Beef Cattle Genomic Tools: How Do They Help?

Bob Weaber, Ph.D.

Professor and Head,

Eastern Kansas Research and Extension Centers

Kansas State University

WHAT'S THE BIGGEST CHALLENGE SEEDSTOCK PRODUCERS FACE?

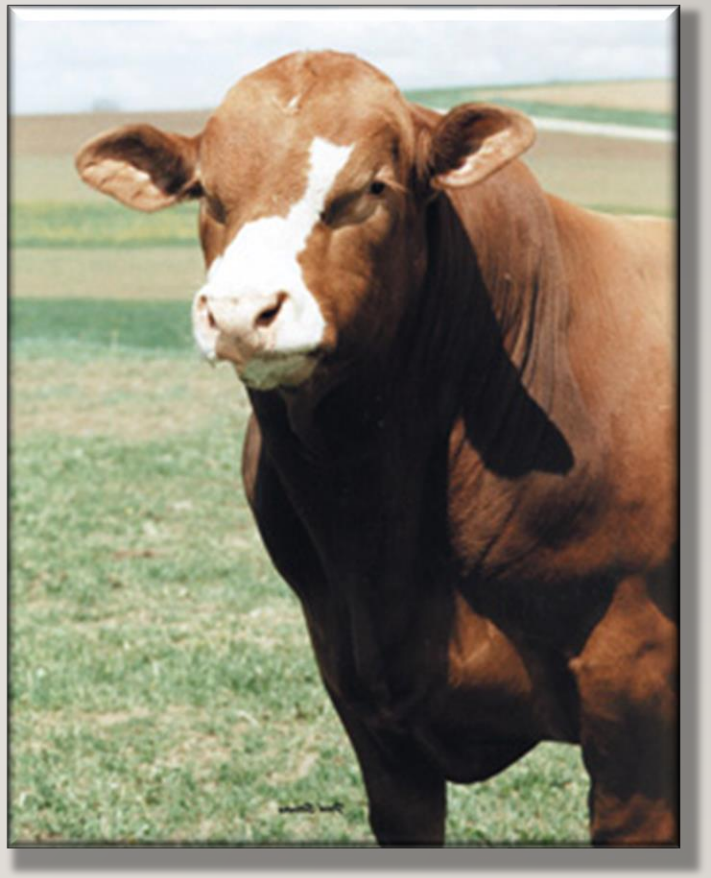
- Competition from other breeds?
- Competition from other breeders?
- Understanding the marketplace and commercial bull buyer needs/wants?
- **Technology adoption?**
- **Integration of new sources of information into decision stream?**

SHOULD YOU USE GENOMIC TOOLS IN YOUR SEEDSTOCK OPERATION?

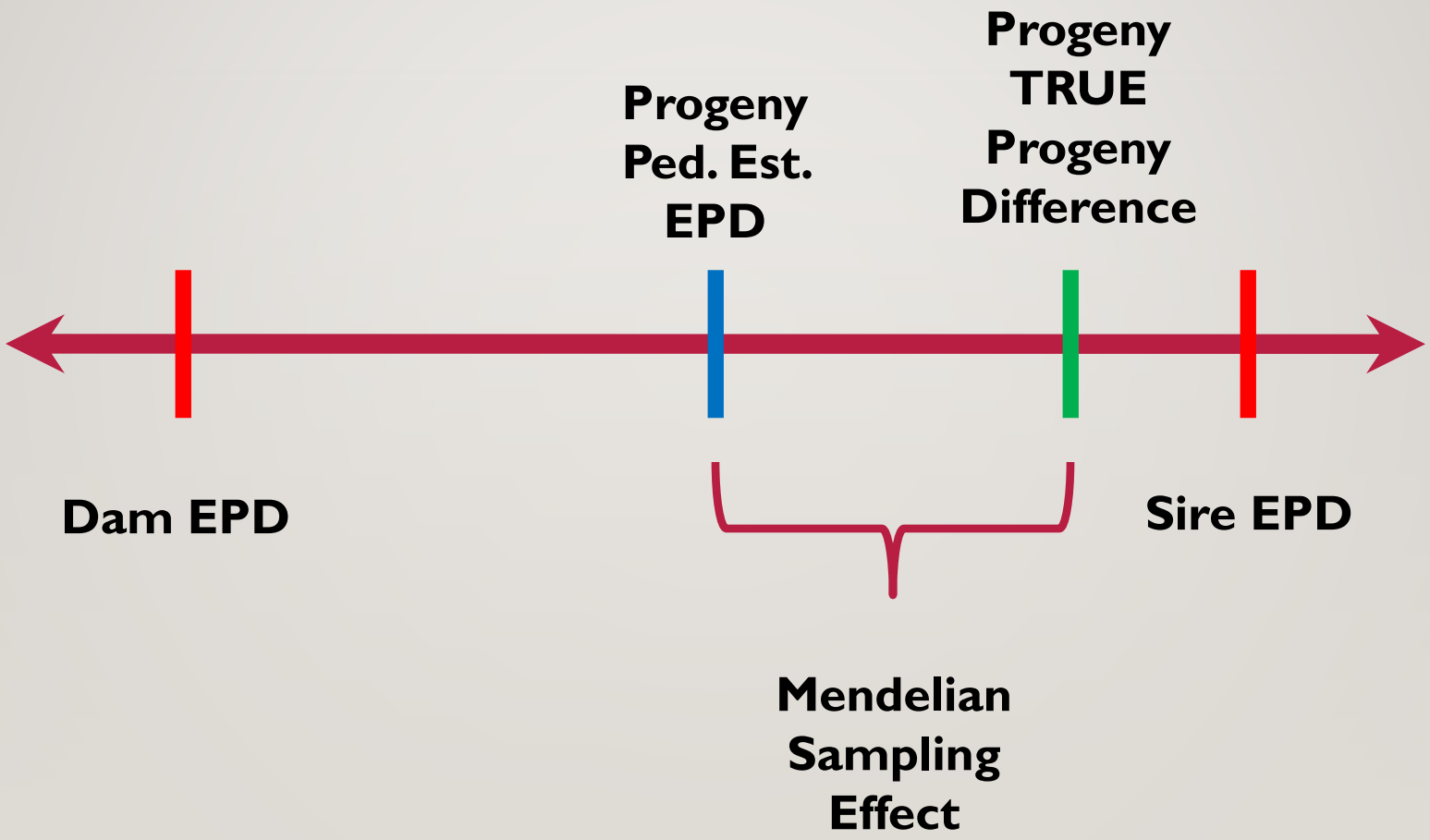
YES!!!!

Any questions?

HOW MANY OF YOU ARE COMFORTABLE USING EPD OR INDEXES IN SELECTION?



FINDING TRUE GENETIC MERIT

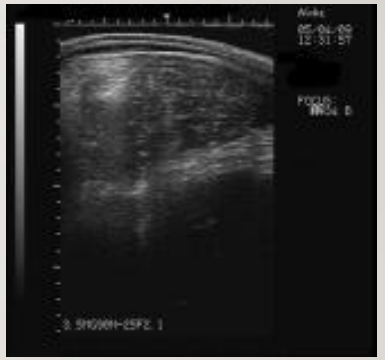


SOURCES OF VALUE

Moser, 2011

		D H D Traveler 6807	AAA #10858958 [AMF-NHF]
	S S Traveler 6807 T510	AAA #12502030 [AMF-CAF-NHF]	
		S S Miss Hi Spade A114	AAA #11665432
S S Objective T510 0T26	AAA #13776378 [AMF-CAF-NHF]		
		S S Rito Rito R76 R011	AAA 11494687
	S S Miss Rita R011 7R8	AAA 12958951 [AMF-NHF]	
		S S Miss Ultress U56	AAA 12490161
		B/R New Design 036	AAA #11418151 [AMF-CAF-NHF]
	G A R Predestined	AAA #13395344 [AMF-CAF-NHF]	
		G A R Ext 4206	AAA #+12716727
KSU Miss Predestined 7166	AAA +15789915 [NHC-AMF]		
		Whitestone Precision H141	AAA #12527924 [AMC-NHC-CAF]
	G A R H141 Precision 03	AAA +14506130 [AMC-NHC]	
		G A R Prime Time 2409	AAA 13395458 [AMF-NHF]

 # Pathfinder + Embryo Transplant



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<< Prev Page | Search Again | Home | Breed Association Codes | Defect Codes

KSU Objective 0183 Reg: AAA 16754371 [NHF] Bull

Birth Date: 02/09/2010 **Tattoo:** 0183
Breeder: 296850 - Kansas State University, Manhattan KS
Owner(s): 296850 - Kansas State University, Manhattan KS

EPD Percentiles

As of 01/11/2011

Production								Maternal					
CED Acc	BW Acc	WW Acc	YW Acc	RADG Acc	YH Acc	SC Acc	Doc Acc	CEM Acc	Milk Acc	MkH MkD	MW Acc	MH Acc	$EN
+9 .29	+1.9 .34	+62 .25	+111 .19		I+.2 .05		I+8 .05	+8 .19	+27 .20		I+63 .05	I+.7 .05	-10.38

Carcass					
CW Acc	Marb Acc	RE Acc	Fat Acc	Carc Grp Carc Pg	Usnd Grp Usnd Pg
I+15 .05	I+.76 .05	I+.43 .05	I+.003 .05		

$Values					
$W	$F	$G	$QG	$YG	$B
+31.57	+45.99	+38.72	+30.74	+7.98	+66.14

296850 BO 11222010

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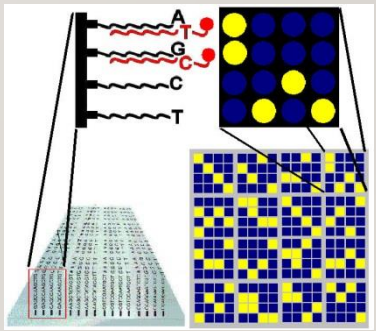
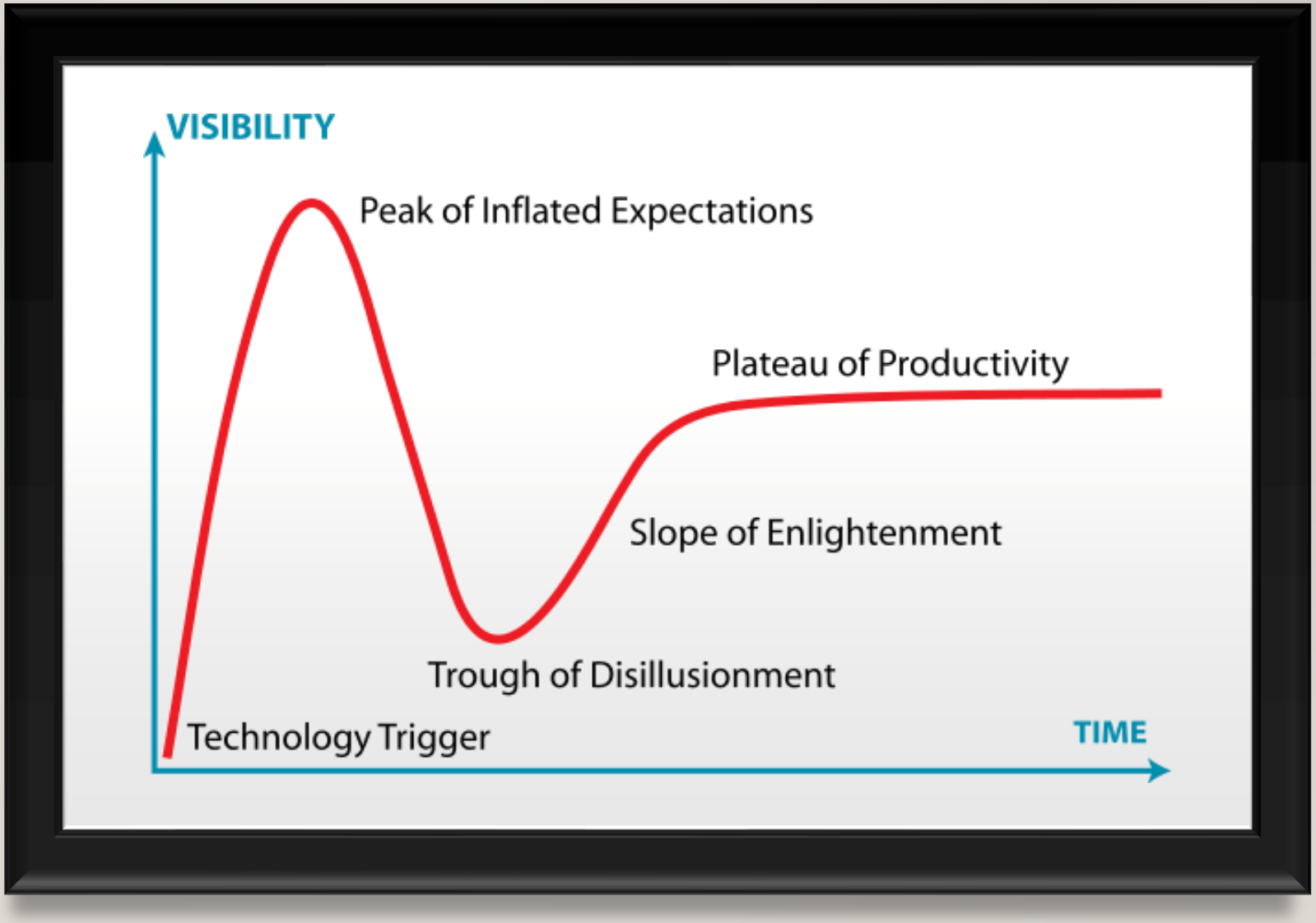


GENOMIC TECHNOLOGY ADOPTION IN BEEF INDUSTRY

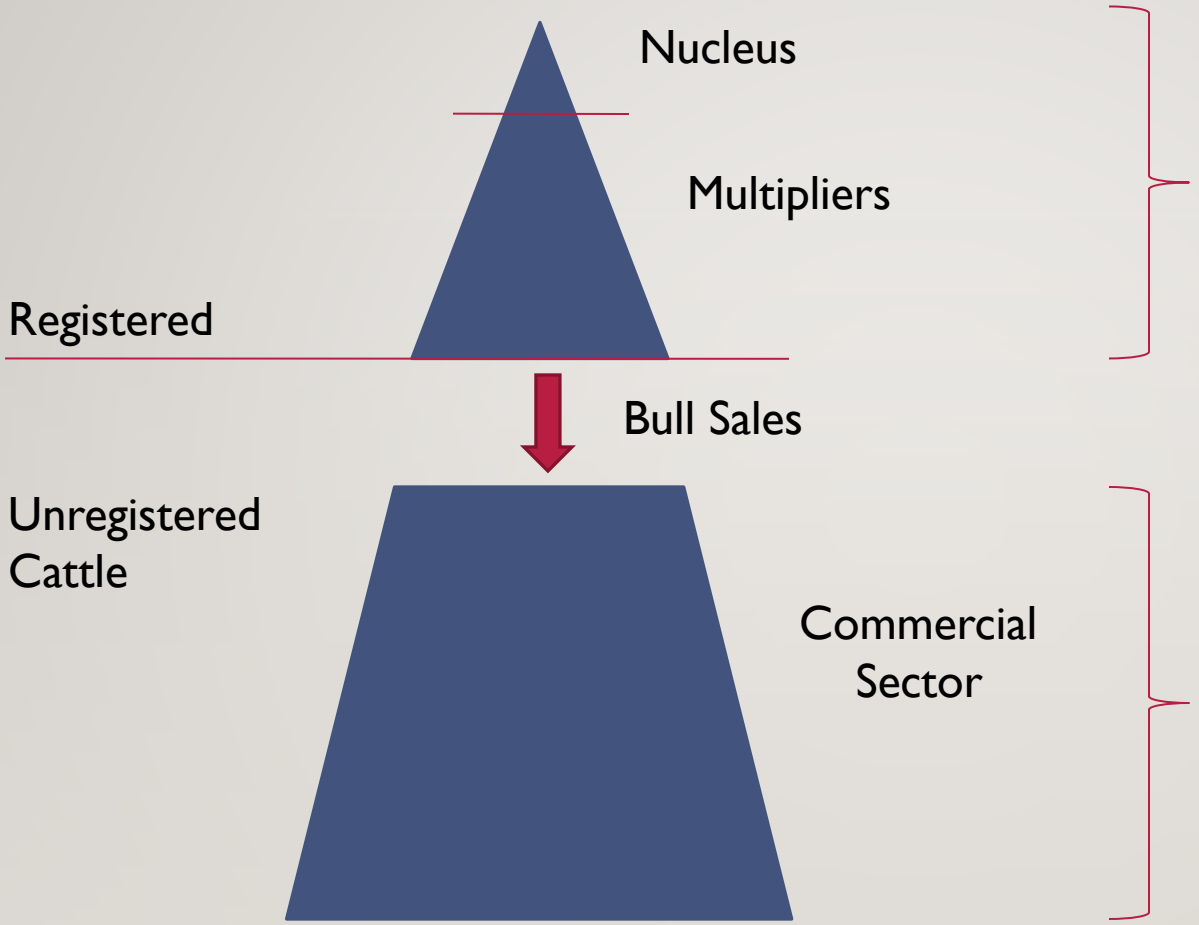
THE GARTNER HYPE CYCLE



NEW TOOLS
NEW OPPORTUNITIES

- Genotyping platforms
  - ULD;Low cost/imputation optimized
- Single Step Genetic Evaluation
  - Glean more information from genotypes
  - Genotypes for all
  - Novel traits/improved models
- Repro Management
  - Gender selected semen
  - IVF
  - MOET
  - Genotyped embryos
  - Clones
  - Genome Editing

SCHEMATIC STRUCTURE & GOAL



$$$$$$
Improvement costs from collection of ancestry, phenotypic and genotypic information

$$$$$$$$$$$$$$$$
Productive benefits from improved cattle (more efficient and/or higher quality)

Net Industry Benefit

$$$$= $$$$$$$$$$$$$$$$-$$$$$$

Garrick, 2007

NUCLEUS RATE OF GENETIC GAIN

$$\Delta G = \frac{[(ir_{TI})_S + (ir_{TI})_D]\sigma_g}{L_S + L_D}$$

Garrick, 2007 Simplistic – two selection paths S=Sires, D=Dams

NUCLEUS RATE OF GENETIC GAIN

intensity of selection dictated by proportion of candidates selected

accuracy of selection

amount of genetic variation in population

$$\Delta G = \frac{[(ir_{TI})_S + (ir_{TI})_D]\sigma_g}{L_S + L_D}$$

Annual Change in Merit/Performance

average ages of selected sires (& dams) when offspring are born

Garrick, 2007

Simplistic – two selection paths

S=Sires, D=Dams

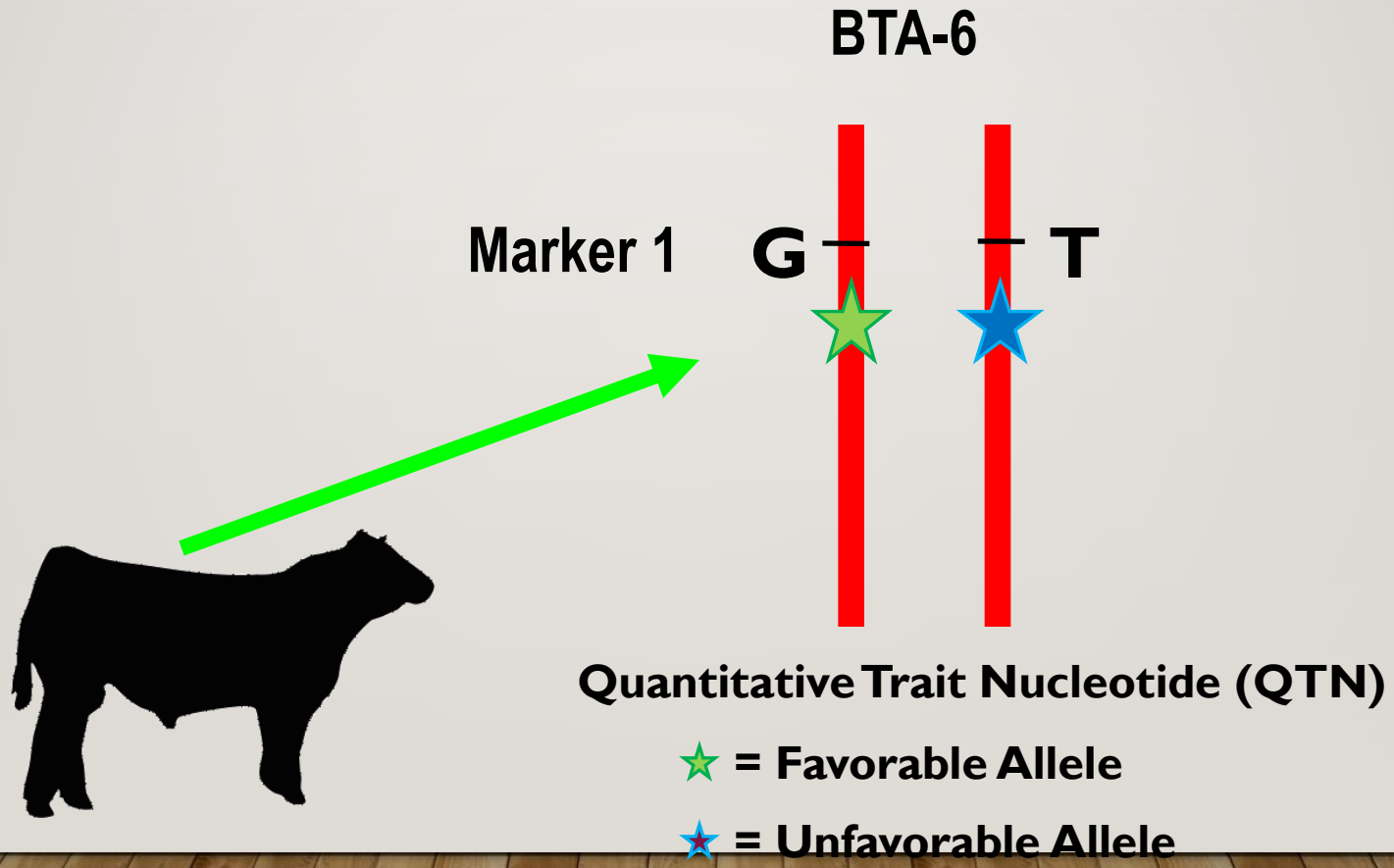
WHAT IS A SNP?

SINGLE NUCLEOTIDE POLYMORPHISM (SNP) DNA MARKER EXAMPLE

G/T SNP

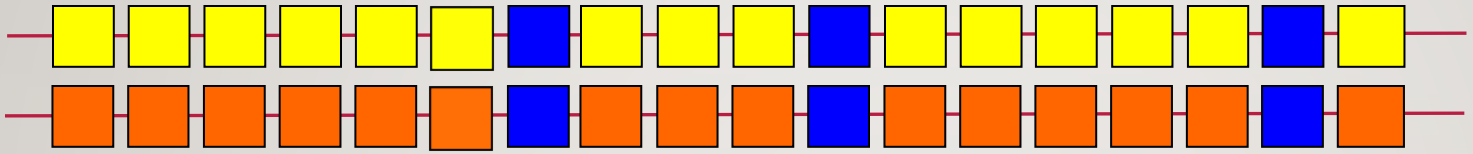
- **Mutation may be in exon (coding sequence; possibly causal) or in intron (non-coding sequence) of gene**

18 SNPS AND QTNS



GENOMICALLY ENHANCED EPD

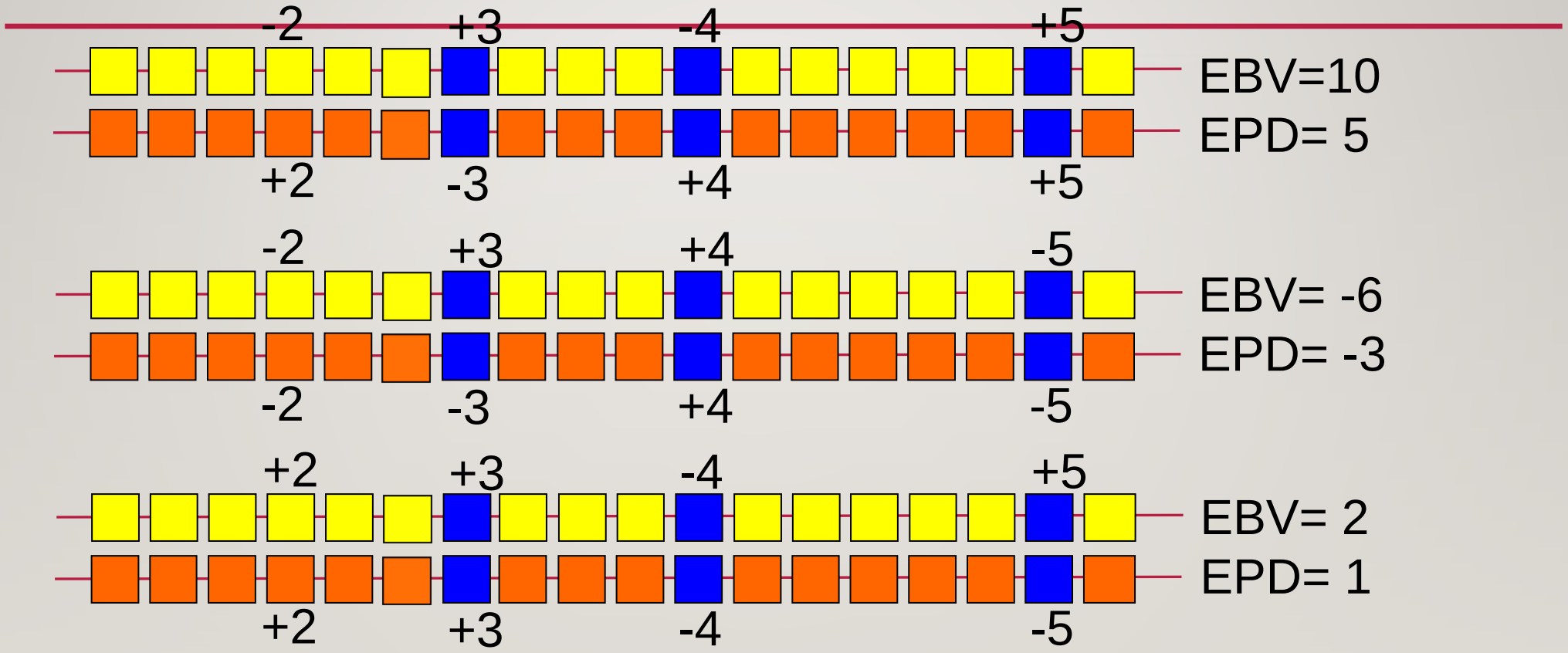
CHROMOSOMES ARE A SEQUENCE OF BASE PAIRS



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

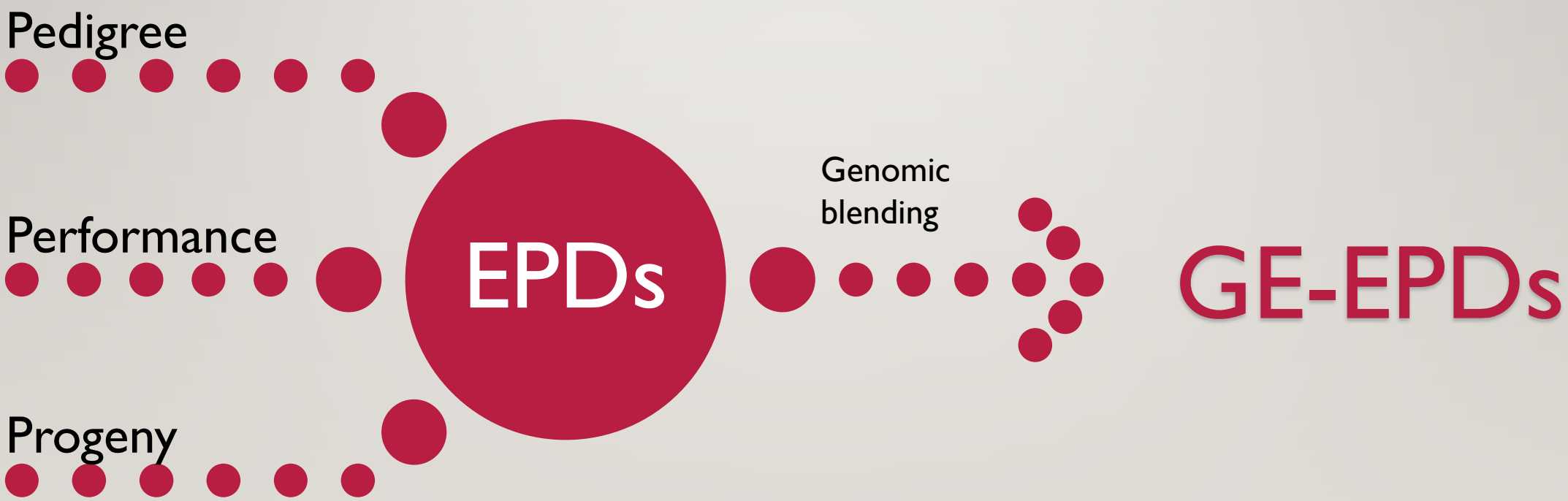
- Blue base pairs represent genes
- Yellow represents the strand inherited from the sire
- Orange represents the strand inherited from the dam

CONSIDER 3 ANIMALS (THINK ACCURACY VERSUS PRECISION)

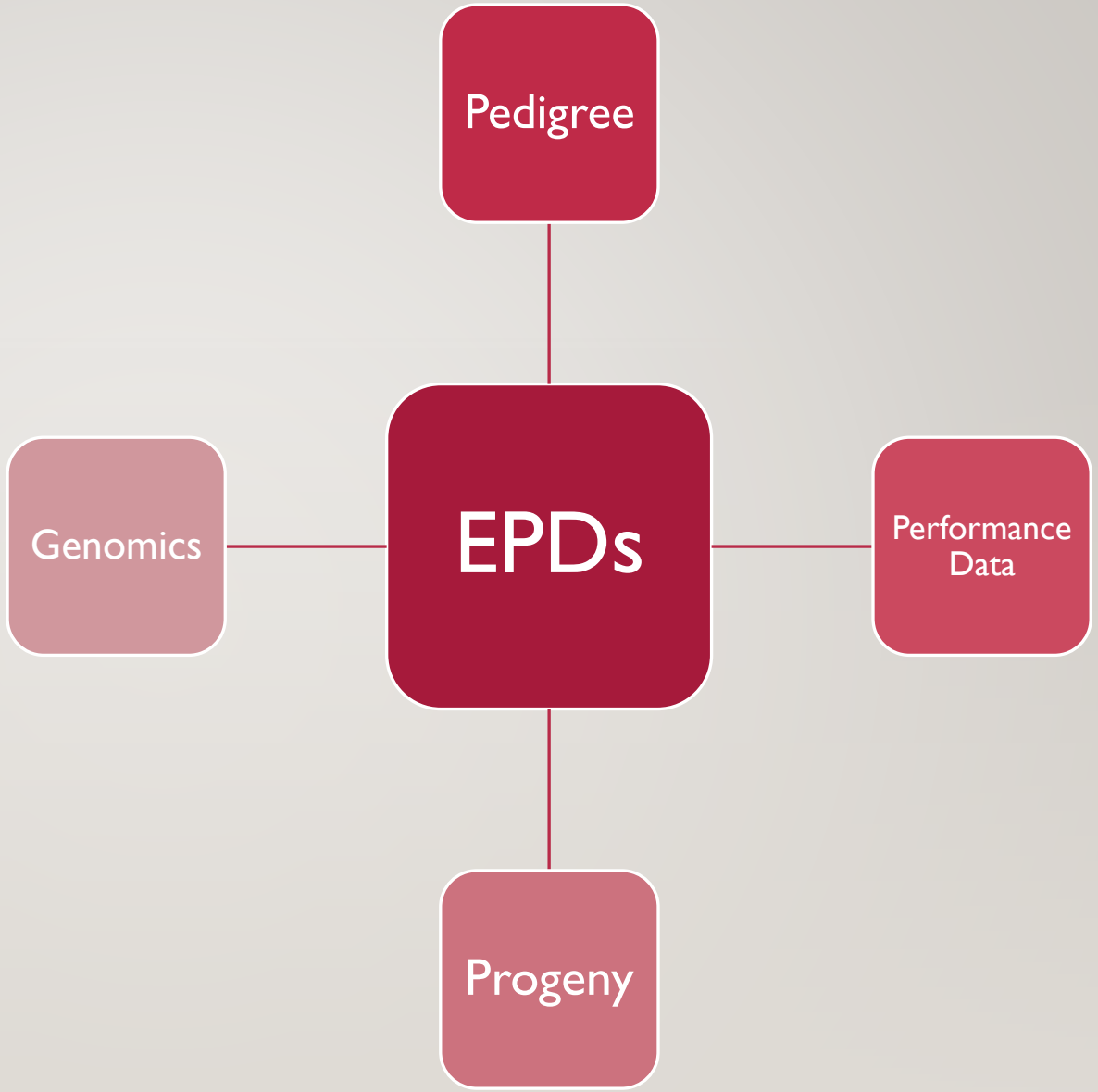


Below-average bulls will have some above-average alleles and vice versa!

TWO STEP METHOD TO COMPUTE GENOMICALLY ENHANCED EPD



SINGLE STEP EPDS



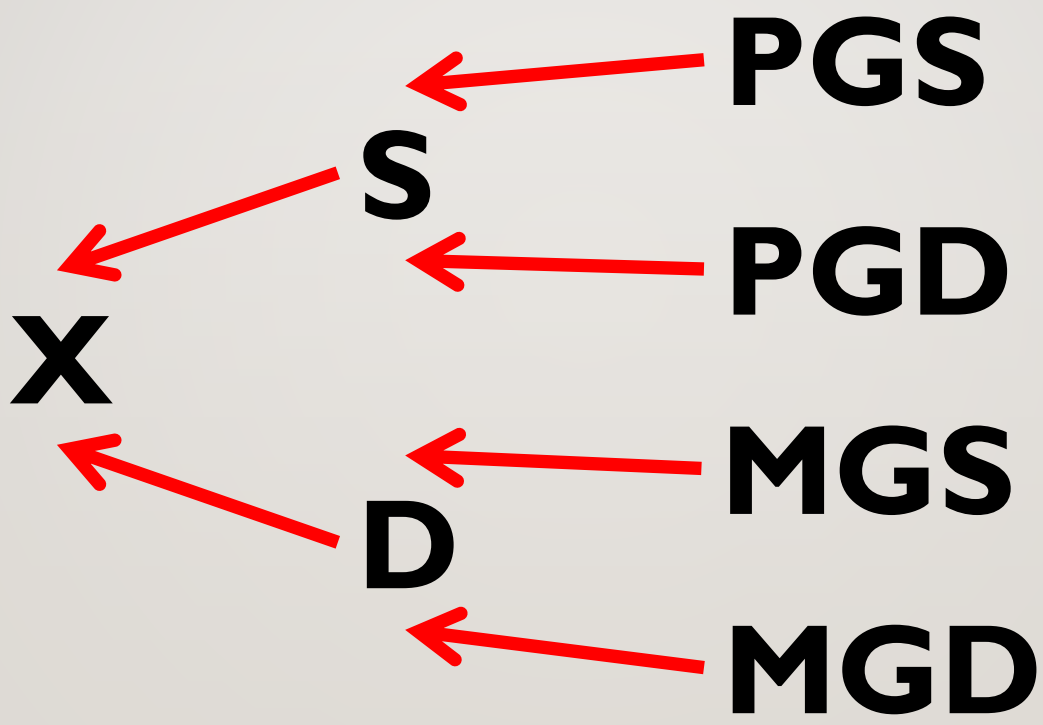
CHANGES IN RATE OF GENETIC GAIN THROUGH IMPROVED ACCURACY OF SELECTION (OLD BLENDING METHOD)

Source of Information	BIF Acc	r_{TI}	Selected %	Intensity	Genetic SD	L (yr)	DeltaG	Rate Increase
PA	0.05	0.31	5	2.06	28	7	2.6	--
Own Record	0.30	0.71	5	2.06	28	7	5.9	1.29
Genomic	0.30	0.71	5	2.06	28	7	5.9	1.29
Own Record + Genomic	0.40	0.80	5	2.06	28	7	6.6	1.56
Progeny	0.65	0.94	5	2.06	28	7	7.7	2.00

SELECTION EFFICIENCY PATHWAYS OF SELECTION

- Genetic gain in population driven by intensity and accuracy of selection of parents and generation interval
- The FOUR paths:
  - Sires of Sires (Paternal Grand Sires)
  - Dams of Sires (Paternal Grand Dams)
  - Sires of Dams (Maternal Grand Sires)
  - Dams of Dams (Maternal Grand Dams)
- Which are the longest generation interval? Highest intensity? Lowest Accuracy?

PATHS OF SELECTION



GENOMIC IMPACT ON SELECTION EFFICIENCY AND RATE (OLD BLENDING METHOD)

Scenario 1: Traditional Selection Using EPD

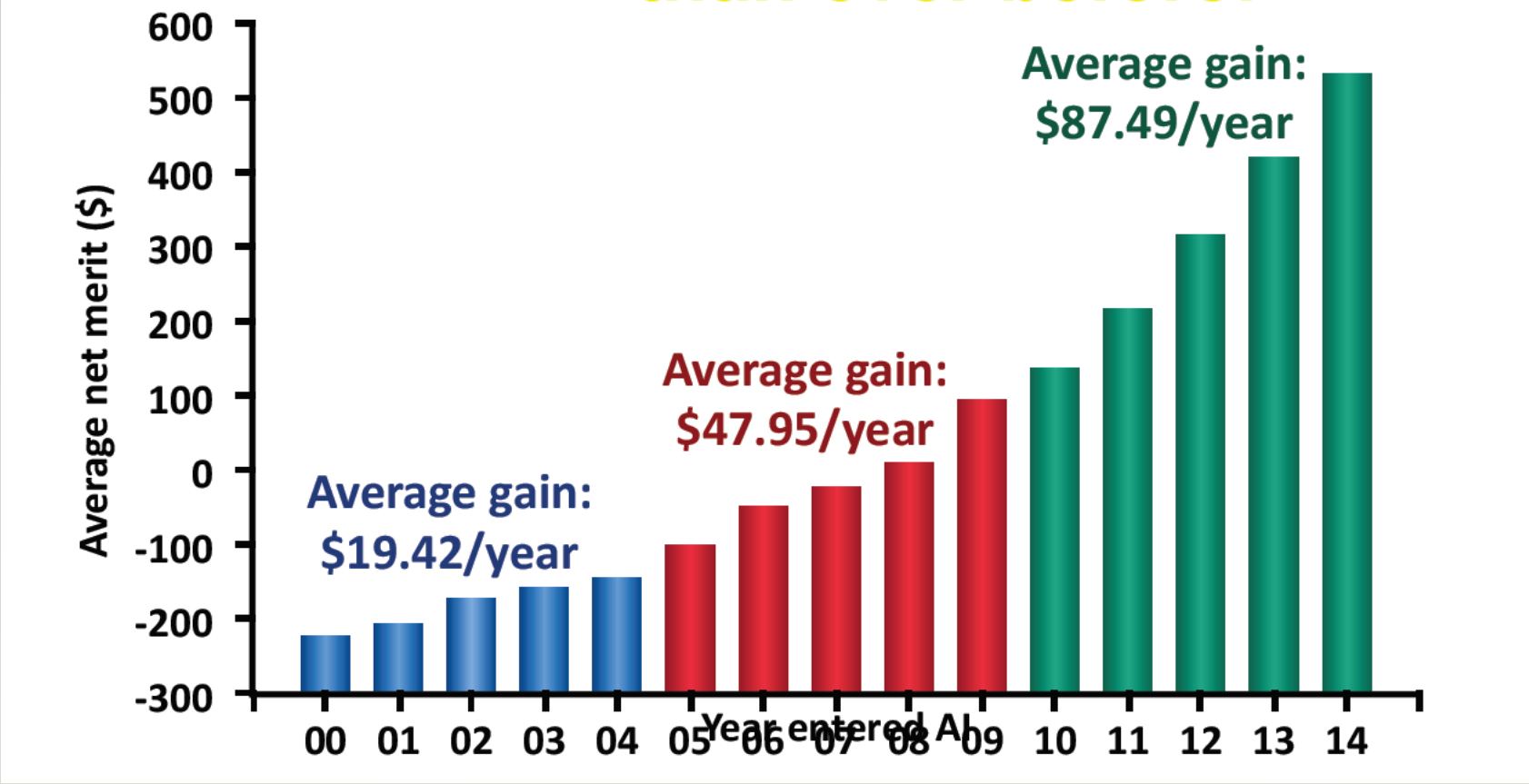
Path	Selection %	Intensity	BIF Acc	Acc (rTI)	Gen. Int (L)	i * rTI
Sires of Bulls	5	2.06	0.65	0.94	10	1.93
Dams of Bulls	10	1.75	0.10	0.44	5	0.76
Sires of Cows	20	1.40	0.15	0.53	6	0.74
Dams of Cows	20	1.40	0.05	0.31	6	0.44
Genetic Gain (sd units)		**0.14**		Totals	27	3.87

Scenario 2: Selection Using Genomically Enhanced EPD

Path	Selection %	Intensity	BIF Acc	Acc (rTI)	Gen. Int (L)	i * rTI
Sires of Bulls	5	2.06	0.66	0.94	7	1.94
Dams of Bulls	10	1.75	**0.29**	0.70	5	1.24
Sires of Cows	20	1.40	0.31	0.72	5	1.01
Dams of Cows	20	1.40	**0.26**	0.67	6	0.94
Genetic Gain (sd units)		**0.22**		Totals	23	5.13

Rate Improvement 56%

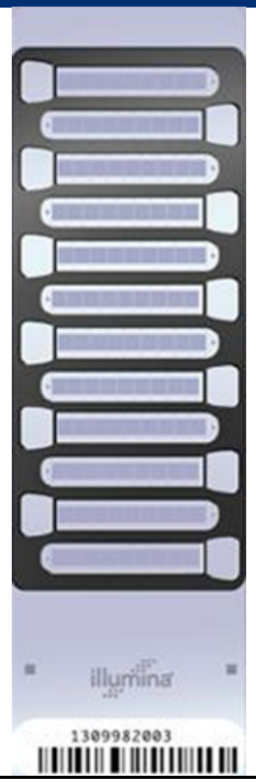
IMPROVEMENT IN NET MERIT ($) IN HOLSTEIN DRIVEN BY GENOMICS



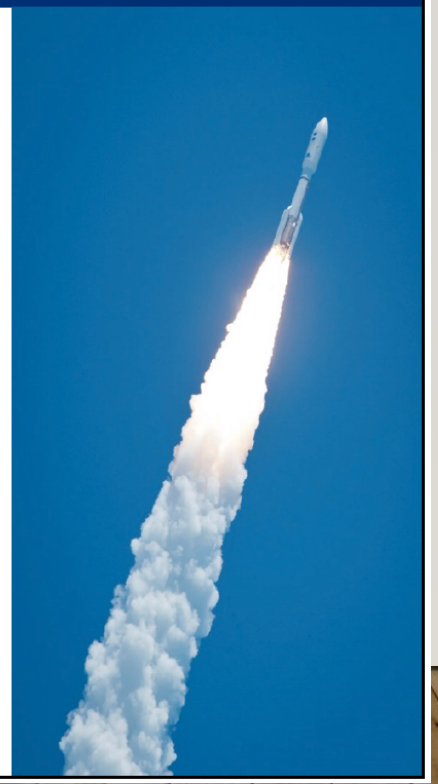
Lawlor, 2017

GENOMICS DRIVES IMPROVEMENT IN LOW HERITABILITY ERTS IN DAIRY

Genomic testing gives us an extra boost in improving the lowest heritable traits



Trait	Extra Daughter Equivalents from SNP effects
Production	25
Conformation	25
Calving Ease	38
Somatic Cell Score	58
Productive Life	80
Fertility	140



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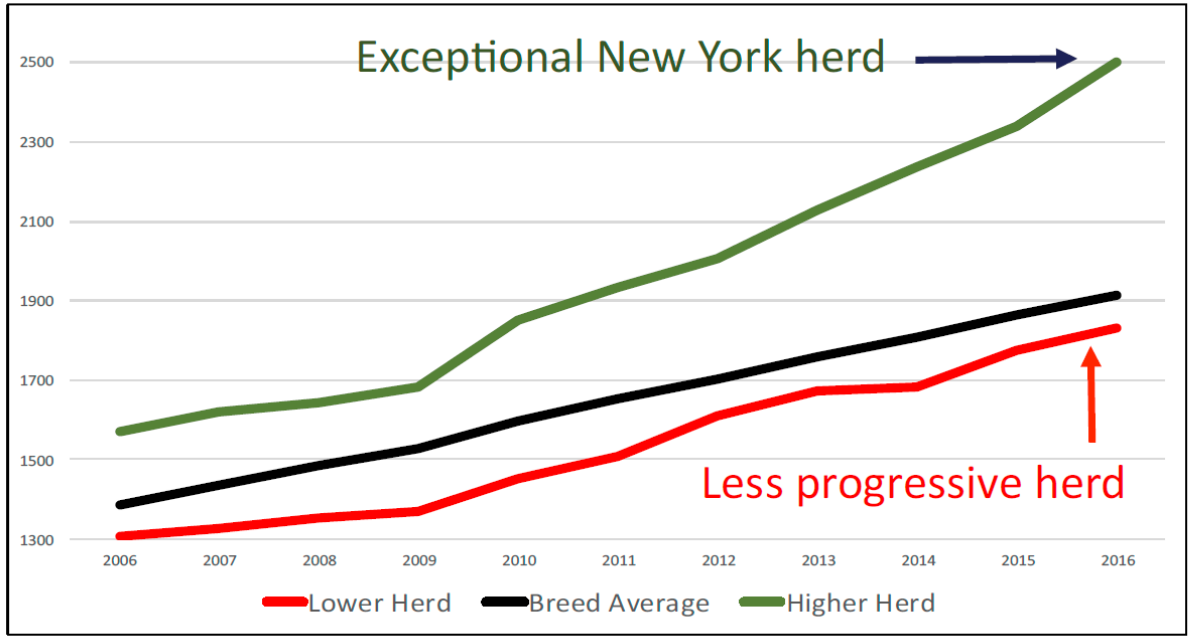
HOW MUCH IS INVESTMENT IN GENOMICS WORTH? THE WIDENING GAP IN DAIRY HERDS…

Greater differences between herds
HIGH herd make $1012 more lifetime profit per cow



Genomic testing,
In vitro fertilization,
Embryo transfer,
Sexed semen

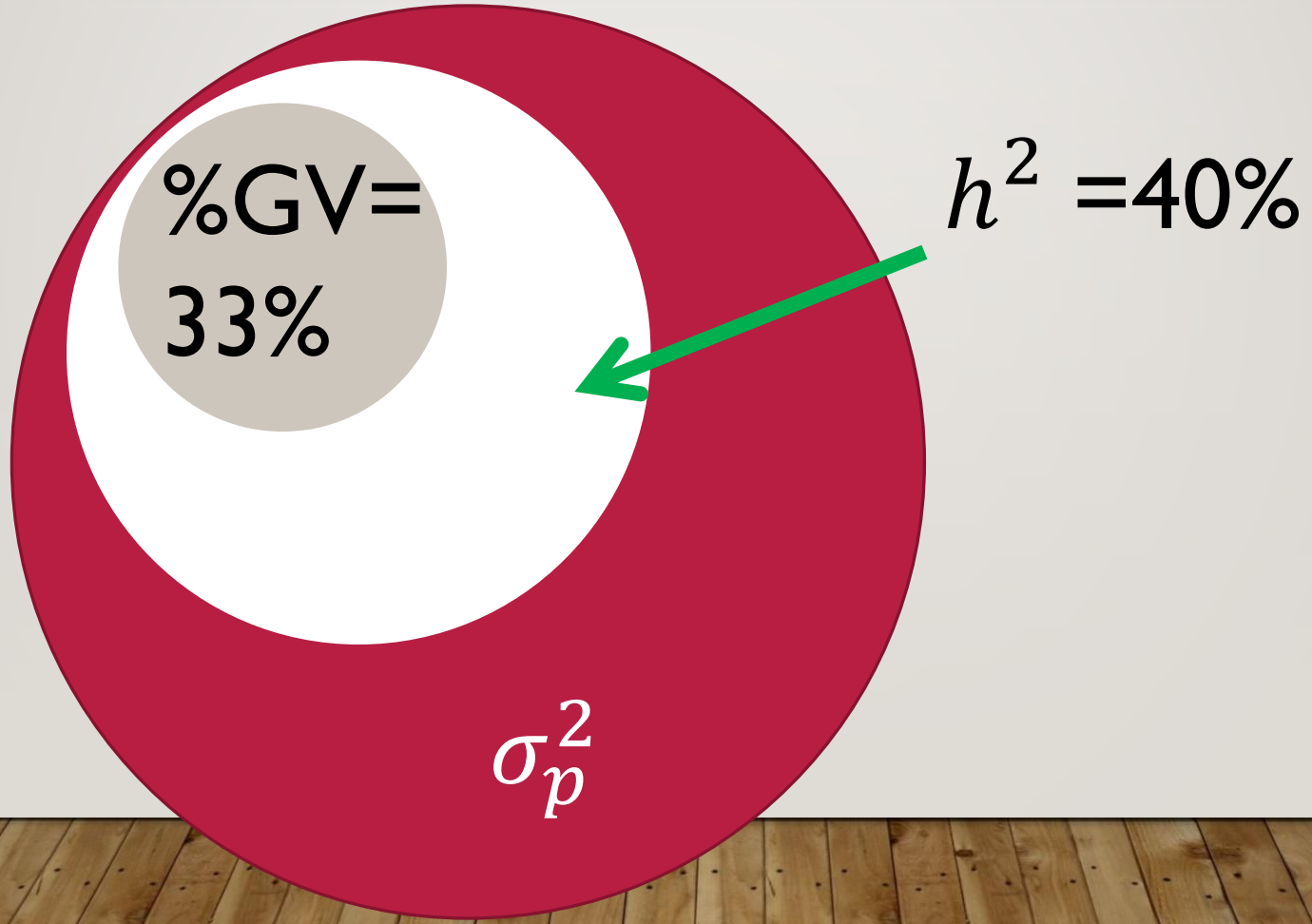
Using older bulls and little genomic testing

Lawlor, 2017

BEEF GENOMICS FUTURE

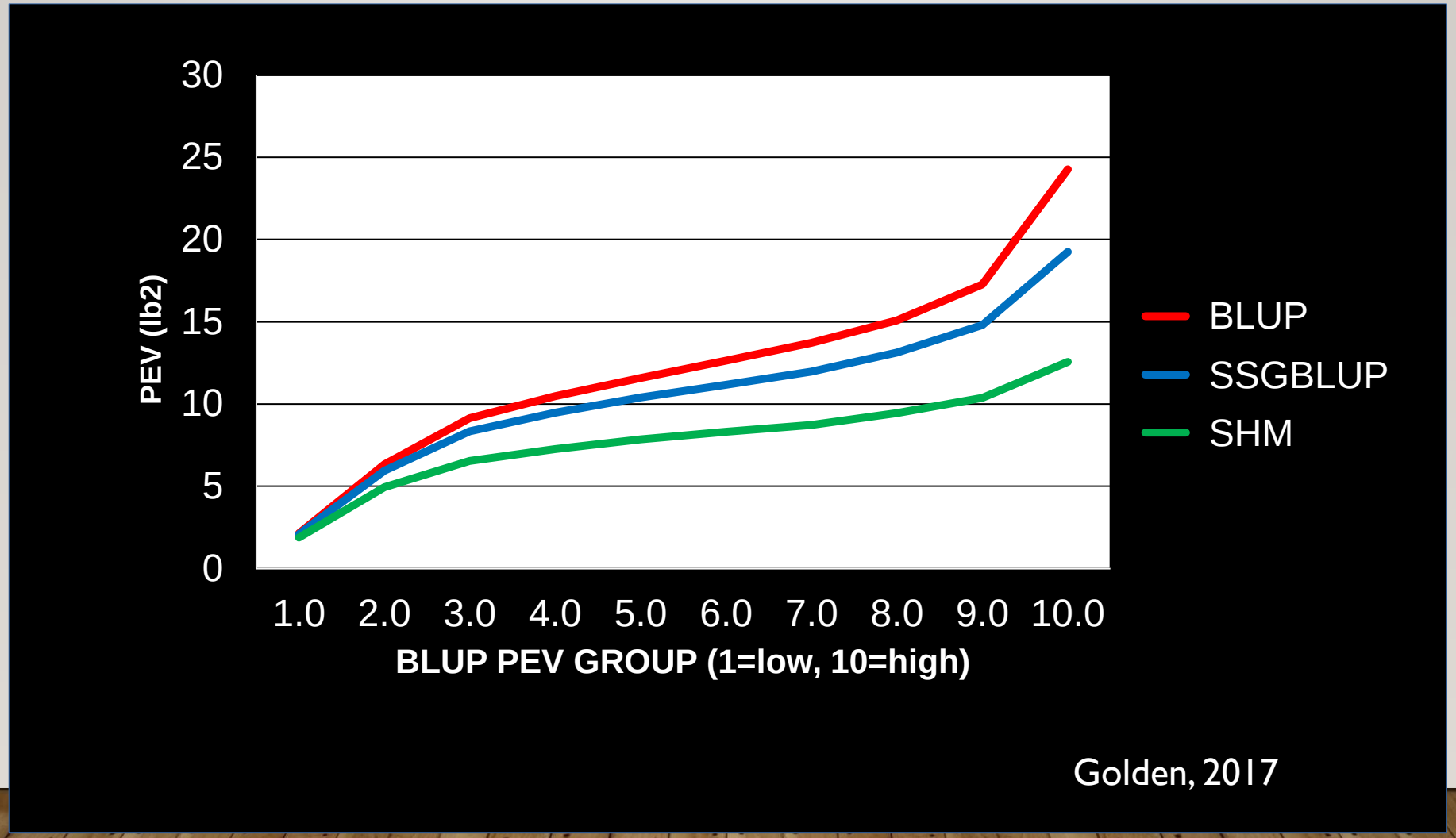
SINGLE STEP EVALUATIONS

PANEL %GV = 33%



Trait	2020 Estimated Progeny Equivalents
Calving Ease (Direct)	25+
Calving Ease (Total Maternal)	4
Birth Weight	22
Weaning Weight	25+
Yearling Weight	25+
Milk	19
Stayability	15
Docility	25+
Carcass Weight	5
Marbling	8
Rib Eye Area	6
Back Fat	8

BAYES Cπ MARKER SELECTION SQUEEZES OUT MORE ACCURACY



STRATEGERY!

Genotype

- Replacement heifer candidates
  - Control of genetic destiny; validate pedigree
- Bull offering
  - Validate pedigree; add accuracy to EPDs your clients use in selection
- Cows
  - Improved accuracy of progeny EPD, validate pedigree, discovery (new/novel traits)

Phenotype

- Deeply for conventional traits, novel traits
- Genos with no phenos is no Buenos! ☺

ASSOCIATION SPONSORED PROGRAMS

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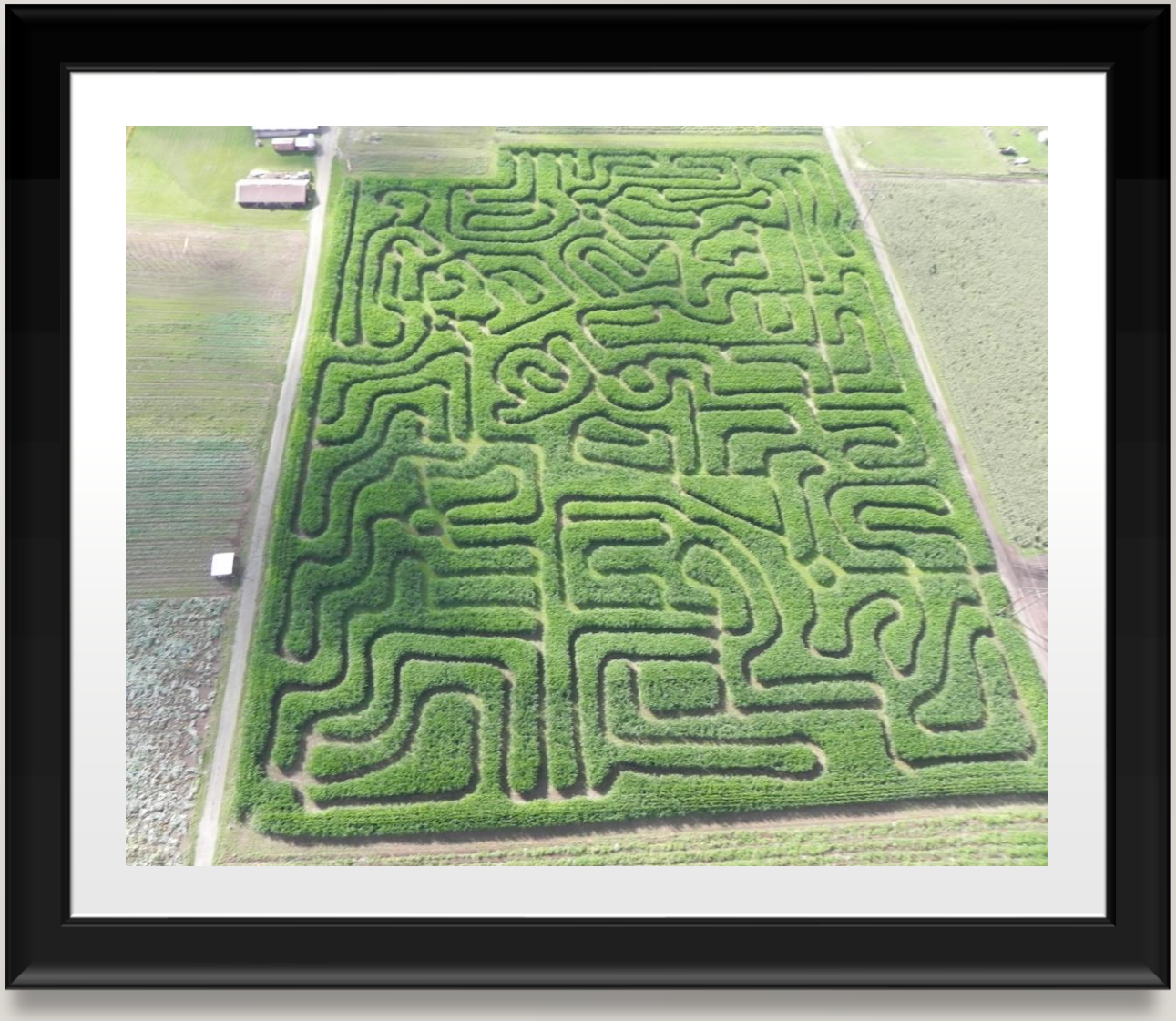
DRONE IMPACT ON CORN FARMER

- Our traditional view of the corn field…

DRONE IMPACT ON CORN FARMER

- Change Your Perspective?



How does new information and new technology change your view of genetic improvement?

Your product?




PREMISE: MAKE SUSTAINED GENETIC IMPROVEMENT IN YOUR PRODUCT

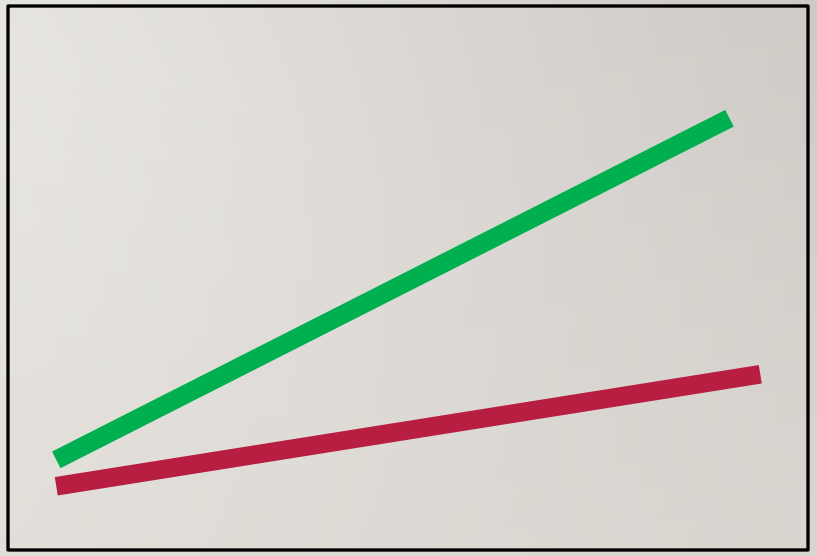
- Deming cycle
- Plan the work; work the plan
- Failure to plan is planning to fail
- You can't manage what you don't measure

ANIMAL VS. POPULATION PERSPECTIVE

- **M**arker **A**ssisted **M**arketing vs **M**arker **A**ssisted **S**election
  - If we don't change the behavior 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

MIND THE GAP!!

- Widening gap in genetic merit
  - Across breeds
  - Within breed
  - Among breeders
- Genomic Selection: Winners and less-than-winners (losers?)



- Are you widening the GAP? At the top or the bottom?

ADOPTION OF COMPLIMENTARY TOOLS

- Genomics
- Novel phenotypes/Essential ERT
- Advanced Repro Technologies
  - MOET
  - IVF
  - Gender Selected Semen

Avoid:

More mistakes faster.

–Lewis Weaber

HOW WILL YOU GET TO THE OTHER SIDE?

HOW WILL YOU GET TO THE OTHER SIDE?

HOW WILL YOU GET TO THE OTHER SIDE?

THANK YOU!

QUESTIONS?

BOB WEABER, PH.D.

KANSAS STATE UNIVERSITY

785-532-1460

BWEABER@K-STATE.EDU