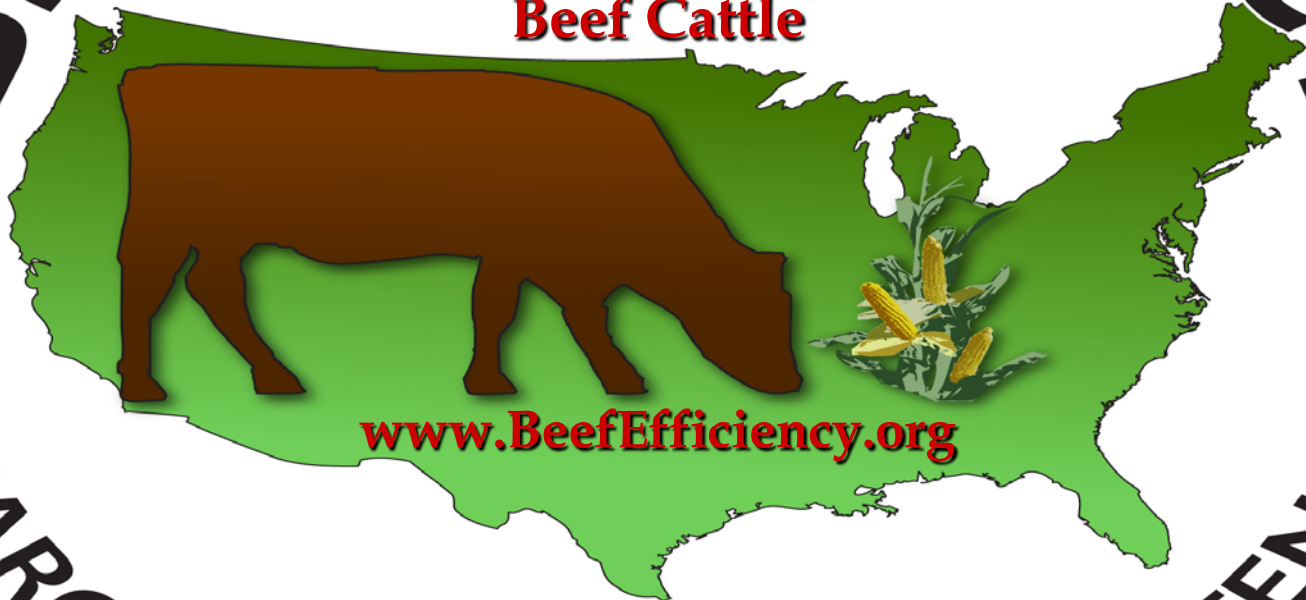


BEEF EFFICIENCY

**National Program for Genetic
Improvement of Feed Efficiency in
Beef Cattle**

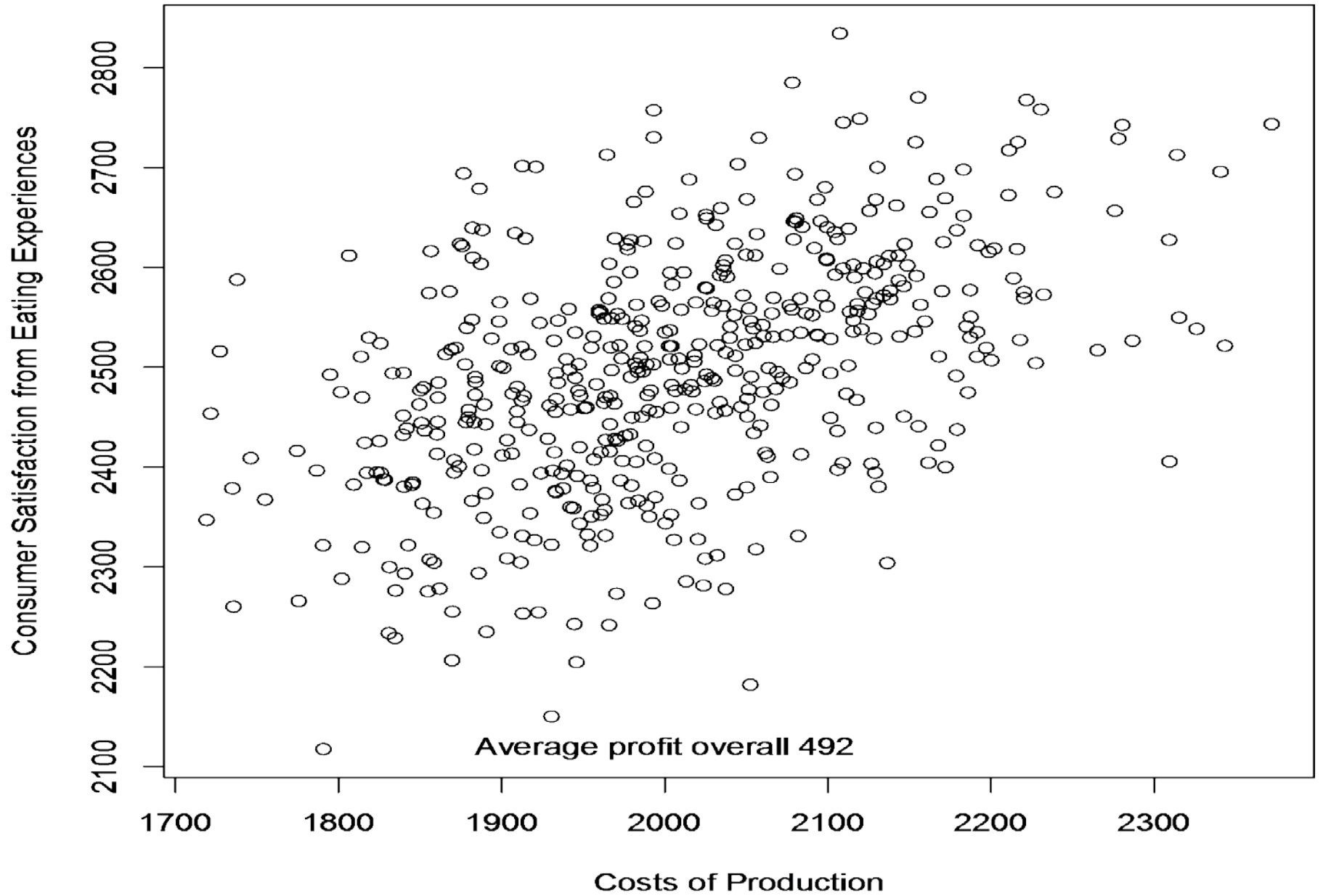


www.BeefEfficiency.org

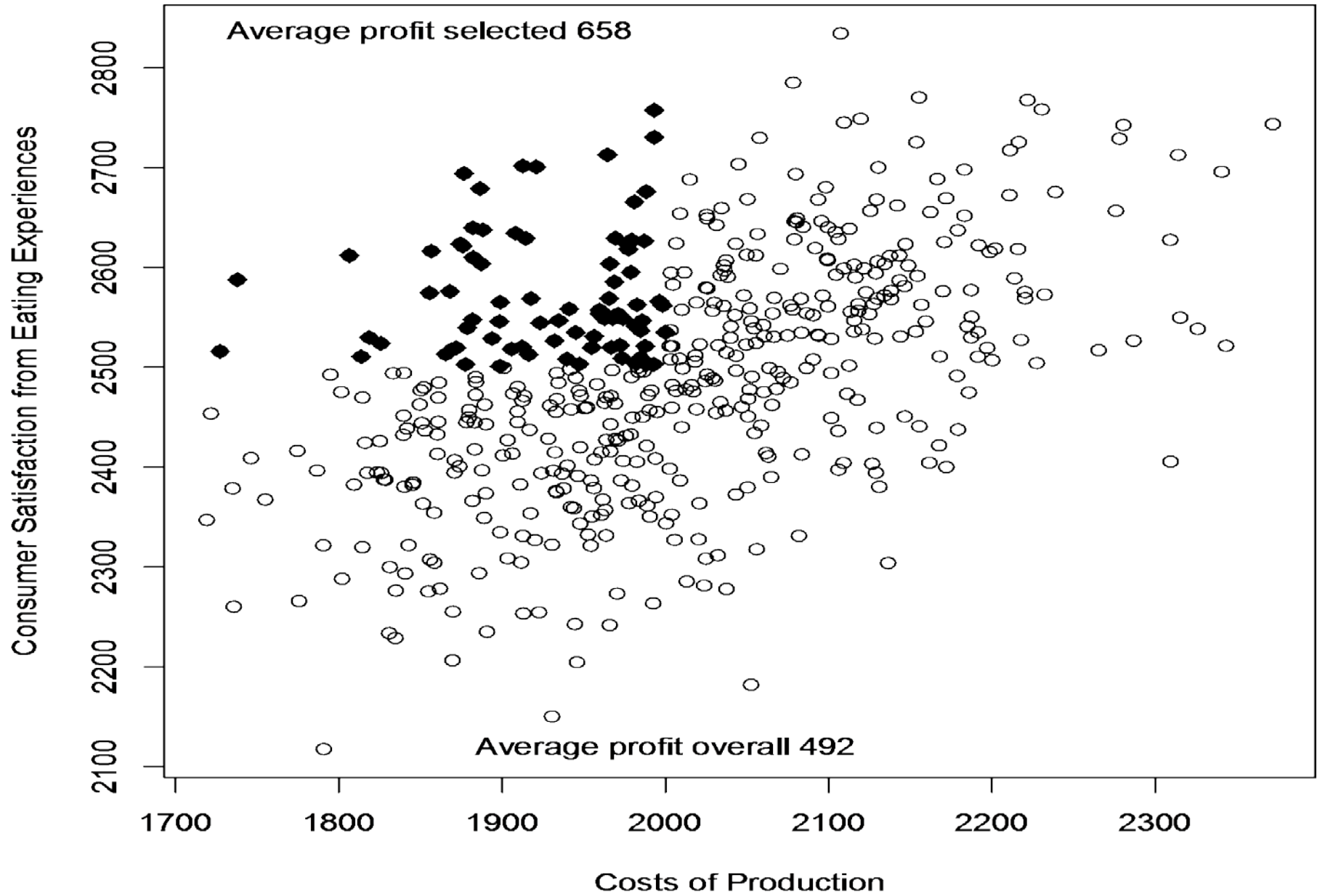
RESEARCH - EDUCATION - EXTENSION

BrownBagger
October 29 2014

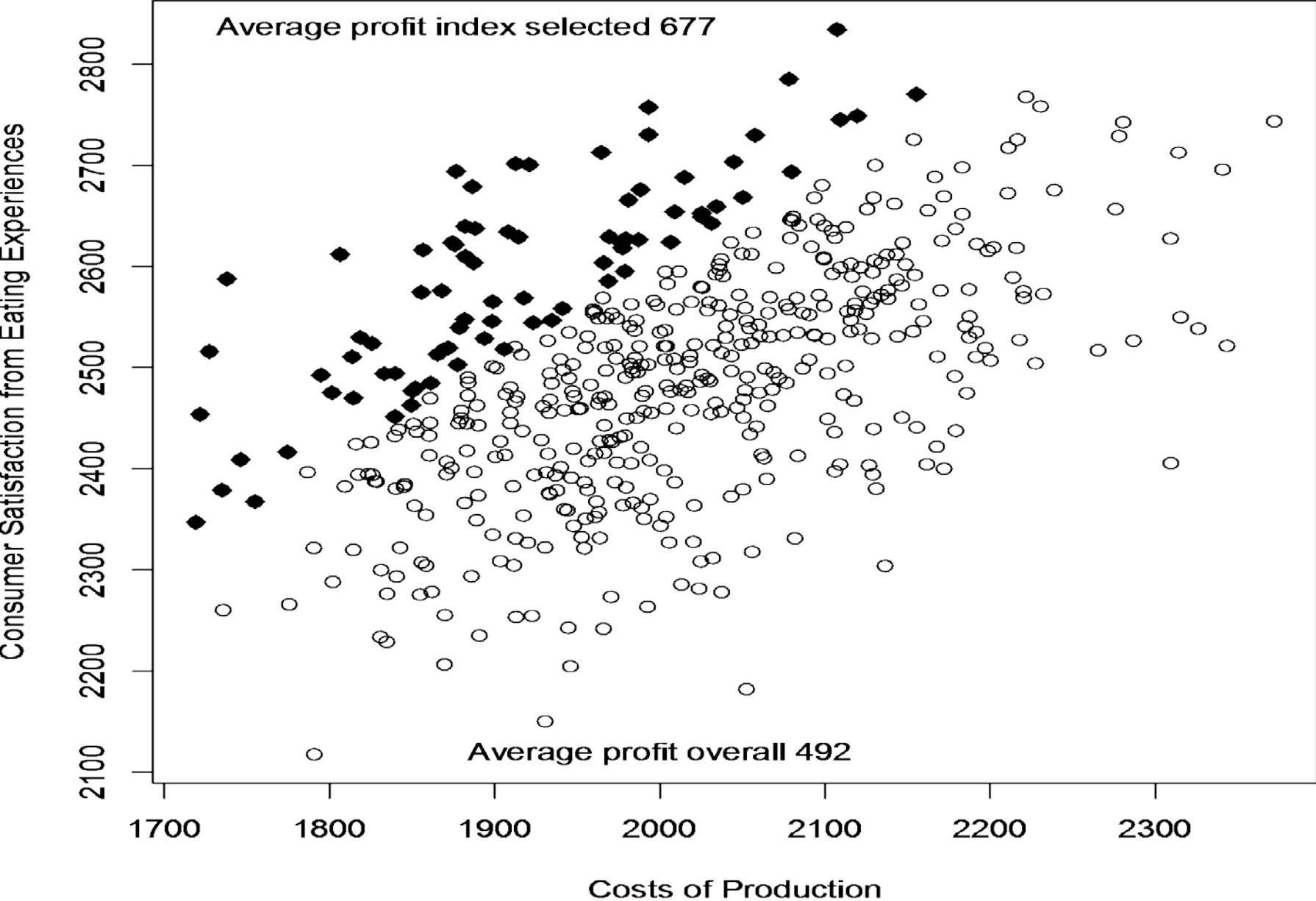
Sire Progeny Means



Independent Culling Levels



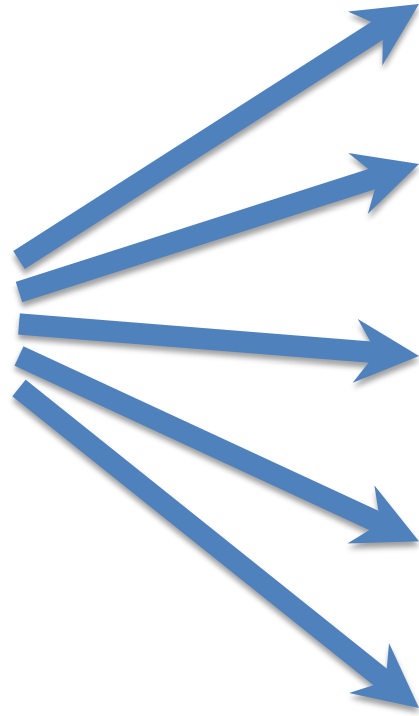
Index Selection



Suppose we generate 100 progeny on
1 bull



Sire

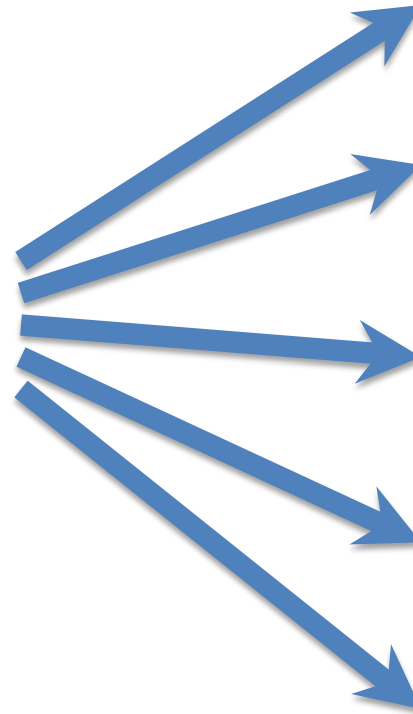


Progeny

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 $\frac{3}{4}$ diversity of the entire population

We learn about parents from progeny



Sire



+30 lb



+15 lb



-10 lb



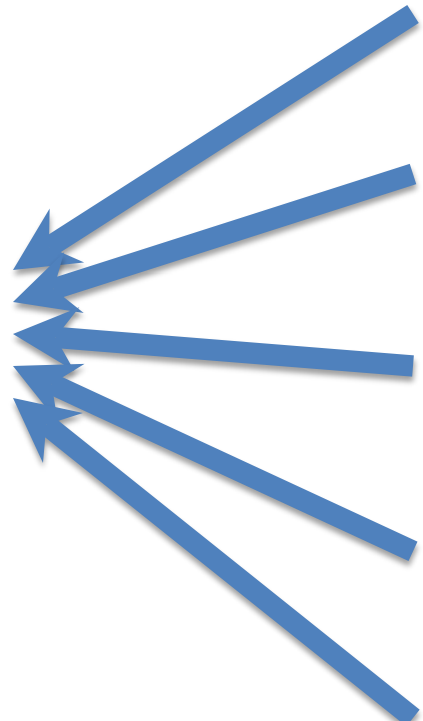
+ 5 lb



+10 lb

Sire EPD +8-9 lb (EPD is "shrunk")

Progeny +10 lb

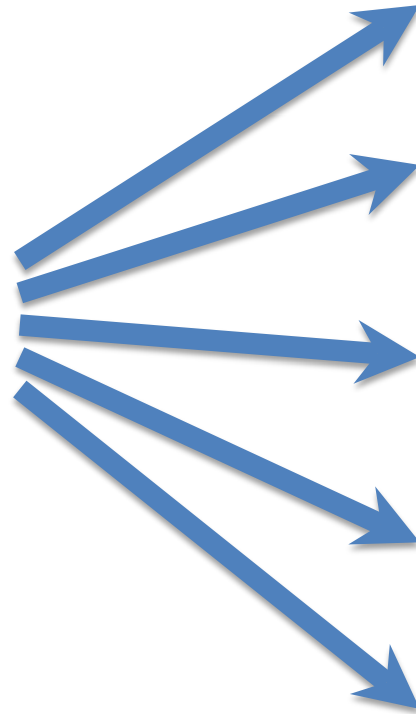


Suppose we generate new progeny



Sire

Sire EPD +8-9 lb



Progeny

Expect them to be 8-9 lb heavier than those from an average sire

Some will be more others will be less but we cant tell which are better without "buying" more information

Four Datasets

- Hereford Cattle fed at Olsens (HD)
 - 847 animals in 10 contemporary groups
- F1² composites fed at USMARC (50k)
 - 1,160 animals in 15 contemporary groups (+9)
- Legacy Simmental cattle fed at Illinois (HD)
 - 1,444 animals in 202 contemporary groups
- Legacy Angus cattle fed at Circle A (HD)
 - 1,580 animals in 102 contemporary groups

Dry Matter Intake

Study	Genetic Var	Residual Var	Heritability
Hereford	3.2	4.6	0.41
USMARC	1.9	3.4	0.35
Simmental	1.35	3.65	0.27
Angus	4.1	7.5	0.35

Mid-test Metabolic Weight

Study	Genetic Var	Residual Var	Heritability
Hereford	79	78	0.50
USMARC	84	97	0.47
Simmental	28	36	0.48
Angus	125	130	0.49

Gain on Test

Study	Genetic Var	Residual Var	Heritability
Hereford	.09	.23	0.27
USMARC	.07	.16	0.30
Simmental	.04	.13	0.23
Angus	.06	.24	0.19

Residual Feed Intake

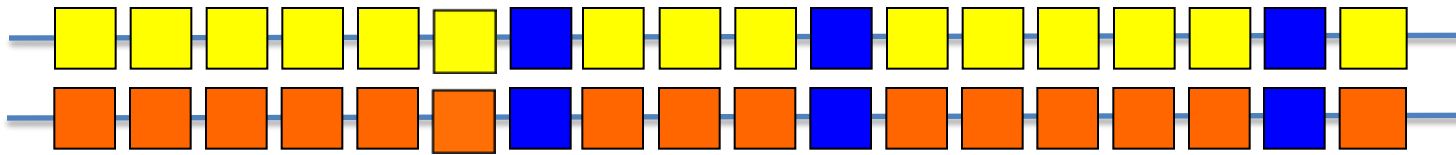
Study	Genetic Var	Residual Var	Heritability
Hereford	1.6	1.9	0.45
USMARC	0.91	0.94	0.49
Simmental	0.96	2.02	0.32
Angus	1.3	4.8	0.21

Background

- Feed Intake (FI), required along with output production measures to characterize efficiency, is heritable but not cost-effective or practical for routine measurement across the national spectrum of seedstock and commercial cattle

Chromosomes are a sequence of base pairs

Part of 1 pair
of chromosomes



Cattle usually have 30 pairs of chromosomes

One member of each pair was inherited from the sire, one from the dam

Each chromosome has about 100 million base pairs (A, G, T or C)

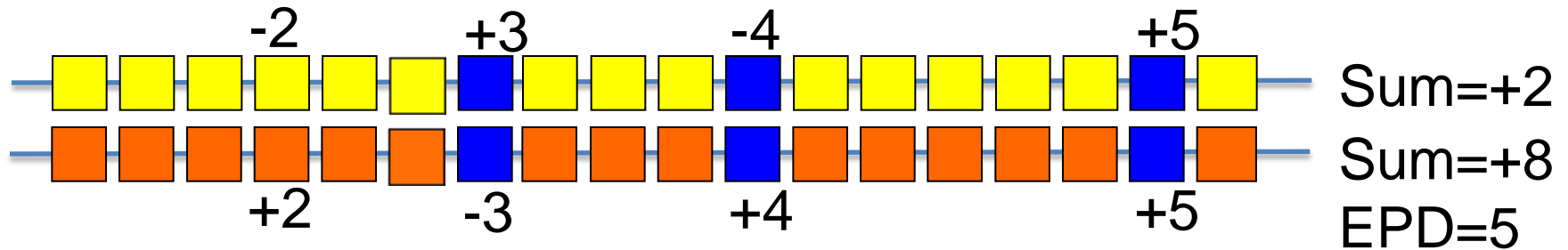
About 3 billion describe the animal

 Blue base pairs represent genes

 Yellow represents the strand inherited from the sire

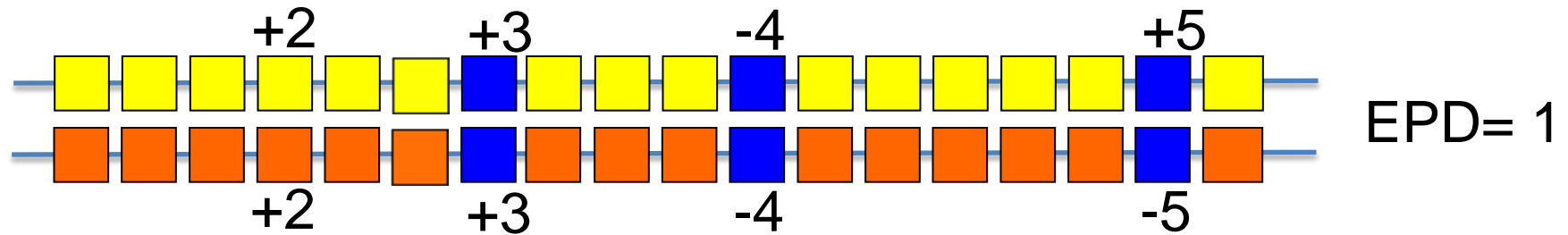
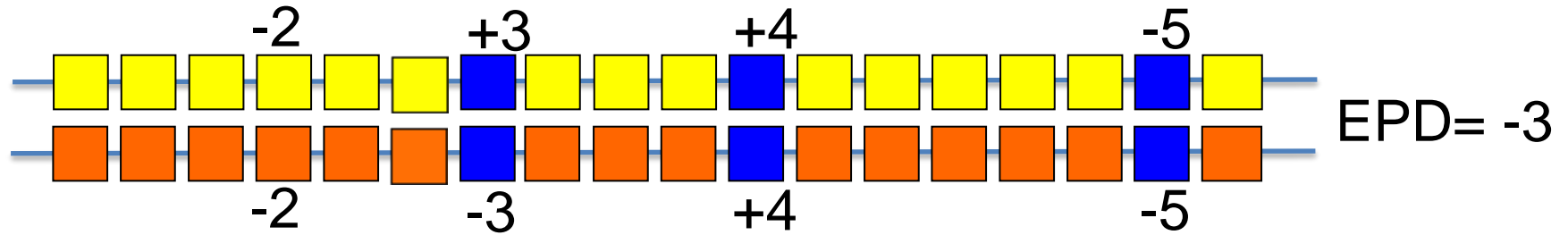
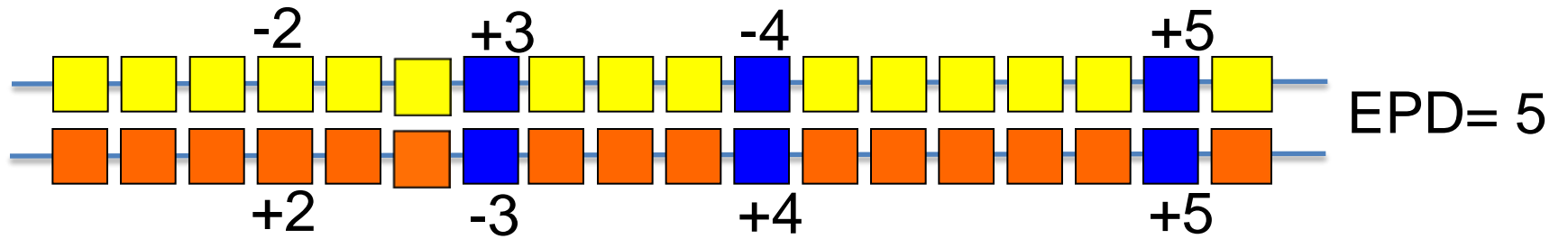
 Orange represents the strand inherited from the dam

EPD is half sum of average gene effects



Blue base pairs represent genes

Consider 3 Bulls



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

Goal

Predict components of feed efficiency
in animals without phenotypic data
based on knowledge of their genome

Approach

- Develop prediction equations based on joint analyses of phenotypic and genomic data
 - Variety of breeds and diets etc
- Apply those prediction equations to new animals
 - Validate predictions

Alleles are inherited in blocks

paternal



maternal



} Chromosome
pair

Alleles are inherited in blocks

paternal



maternal



} Chromosome
pair

Occasionally (30%) one or other chromosome is passed on intact

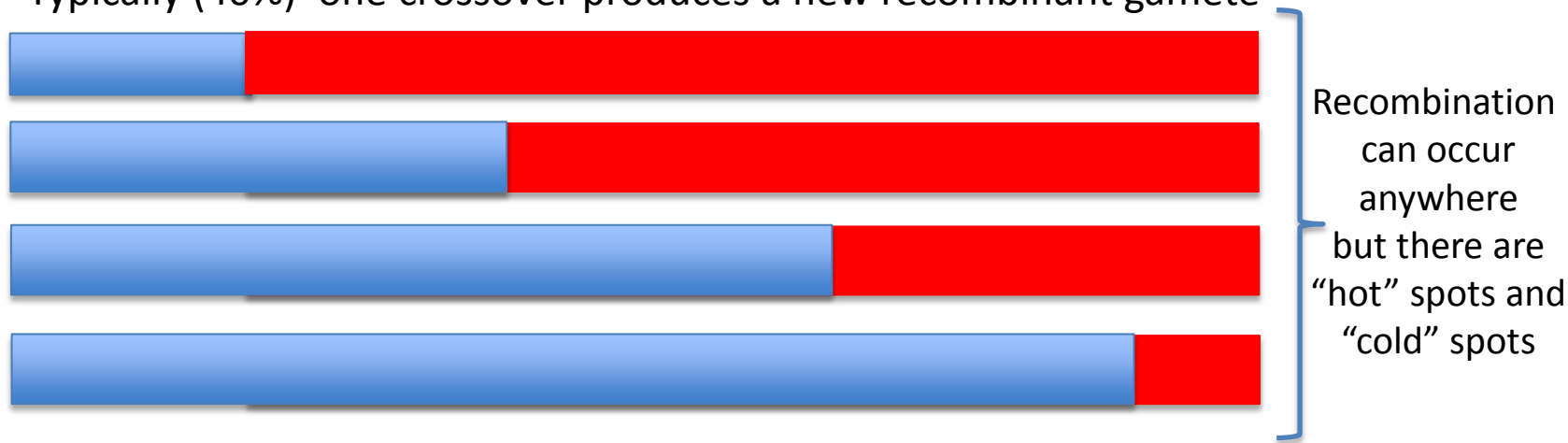
e.g



Alleles are inherited in blocks



Typically (40%) one crossover produces a new recombinant gamete



Alleles are inherited in blocks

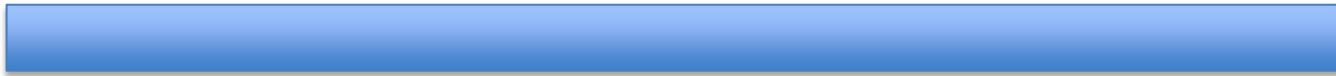


Sometimes there may be two (20%) or more (10%) crossovers



Alleles are inherited in blocks

paternal



maternal



Chromosome pair

Interestingly the number of crossovers varies between sires and is heritable



On

average



1 crossover

per

chromosome



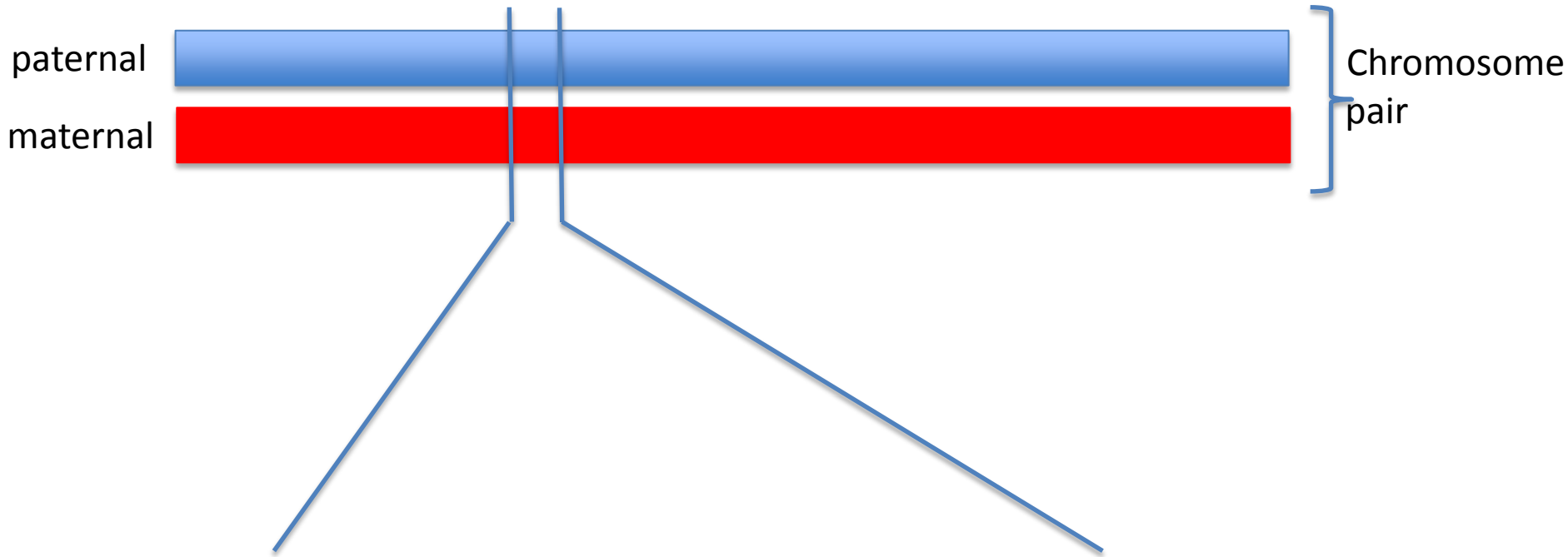
per

generation



Possible offspring chromosome inherited from one parent

Alleles are inherited in blocks

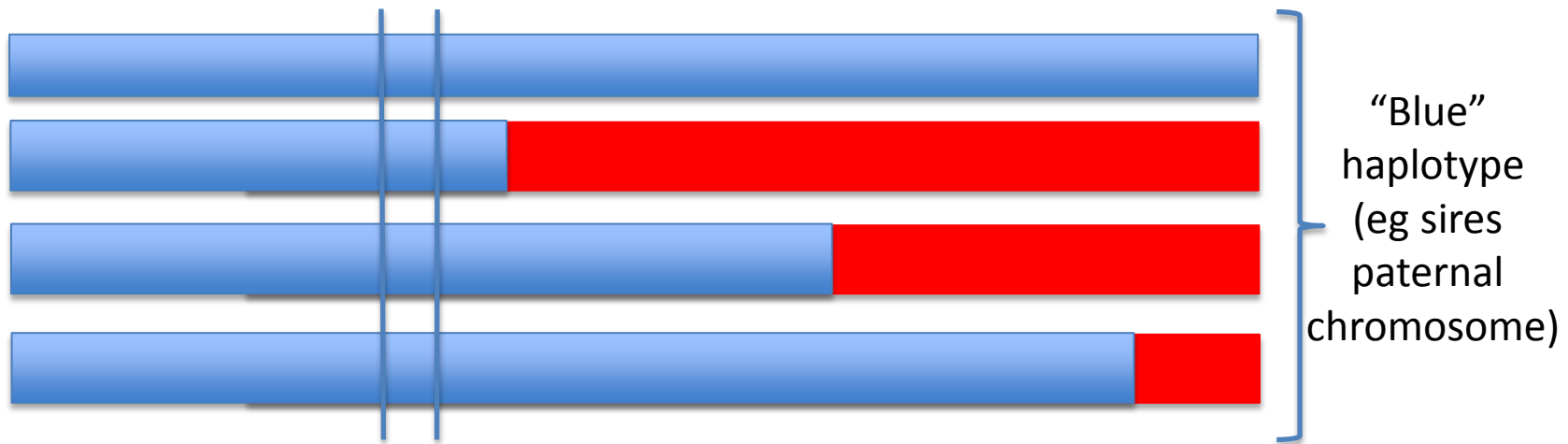


Consider a small window of say 1% chromosome (1 Mb)

Alleles are inherited in blocks



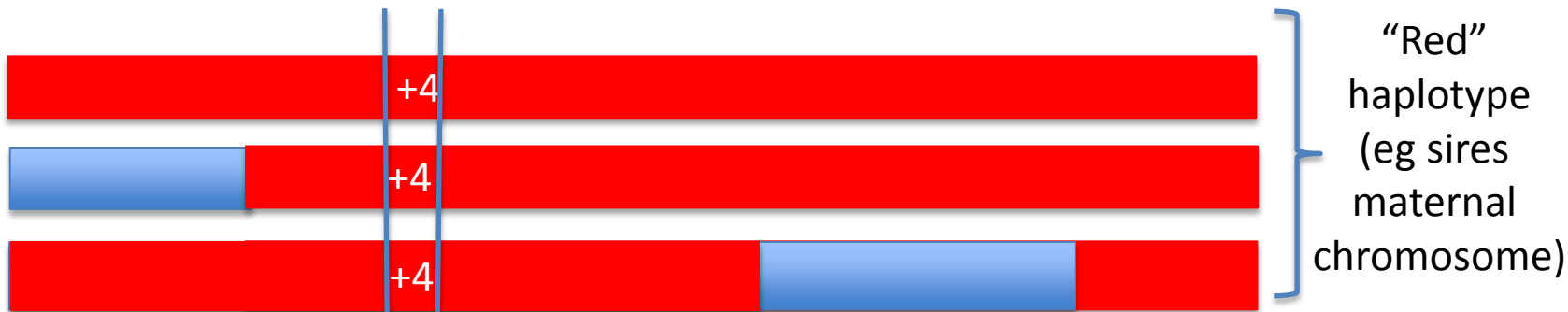
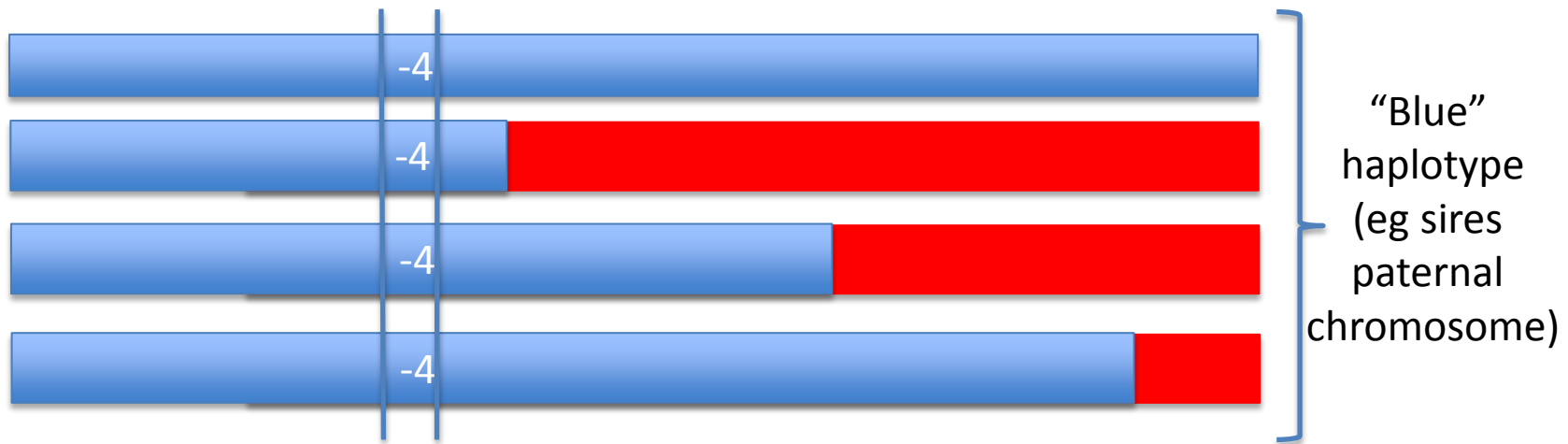
Offspring mostly (99%) segregate blue or red (about 1% are admixed)



Alleles are inherited in blocks



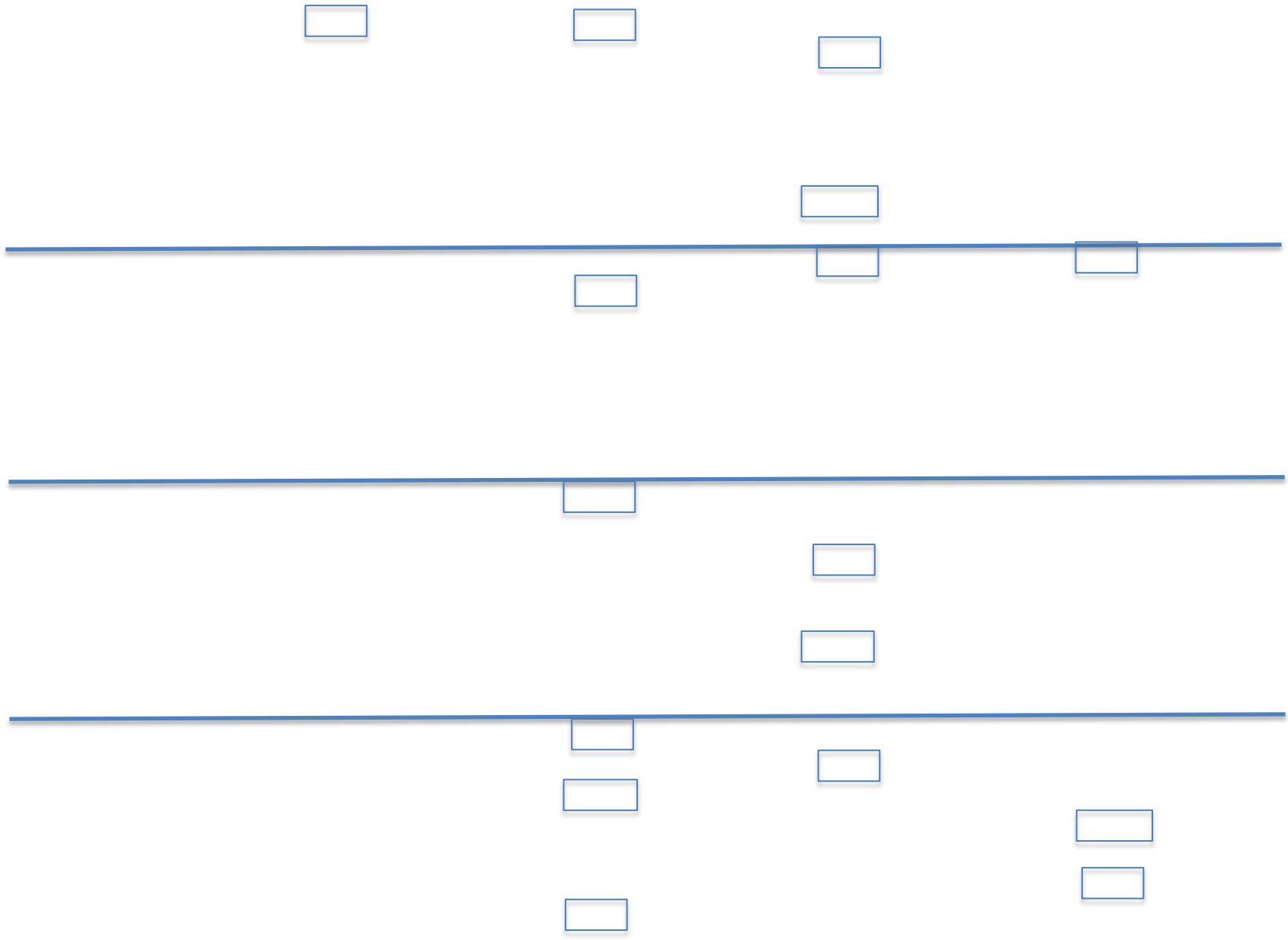
Offspring mostly (99%) segregate blue or red (about 1% are admixed)



Major Gene Results

Genome-Wide Association Study (GWAS)

Genomic regions
or Quantitative Trait Loci (QTL)
accounting for
 $\geq 1\%$ genetic variance



0 0.55 7_93

23 0.60 5_4

Across-breed Prospects

Across-breed prediction requires
having the same gene/feature
causing variation in different breeds

And having a marker that can identify the
favorable allele(s) regardless of breed

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Industry Roll out

- Angus (AAA)
 - Use Residual Average Daily Gain (RADG) EPD predicted from intake and growth information as well as genomic information
- Hereford (AHA)
 - Prototype EPD based on measured DMI that will include genomic information in the near future
- Simmental (and its affiliate breeds)
 - Red Angus, Gelbvieh, Limousin, Maine Anjou, Shorthorn etc)
 - Current DMI EPD used in indexes that is based on predicted DMI from production phenotypes and will include measured DMI and genomic information in future

Summary

- This multi-institutional 5-Year national project is
 - Undertaking basic and applied research related to identifying factors that improve feed efficiency
 - Extending its findings to stakeholders using a variety of communication approaches
 - Implementing its discoveries within the context of the beef industry infrastructure

The Participants



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United States Department of Agriculture
National Institute of Food and Agriculture

20 investigators 10 institutions

