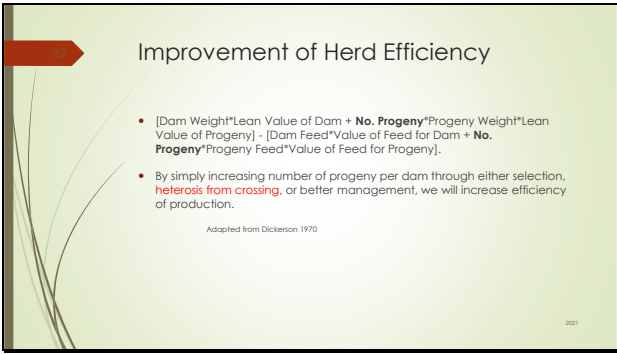_____

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iGenDec Impetus

- The impetus for this project is **not** the belief that currently available selection indices are so inherently flawed that they are of little value.
- We believe that allowing beef cattle producers to take part in the creation of their own selection index has the potential to increase the rate of technology adoption.
- The other primary improvement is in the ability to combine multiple partial solutions (e.g., additive and non-additive genetic effects) to enable sire selection across breeds in an economic framework.

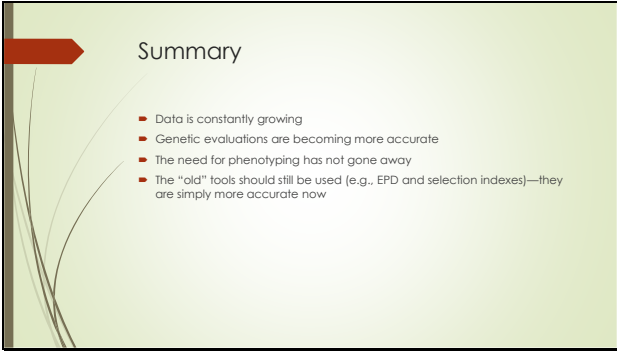**Slide 32**

Improvement of Herd Efficiency

- [Dam Weight*Lean Value of Dam + **No. Progeny***Progeny Weight*Lean Value of Progeny] - [Dam Feed*Value of Feed for Dam + **No. Progeny***Progeny Feed*Value of Feed for Progeny].
- By simply increasing number of progeny per dam through either selection, heterosis from crossing, or better management, we will increase efficiency of production.
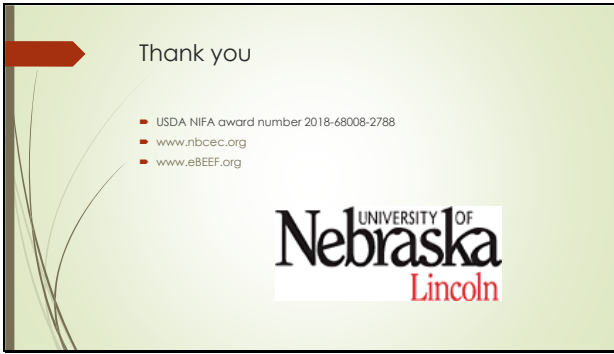
Adapted from Dickerson 1970

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Summary

- Data is constantly growing
- Genetic evaluations are becoming more accurate
- The need for phenotyping has not gone away
- The "old" tools should still be used (e.g., EPD and selection indexes)—they are simply more accurate now

Thank you

- USDA NIFA award number 2018-68008-2788
- www.nbcec.org
- www.eBEEF.org

UNIVERSITY OF Nebraska Lincoln

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