



General Overview of Genomics

K-STATE
Research and Extension

Bob Weaber, Ph.D.

Cow-Calf Extension Specialist

Assistant Professor

Dept. of Animal Sciences and Industry

bweaber@k-state.edu



Overview

- Why might genomics be important for the genetic improvement of beef cattle?
- Definitions/glossary
- Organization of cattle genome
- Tools in the toolbox
 - SNP markers
 - High density assays
- How we use the tools to detect and exploit genetic variation
 - Linkage Disequilibrium
 - Linkage
 - Genome Wide Association Studies (GWAS)

Why might genomics be important for genetic improvement of beef cattle?

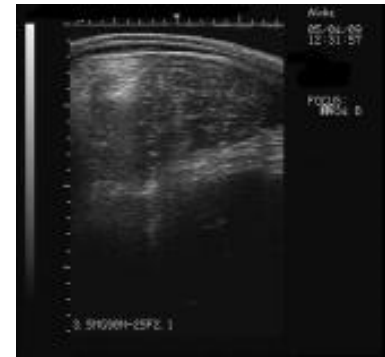




Sources of Value

Moser, 2011

D H D Traveler 6807 AAA #10858958 [AMF-NHP]
 S S Traveler 6807 T510 AAA #12502030 [AMF-CAF-NHP]
 S S Miss Hi Spade A114 AAA #11665432
 S S Objective T510 OT26 AAA #13776378 [AMF-CAF-NHP]
 S S Rito Rito R76 R011 AAA 11494687
 S S Miss Rita R011 7R8 AAA 12958951 [AMF-NHP]
 S S Miss Ultress U56 AAA 12490161
 B/R New Design 036 AAA #11418151 [AMF-CAF-NHP]
 G A R Predestined AAA #13395344 [AMF-CAF-NHP]
 G A R Ext 4206 AAA #*12716727
 K S U 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-NHP]
 # Pathfinder + Embryo Transplant



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

K S U Objective 0183 Reg: AAA 16754371 Bull [NHP]

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

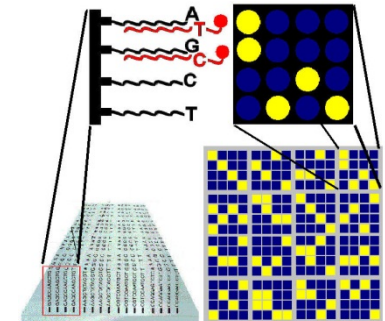
Production							Maternal						
CEA Acc	BW Acc	WW Acc	YW Acc	RADG Acc	YH Acc	SC Acc	Doc Acc	CEM Acc	Milk Acc	M&M M&D	MW Acc	MH Acc	SEN
+9	+1.9	+62	+111		I+1.2	I+8	+8	+27	I+63	I+7			-10.38
.29	.34	.25	.19		.05	.05	.19	.20	.05	.05			

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

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

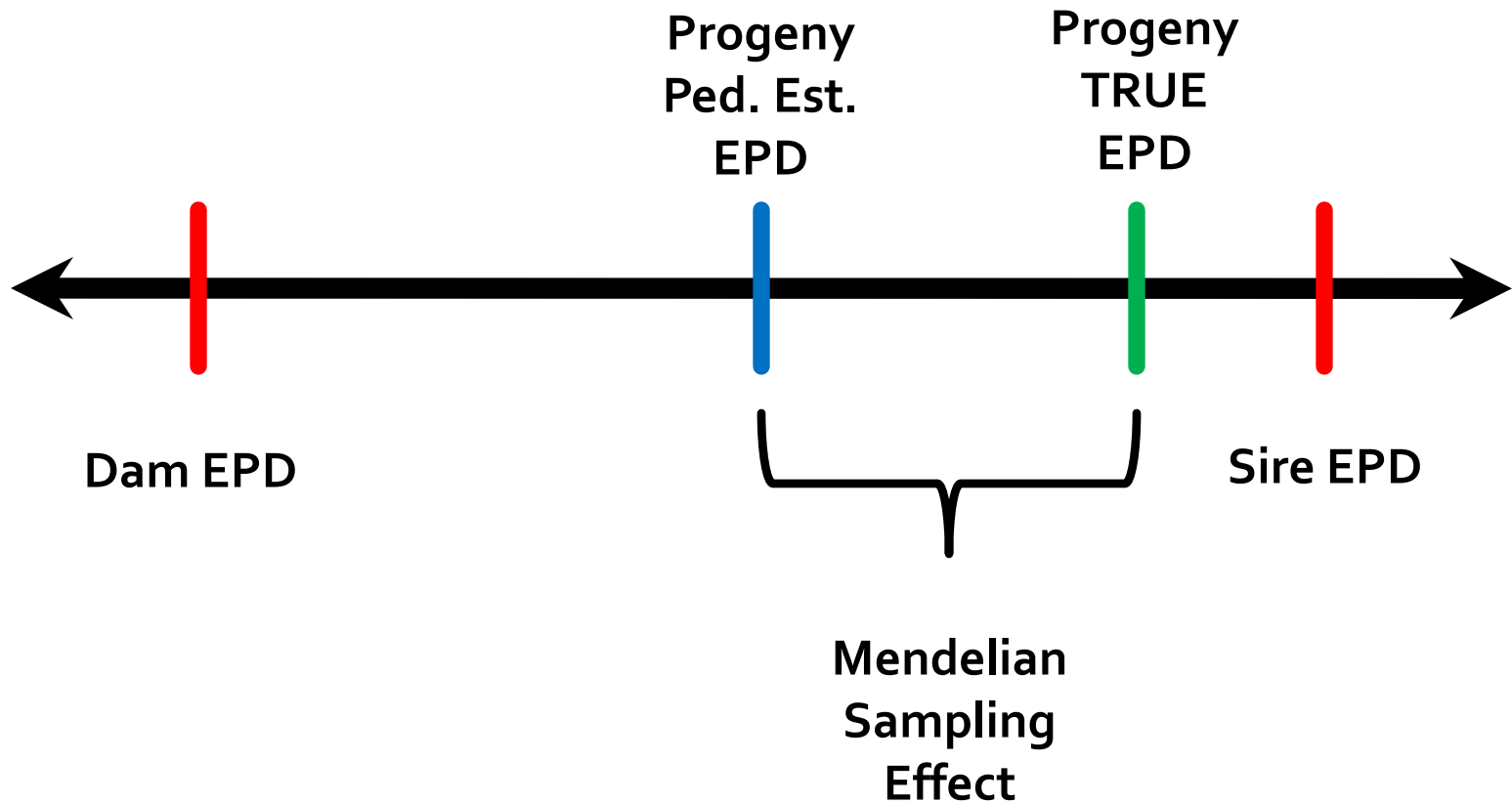
296850 BO 11222010

American Angus Association® 3201 Frederick Ave. St. Joseph, MO 64506





Finding True Genetic Merit





So When Are Markers Helpful?

- Traits that are hard/expensive to measure
 - Disease, reproduction, stayability, etc.
- Qualitative traits with economic impact
 - Horned/polled, color
- Collectively account for large portion of genetic variation of trait, inexpensive to test
- Results incorporated into NCE programs
 - Markers are not a substitute for EPDs
- Very useful for parentage identification and pedigree validation (seedstock)

Definitions/Glossary





Define: genomics

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)—compare proteomics



Glossary of Genetic Terms

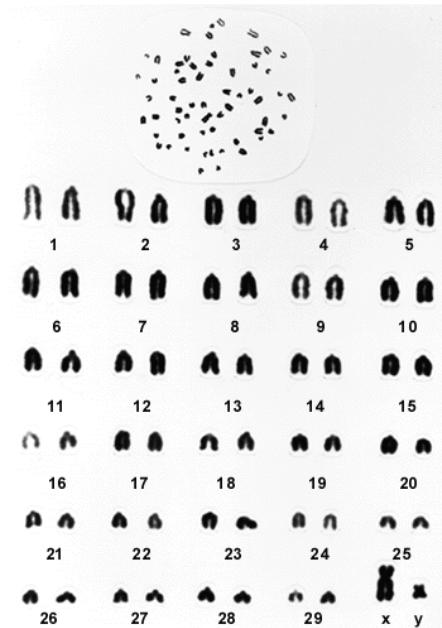
- **Genome:** the genetic material of an organism.
- **Chromosome:** organized compaction of DNA in nucleus of cell that contains genes; occur in homologous pairs in cattle.
- **Locus:** position in a chromosome of a specific gene.
- **Intron:** polynucleotide sequence that does not code for a protein or other gene product.
- **Exon:** polynucleotide sequence that is copied and spliced together to form messenger RNA and ultimately a protein or other gene product.



Glossary of Genetic Terms

- **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.
- **Allele:** any of the alternate forms of a gene.
- **Nucleotide:** basic structural units of DNA (A, C, G, T)
- **Codon:** a specific sequence of three consecutive nucleotides that specifies a specific amino acid in a protein, or starts or stops protein synthesis
- **QTL:** Quantitative Trait Locus, region of chromosome associated with variation in a trait

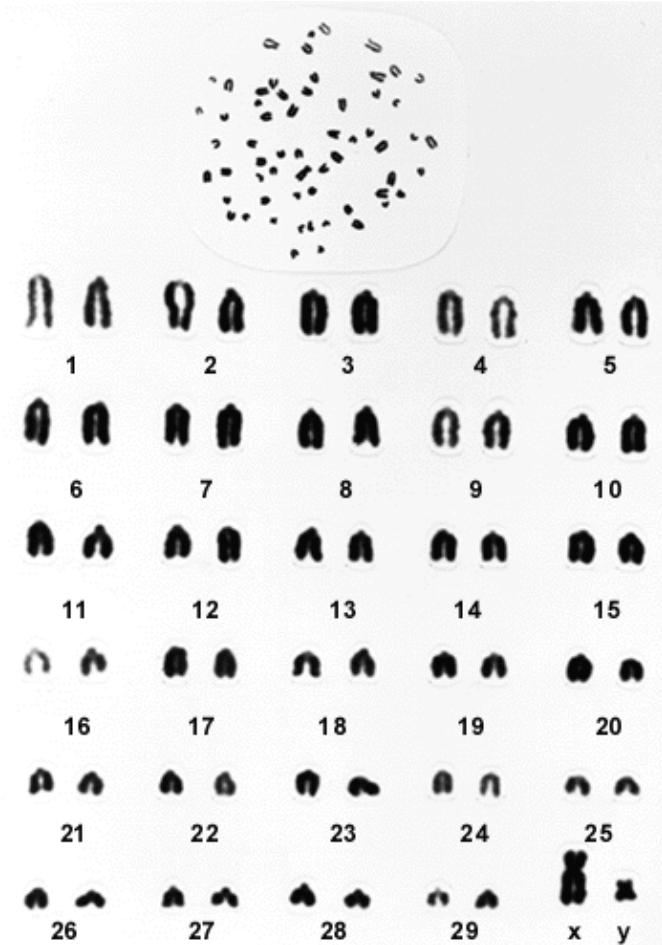
Organization of Cattle Genome





The Biology Assures Variation in Progeny

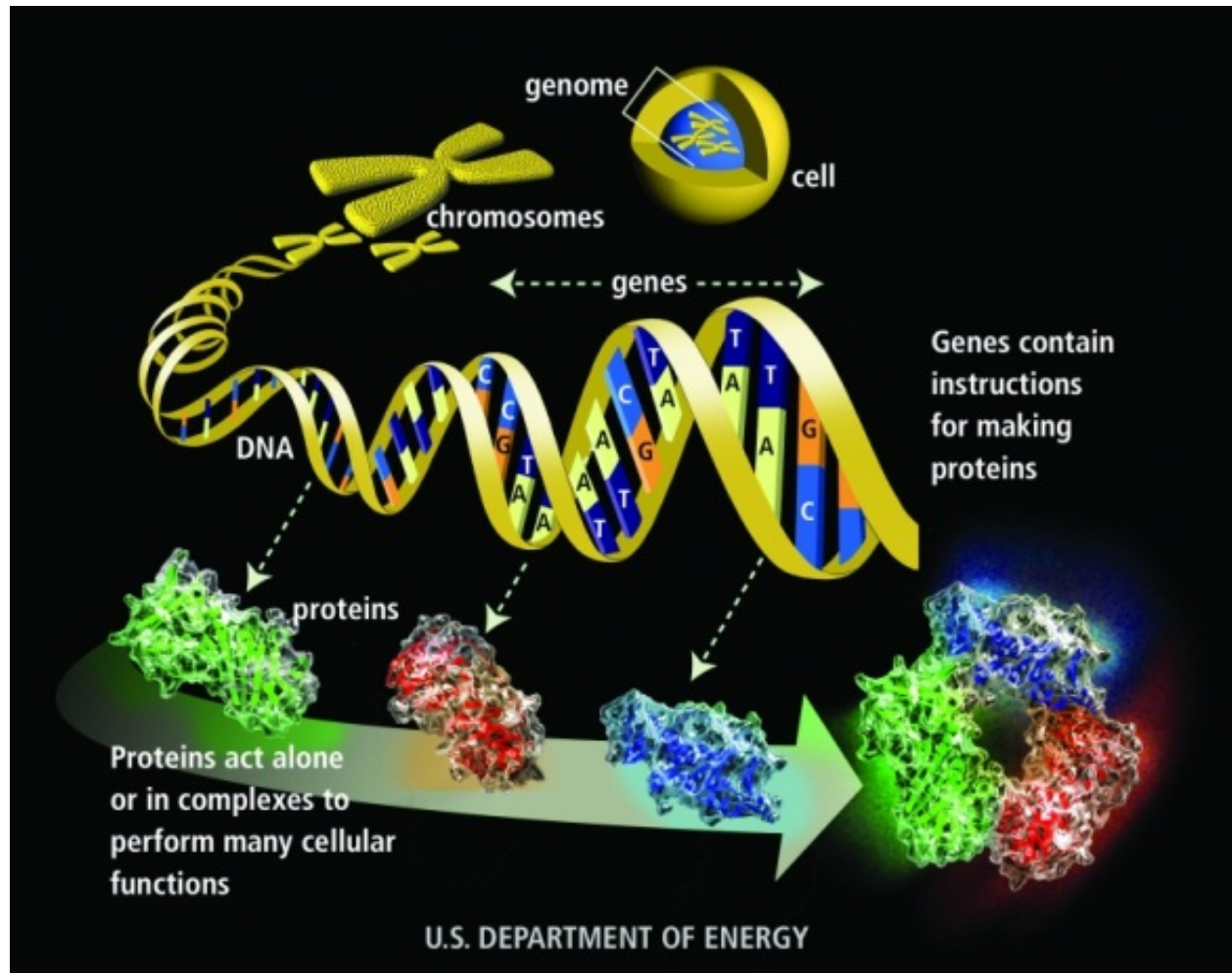
- Cattle have 30 pairs of chromosomes
 - 29 autosomes, 1 sex determining
 - Diploid (2 copies of each chromosome)
 - ~3.5 Billion base pairs
- Meiotic cell division forms gametes
 - Eggs and sperm are haploid
 - 1 chromosome from each pair; random
 - Recombination or cross-over events
- Fertilization restores diploid chromosome count
- Two copies of each gene
 - Alternate forms are called alleles



Genet. Mol. Biol. 1999, vol.22, n.3, pp. 369-373



Worth a 1,000 words?



Tools in the Genomics Tool Box





Single Nucleotide Polymorphism (SNP) DNA Marker Example

G/T SNP

1 BTA-6

...ATCGTAG**G**ATATTGGCC...

...TAGCAT**C**TATAACCGG...

2 BTA-6

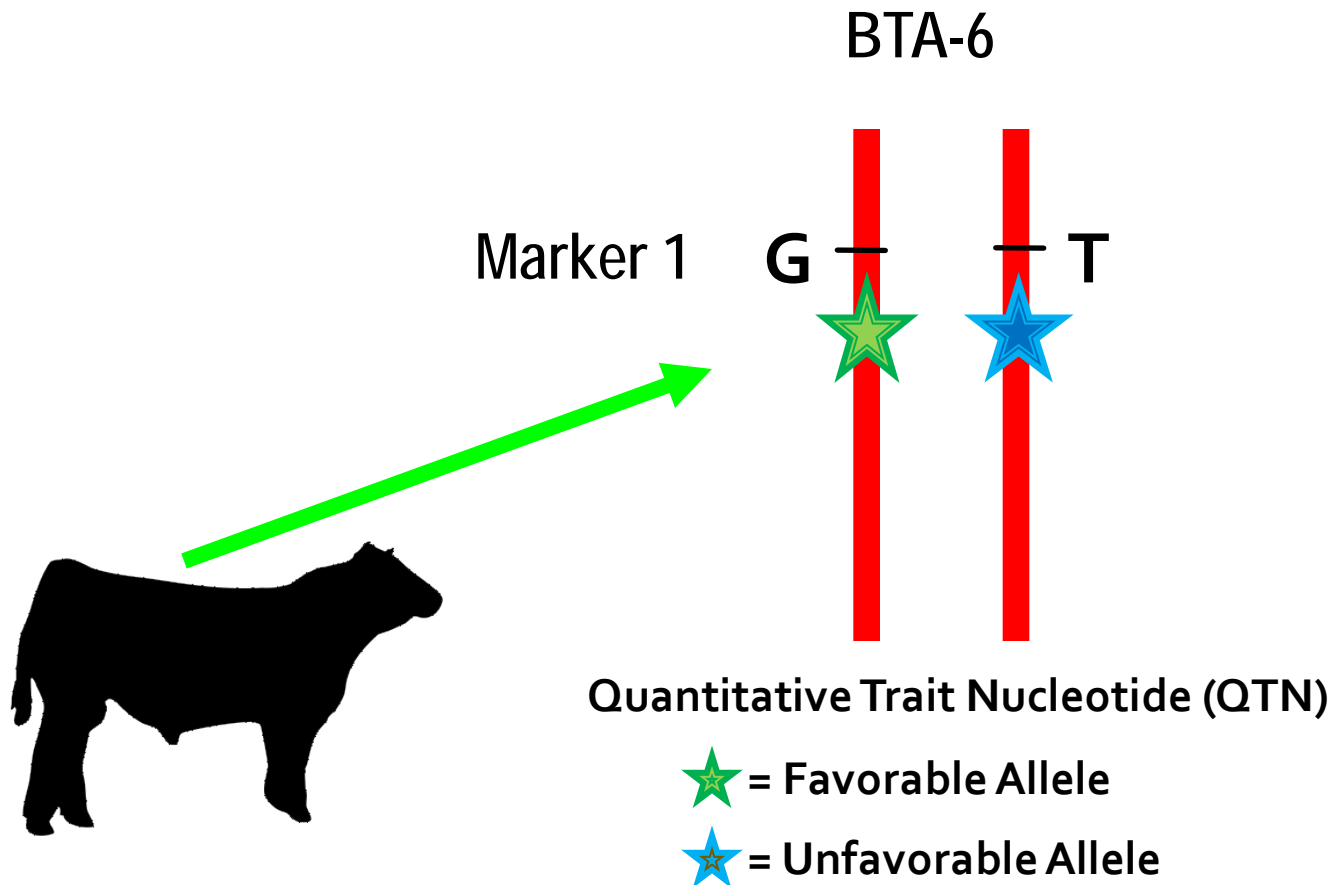
...ATCGTAT**T**ATATTGGCC...

...TAGCAT**A**TATAACCGG...

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



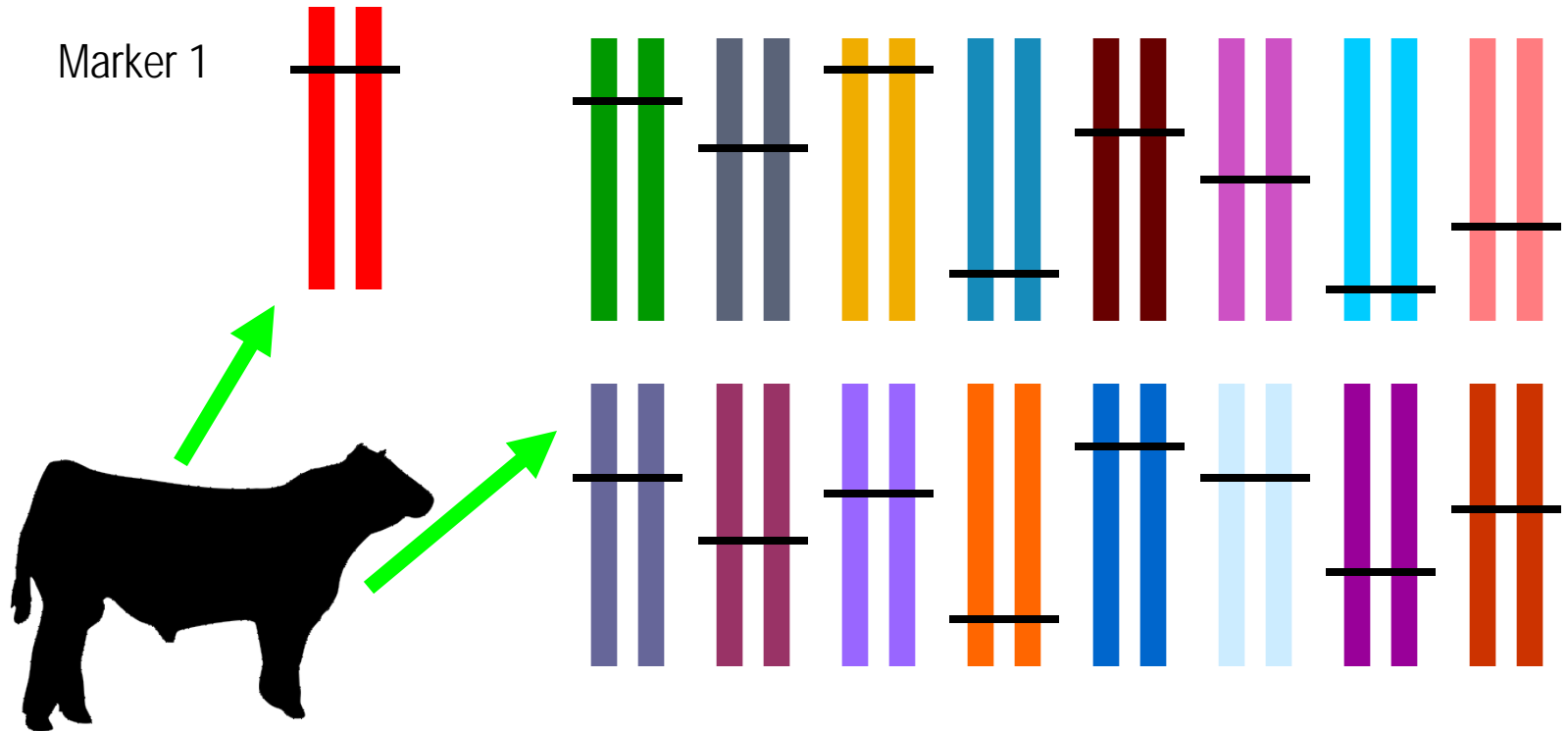
SNPs and QTNs





What a Marker Test Tells You:

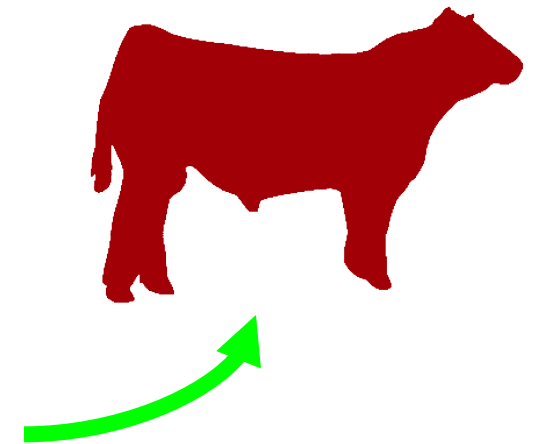
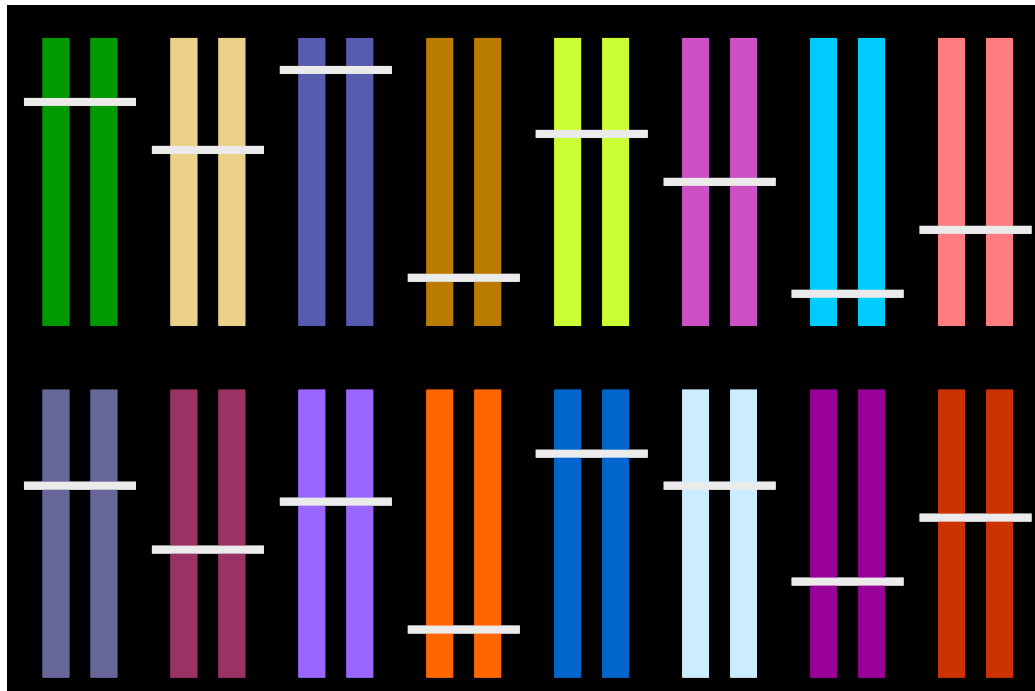
But What About These Genes?





What an EPD Tells You:

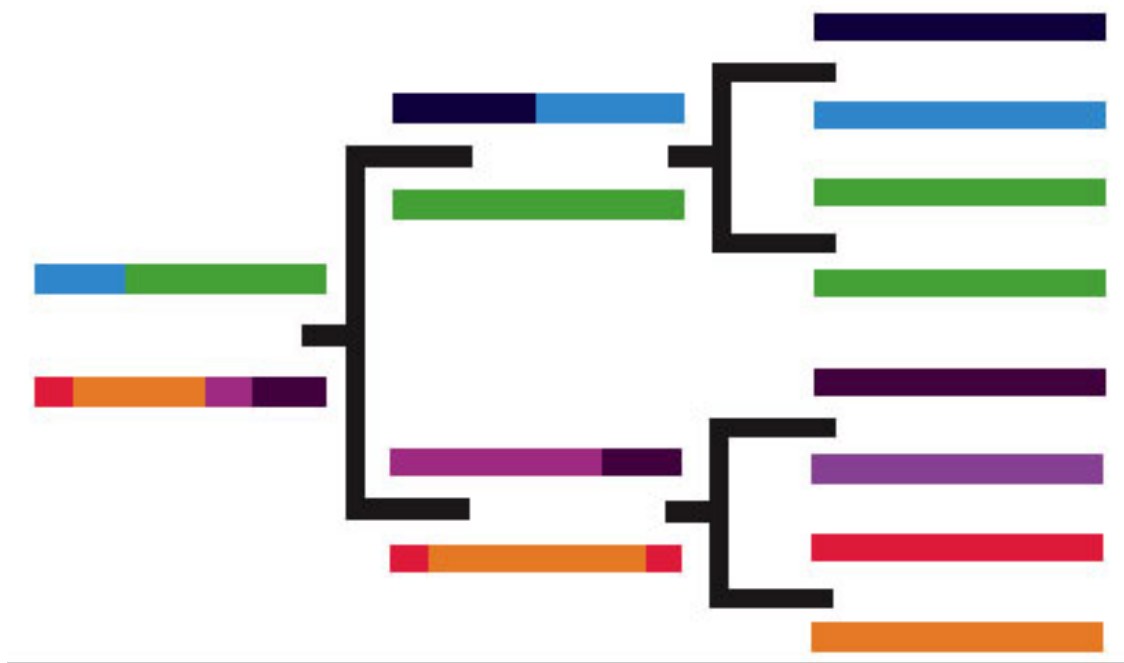
Cumulative effect of all genes and their interactions on a trait.





A genomic pedigree

SNP markers allow identification of regions of chromosome and tracking of inheritance of specific region





A Question of Resolution

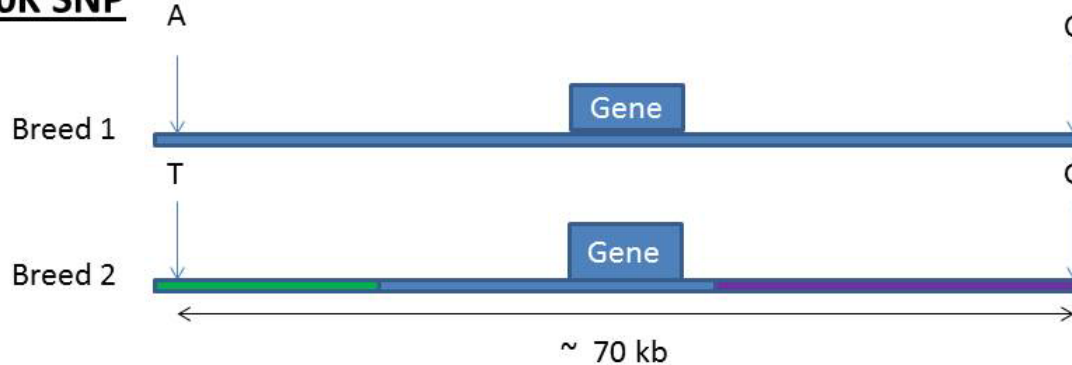
- Think of Bovine Genome as distance from Washington DC to Anchorage, AK ~3,300 miles
- 3K panel is equivalent to marker every mile
- 50K panel is marker every 100 yards
- 700K panel is marker every 22 feet



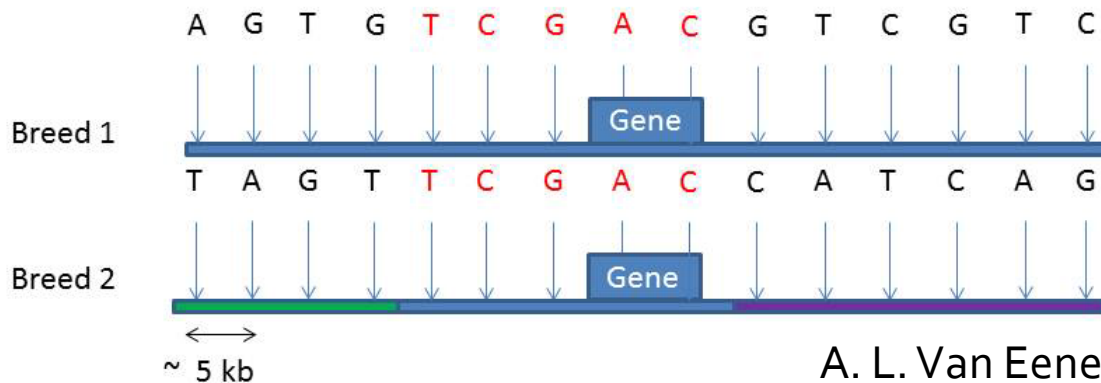


Research Will Transition to Higher Density Panels

A. 50K SNP



B. 700K SNP



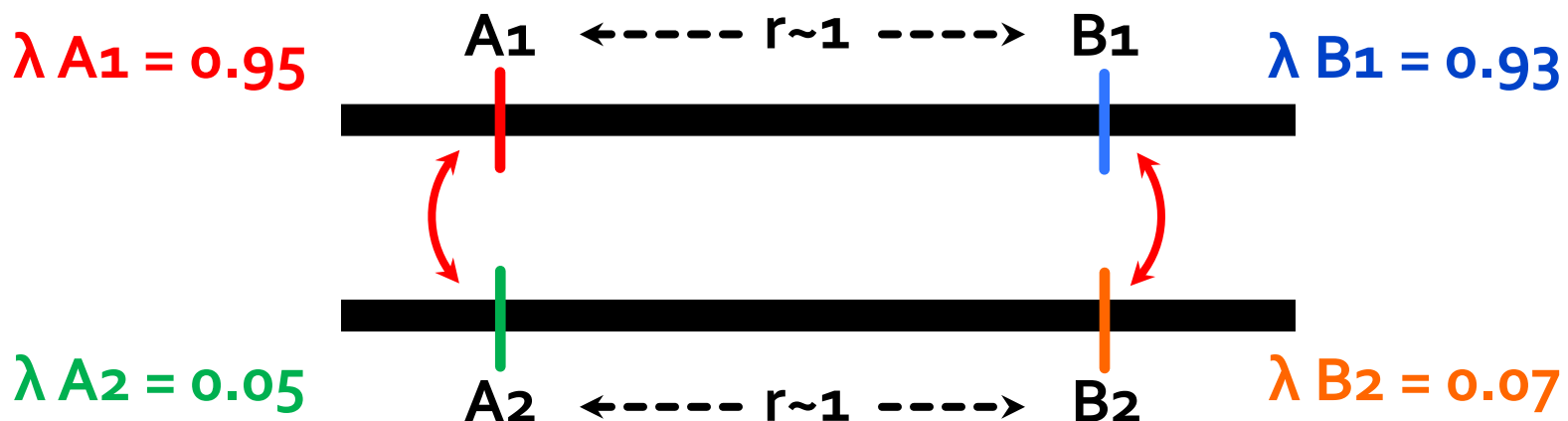
A. L. Van Eenennaam, 2011

Bovine Genome ~3.5 Billion bp; 3K SNP/1.17 Mb



Linkage Disequilibrium (LD)

- LD is the non-random association of alleles (markers) at two or more loci.
- LD describes the ability of SNP at one locus to act as surrogates for SNP at another locus
- Think correlation...ability of SNP at locus 1 to predict SNP at locus 2... 0 = independent, 1 = dependency





Linkage Disequilibrium (LD)

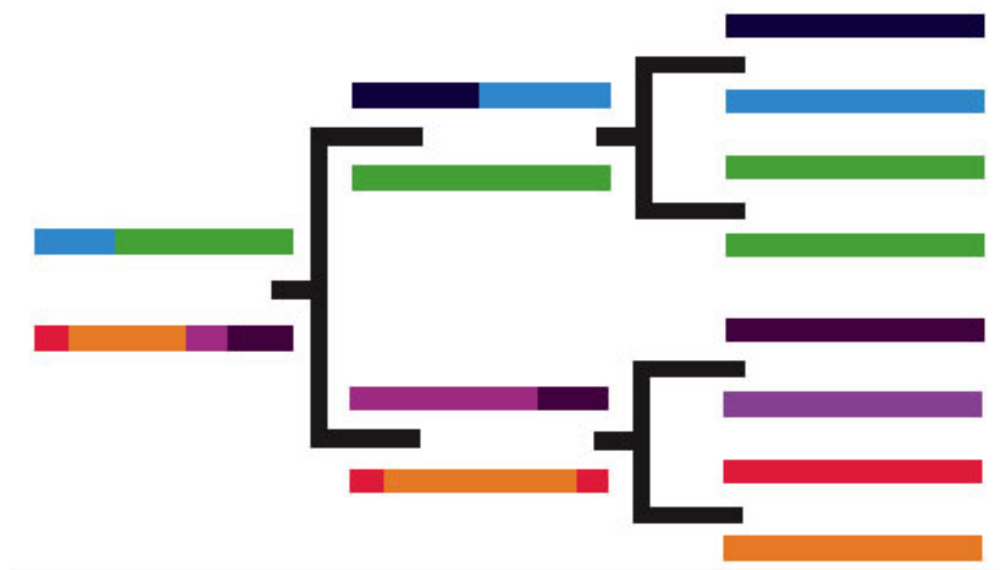
- Influenced by a variety of phenomena:
 - Linkage
 - Recombination rate
 - Genetic drift
 - Non-random mating
 - Population structure



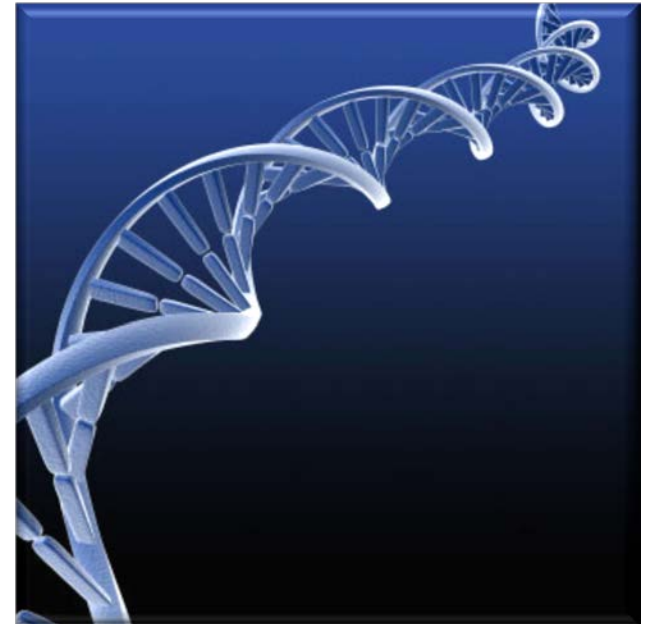


Linkage

- The tendency of certain loci to be inherited together
- Loci that are close to each other on chromosome tend to stay together during meiosis.
- Crossing over (recombination) breaks up linkage.



How do we use these tools?





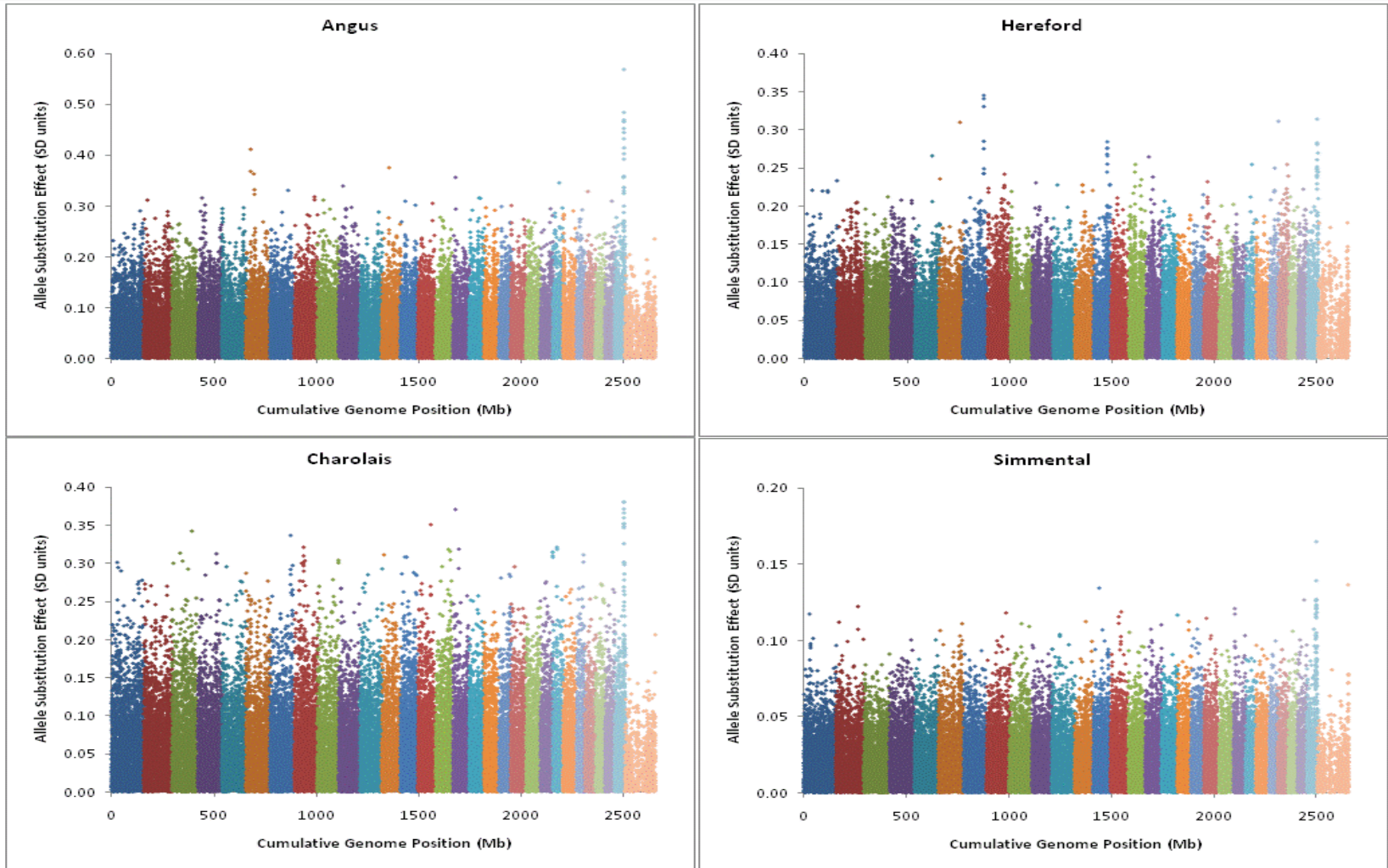
Genome Wide Association Study (GWAS)

- Find associations between a subset of markers (from a panel of markers) that are associated with variation in a trait(s)
- Variety of methods available to identify markers with statistically significant associations and to estimate the allele substitution effects.
- Summation of effects yields Molecular Breeding Value
- Not all markers on 50K panel associated with a trait(s), in fact many are not...
- MBVs used as data for computation of Genomically Enhanced – Expected Progeny Differences (GE-EPD)



WBSF GWAS NCBA CMP

McClure et al., 2011





Thank You!
Questions?

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