

# Utilization of Genomic Information to Accelerate Soybean Breeding and Product Development through Marker Assisted Selection

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MONSANTO



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# Presentation Overview

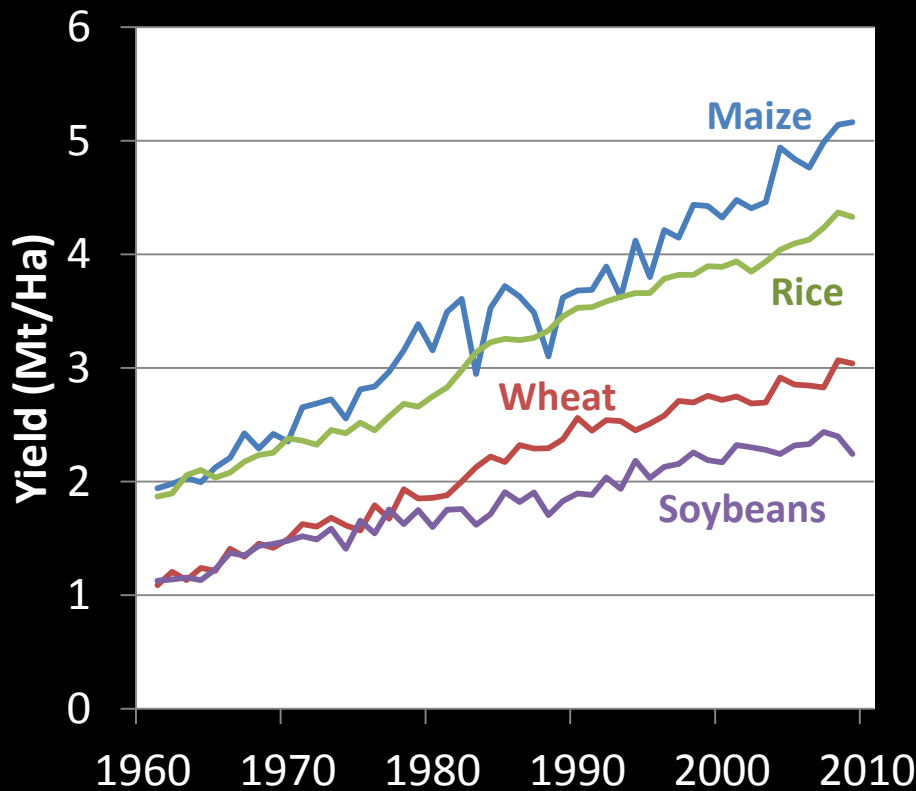
**Molecular Breeding in the Ag Industry**

**Technology Application for Accelerating Trait Mapping**

**Marker Deployment in Commercial Product Development**

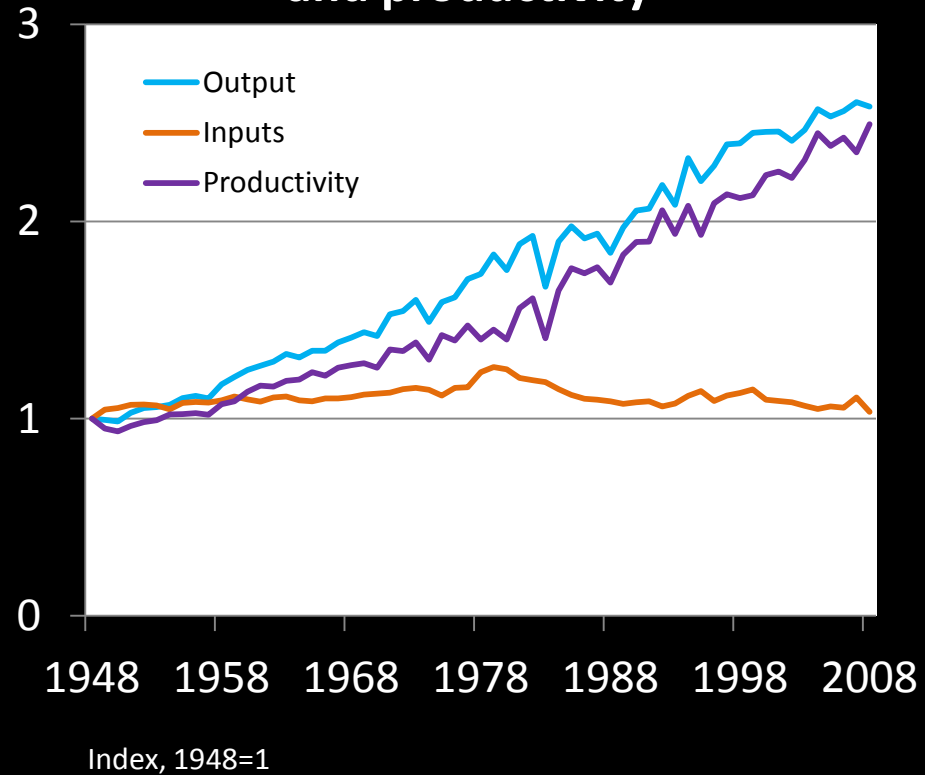
# The Application of Science and Technology in Agriculture has Helped Deliver Increased Productivity and Resource-Use Efficiency

## World Yields of Staple Food Crops



Source: FAOSTAT

## U.S. agricultural output, inputs and productivity



Source: USDA-ERS data product, Agricultural Productivity in the U.S. (2010)

# To Further Improve Performance, We Must Identify and Create Better Genetic Combinations

## Existing Genetic Variation

Yield, Stress  
Tolerance, etc.

Disease Resistance, etc.

Yield, Quality  
Traits, etc.

Tolerance to Herbicides,  
Insects, etc.

## Transgenic Genetic Variation



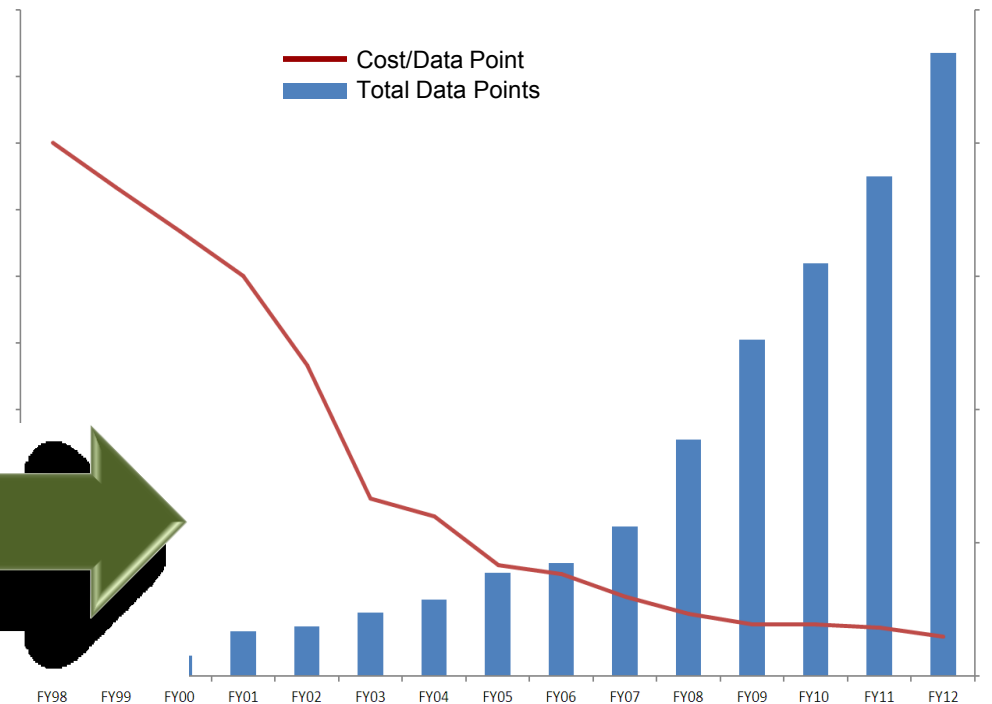
# The Evolution of the Use of Molecular Markers

## *Increased Capacity and Decreased Cost Enables Large Scale Plant Breeding Applications*

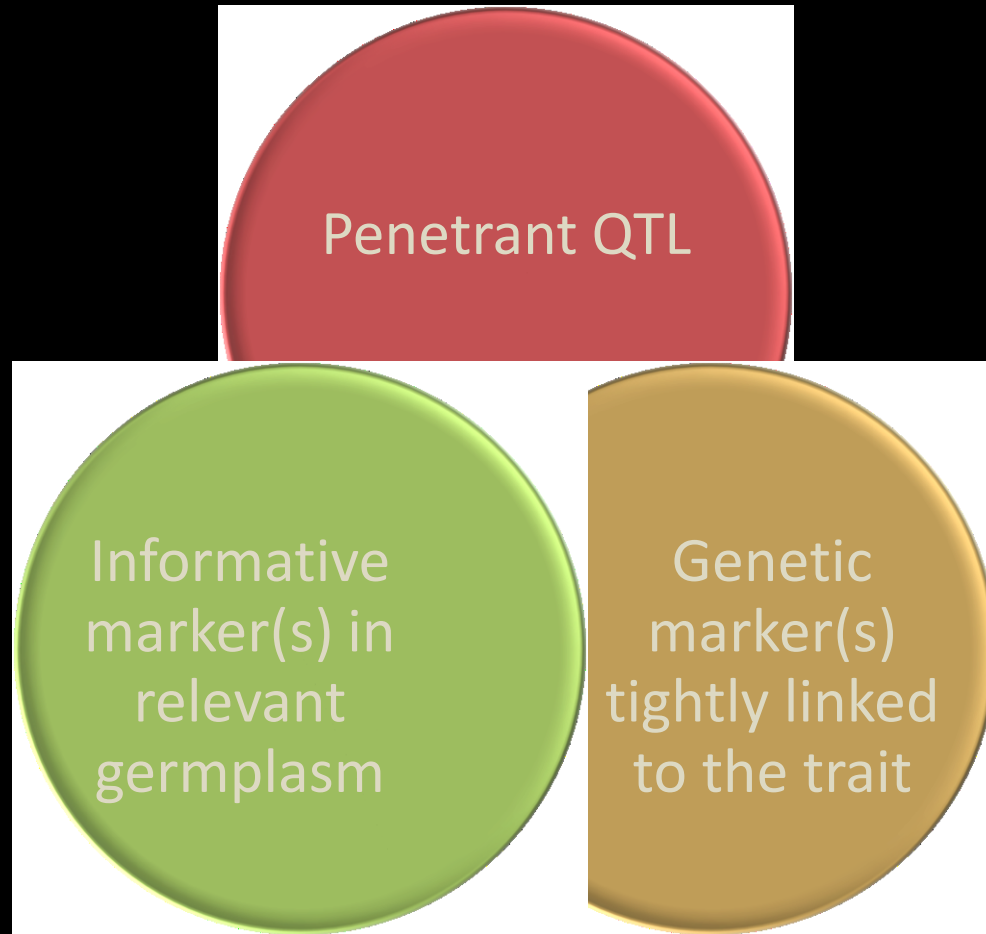
In era of gene-based breeding, the amount of data explodes, accelerating the ability to realize step-change improvements

### Key growth drivers

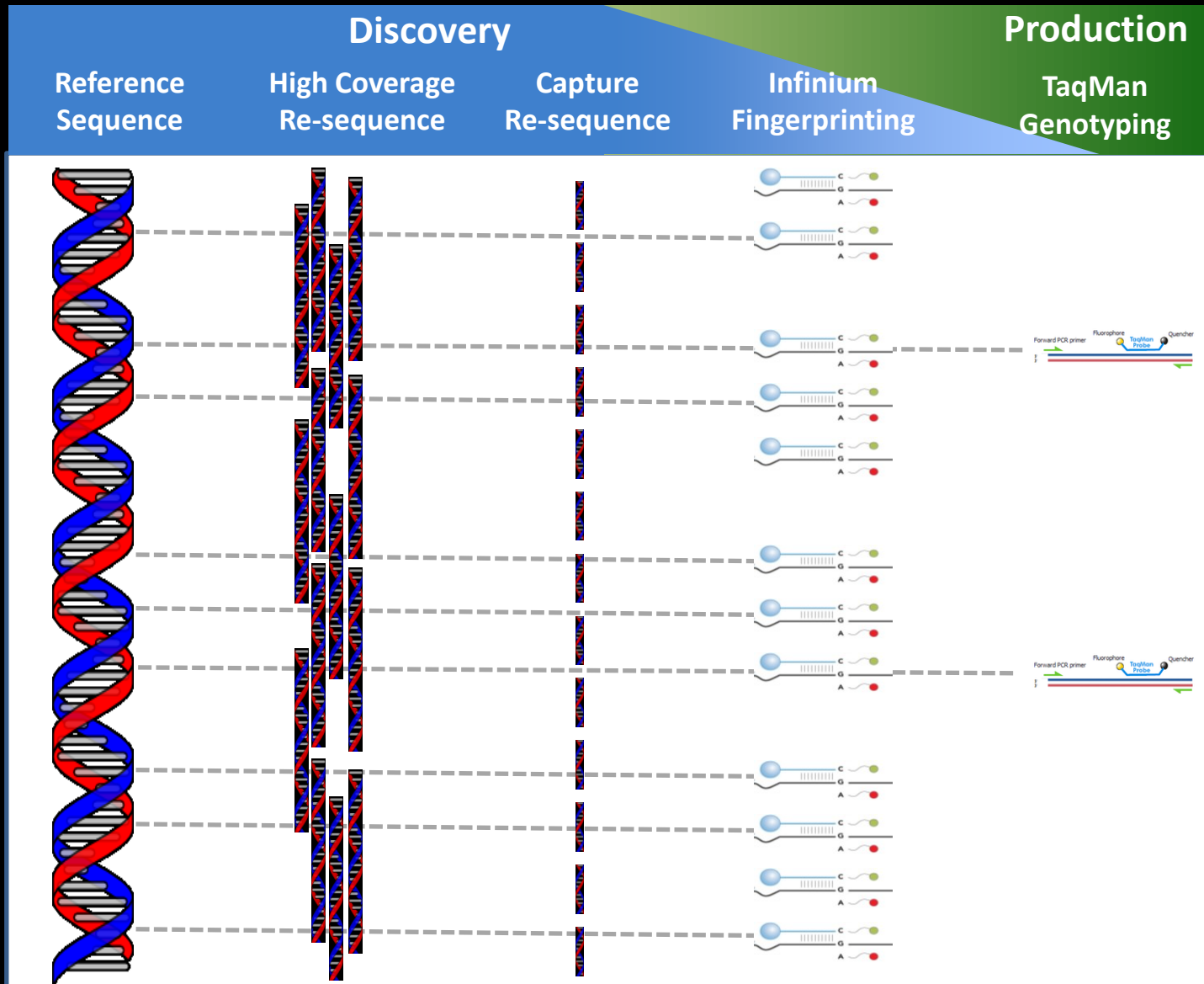
- Automation
- Technological Advances



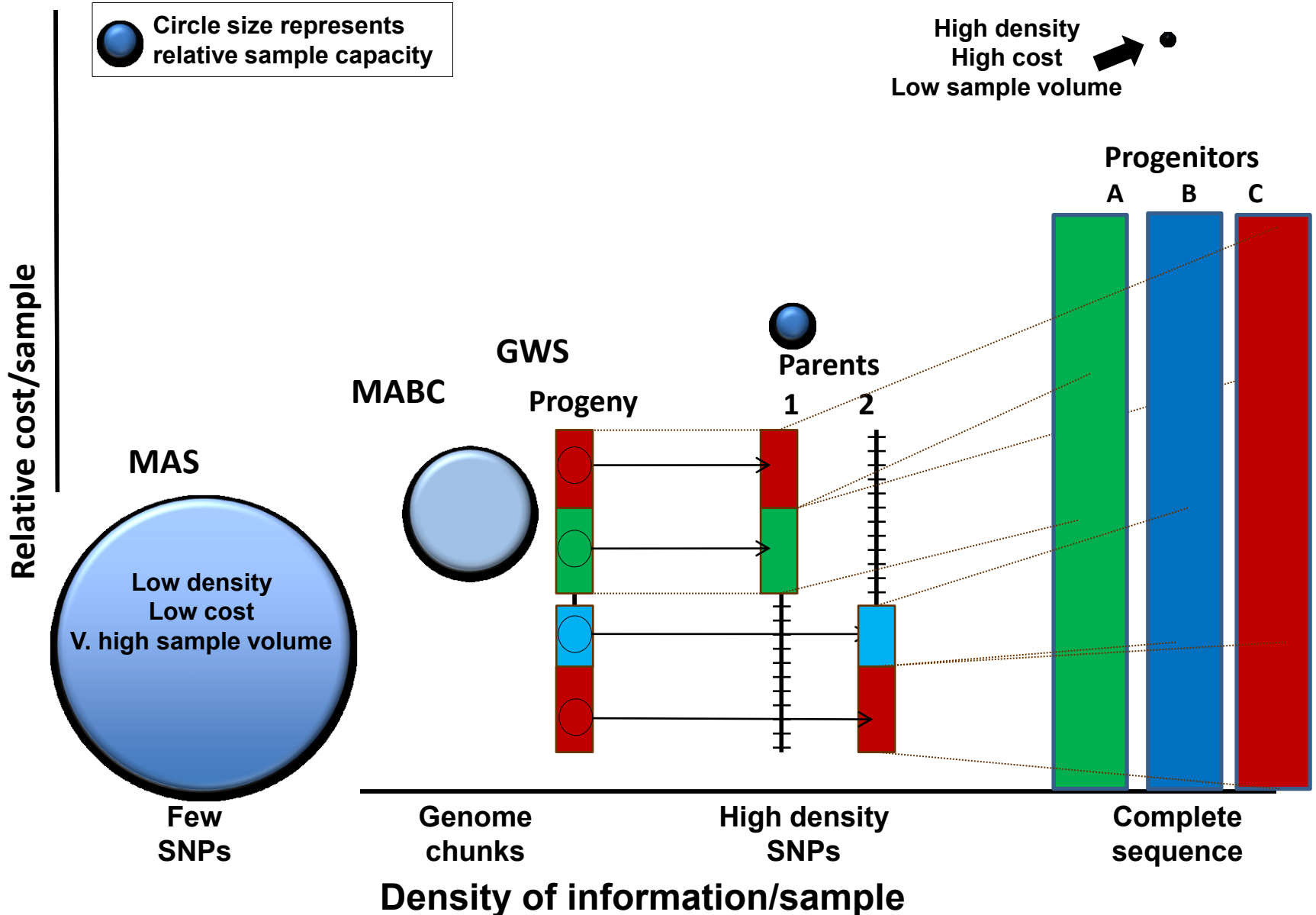
# Effective Markers for MAS breeding require multiple components



# Alignment of Technology Platforms Enables Cross-Talk

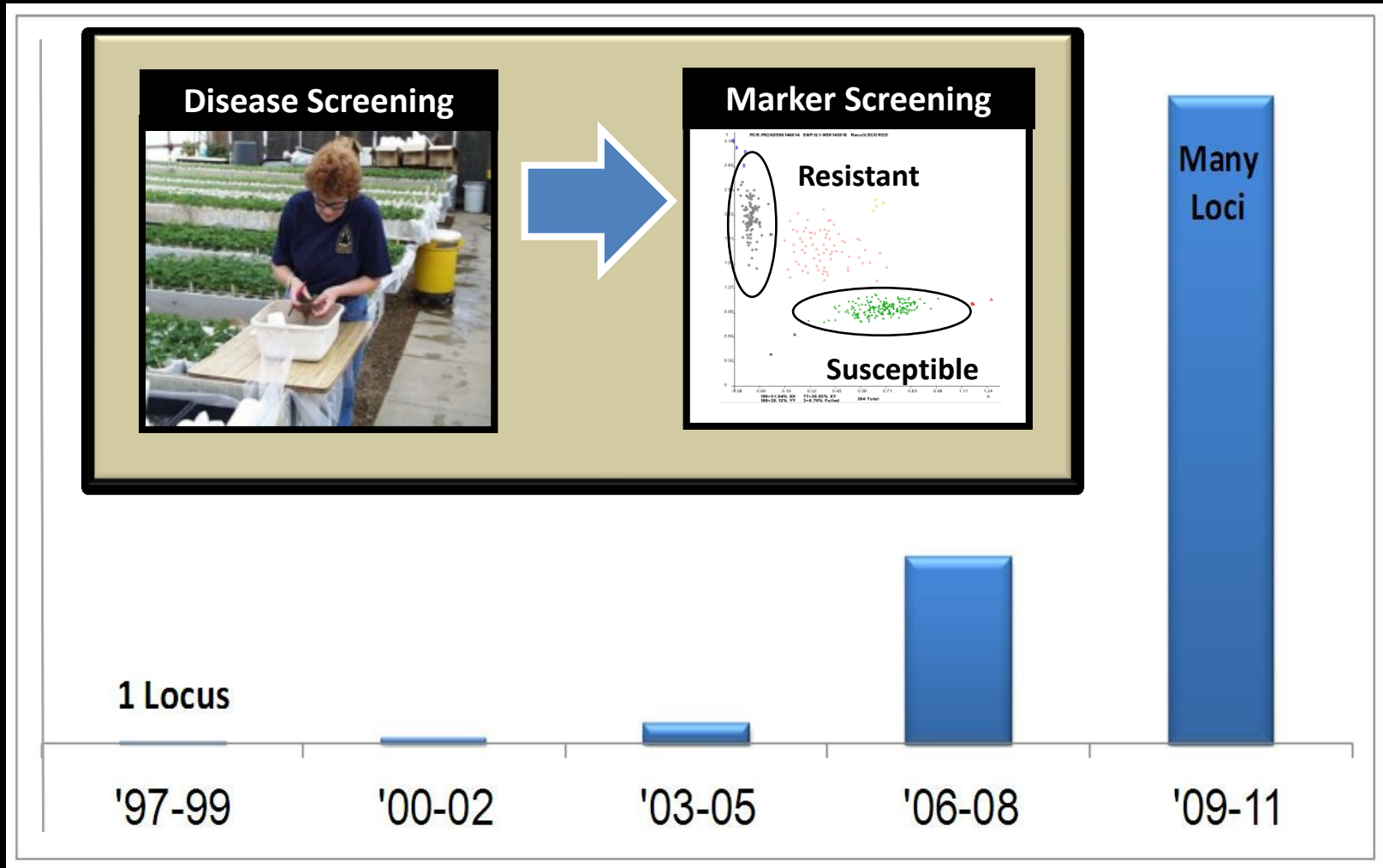


# Efficiency is Achieved by Aligning Technologies with Desired Outcomes

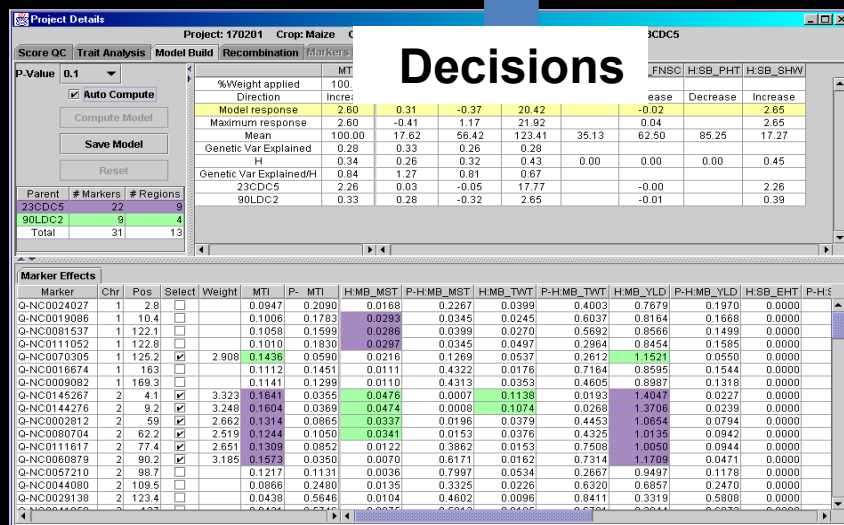
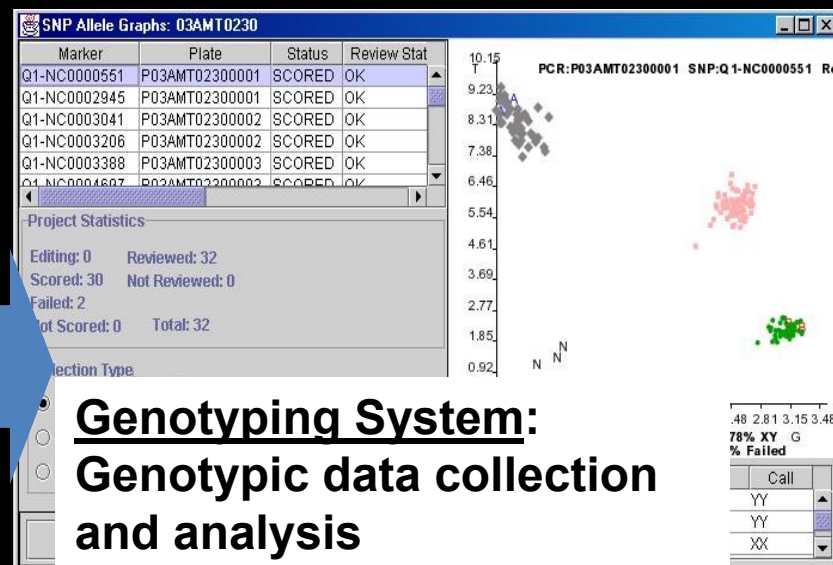
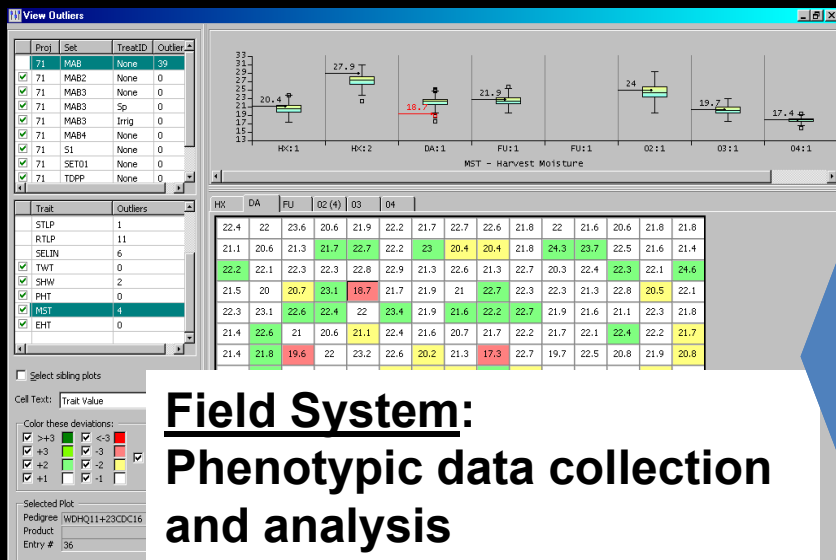




# Marker-Assisted Selection (MAS) For Simple Traits in Soy Expands Breeding Pipeline and Decreases Cost



# Integrated Data Analysis and Decision Making System Is Needed



**Analysis System: Integrate and analyze phenotypic and genotypic data**

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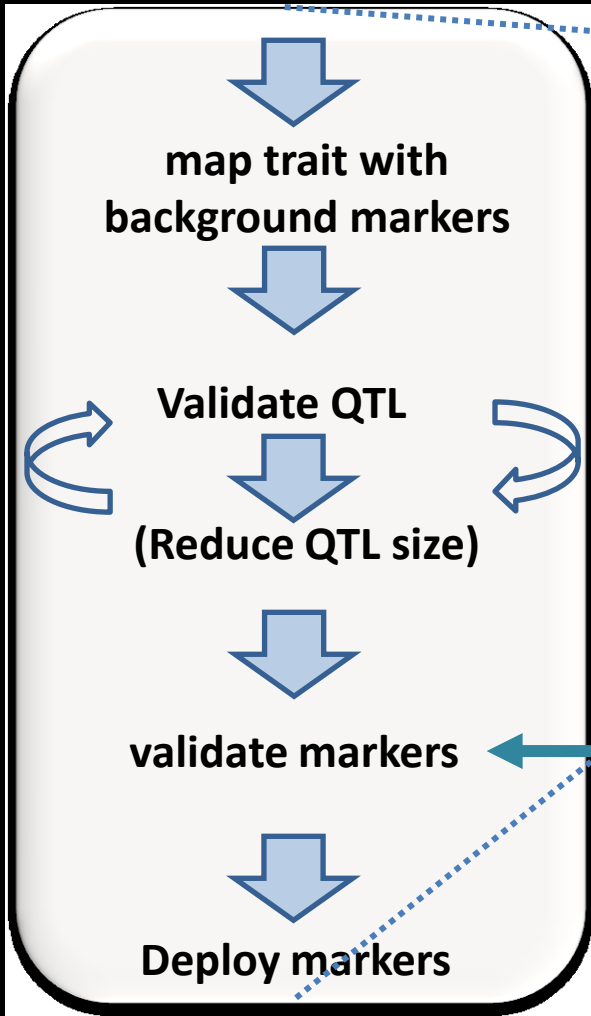
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# Leveraging Available Public Data Accelerates Trait Marker Development

## 1. Classic QTL Mapping

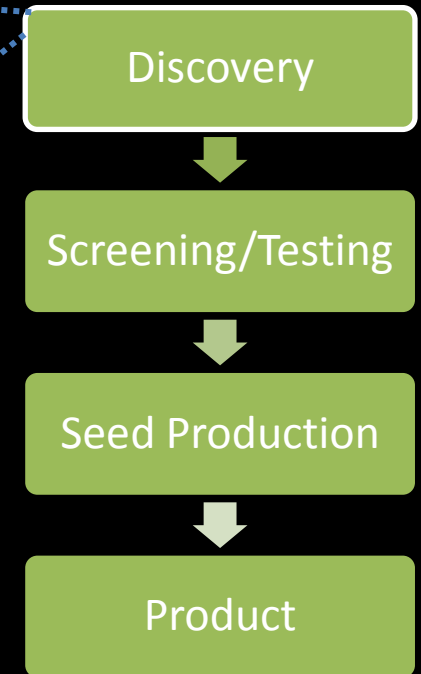


## 2. Leverage available data (public literature)

Validate QTL in breeding germplasm

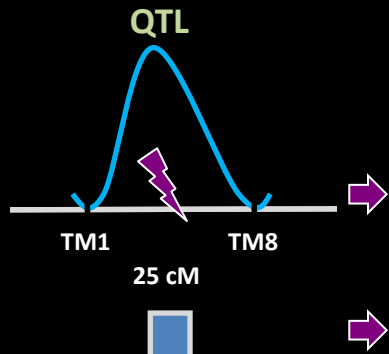
(joint linkage mapping, association mapping)

## Breeding Pipeline



# Leveraging Technology: Higher marker density improves resolution

⚡ Recombination break point, Red: donor allele, Blue: RP allele, S: susceptible, R: resistant, TM: Taqman marker



M1 100 cM	M2 105	M3 107	M4 110	M5 115	M6 120	M7 123	M8 125 cM	Phenotype
0	0	0	0	0	0	0	0	S
2	0	0	0	0	0	0	0	S
2	2	2	2	0	0	0	0	S
2	2	2	2	2	2	2	0	R
0	0	0	0	0	0	0	2	S
0	0	0	0	0	2	2	2	S
0	0	0	0	2	2	2	2	R
0	2	2	2	2	2	2	2	R
2	2	2	2	2	2	2	2	R

- QTL TM1-TM8
- New markers between
- 7 recombinant groups by TM
- Refine QTL to TM4 and TM6 (25 cM → 10 CM)
- If more markers are needed, repeat the process



Chip and genotype with M4, M5

Apply hi res markers only selected seed QTL

2	0	0	0	0	0	0	0	0
2	2	0	0	0	0	0	0	0
2	2	2	0	0	0	0	0	0
2	2	2	2	0	0	0	0	0
2	2	2	2	2	0	0	0	0
2	2	2	2	2	2	0	0	0
2	2	2	2	2	2	2	0	0
2	2	2	2	2	2	2	2	0
0	0	0	0	0	0	0	0	2
0	0	0	0	0	0	0	2	2
0	0	0	0	0	0	2	2	2
0	0	0	0	0	2	2	2	2
0	0	0	0	2	2	2	2	2
0	0	0	2	2	2	2	2	2
0	0	2	2	2	2	2	2	2
0	2	2	2	2	2	2	2	2

Recombinant #1  
Recombinant #2  
Recombinant #3  
Recombinant #4  
Recombinant #5  
Recombinant #6  
Recombinant #7  
Recombinant #8  
Recombinant #9  
Recombinant #10  
Recombinant #11  
Recombinant #12  
Recombinant #13  
Recombinant #14  
Recombinant #15  
Recombinant #16

**Recombinant group 2**

**Recombinant group 6**

# Leveraging Technology: Sequence Capture

## Southern Stem Canker (SSC)

Malvick, 2002

### **Pathogen Facts**

- Causative agent:  
*Diaporthe phaseolorum* f. sp. *Meridionalis*
- Soybean losses from SSC totaled approximately \$67.1 million in 2003 (Wrather, 2004)
- SSC infects the plant early in its vegetative growth, but symptoms don't appear until reproductive stages (Ploetz and Shokes, 1985)
- Because of the long asymptomatic latent period, genetic resistance is the best option
- **Six independent dominant resistance factors have been reported: *Rdc1*, *Rdc2*, *Rdc3*, *Rdc4*, and two unnamed loci** (Tyler, 1995)
- **Phenotyping is tedious, time-consuming, and often unreliable and has hampered the use of markers for marker-assisted selection (MAS).**
- **A highly effective 5 week greenhouse assay was implemented in 2006.**



# Experimental workflow for SSC



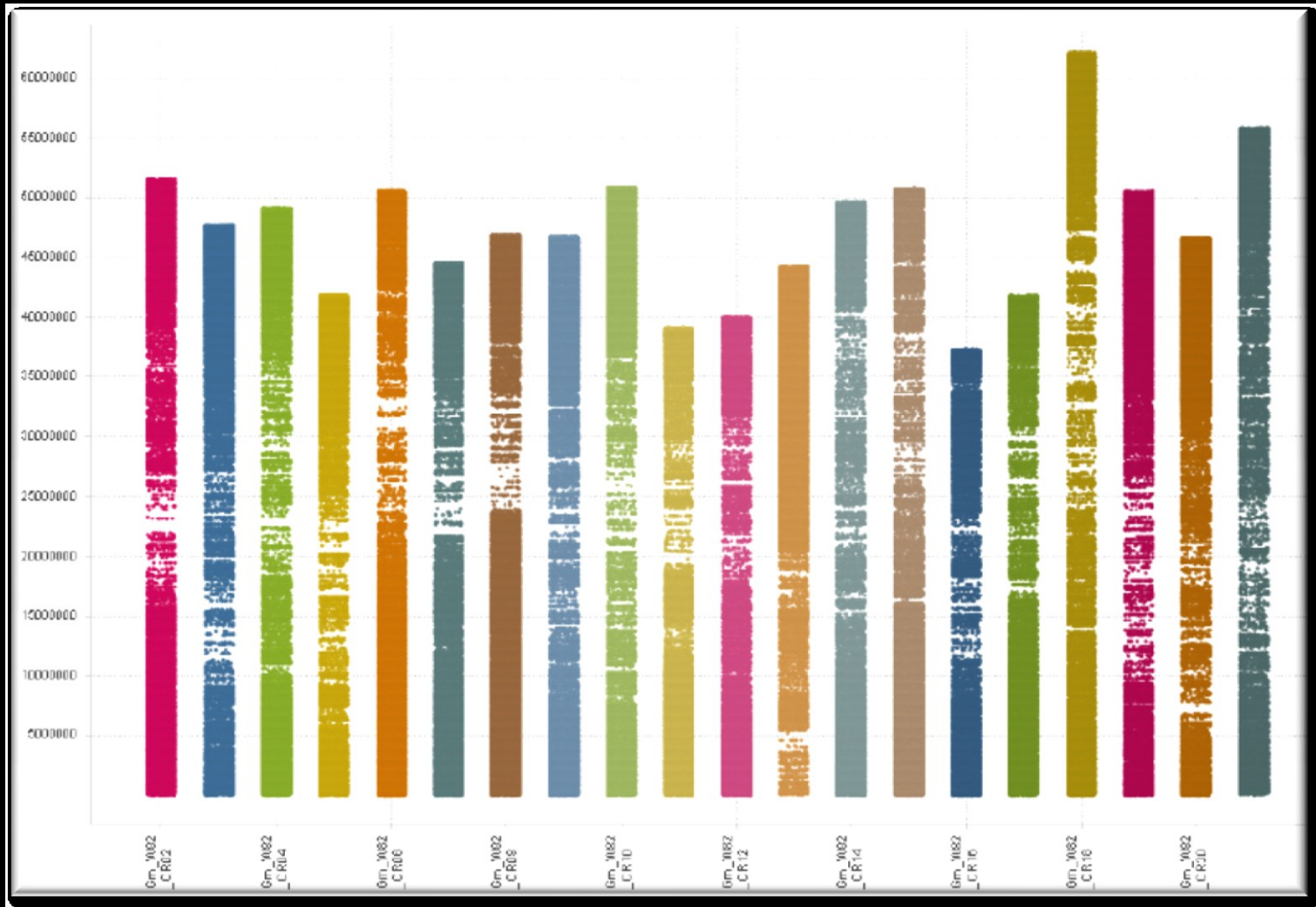
SSC Susceptible

F2:F3 family phenotyping

Pool Creation and Sequence Capture  
-F4 derived DNA mixed in in  
equimolar amounts

Quantitative Sequencing and  
Mapping  
-Single lane per sample on GAllx

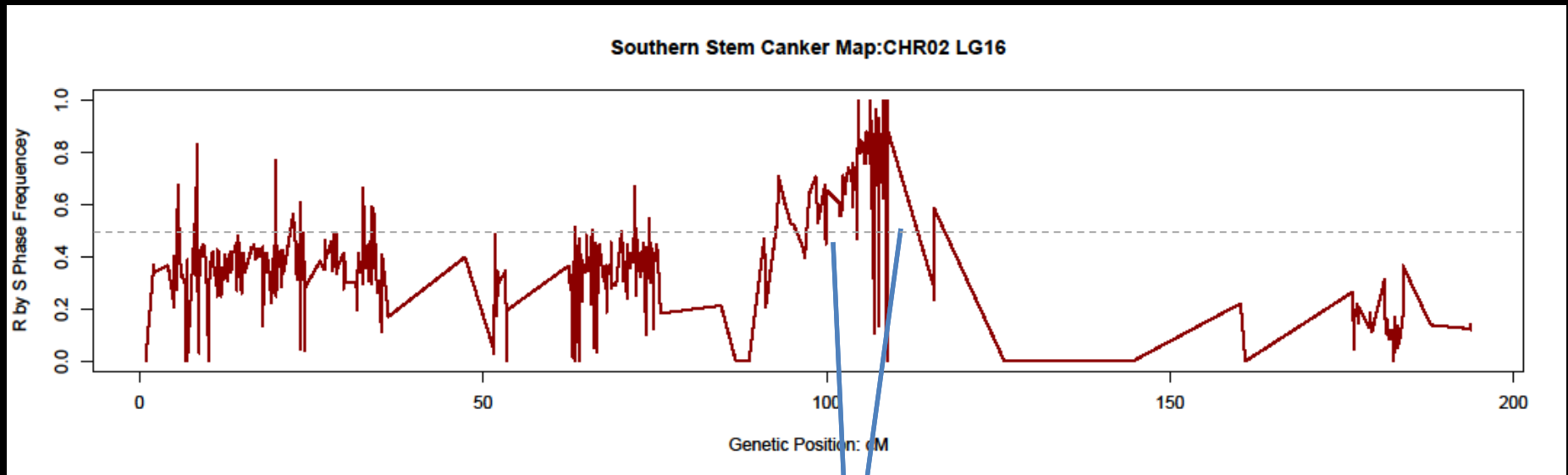
# Sequence Capture Allows Even, High-definition Interrogation of the Entire Genome



*Over 330,000 unique probes completely cover the soybean genome*



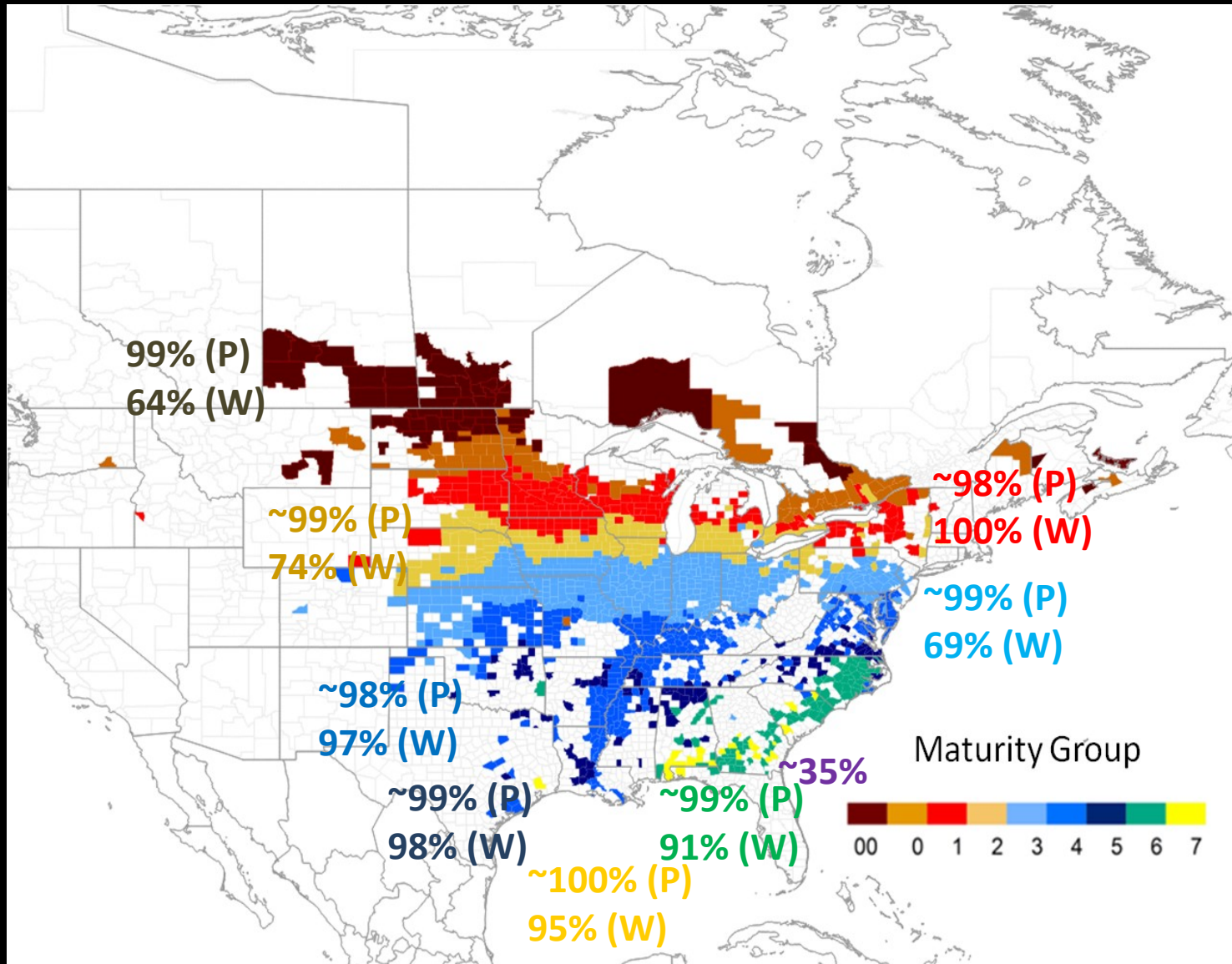
# Comparing Allele Frequency in Resistant vs. Susceptible Pools Efficiently Identifies the Trait Region



***Trait Target Region***

# Even Great Technology Isn't Perfect!

*In-Gene Marker Performance Varies Across Maturity Groups for Flower Color*



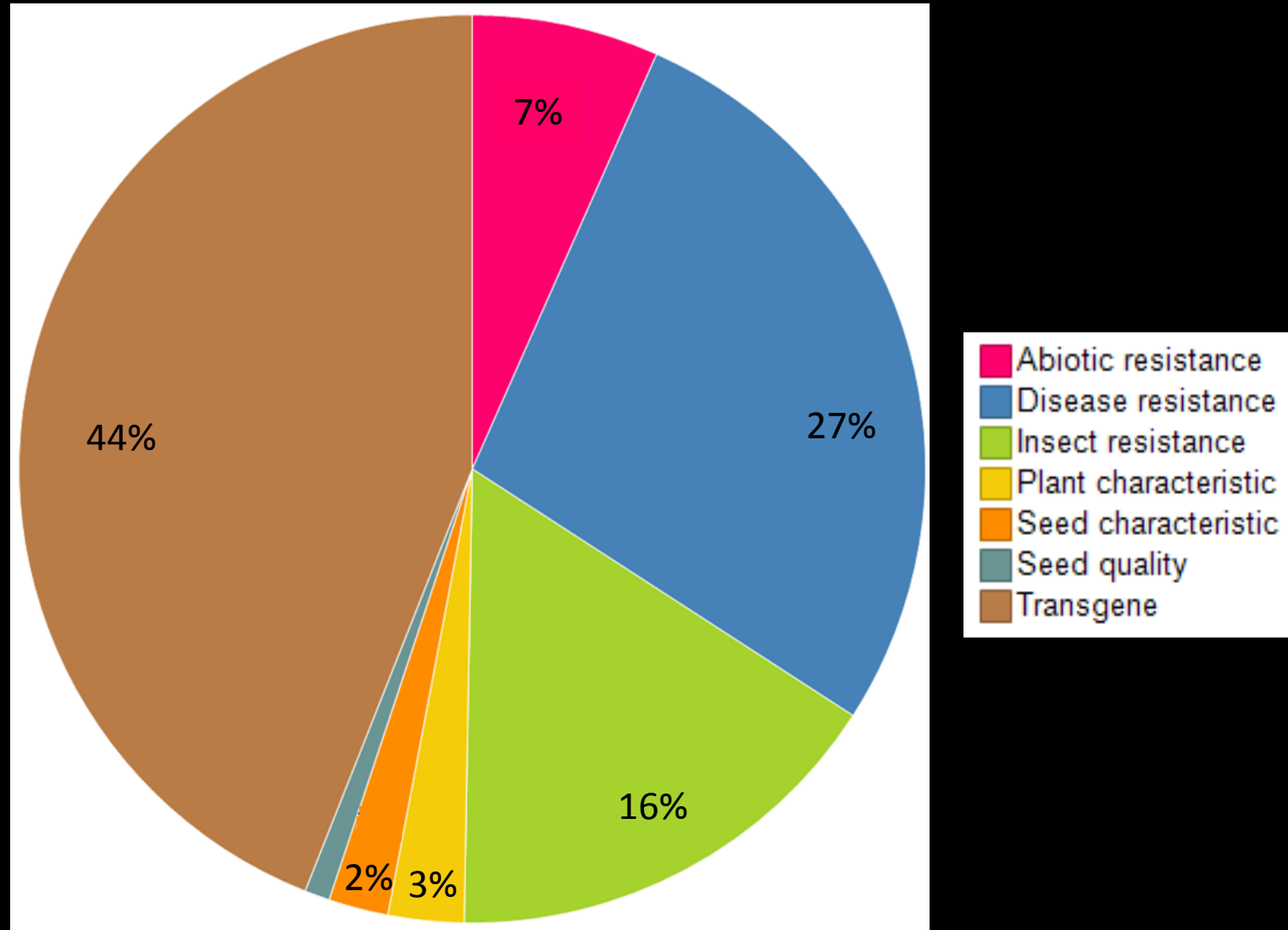
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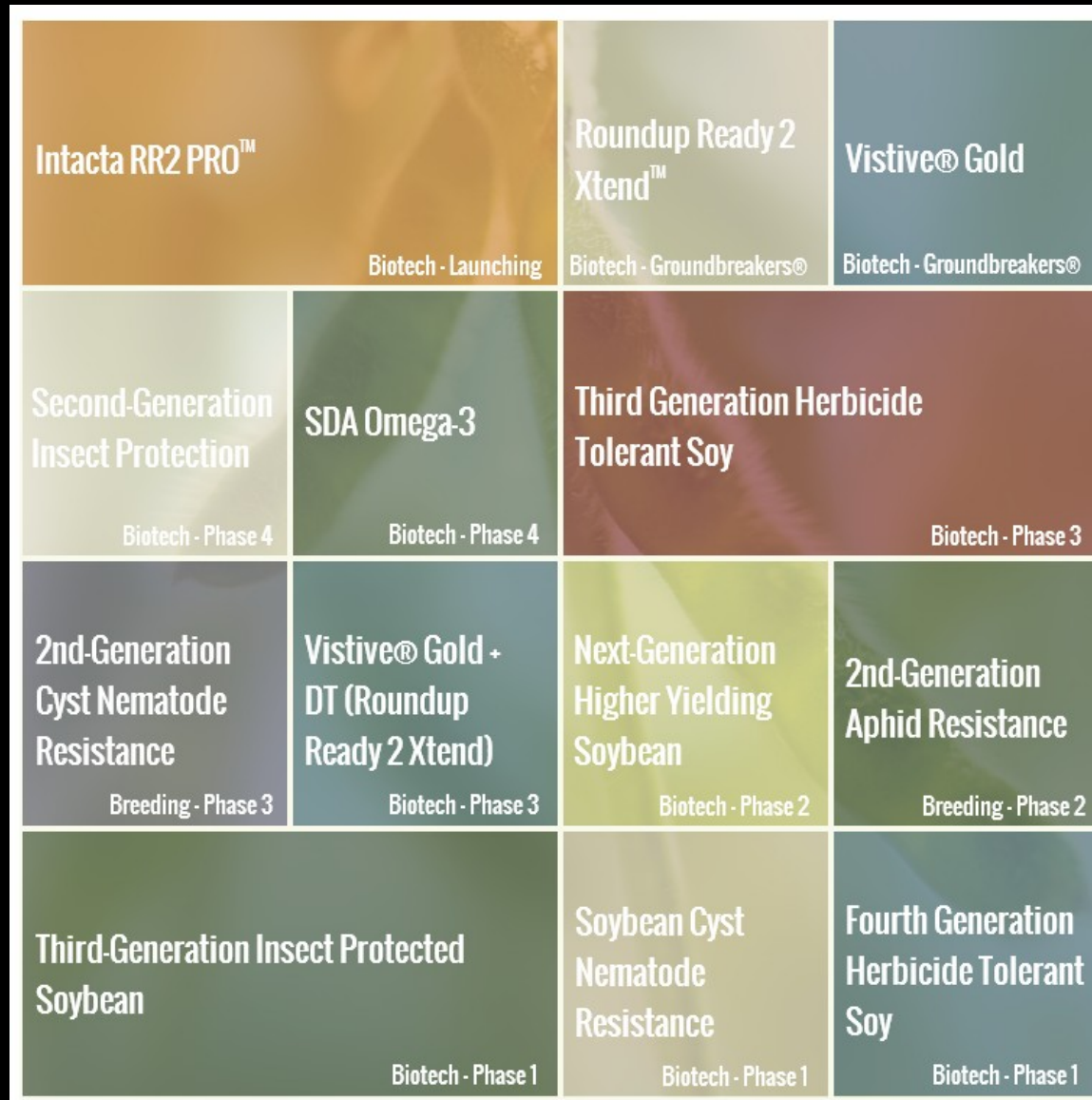
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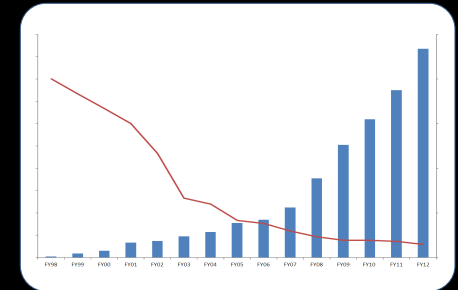
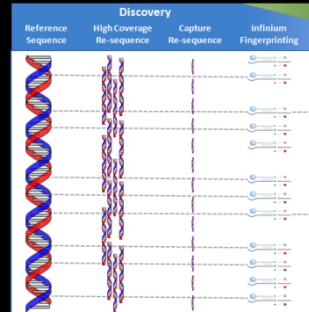
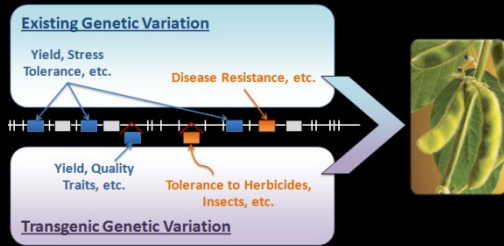
# Tens of Millions Genotyping Data Points Were Collected for Soy Traits in 2013



# Technology Pipeline



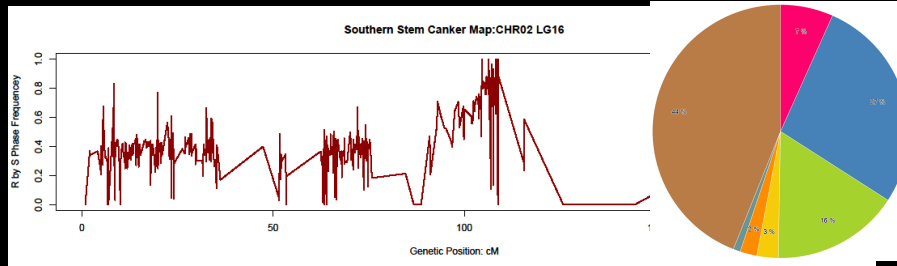
# Key Message



Combining genome wide selection with marker-assisted breeding...

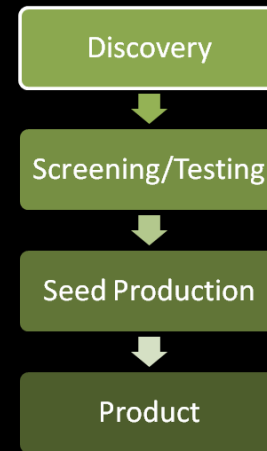
Using multiple technologies and *new* technologies...

While increasing capacity and reducing costs...



Allows us to map traits efficiently and track them in our germplasm...

## Breeding Pipeline



**Thereby Increasing Our Speed to Product Development**

Intact... Biotech - Phase 1	Roundup Ready 2 Xtend™ Biotech - Phase 2	Vistive® Gold Biotech - Groundbreakers®
Second Generation... Biotech - Phase 3	SDA Omega-3 Biotech - Phase 4	Third Generation Herbicide Tolerant Soy Biotech - Phase 3
Zinc... Biotech - Phase 3	Older... Biotech - Phase 2	2nd-Generation Aphid Resistance Breeding - Phase 2
Third Generation Insect Protected Soy... Biotech - Phase 1	Soybean Cyst Nematode Biotech - Phase 1	Fourth Generation Herbicide Tolerant Biotech - Phase 1