



## Types of Markers

↳ We represent DNA like a long string of letters (ACTG)

↳ SNPs

- Single Nucleotide Polymorphism
- Single Base Change in DNA
- Like a typo in the phone book
- Millions in the bovine genome
- Now more commonly used for DNA tests
  - Easier to assay
  - Cheaper!

Chromosomes

|          |          |
|----------|----------|
| A        | A        |
| C        | C        |
| T        | T        |
| G        | G        |
| A        | A        |
| A        | A        |
| A        | A        |
| G        | G        |
| <b>G</b> | <b>T</b> |
| G        | G        |
| A        | A        |
| G        | G        |
| C        | C        |
| T        | T        |
| G        | G        |

Rolf M

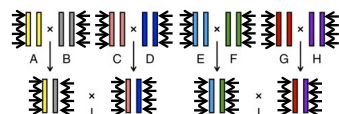
Roff M 55

Rose  
1019  
Ross

## What is so Important about DNA Markers?

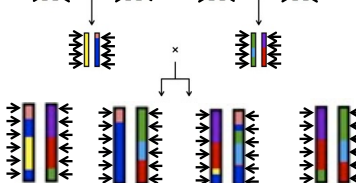
↳ Not the Causal Mutation (unfortunately)

- Can't test directly



↳ Independent assortment

- Many possible combinations
- Recombination
- Track inheritance



## Independent Assortment

↳ Genes assort independently into gametes

- Every mating can produce 1,152,921,504,606,846,976 genetically distinct full siblings!!!
- DNA markers can help us figure out what was inherited by each animal



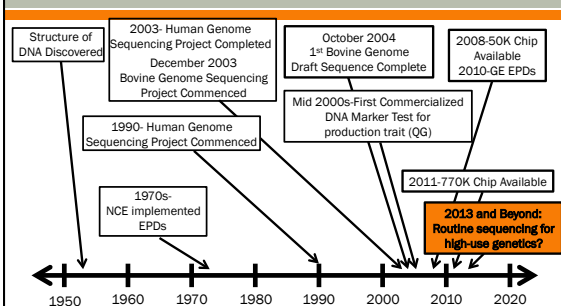
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## Timeline



## Evolution of DNA Technology

↳ Mid 2000s

- First DNA marker test for a production trait
- GeneStar Quality Grade
- 4 markers by 2007

↳ 2008

- 50K SNP Chip

↳ 2011

- 770K SNP Chip

↳ 2013

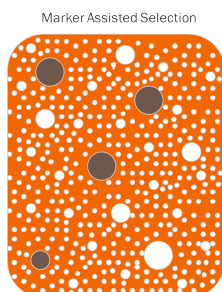
- Genome sequencing includes all possible DNA markers!
- Exome Sequencing
- Gene Expression (RNA)
- Rumen Microbes (Microbiome)



↳ Prices are Dropping as amount of data and adoption (volume) increases!!!

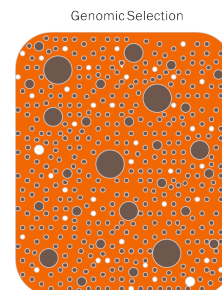
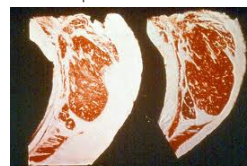
## Marker Tests: Then vs. Now

- Then: Marker Assisted Selection
- A few markers
- Large effects



## Marker Tests: Then vs. Now

- Now: Genomic Selection
- Thousands of Markers
- SNP Markers
  - Cheap(er)
- More Options!



## Marker Tests: The Options

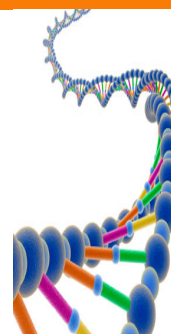
- Parentage
- Simple Traits:
  - Genetic Defect testing
- Complex Traits:
  - Genomic data into NCE (for some panels)
  - Targeted panels
    - GeneMax (not in NCE) + Others
  - Small Chips
    - 9K
  - Large panels
    - 50K



- Sequencing was key to developing all of these tools!

## Where do we go from here?

- Maintaining current prediction accuracy will require constant phenotype collection and retraining with more genotypes
- Adding more markers on a larger chip will most likely show diminishing returns
  - 50K to 770K ~3-5% increase in prediction accuracy (Kachman)
    - Strategies for improvement?
  - Still markers, not causal mutations
  - Only a subset of all the mutations in the genome
- Whole Genome Sequencing
  - All mutations at one time (could be millions!)
  - Not just what is on the chip
  - Includes causal and rare mutations
  - Find regions (chip) vs. Find Causal Mutations (sequencing)



## Sequencing Projects

### 1990-2003: Human Genome Sequencing Project

- 13 years
- ~\$437 Million ([http://www.ornl.gov/sci/techresources/Human\\_Genome/project/budget.shtml](http://www.ornl.gov/sci/techresources/Human_Genome/project/budget.shtml))
- More than \$3 Billion by some estimates!

### 2003-2005: Bovine Genome Sequencing Project

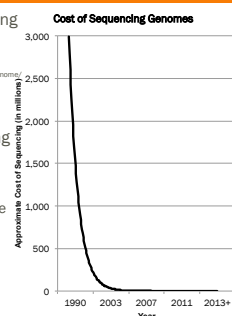
- ~2 years (to get 6x draft assembly)
- \$53 million (<http://www.genome.gov/12512874>)
- Still working to improve assembly and gene annotations

### Current Cost for 1 Genome: ~\$10,000

- Data only, no assembly

### Rumored cost for 1 Genome: ~\$1,000

- Data only, no assembly



## How Big is the Genome?

### How much information are we talking about?

- 3,200 bases/sheet of paper
- 1 copy of each chromosome
  - 3 billion base pairs
- 4.6 pallets of paper
- Each cell has 2 copies of each chromosome



## Genome Sequencing Limitations

- ✎ Limited more by data storage requirements and computing power for analysis than by data generation
  - Like putting together a puzzle with millions of small pieces and no picture to tell you what it looks like
  - Need to use computer to predict where genes are
  - Identify mutations



## Uses of Sequencing Data

- ✎ Causal mutations
  - Are all included in the genome sequence
    - Develop better marker panels in the future
  - No need for additional DNA testing
- ✎ Genetic evaluation
  - Information can be used in genetic evaluation
  - Can also be used to augment DNA testing information for relatives
    - Fill in the gaps (imputation)
- ✎ Fertility
  - Address early embryonic mortality by combo sequencing and DNA chips
- ✎ Data repository
  - Each carrying ~8 recessive lethal mutations
  - If issues do arise, already have the tools needed to solve the problem quickly

## Questions?



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