GENOMICS?
WHY?

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DEFINED

Genomics: a branch of biotechnology concerned with applying the techniques of genetics and molecular biology to the genetic mapping and DNA sequencing of sets of genes or the complete genomes of selected organisms using high-speed methods, with organizing the results in databases, and with applications of the data (as in medicine or biology).

GLOSSARY OF TERMS

- **Genome:** the genetic material of an organism.
- **Chromosome:** organized compaction of DNA in nucleus of cell that contains genes; occur in homologous pairs in cattle.
- **Gene:** a specific sequence of nucleotides that is the functional unit of inheritance controlling the transmission and expression of one or more traits by specifying the structure of a protein or controlling the function of other genetic material.
- **Locus:** location within the genome
- **Allele:** any of the alternate forms of a gene/SNP/DNA variant
- **Nucleotide:** basic structural units of DNA (A, C, G,T)
- **SNP:** single nucleotide polymorphism

A QUESTION OF RESOLUTION

- Think of Bovine Genome as distance from Washington DC to Anchorage, AK ~3,300 miles

- 3K panel is equivalent to marker every mile

- 50K panel is marker every 100 yards

- 700K panel is marker every 22 feet

- Cattle genome: 3Gb, 22K genes, 14K conserved mammalian species

3,300 mi.

Slide provided by Bob Weaber
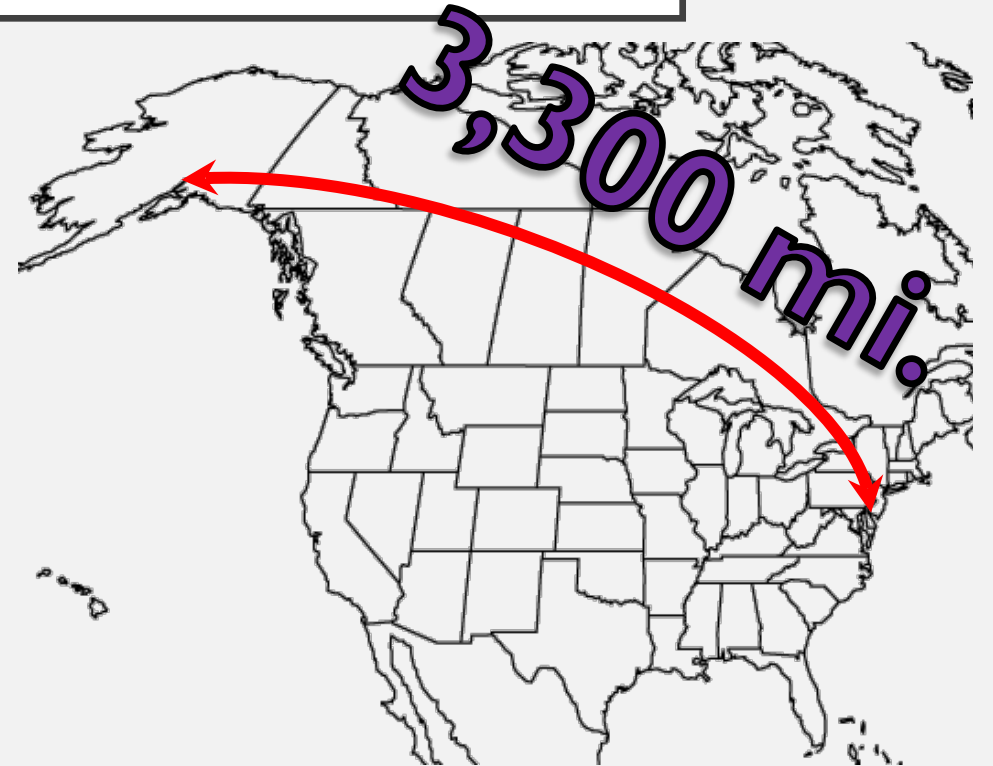
SOURCES OF DATA

- Records from relatives
- Records from an individual
- Genomic data
- Records from descendants

NOT ALL DATA ARE EQUALLY INFORMATIVE

- Data are weighted proportional to their contribution to determining an animal's cumulative genetic worth for a given trait.
  - Heritability
  - Kinship
  - Genetic (co) variation among animals via genomic markers
  - Genetic correlations among traits
  - Confidence in the observation
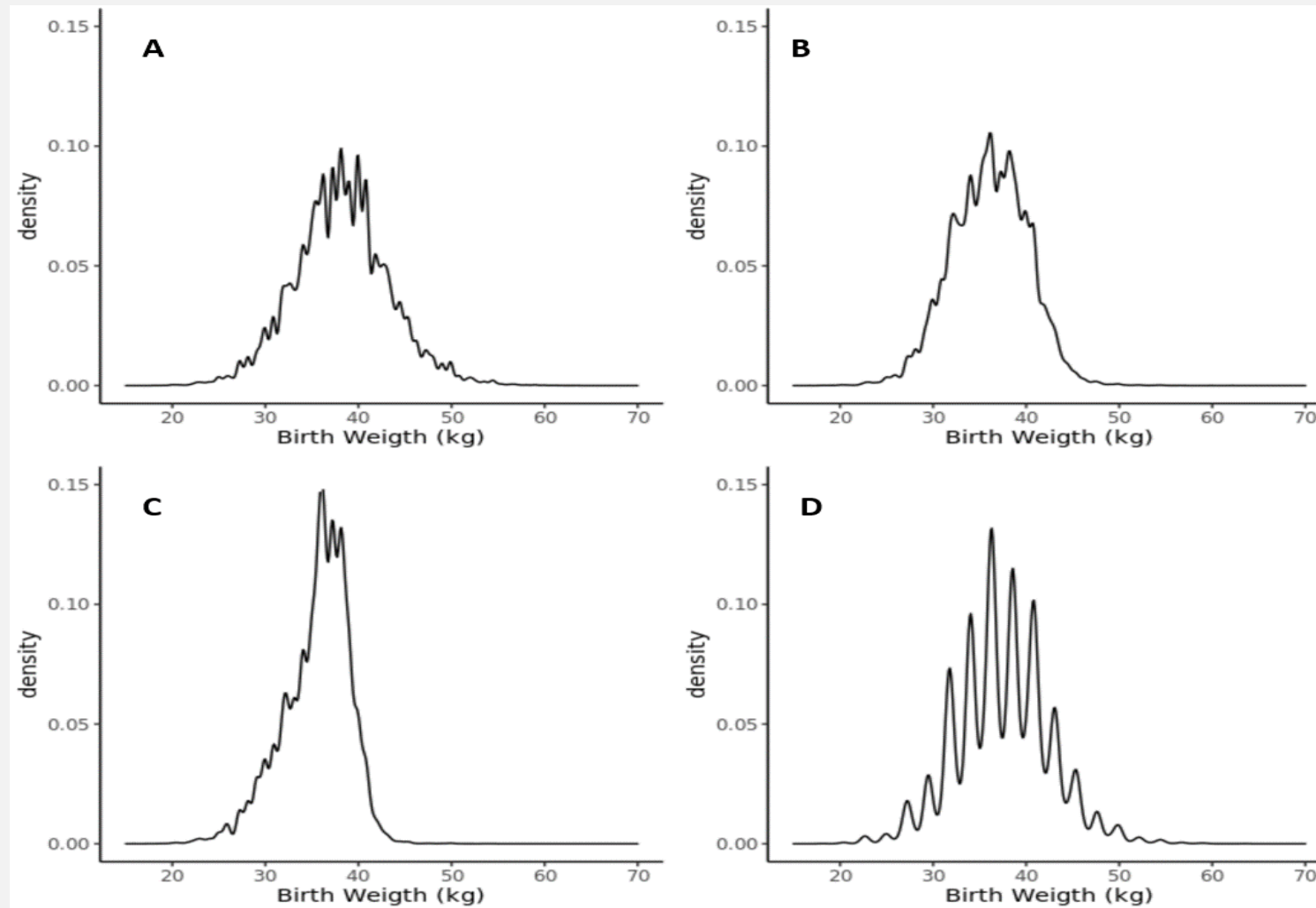
Birth weight distributions for animals in contemporary groups classified as Real (**A**), Tape (**B**), Fabricated (**C**) and Dirty (**D**).

KINSHIP

- Generally thought of as pedigree

- Critical for prediction of genetic merit

- Flow of information among relatives

- Allows EPD for:

  - Parents from progeny records

  - Sex-limited traits

IMPACT OF SIRE MISIDENTIFICATION

- Sire misidentification has been a substantial issue in some populations
  - 7.6% to 10.0% in sheep (Berry et al., 2016)
  - 10.00% to 13.28% in cattle (Vissher et al., 2002; Purfield et al., 2016; Řehout et al., 2006)
  - 8.4% to 14.6% in goats (Bolormaa et al., 2008).
- Breaks true kinship ties and creates false ones
  - Decrease in heritability estimates
  - Incorrect assignment of phenotypic information to relatives
    - Incorrect selection decisions
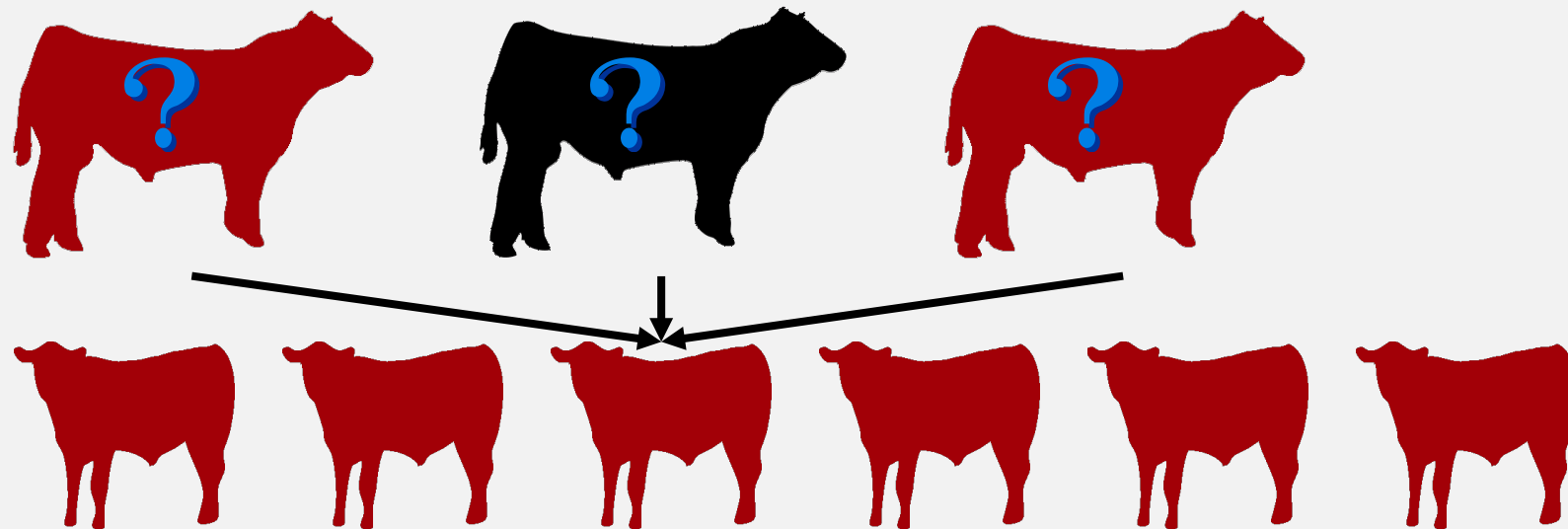   - Problem is most severe if (heavily used) bulls have incorrect pedigree

VALIDATION VS. TESTING (DISCOVERY)

- ## Validation
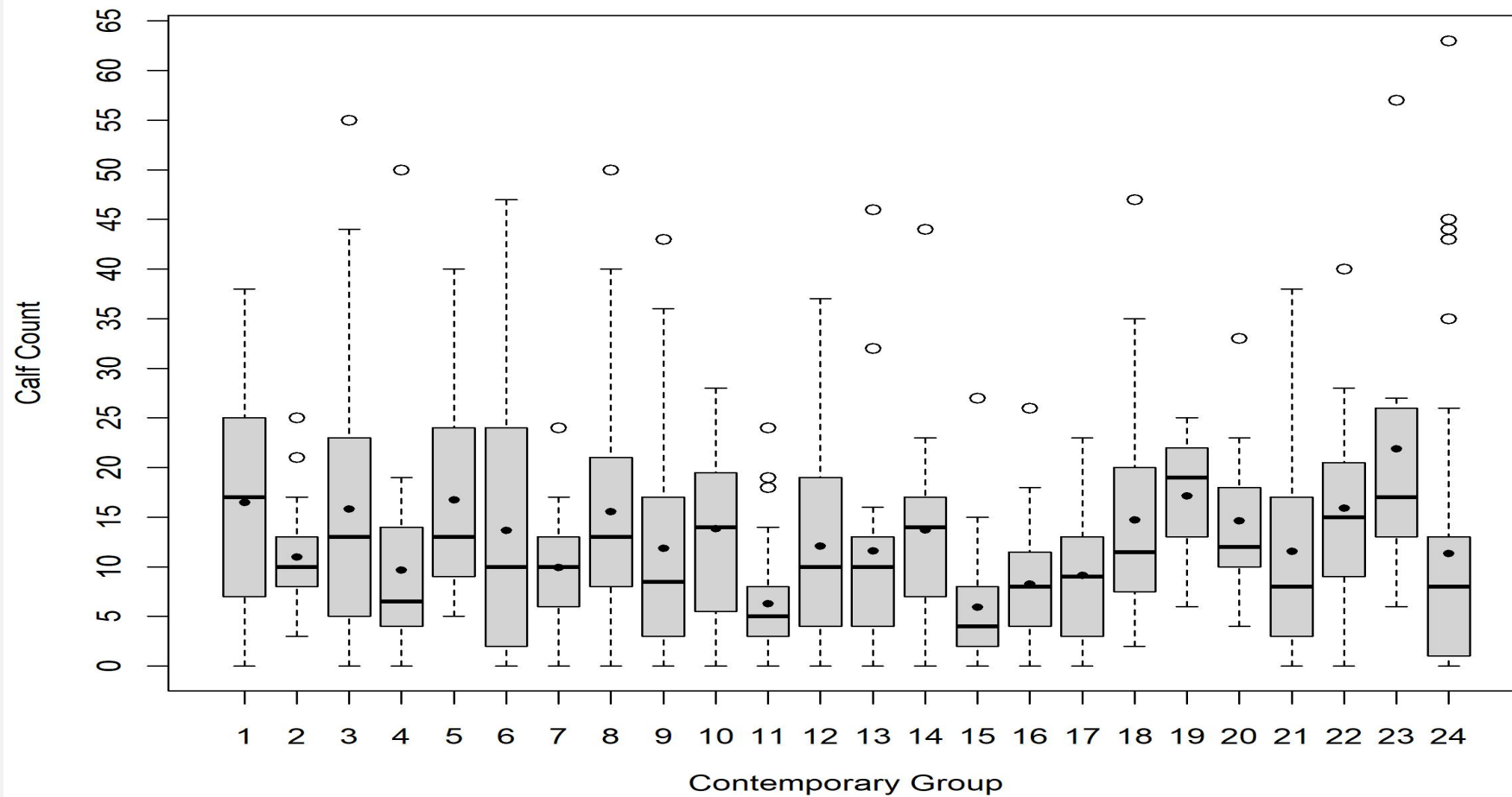 - Given progeny, do sire and dam qualify as parents (non-exclusion)
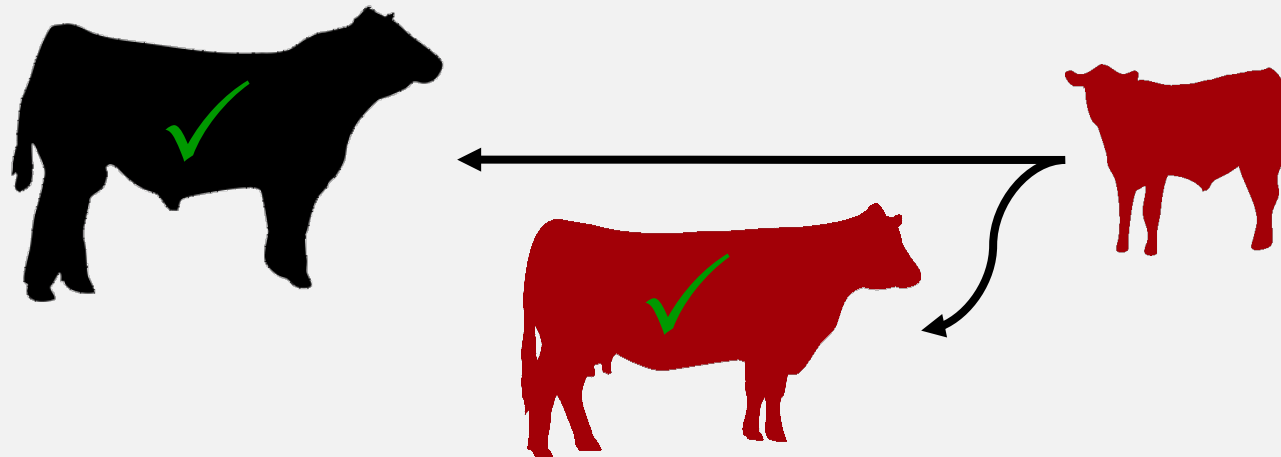
VALIDATION VS. TESTING (DISCOVERY)

- ## Testing/Discovery
  - Assignment of paternity (or maternity)
  - One or both alleged parents unknown

VARIATION IN CALVES PER SIRE
$h^2 \sim 18\%$

PRINCIPLE OF EXCLUSION

Possible Sires:

Bull A: AA BB   Bull B: Aa bb   Bull C: aa bb

??   ??   ??

Progeny Genotype: AA bb

PRINCIPLE OF EXCLUSION
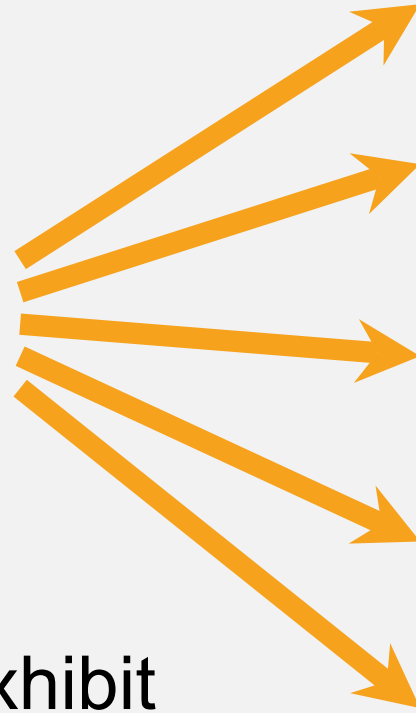
Possible Sires:
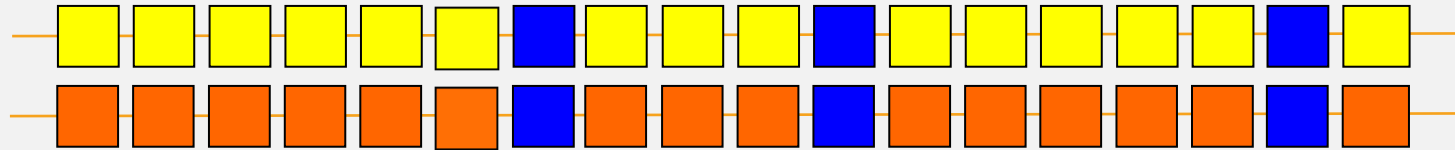
Bull B: Aa bb

Progeny Genotype: AA bb

PERFORMANCE OF THE PROGENY

Sire

+30 lb

+15 lb

-10 lb

+ 5 lb

+10 lb

Progeny +10 lb

Offspring of one sire exhibit more than ¾ diversity of the entire population

CHROMOSOMES ARE A SEQUENCE OF BASE PAIRS

Cattle usually have 30 pairs of chromosomes (29 autosomes and 1 sex)
Half of the pair from sire and half of the pair from dam
Each chromosome has about 100 million base pairs (A, G, T or C)
~ 3 billion base pairs per animal

Blue base pairs represent genes

Yellow represents the strand inherited from the sire

Orange represents the strand inherited from the dam

CONSIDER 3 ANIMALS
(THINK ACCURACY VERSUS PRECISION)
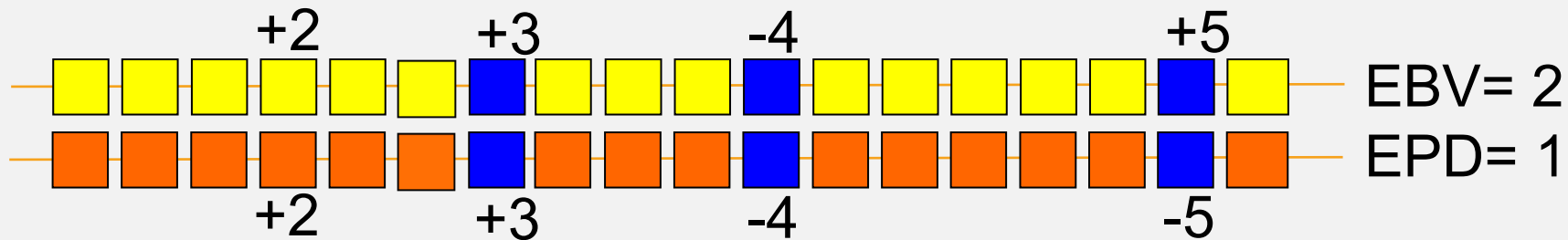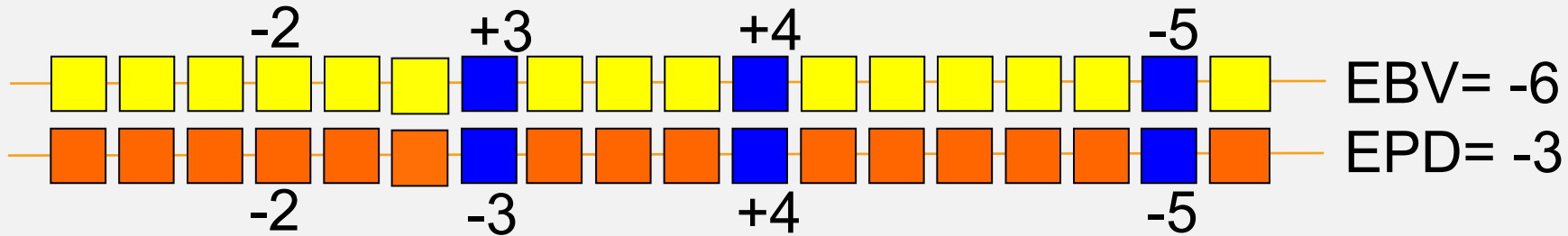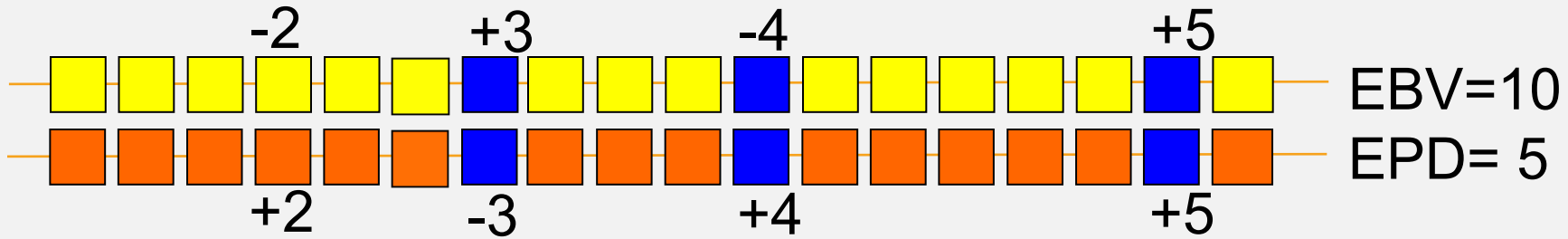
Below-average bulls will have some above-average alleles and vice versa!

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
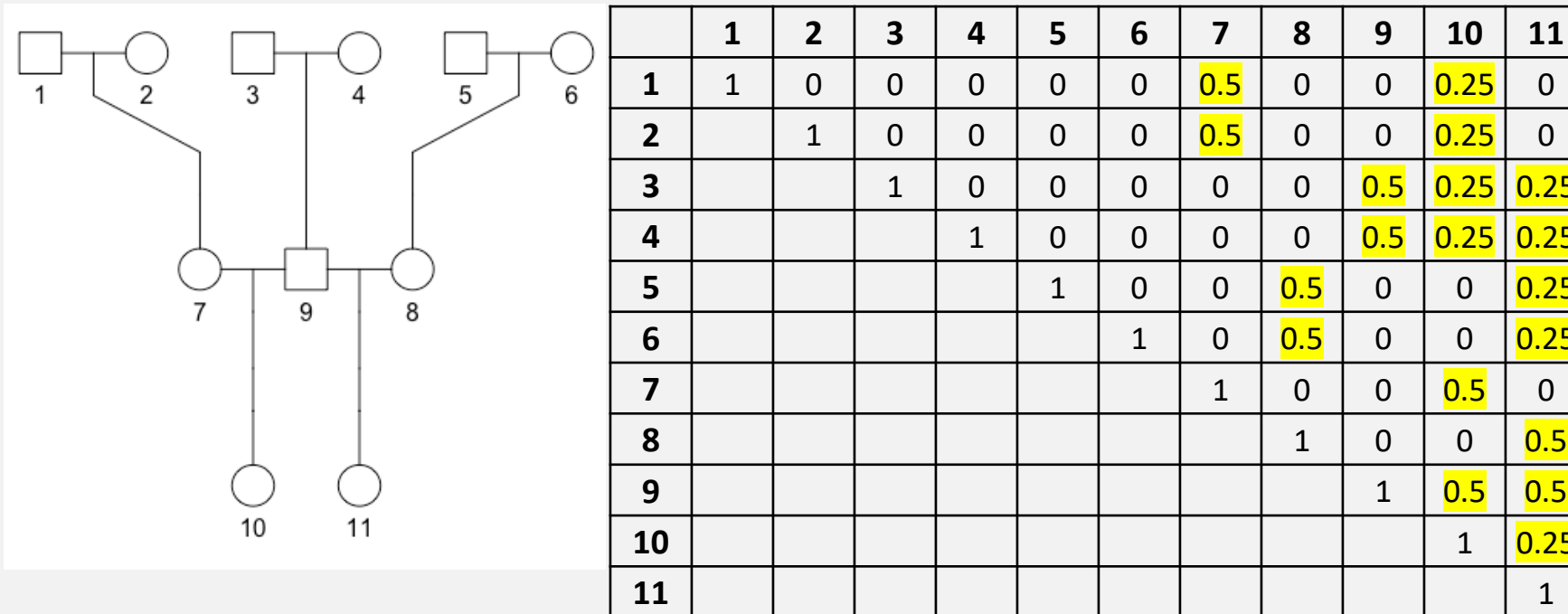
UNDERSTANDING RELATIONSHIPS AMONG ANIMALS
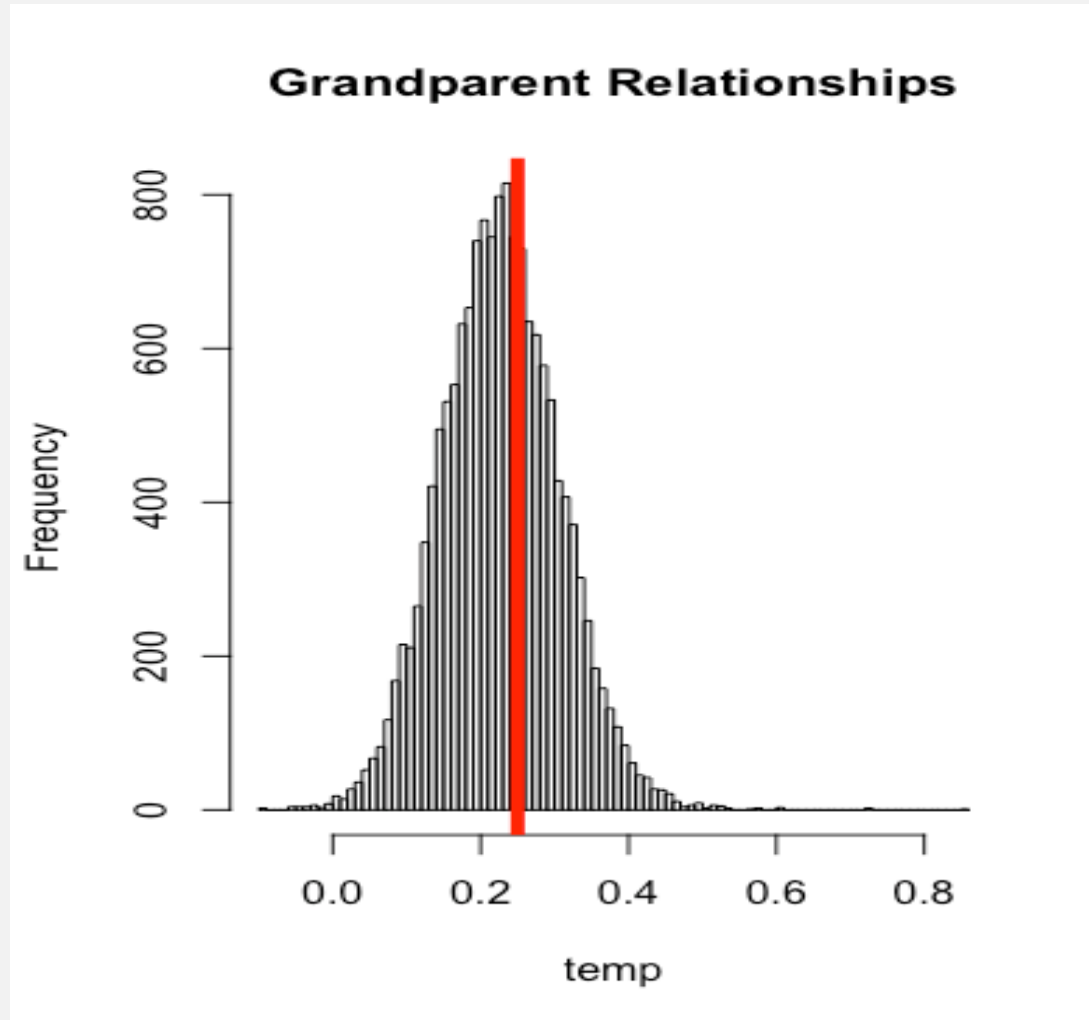
SOURCES OF INFORMATION
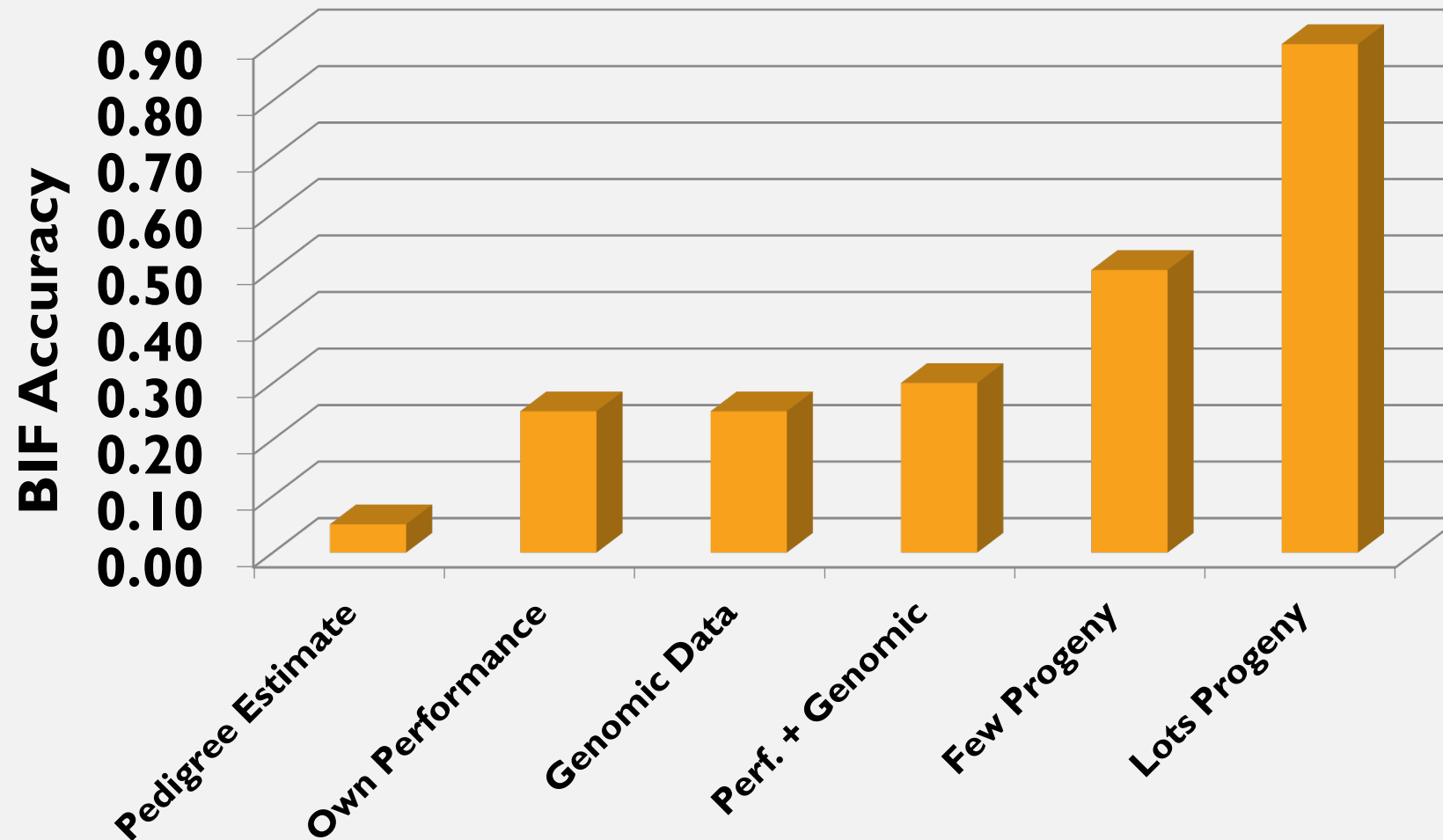
PHENOTYPES WILL ALWAYS BE KING

- Genetic evaluations will be best if there is a *continuous* flow of phenotypes
  - PAP
  - Foot and leg
  - Mature weight
  - Carcass traits

  Best way to tackle "novel" traits is to make them less "novel"

  Quality phenotypes, near the selection candidates, are most important.

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

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

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

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	---	-----	15
Marbling	9	3	8

HOW ARE GENOMIC EPD BEING USED?

- For selection?

  - If so, then you genotype every calf born

  - If we don't change the behavior of producers doing selection we have no chance of changing the genetics

  - Appropriate use (and capture of gain) requires that we actually use the tools to inform selection

- For marketing?

  - Genotyping selected animals

  - Reduces the amount of data such that GE-EPD may not be possible (or impactful) for maternal traits.
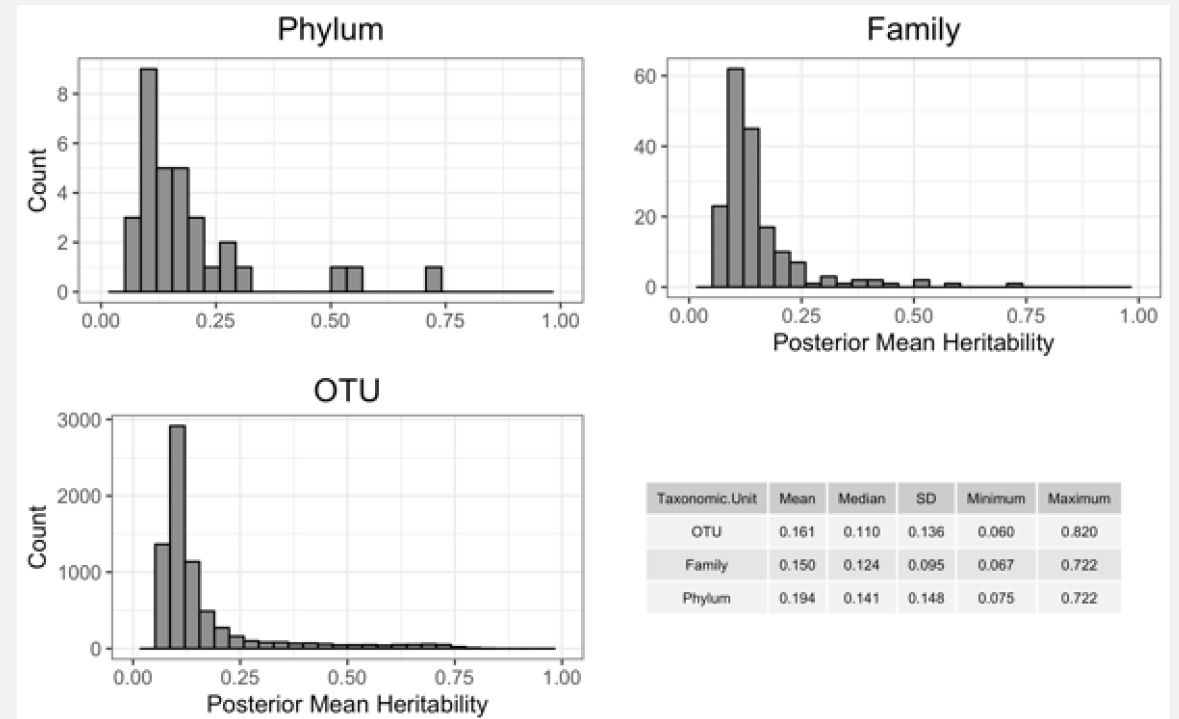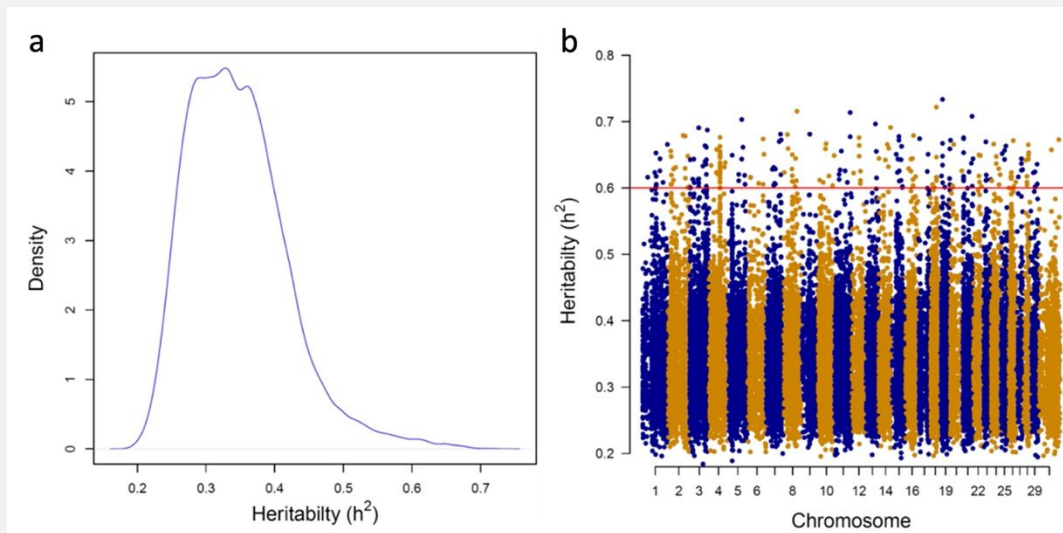
PRACTICAL EXAMPLE
UNL SEEDSTOCK HERD

- AI once and turn out natural service sires in multi-sire groups
- Target sample collection via tsu at branding
  - Additional opportunities at branding and weaning
- Have ~120 bull calves born and room to place ~90 on feed
  - Market ~60-70 bulls
  - Need earlier predictors to help sort
  - Multi-sire pastures decrease risk of open cows and increase uncertainty in pedigree
  - Not all cows gestate for the same length of time (i.e., mistakes even if single-bull pastures)
  - Mistakes in AI assignment do happen
  - Dams get switched too

GENOMICS AND NOVEL TRAITS

- Genomics has allowed for the discovery of genetic components related to:
  - Disease susceptibility
  - Fertility
  - Feed efficiency
  - Microbiome
  - Healthfulness of meat
    - Mineral content
    - Fatty acid profiles

"NEW" PREDICTORS ARE HERITABLE

Ribeiro et al., 2022

Waseem et al., 2020

Taxonomic.Unit	Mean	Median	SD	Minimum	Maximum
OTU	0.161	0.110	0.136	0.060	0.820
Family	0.150	0.124	0.095	0.067	0.722
Phylum	0.194	0.141	0.148	0.075	0.722

TAKE AWAYS…

- The study of genetics, and more specifically genetic evaluation of cattle, has been an evolutionary process

- As tools evolve and become more accurate, the risk of not using them becomes greater.

- Genomic tools work and have growing application in seedstock sector

- https://ebeef.ucdavis.edu/2021-nbcec-beef-cattle-sire-selection-manual
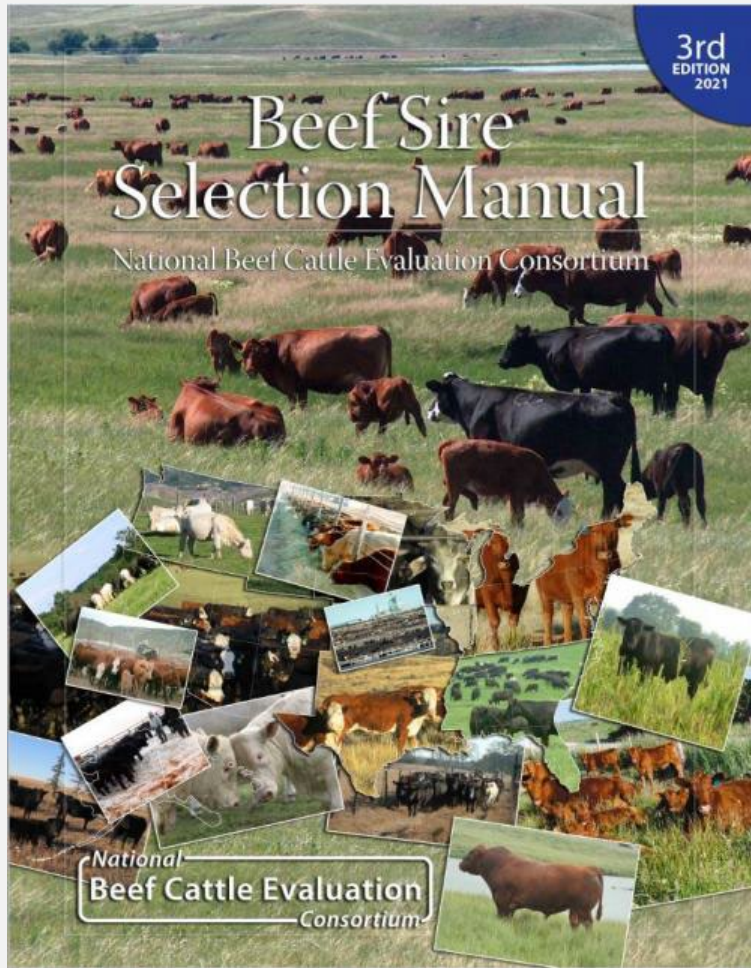
THANK YOU

- www.eBEEF.org
- http://beef.unl.edu
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