

# Genetic Architecture of Maize and Teosinte

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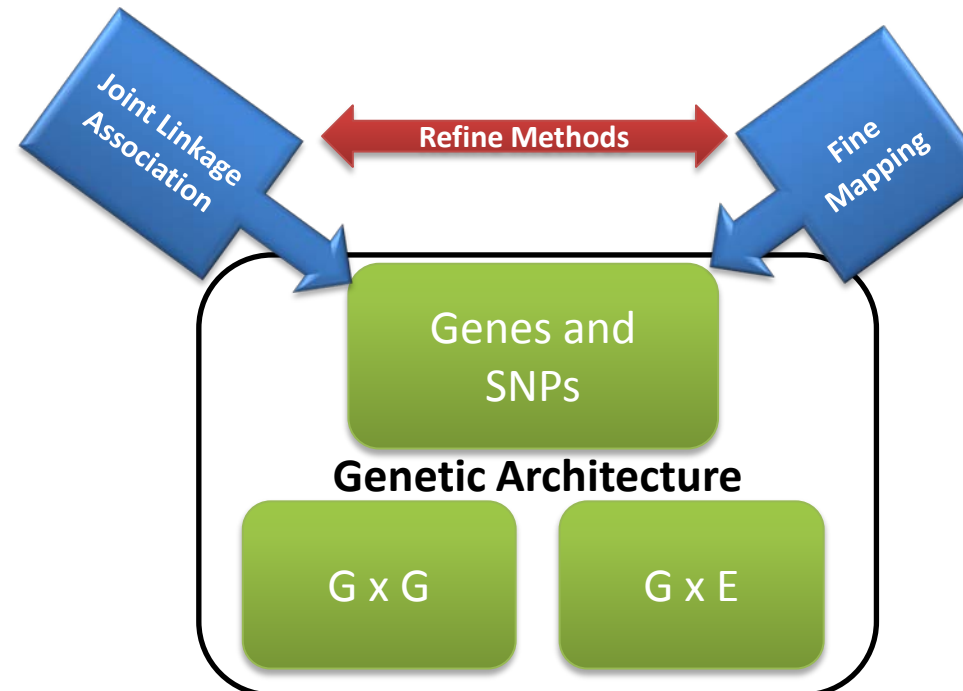


## Summary

This NSF project (DBI 0820619) will improve our understanding of the genetic architecture of complex traits in maize and its wild relative, teosinte. We are identifying genes that control domestication traits and three key agronomic traits: flowering time, plant height, and kernel quality. We are performing genetic linkage, association, and fine mapping analyses in the largest and most diverse set of mapping families publicly available for any species. A large series of isogenic lines are being used to characterize allelic series and epistatic interactions. The genetic architecture of each of the four trait groups will be compared and contrasted, and we will examine the influence of recombination and past domestication bottlenecks on the genomic distribution of functional diversity. Finally, we will evaluate the ability of genetic architecture-based models to predict phenotype in a broad range of germplasm, including elite US hybrids. This project will take a step toward the ultimate goal of predicting phenotype from genotype.

## 1. Genetic architecture elements

Finding the genes, alleles & interactions

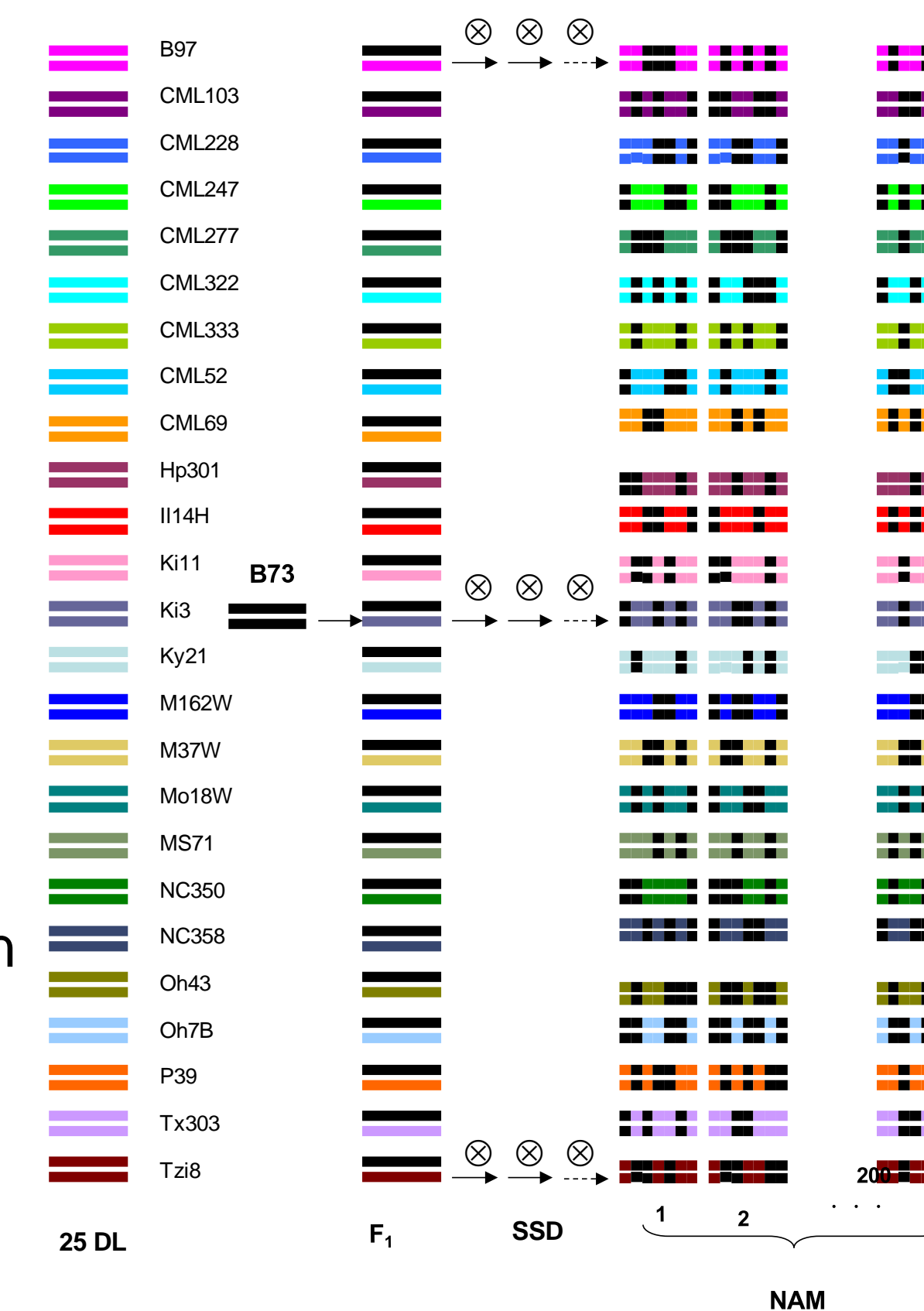


### 1.1. Joint linkage-association mapping

**Core traits:**  
• Flowering time, plant height, kernel quality & domestication syndrome

**Mapping populations:**

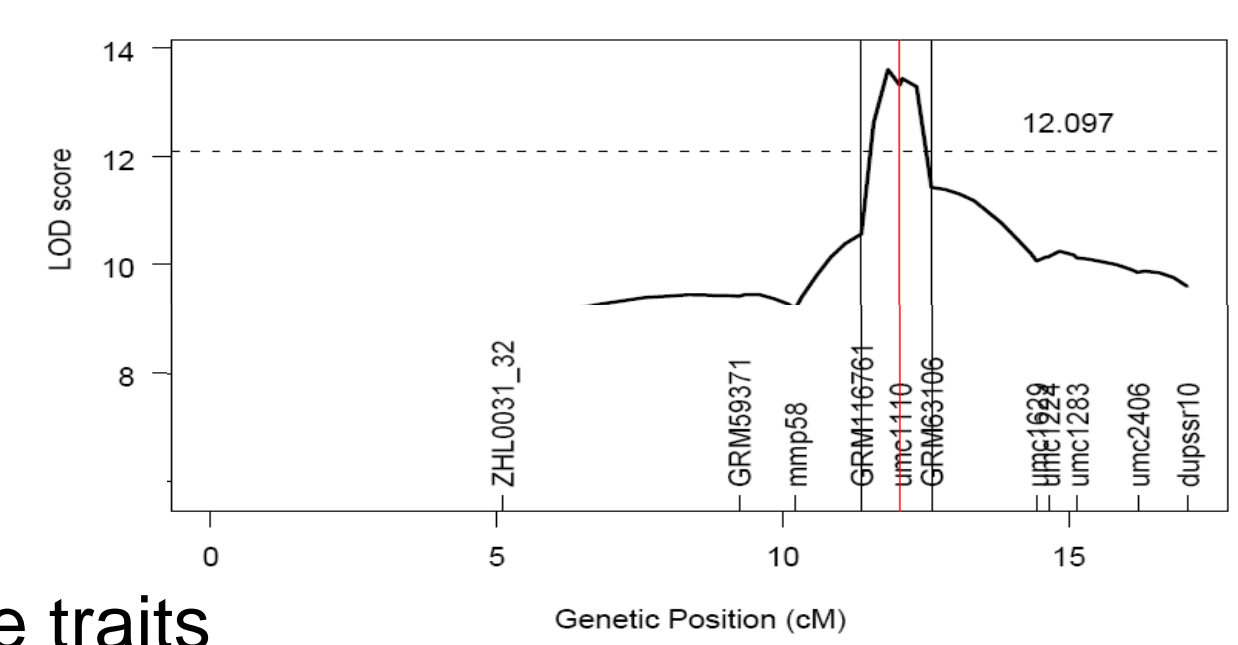
- Nested Association Mapping (NAM) population**
  - Captures 136,000 recombination events
  - Parental (maize HapMap) sequence projected onto 5000 NAM RILs for NAM-GWAS analysis
- Maize Diversity Panel (MDP)**
  - 281 diverse maize lines, 92 ex-PVP lines & 2500 USDA world inbreds
  - Will combine with NAM in a joint linkage-association mapping analysis
- Maize-teosinte backcrosses**
  - In B73 or W22 background (>850 NILs each)
  - Using to map domestication & kernel quality traits



### 1.2. QTL fine mapping

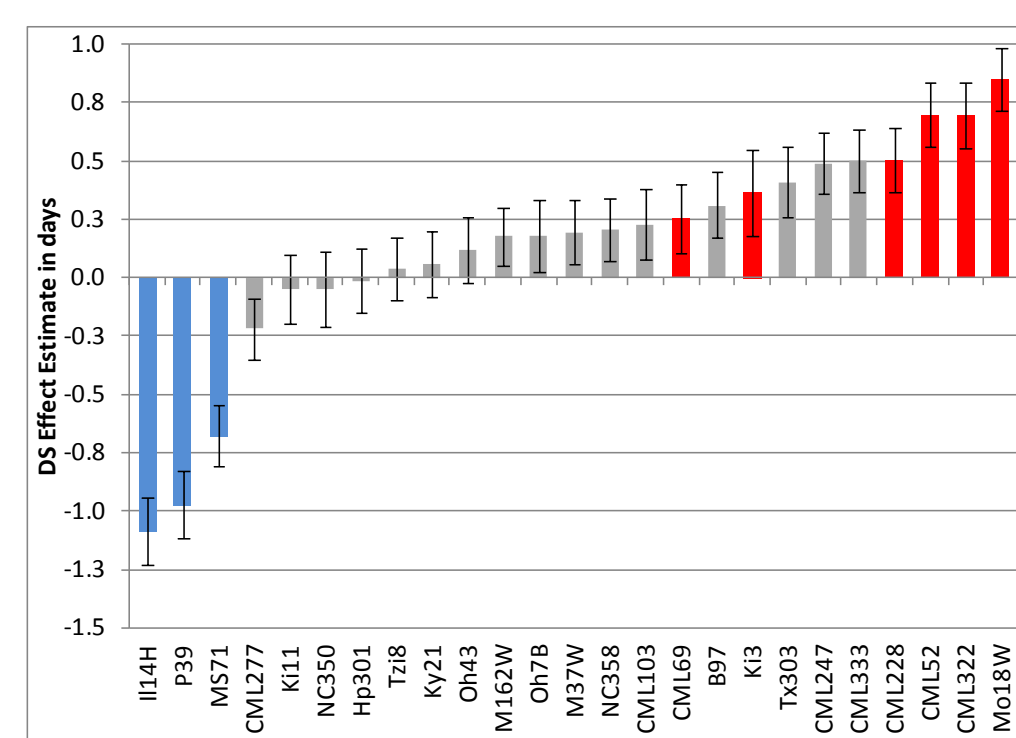
**Why?**  
• Formal proof that QTL represent specific genes  
• Positive controls for GWAS

**How?**  
• Attempting to fine map 4-6 QTL for each of the 4 core traits  
• Using heterozygous inbred families (HIFs) in NAM or teosinte backcross pops, or  
• Near isogenic lines (NILs) provided by Syngenta  
• these Mendelize the phenotypic variation  
• repeated rounds of screening for recombinants  
→ narrow down physical interval



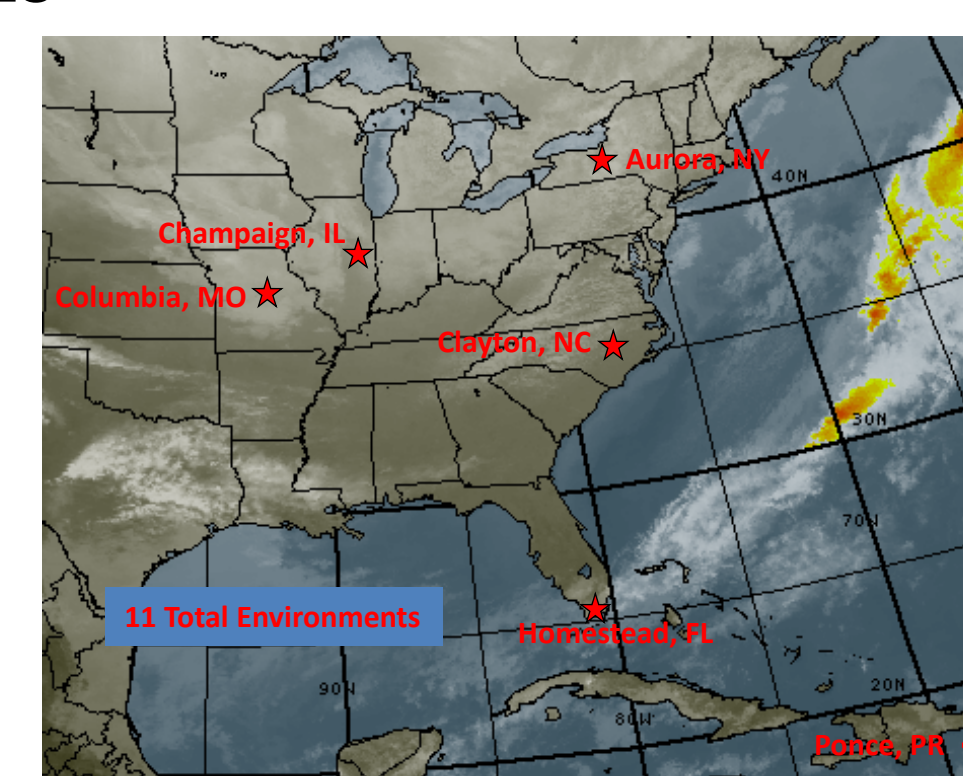
### 1.3. Allelic series & epistasis

• Allele series at a limited number of common QTL?  
• Or numerous QTL each with limited number of alleles?  
• For epistasis, NAM provides high statistical power  
• Allele series & epistatic interactions to be validated using NILs



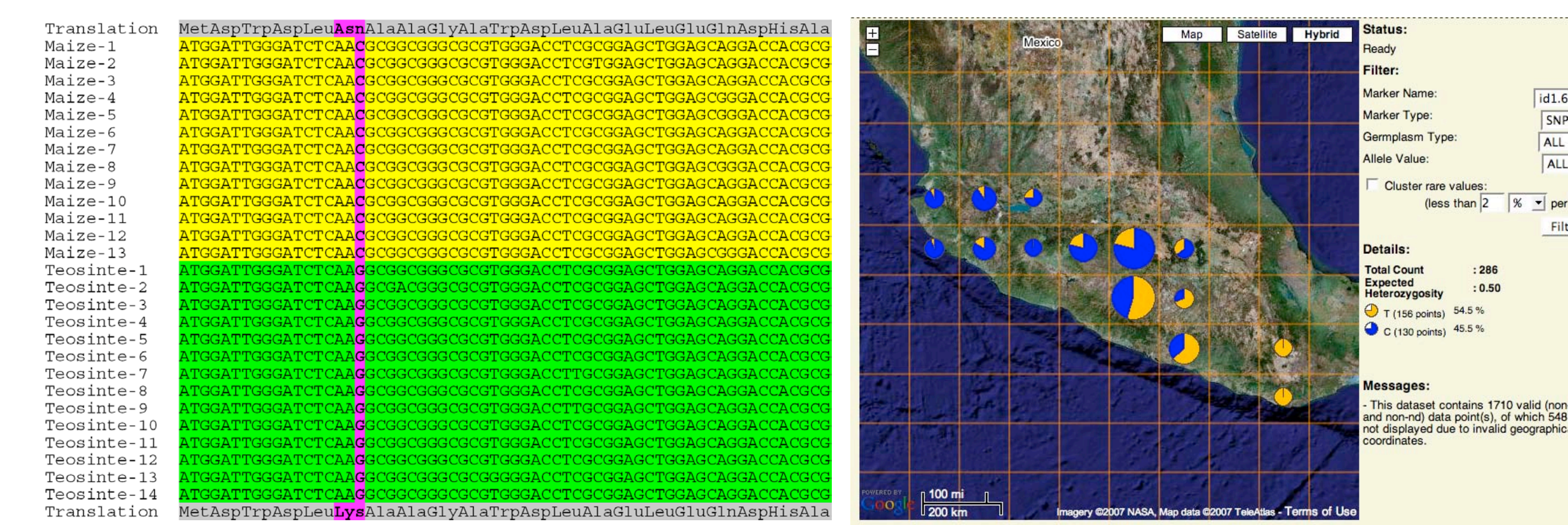
### 1.4. Genotype by environment interaction

• We have grown NAM in 11 environments  
• Does GxE result from a small number of genes?  
• Or is it consistent across QTL for a trait?  
• Are some genes sensitive to specific environmental factors?

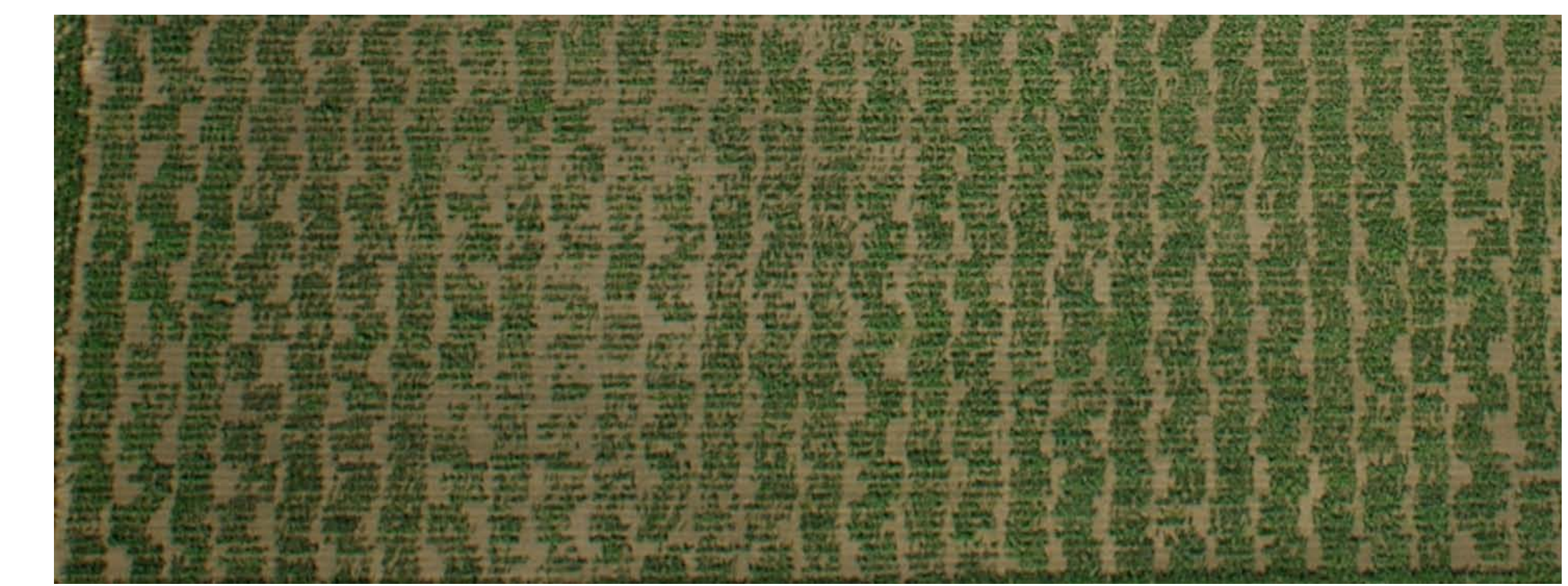


## 2. Molecular characterization of QTL

- Will initiate characterization of a subset of the fine-mapped genes
- Using four approaches:
  - Sequence analysis
  - Analysis of phylogenetic & geographical distribution
  - Allele specific expression in F<sub>1</sub> plants
  - Knock-out lines from TILLing, targeted mutagenesis, Uniform MU, etc.

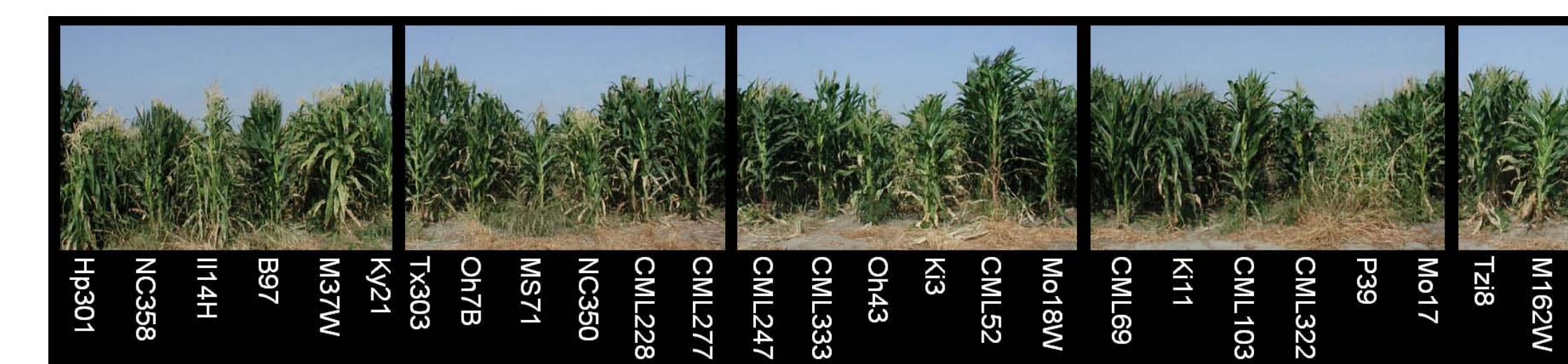


## Community access to NAM



The NAM population grown in Missouri in 2009

- Seed for all or part of NAM available from the Maize Stock Center
- Genotypes at 1106 SNP markers available at [www.panzea.org](http://www.panzea.org)
- Next generation (Maize HapMap) sequencing data will be projected from the parents onto the RILs
- We will host a public grow out of NAM in summer 2012**  
- the maize community is invited to score traits of interest

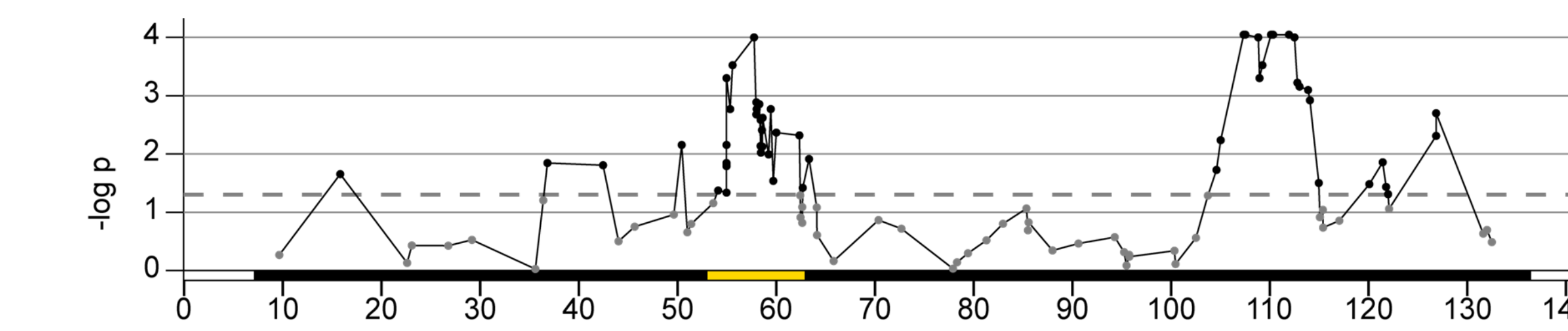
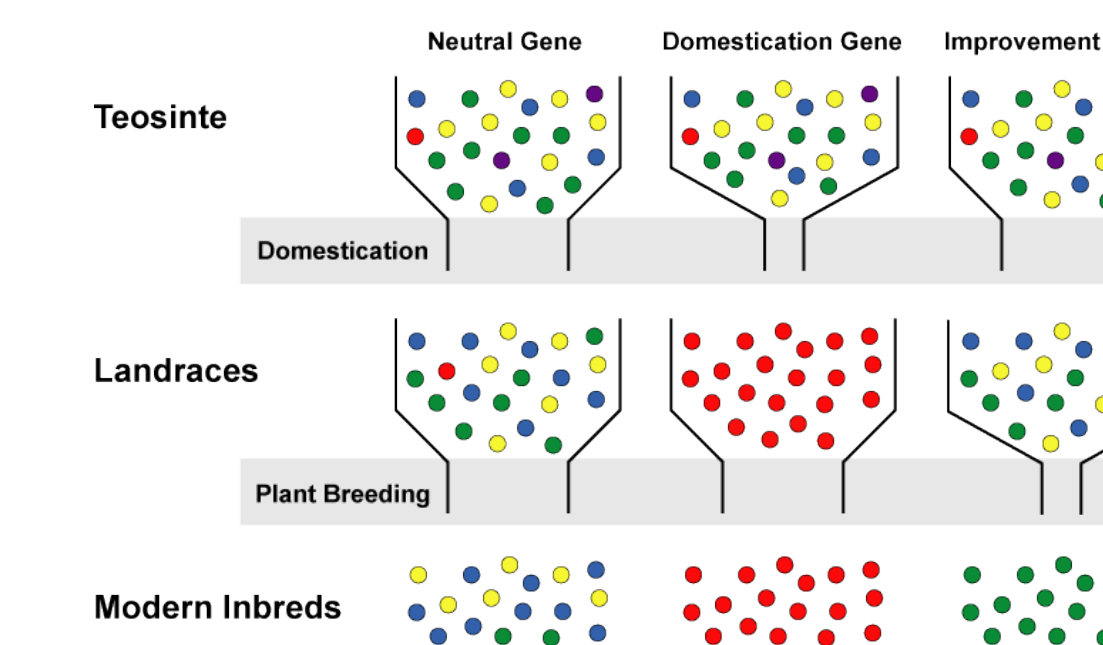


Phenotypic diversity among the NAM parents (25 diverse lines plus M17)

## 3. Effects of recombination & bottlenecks

• How does *functional* & molecular diversity relate to:

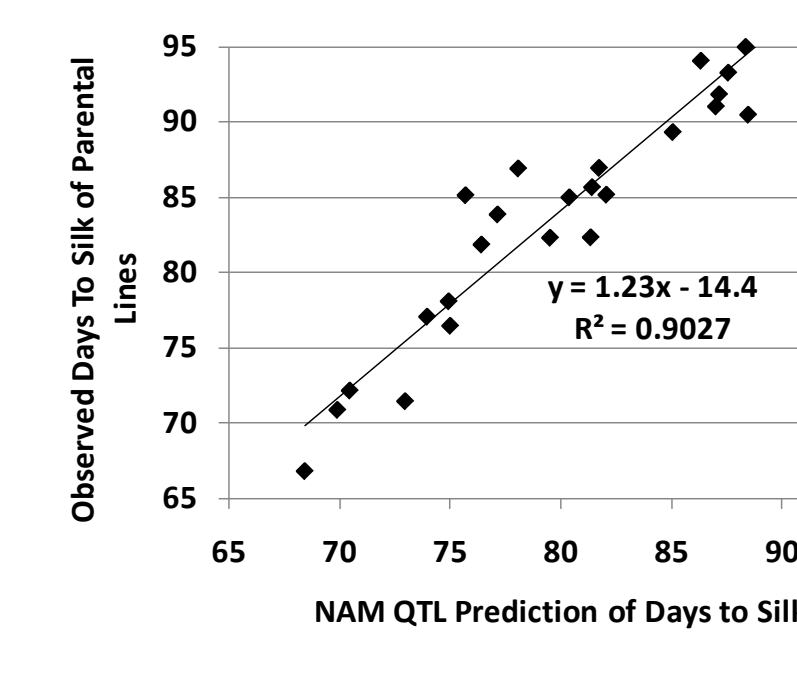
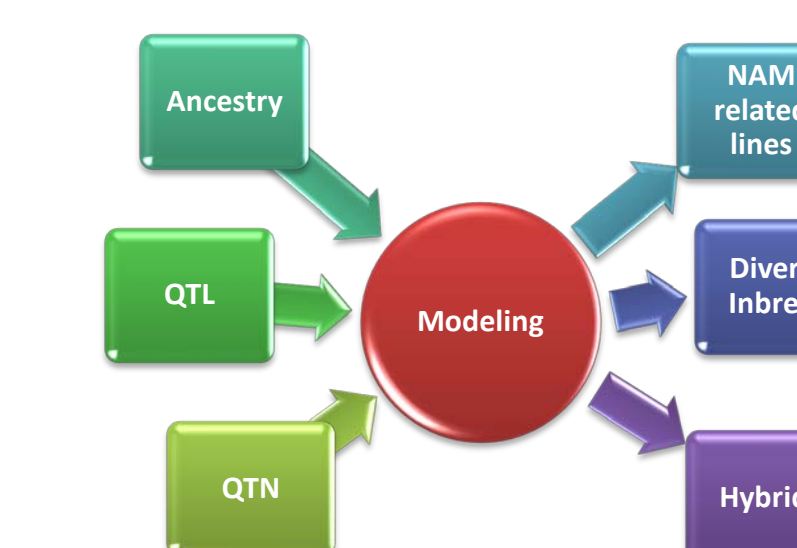
- Recombination rate variation across:
  - the genome?
  - NAM families?
- Historical demographic bottlenecks & founder events?
- Artificial selection during maize domestication and improvement?



Differential recombination in NAM (Chromosome 4)

## 4. Phenotypic prediction

- Will test our ability to predict phenotype in three germplasm sets:
  - NAM** (plus two related RIL families)
    - core association panel (281 lines)
    - 92 ex-PVP lines
    - 27 maize landrace inbreds
  - Maize Diversity Panel (MDP)** which includes:
    - core association panel (281 lines) crosses with B73
    - 300 F<sub>1</sub>'s between ex-PVP heterotic groups
  - F1 hybrids** including:
    - 281 diverse lines crosses with B73
    - 300 F<sub>1</sub>'s between ex-PVP heterotic groups
- Predictions within NAM tested by jackknifing:
  - remove one family at a time
  - predict phenotypes based on remaining families



## Other community resources

- All of our germplasm resources will be genotyped to high density  
- Genotypic data & seed will be made publically available



- Our high density genetic maps will lead to improvements of the maize physical map

## Outreach

Teaching evolution, genetics & diversity to four target audiences:

- The general public** – via a mobile museum display in collaboration with the Museum of the Earth (Ithaca, NY)
- High school teachers** – via summer courses held at NC Ag & Tech State U
- International scientists** – via the African Scientist Fellowship Program at Cornell
- Undergraduates** – via direct participation in our research.

