Genetic Evaluations

Genomic enhanced EPDs

Genetic Evaluations for Beef Cattle

- Majority – carried out by breed associations

  - Different genetic evaluation providers

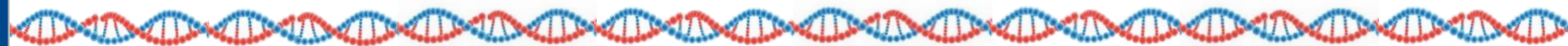 - Different methods to calculate EPDs

    Different EPDs reported for each breed

    challenging to compare data from different evaluations

- Within a breed - EPDs can be directly compared

- Historically - "across-breed" EPD adjustment factors, developed by USDA-MARC

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Whole Herd Recording

- Whole performance records - required on all calves produced by each breeder

- Whether any or all of those calves are registered - the breeder's decision

Collection of phenotypes for development of EPDs for important traits
(heifer pregnancy and stayability)

difficult to produce with incomplete data

Remove selection bias from genetic evaluations

results from only obtaining a select subset of data from superior animals

Interpreting EPDs

- EPD on one animal – no meaning (by themselves)

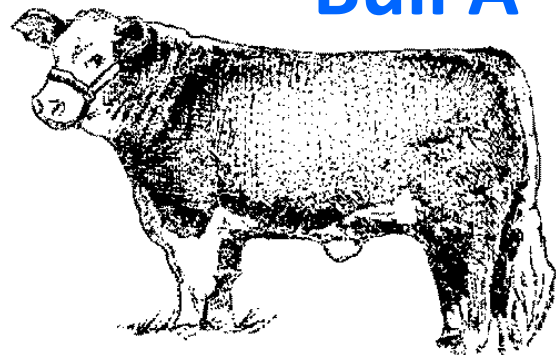- **Deviations** from some preset values (determined individually by each breed)

> **Expected difference** in **future progeny** performance of one individual **compared** to another.

> **EPD ≠ actual performance!**
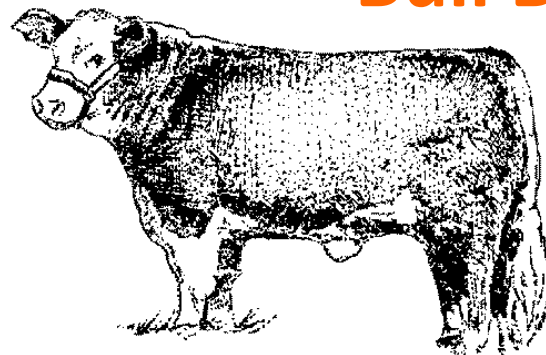> **EPD - do not predict performance!**

Interpreting EPDs
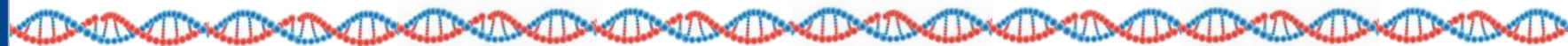
Bull A

Bull B

Weaning Weight

EBV = + 100 lbs
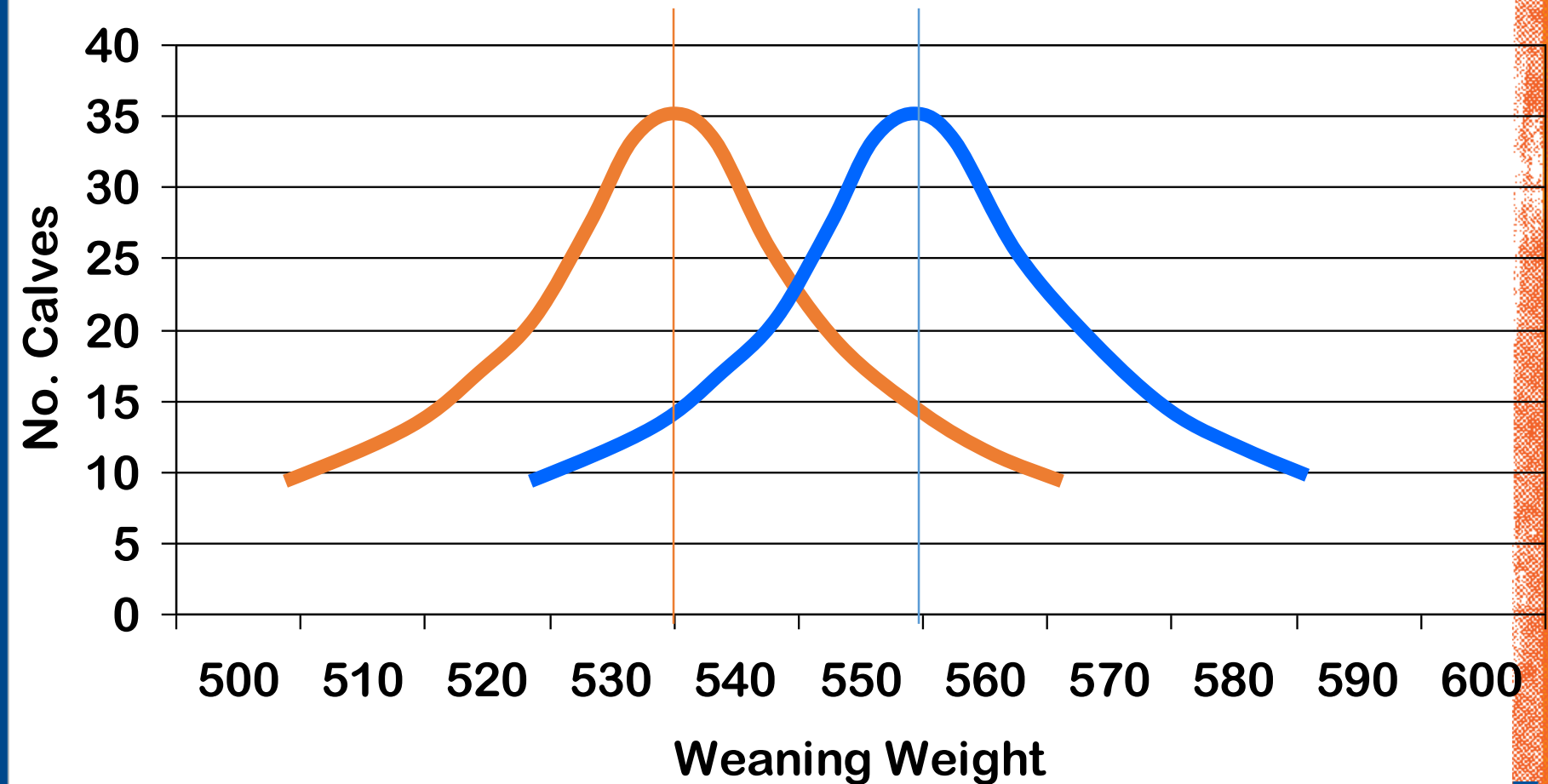
EPD = **+ 50** lbs

EBV = + 60 lbs

EPD = **+ 30** lbs

Calves **expected** to differ, **on average**, by **20** pounds (50 – 30)

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Calves expected to differ, on average, by 20 lb

Bull A: EPD **+50**

Bull B: EPD **+30**

Genomic Testing

- Incorporation of DNA information into genetic evaluations – stepwise evolution since 2000.

- Goal: **increase the accuracy** of predicting genetic merit (EPD)

For breeders to make the **best use of genomic** data, it needs to be **combined** with traditional sources of information (i.e. phenotypes and pedigrees) into traditional genetic evaluations.

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Accuracy of EPDs

- EPDs with low accuracy - still the single best tool for selection

- Associated with wide margins of possible change
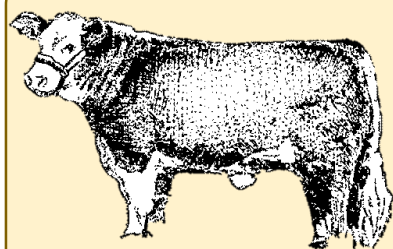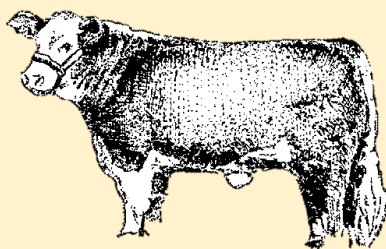
EPD = 0   EPD = 3

Low accuracy

Possible change **± 4** units

-4 to +4   -1 to +7

	Production			
Accuracy	BW	WW	YW	RADG
.05	2.49	11.0	16.2	.082
.10	2.36	10.4	15.3	.078
.15	2.23	9.9	14.5	.074
.20	2.10	9.3	13.6	.069
.25	1.97	8.7	12.8	.065
.30	1.84	8.1	11.9	.061
.35	1.71	7.5	11.1	.056
.40	1.58	7.0	10.2	.052
.45	1.44	6.4	9.4	.048
.50	1.31	5.8	8.5	.043
.55	1.18	5.2	7.7	.039
.60	1.05	4.6	6.8	.035
.65	.92	4.1	6.0	.030
.70	.79	3.5	5.1	.026
.75	.66	2.9	4.3	.022
.80	.53	2.3	3.4	.017
.85	.39	1.7	2.6	.013
.90	.26	1.2	1.7	.009
.95	.13	.6	.9	.004

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Incorporation of genomic information

Which traits?

- Traits **with** routine genetic evaluations obtained from phenotypic and pedigree information.
  - Enhanced **accuracy** of genetic evaluations

- Traits **without** routine evaluations.
  - Will allow selection for **novel** but economically important traits

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- Traits **with** routine genetic evaluations obtained from phenotypic and pedigree information.
  - Enhanced **accuracy** of genetic evaluations

Pedigree estimated EPDs, no ultrasound scan data

OLD	CWT	MARB	RE	FAT
EPD	I +15	I +.79	I +.41	I -.001
Acc	.05	.05	.05	.05

Genomics added

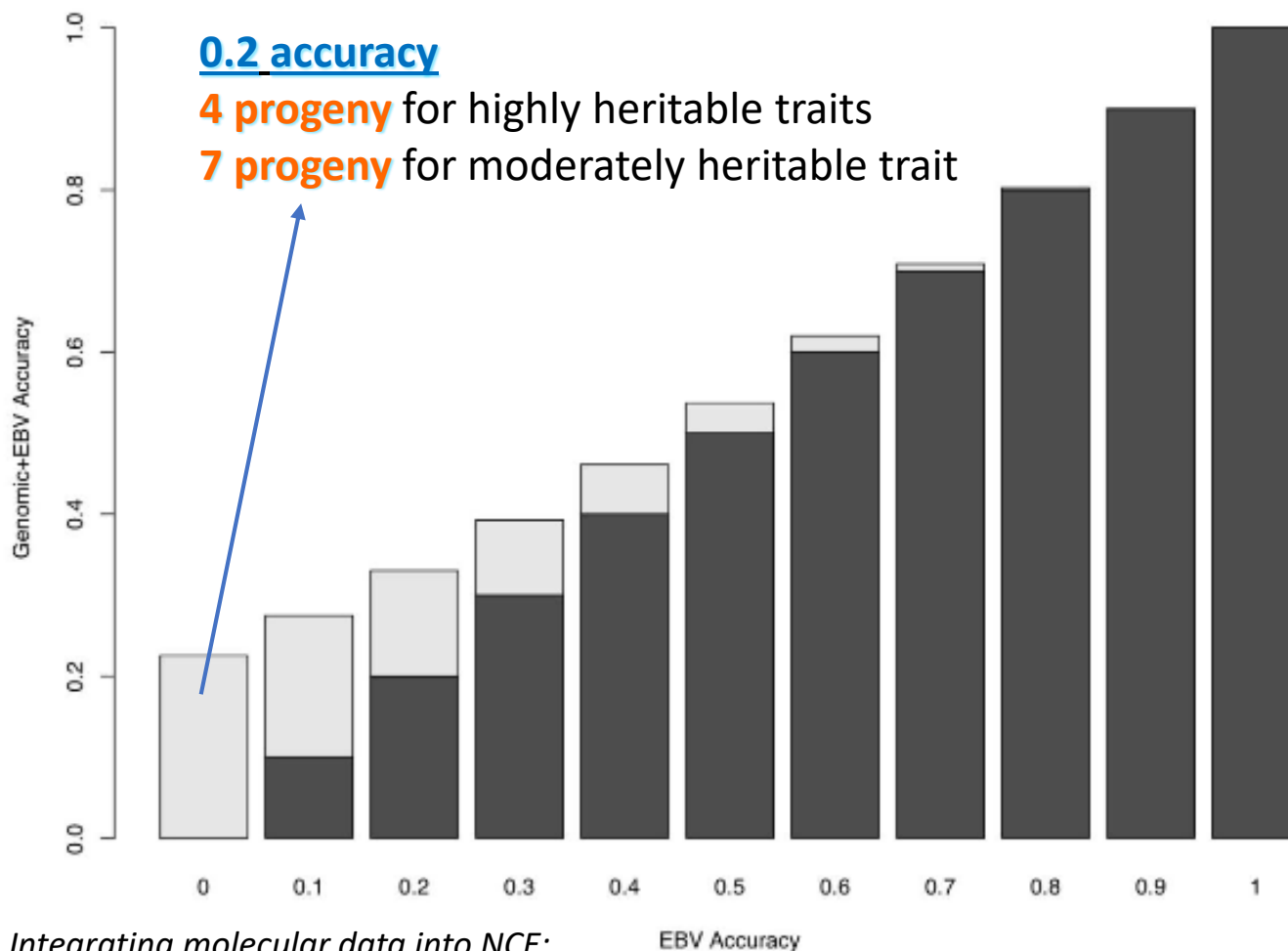| NEW	CWT	MARB	RE	FAT
EPD	+ 18	+ .71	+ .50	+.004
Acc	.30	.38	.35	.28

Traits with current genetic evaluation

Enhanced accuracy of genetic evaluations

- More pronounced in **young** animals with no recorded progeny – high value for selection of replacement animals.

- The increase in **accuracy** will depend on:
  - Available records on relatives
  - Heritability of the trait
  - Proportion of variation accounted for by the test

Adding Genomic Information

- Increase in accuracy from integrating genomic information that explains 40% of the genetic variation into EBV

0.2 accuracy
4 progeny for highly heritable traits
7 progeny for moderately heritable trait

M. Spangler, Integrating molecular data into NCE: expectations, benefits, and needs

Population specific tests

- Current marker panels (genetic tests) are likely to work best in the populations where discovery occurred

- Predictive power decreases as the target population becomes more **genetically distant**

Discovery	**Target**	
Angus	Angus	Closest relationship
Angus	Charolais	
Angus	*Bos Indicus*	Most distant relationship

- Same erosion will occur **over time** (over generations if panels are not retrained).

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Novel traits

- Genomic information (SNPs)

  - Increase the accuracy of EPDs

  - Add "novel" traits to our suite of available EPD (cattle health – BRD, feed efficiency, healthfulness, nutritional value, disease resistance, thermotolerance, reproductive traits)

- Large resource populations with phenotypes are required for discovery and validation.

- Need breed specific prediction equations.