Progress on genomics portion of reducing cost of efficient beef production study

Objective:
Identify association between variations in DNA sequence and animal performance.

(Find DNA MARKERS for traits)

Variation in DNA sequence

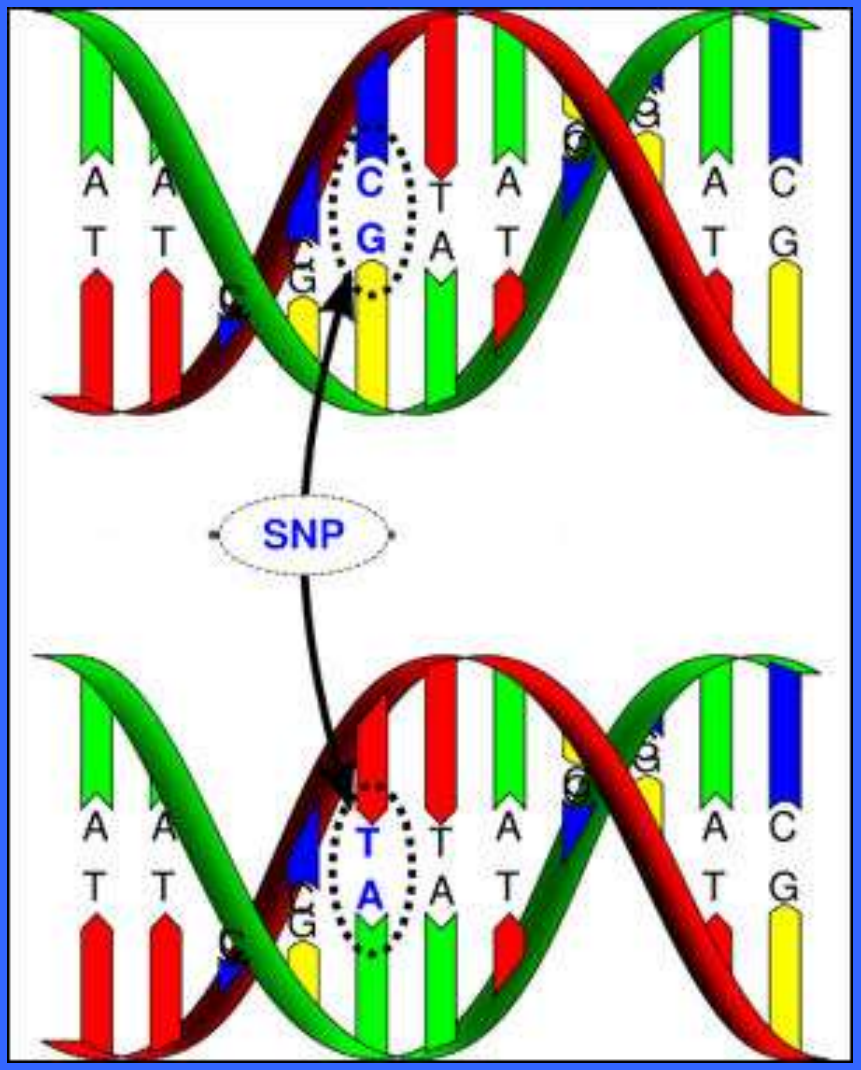
29 Autosomes + X Y

2 DNA strands/ Chromosome

3 Billion base pair

ATCG

TAGC



DNA Marker

- Differences in the sequence (A,T,G,C) of DNA that are associated with variation in a trait.

  - Difference in sequence may cause variation

  OR

  - Difference in sequence may be “marker” of the variation.

Types of Markers

- Single nucleotide polymorphism (**SNP**)

ATTTACA

ATTTGCA

- Microsatellite

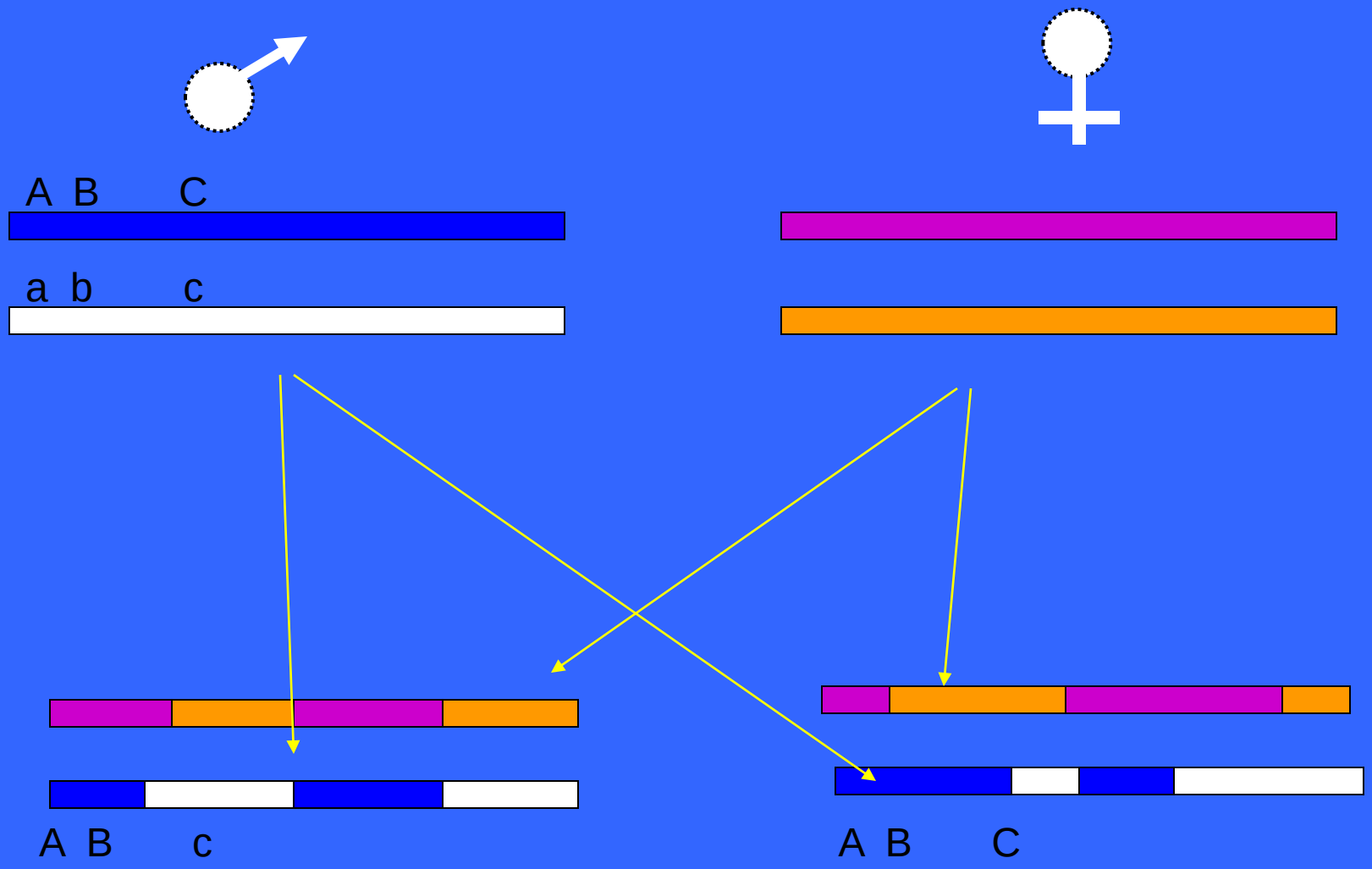
Repeated sequence that differs in length

TGTGTGTGTGTGTGTGT

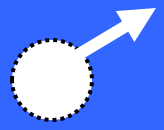
TGTGTGTGTGTGT

Different forms = **Allele**

Recombination & Inheritance

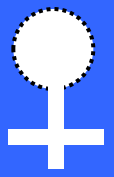


Example of SNP Marker



…ATTTACA…

…ATTTACA…



…ATTTGCA…

…ATTTGCA…

C313Y Allele-Specific Test

A/A G/G A/G

Piedmontese A →

Normal G →

- Piedmontese

- Belgian Blue

What type of traits are DNA markers good for?

Quantitative

- **Growth, carcass, etc.**
- **Many genes**
- **Many Markers**

Qualitative

- **Coat color**
- **Horned/polled**
- **One gene**
- **~ 1 Marker**

SNP options

- 700K (777,962 SNP BovineHD BeadChip, Illumina Inc)
- BOS 1 Array (648,855 SNP chip, Affymetrix) ~**$400**
- 50K (BovineSNP50 BeadChip, Illumina Inc; >54,000 SNP) ~**$150**
- 3K (Bovine 3K BeadChip, Illumina Inc; contains 2900 SNP soon to be replaced by 6 K) ~$38

How many SNPs do we need?

1 base	1 second
• 3 billion bases	• 95 years
• 100 million/ chromosome	• 3.2 years
• 1 SNP every 4286 bp (700 k panel)	• 1.2 hours
• 1 SNP every 60,000 bp (50 k panel)	• 16.7 hours
• 1 SNP every million bp (3k panel)	• 1.7 weeks

Approx # SNP/ chromosome

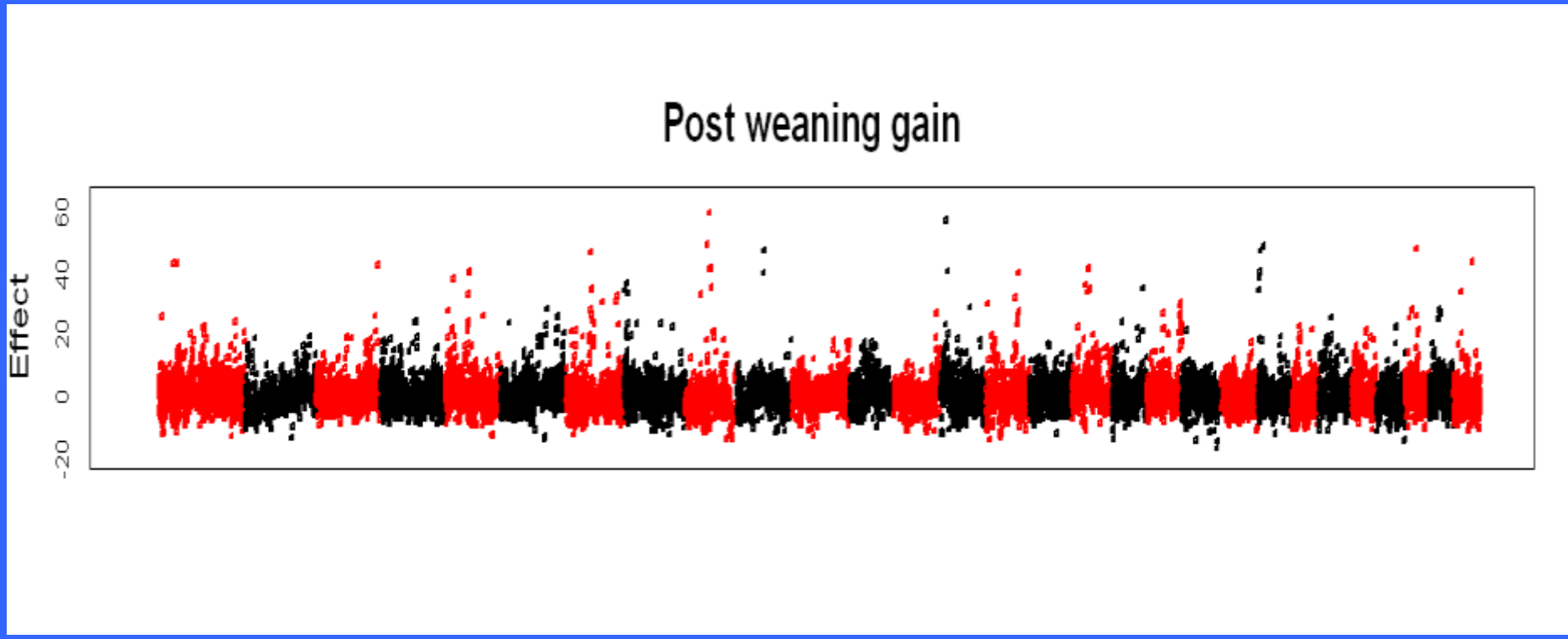
- 700K = 23333 ~$400
- 50K = 1667 ~$150
- 3K = 100 ~$38


Analysis of 50K SNPs on Hereford

July 28th, 2010

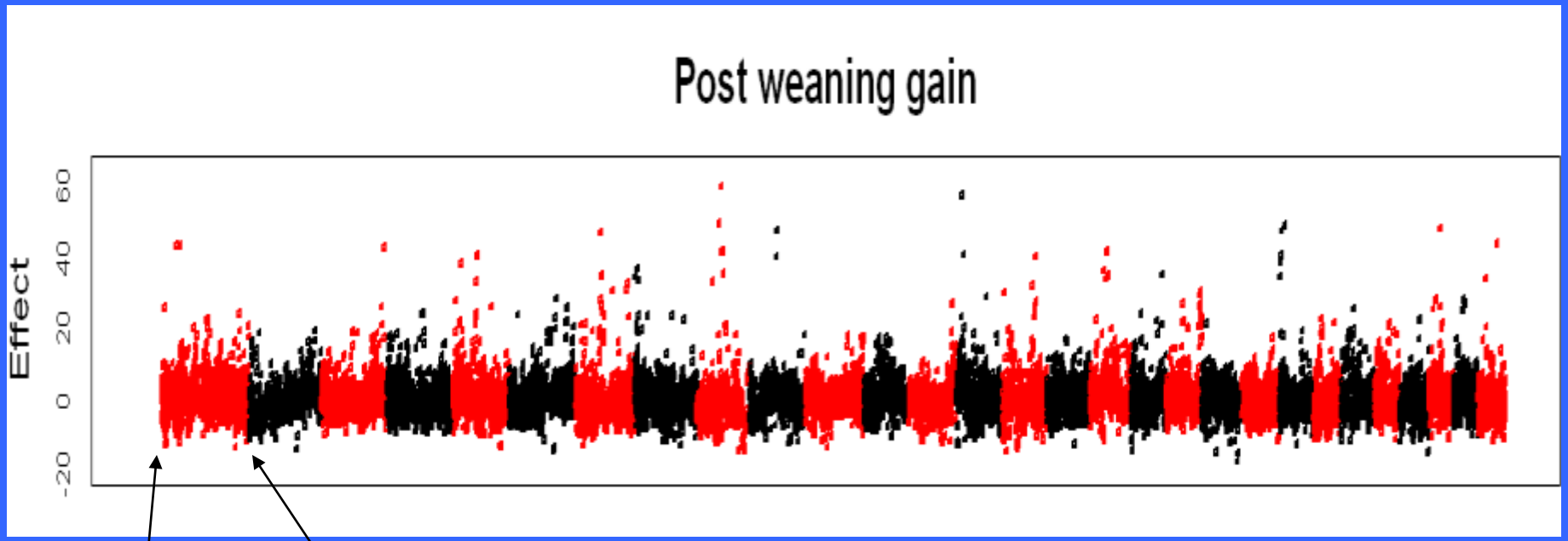
YiJian Huang

North Carolina State University



50K = ~1667 SNP/chromosome

Imputation of 50K from 3K



~100 million bp/ chromosome

50K = ~1667 SNP/chromosome (1 SNP/1851 bp)

3K = ~100 SNP/chromosome (1SNP/34500 bp)

Genomics on CGC study

- 50K chip done on 60 sires
- 3K chip done on ~2000 offspring

- Lee: Imputations of 50K SNP on offspring

- Mike: In Iowa today working on software to do GWAS analysis.

Traits measured in CGC

ALL

- BW
- WW
- Post wean gain
- YW
- Puberty
- US carcass traits
- Horn/poll
- Color

Females

- Post wean feed intake
- Heifer Pregnancy
- BW & BCS 4X/year
- Calving dates
- Longevity
- Reason for cull

Yearling Bulls

- BSE/Semen characteristics