

Next Generation Crop Improvement

Peter L. Morrell
Agronomy & Plant Genetics - Minnesota

REVIEWS

Crop genomics: advances and applications

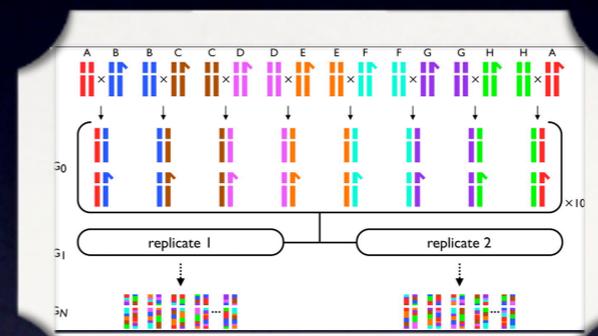
Peter L. Morrell¹, Edward S. Buckler² and Jeffrey Ross-Ibarra³

Soybean Genomics Strategic Plan

- Goal 1: Improve Utility of Genome Sequence
 - Improve bioinformatics resources - practical applications
- Goal 2: Translational Genomics - Optimize Breeding Efficiency

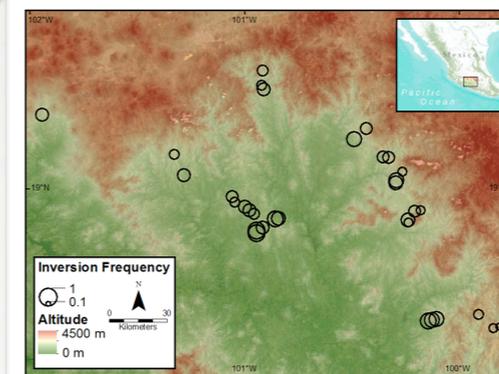
Topics

- Next generation populations
- Selection against deleterious mutations
- Applications of genome-wide SNP data



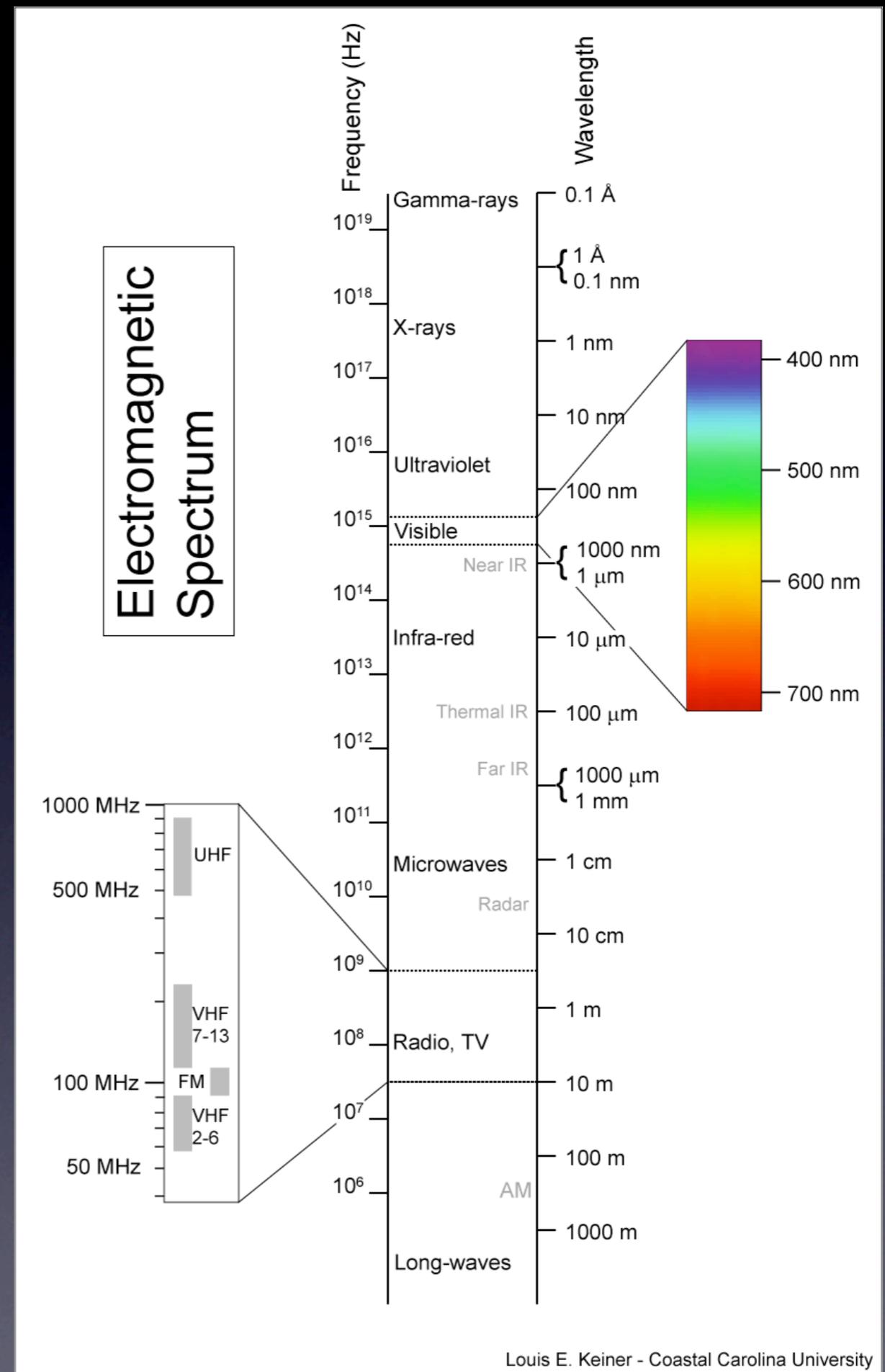
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Rice	... AAC CAC CTT ...
Brachypodium	... AAC CAG CTC ...
Sorghum	... AAT CAT CTC ...
	Asn His Leu
Maize	... AAC GAT CTC ...
	Asn Asp Leu



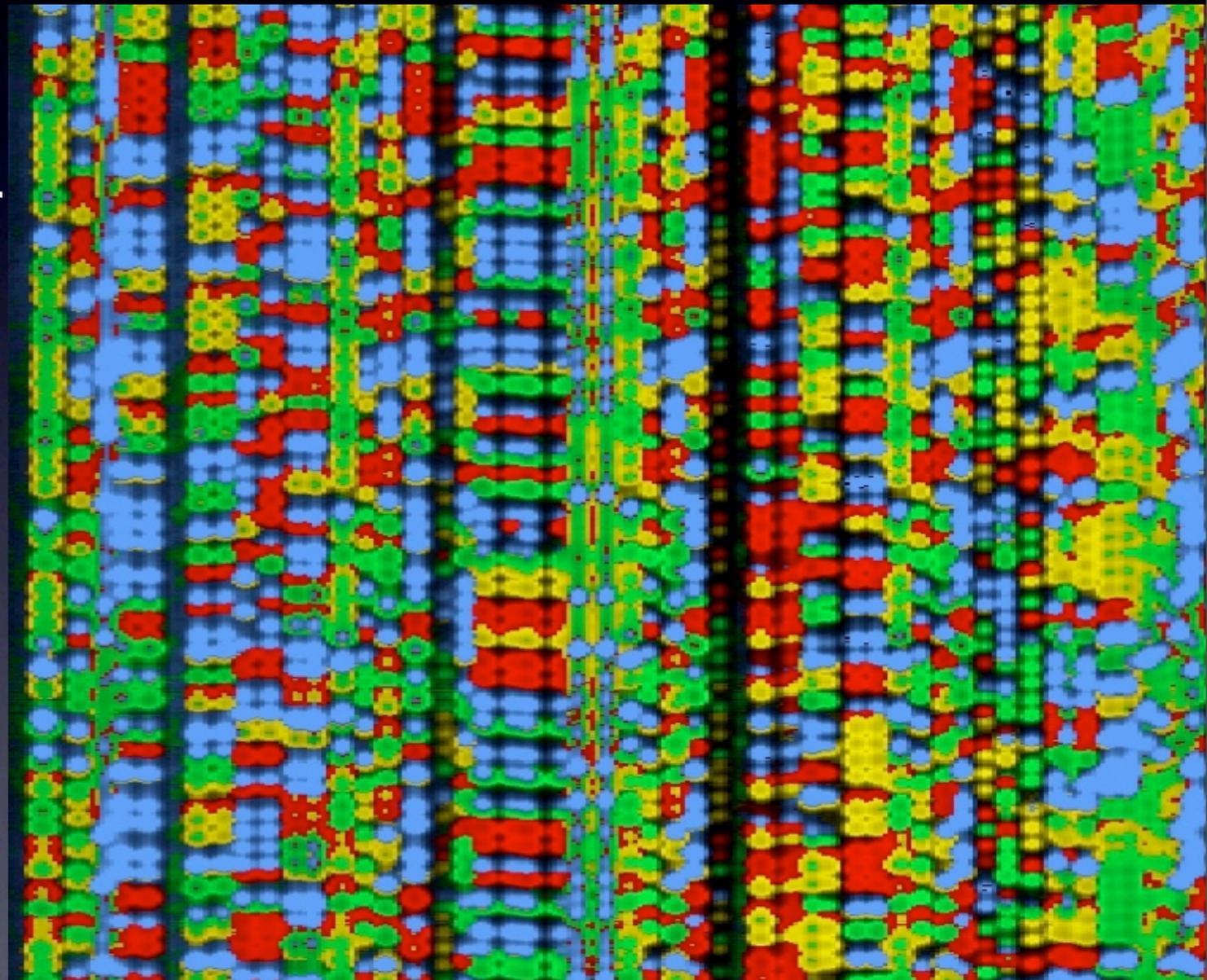
Observational Astronomy

- Information about places we won't ever visit
- The visible portion of the electromagnetic spectrum is only a fraction of what exists
- DNA resequencing data latent with information about the past

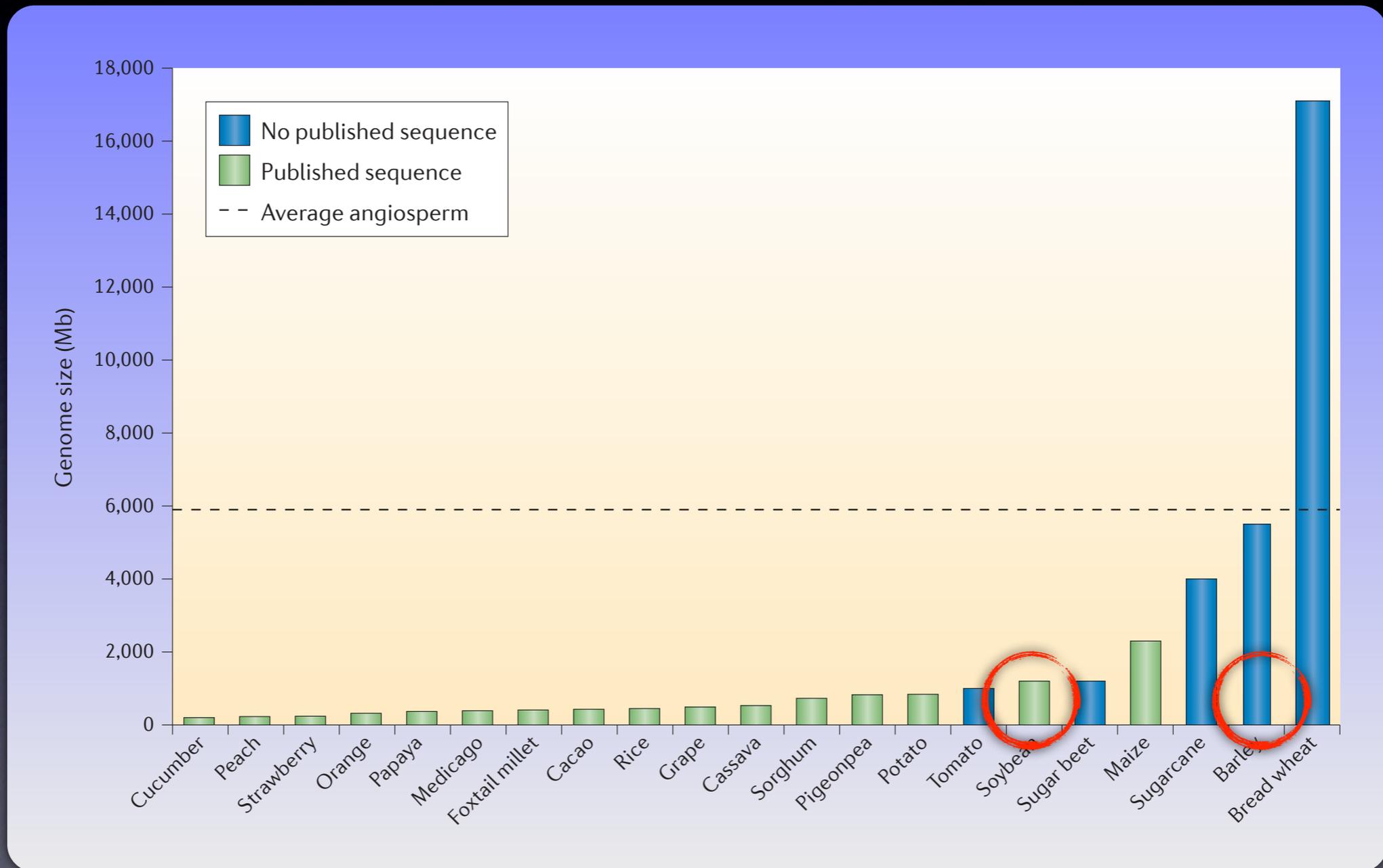


DNA Resequencing

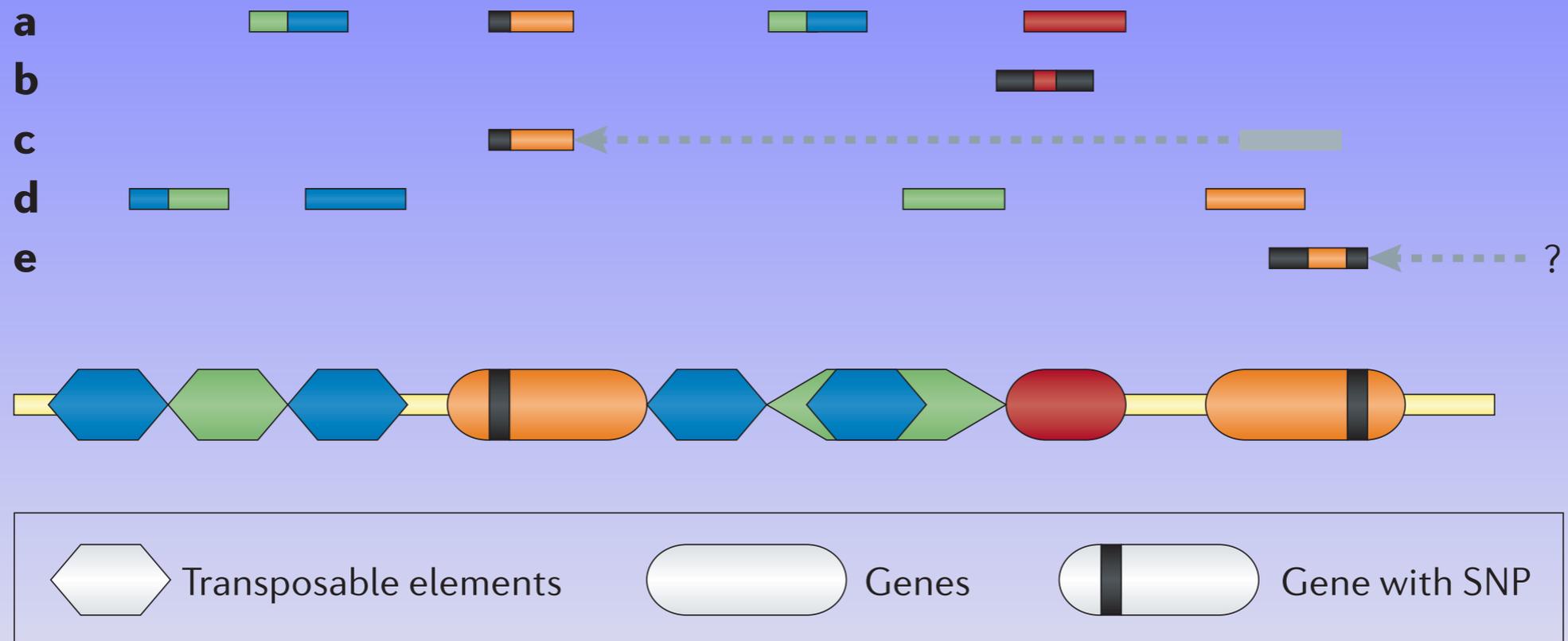
- Most direct measure of genetic diversity
- Can assay all heritable variation
- Can now be collected very rapidly



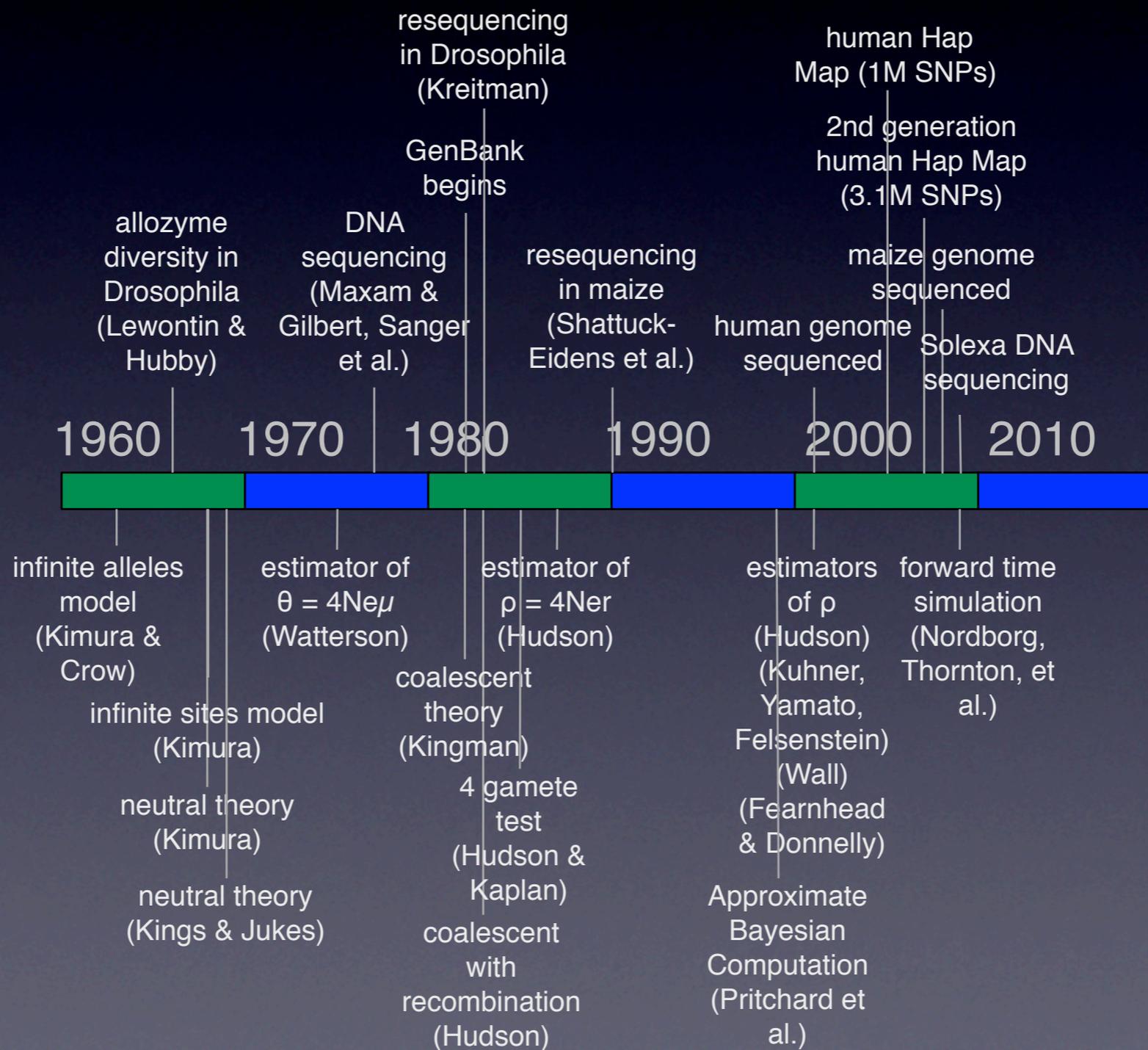
Genome Size



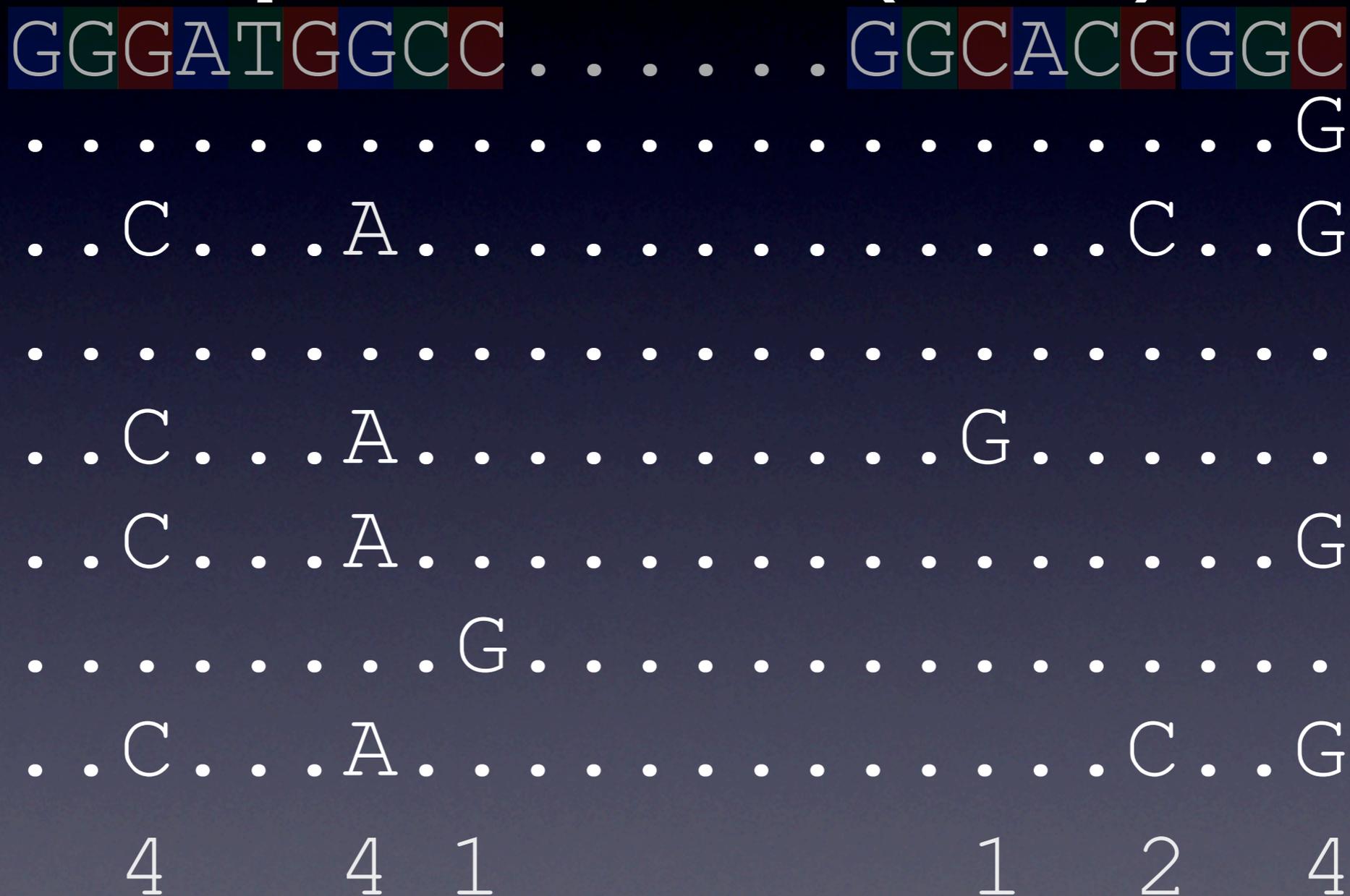
Short Read Mapping

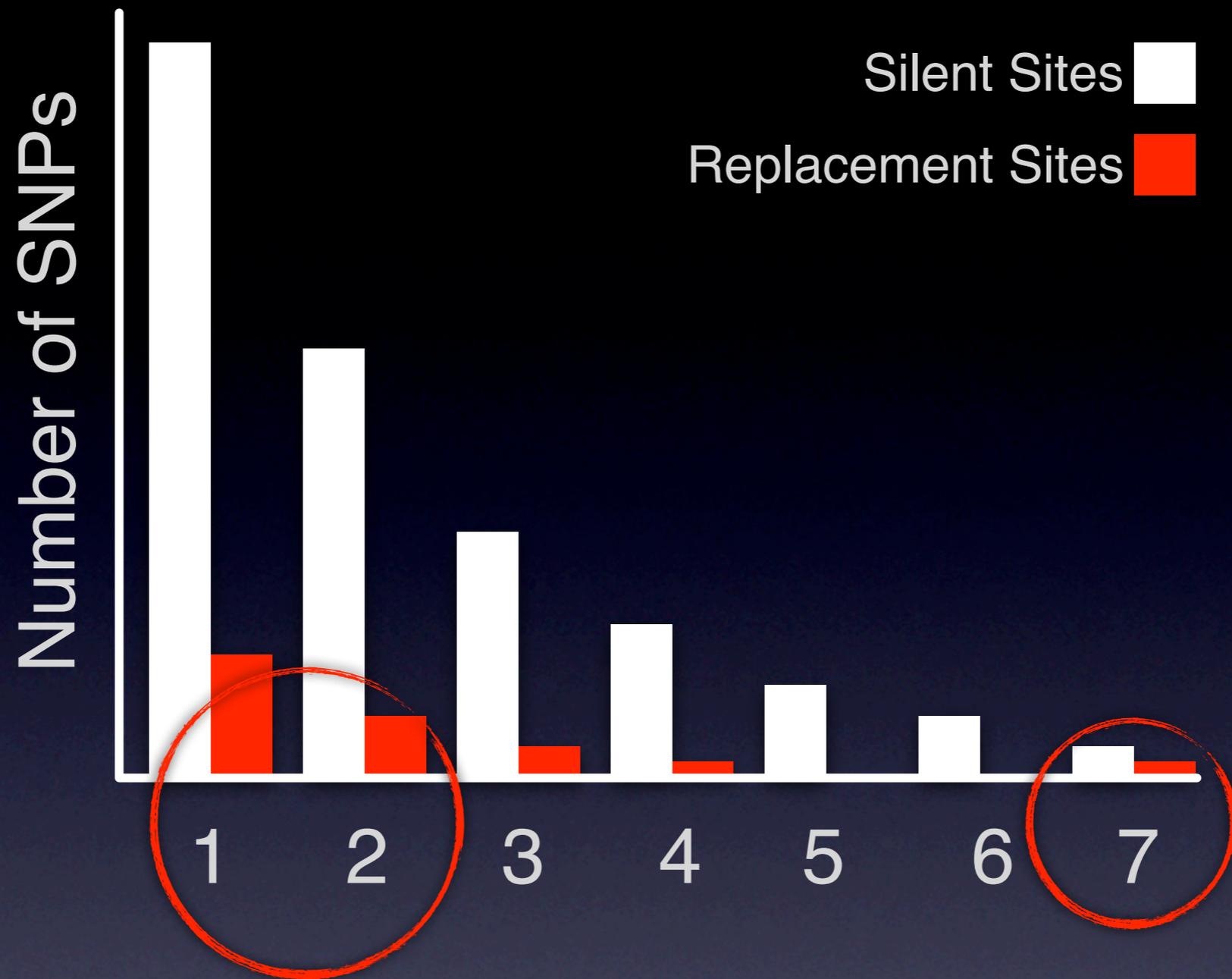


Molecular Population Genetics



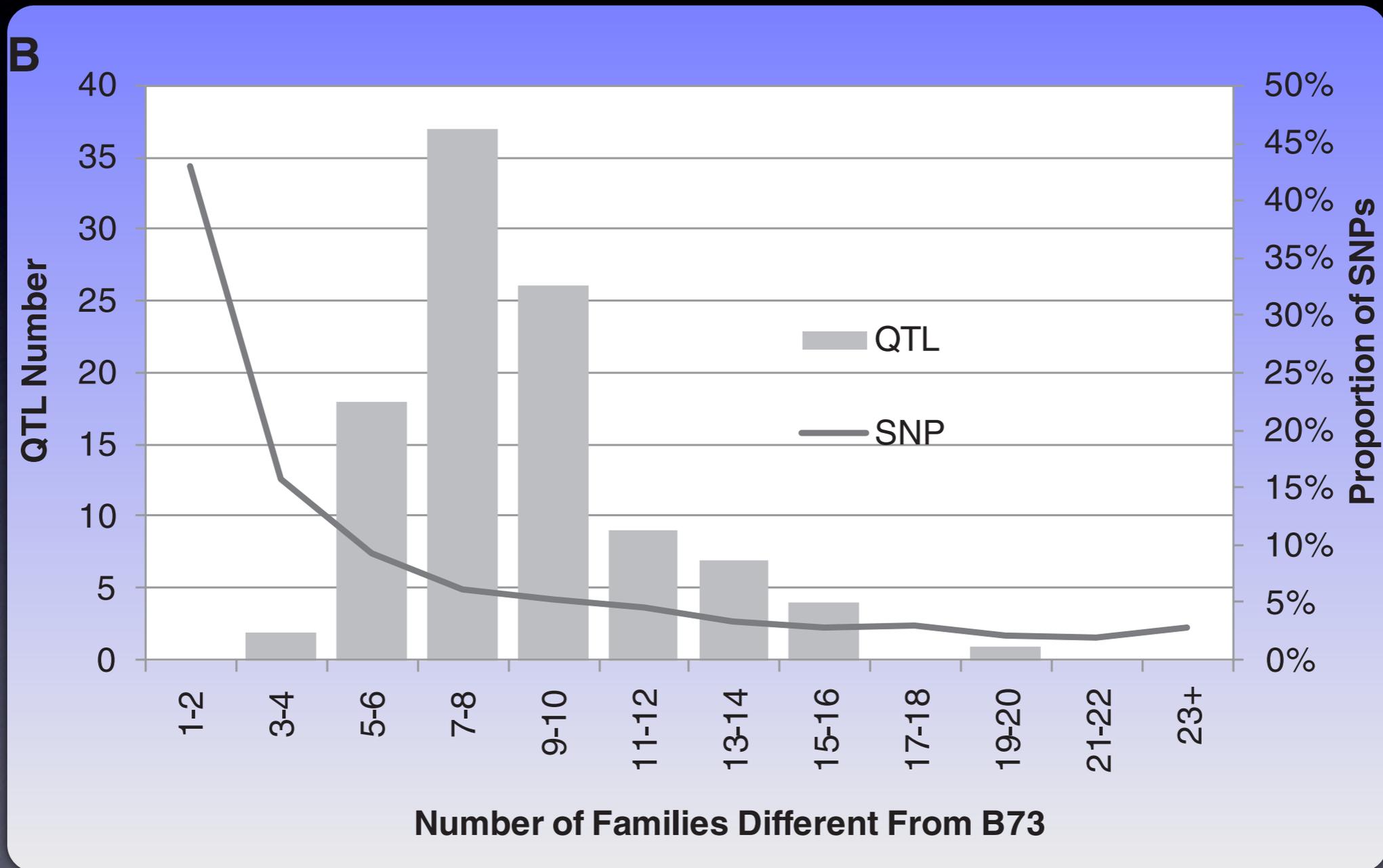
Derived Site Frequency Spectrum (SFS)





Derived SFS

QTL & SNP Frequency



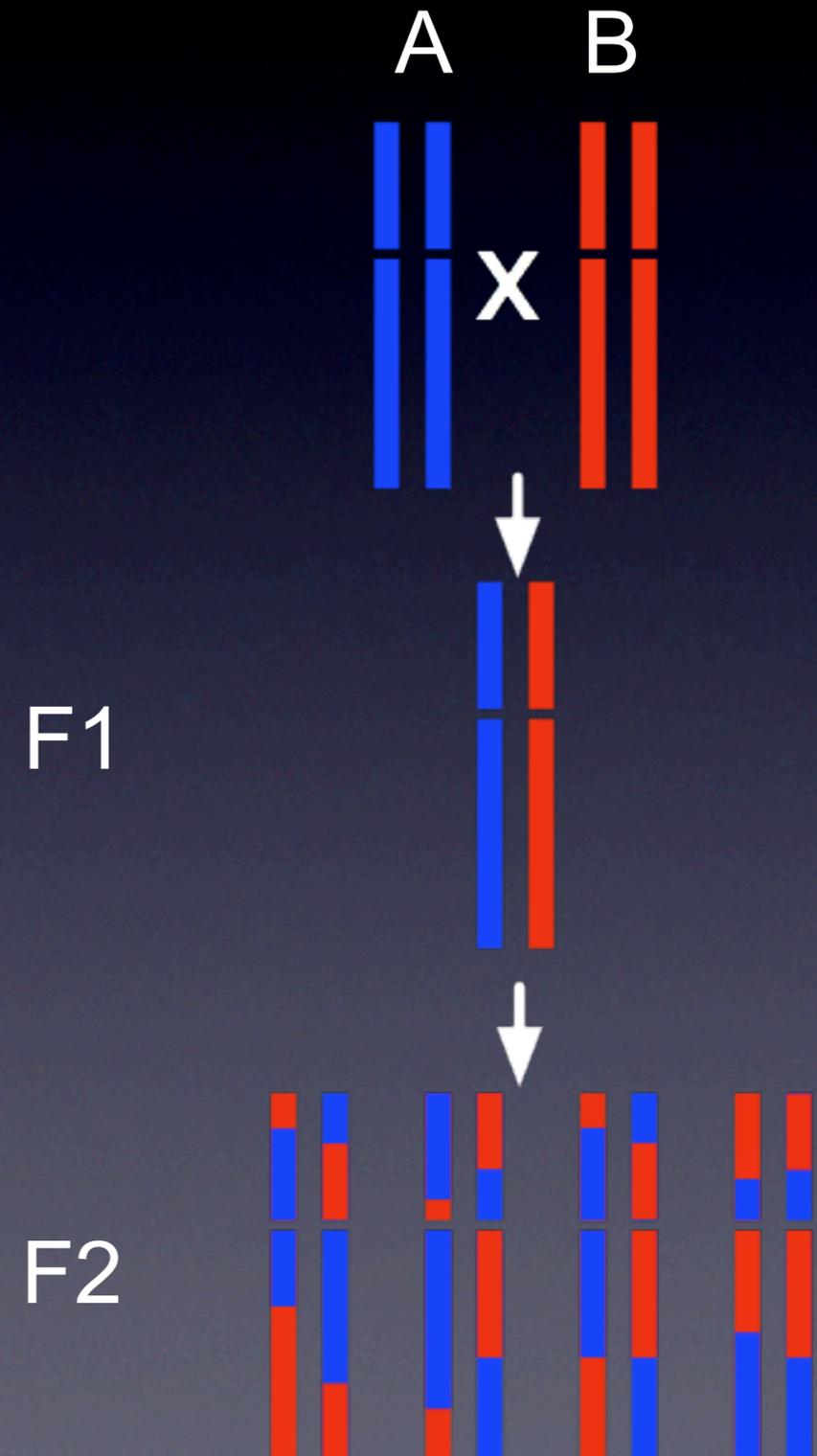
Buckler et al. 2009

Next Generation Populations

- Where are mutations that control quantitative variation?
 - How large an effect do they have?
- What is their frequency in the population?

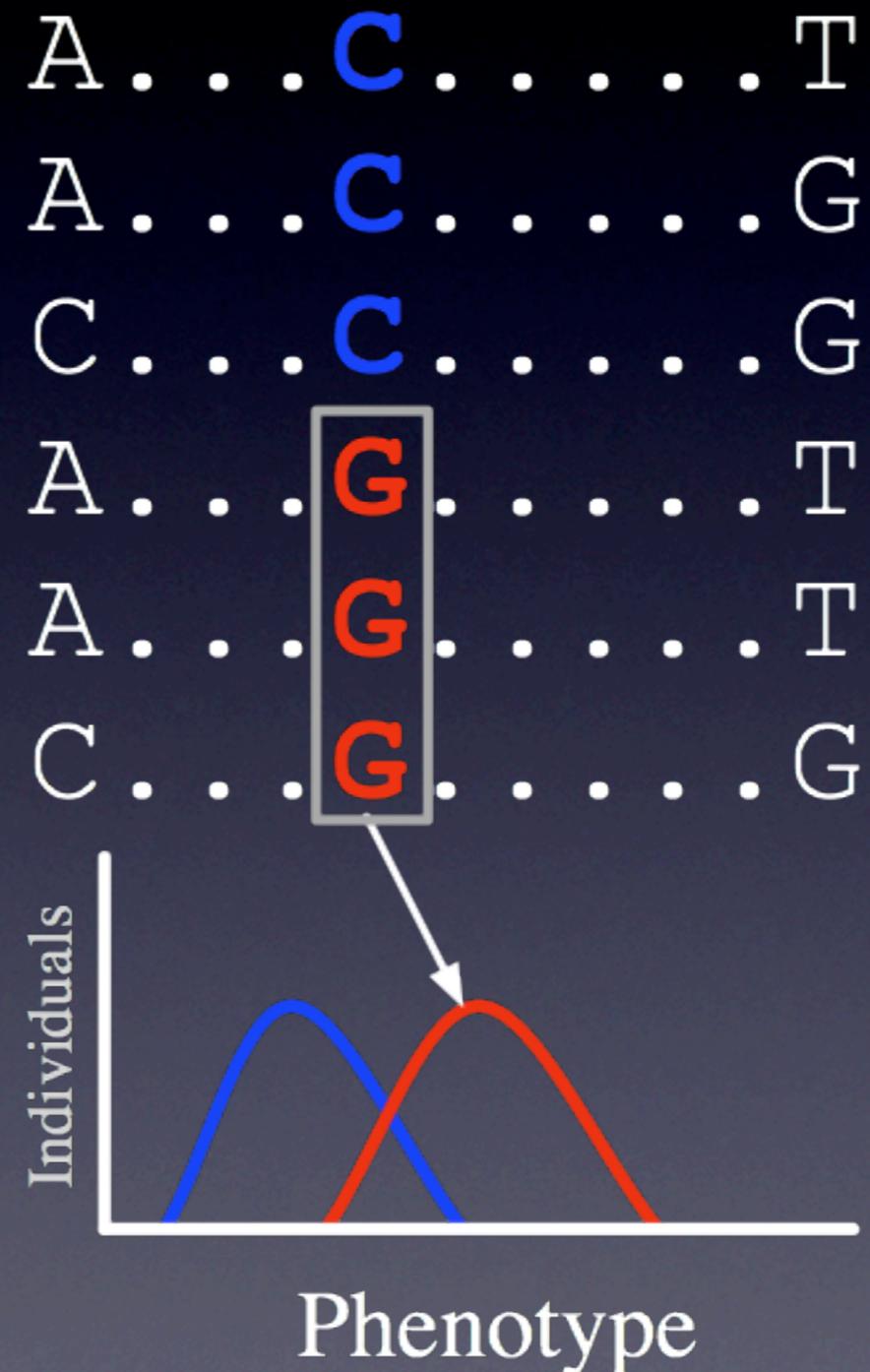
QTL Mapping

- Quantitative Trait Locus mapping
- Progeny segregating for portions of the parental genomes
- Statistical test of association between genotype and phenotype



Association Mapping

- Statistical association between SNPs and phenotype
- Generally assumes common disease (trait) common variant
- Fails under selection mutation balance
 - Constant flux of rare causative mutations

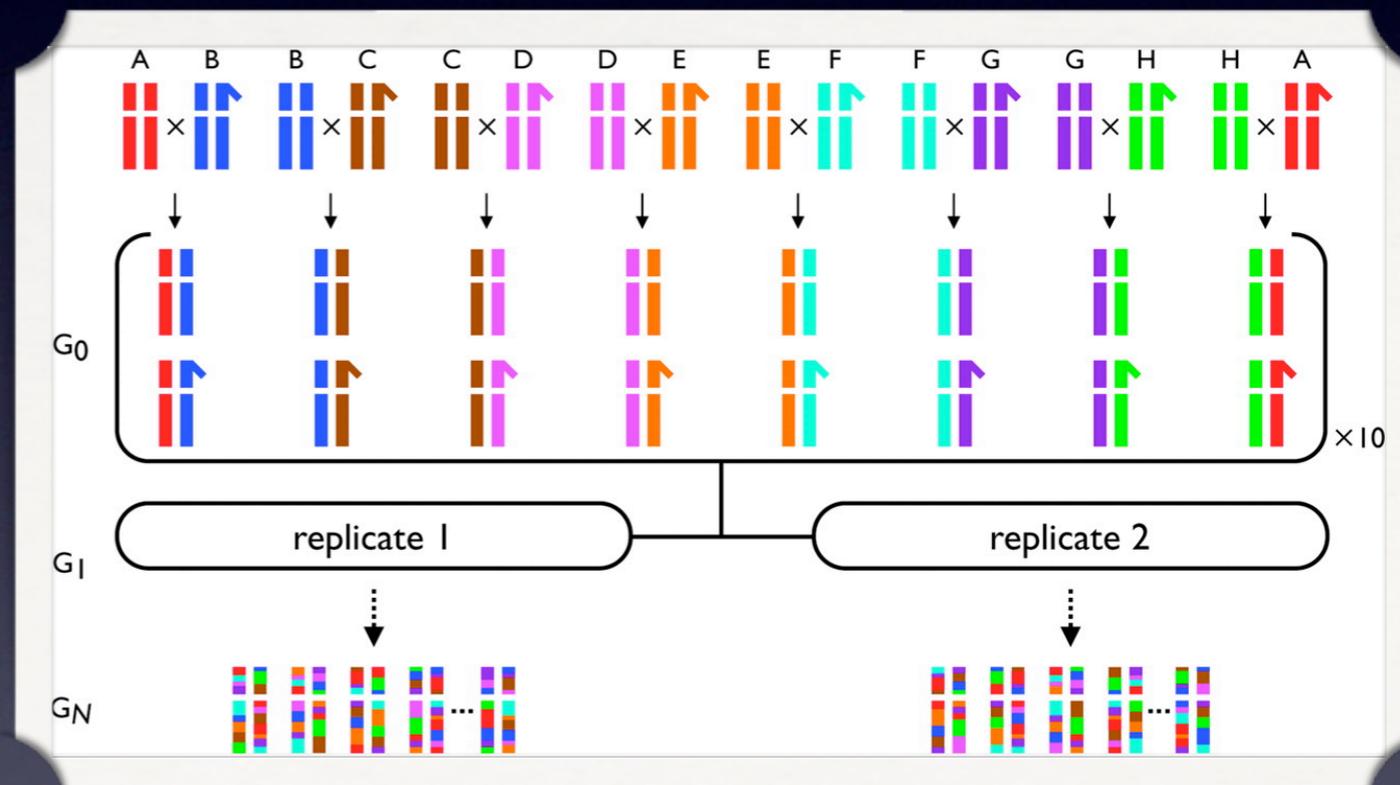


Assumptions

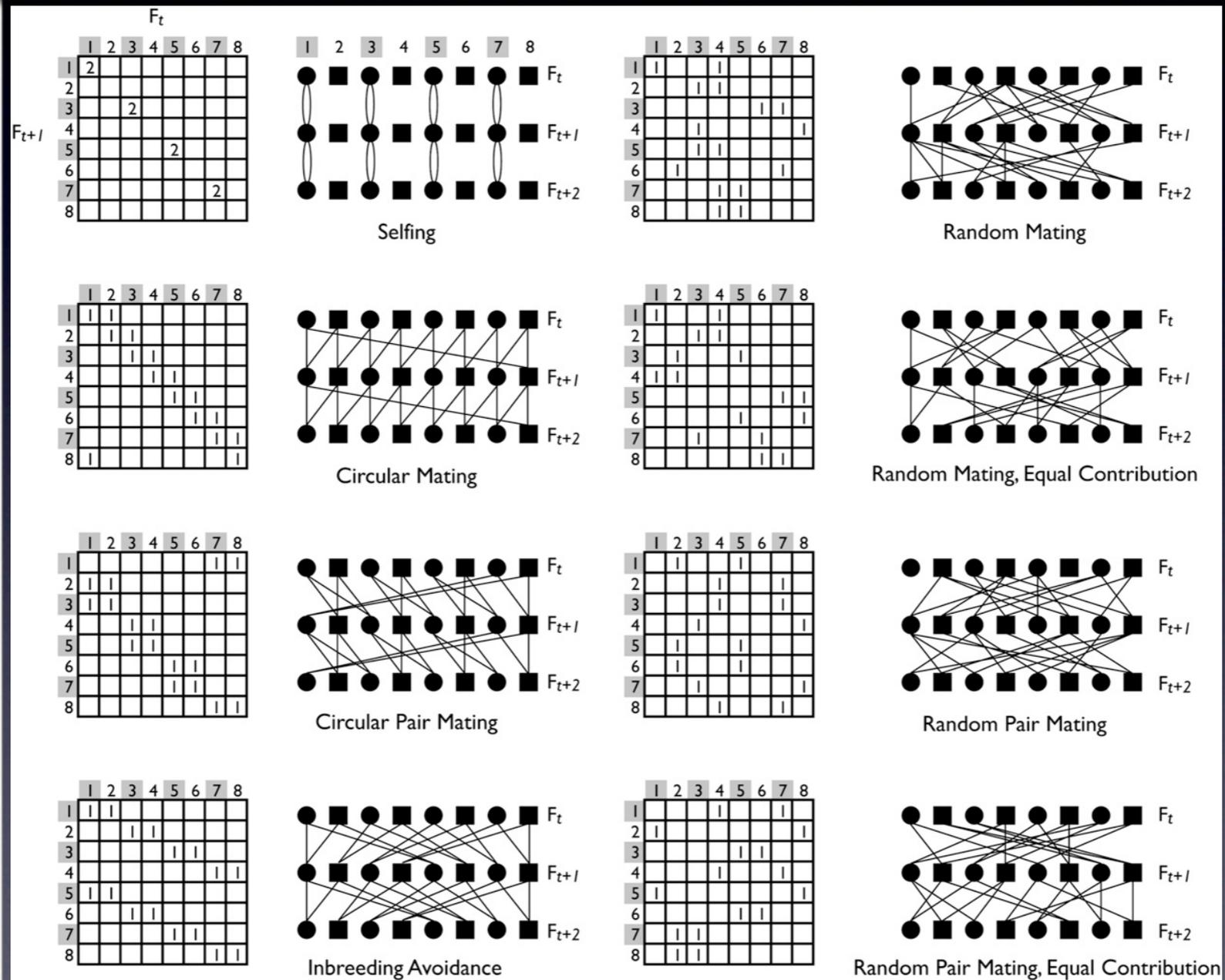
- Future Resources - Next Generation
 - Reference genome sequences and fully resequence genomes for all major crops
 - 10^5 - 10^6 SNPs will be available for inexpensive genotyping in most crops

Multiparent QTL

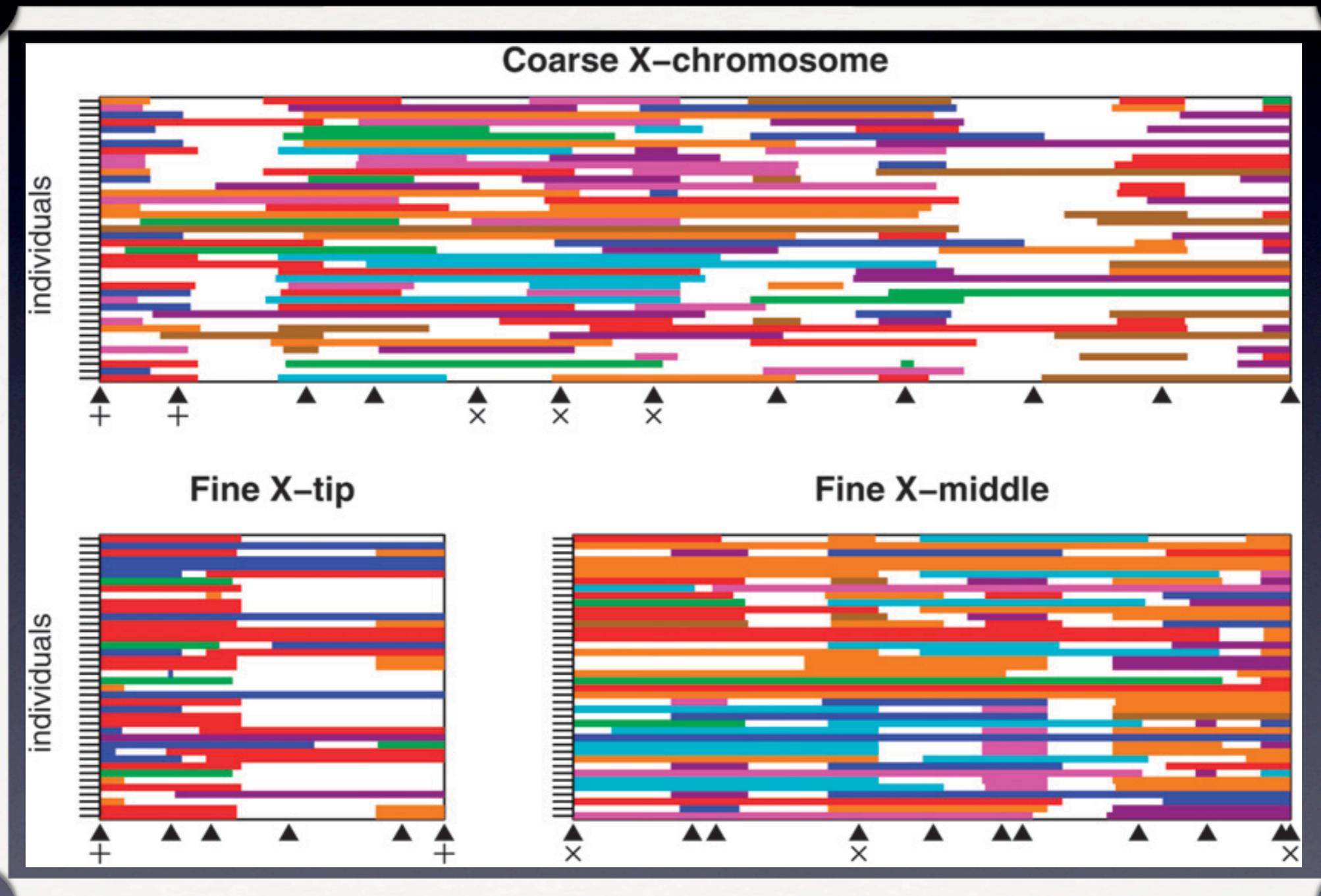
- Multiple parental lines; multiple generations
- Similar to barley composite crosses from 1920's
- *Arabidopsis* MAGIC populations
- *Drosophila* synthetic



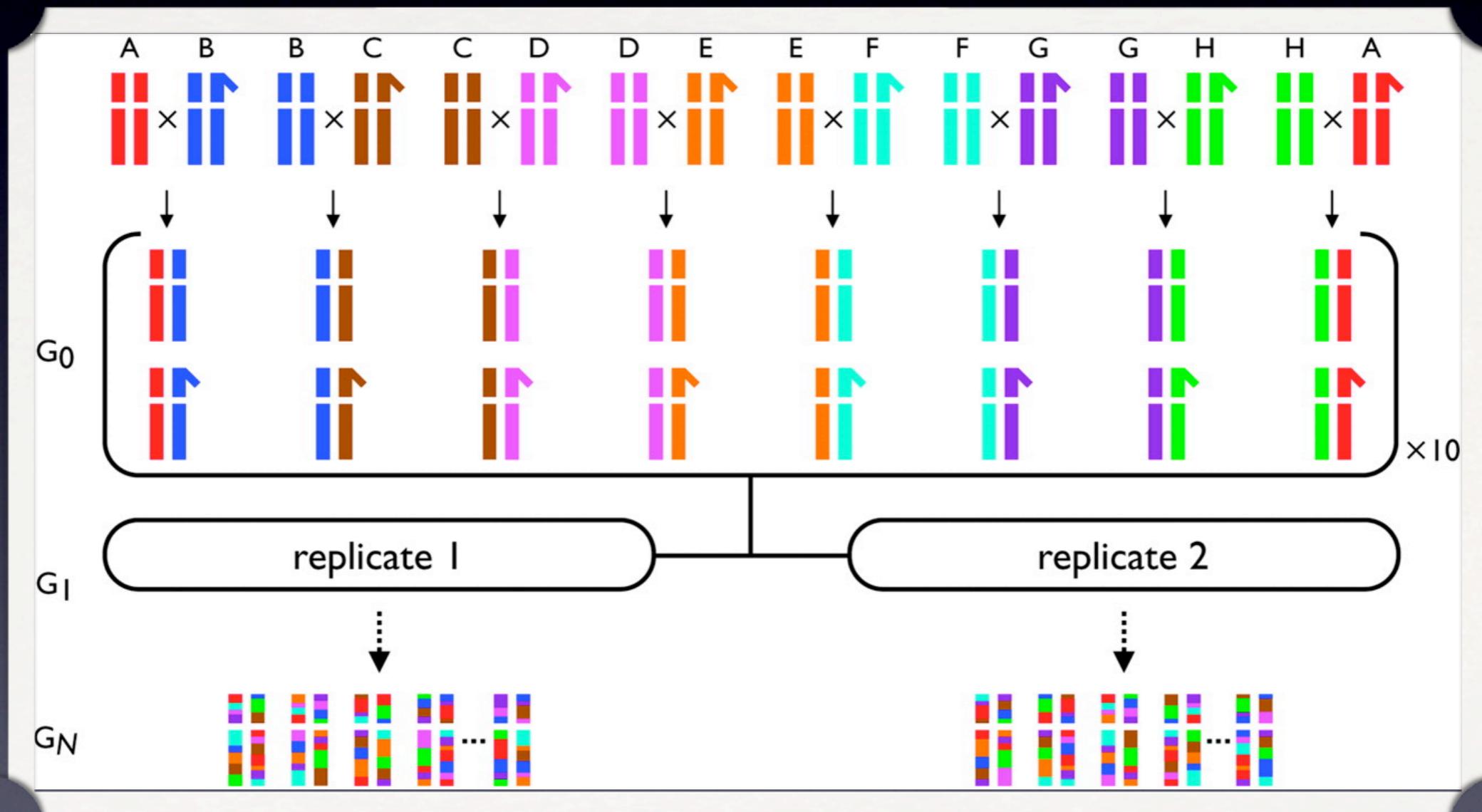
Mating Designs



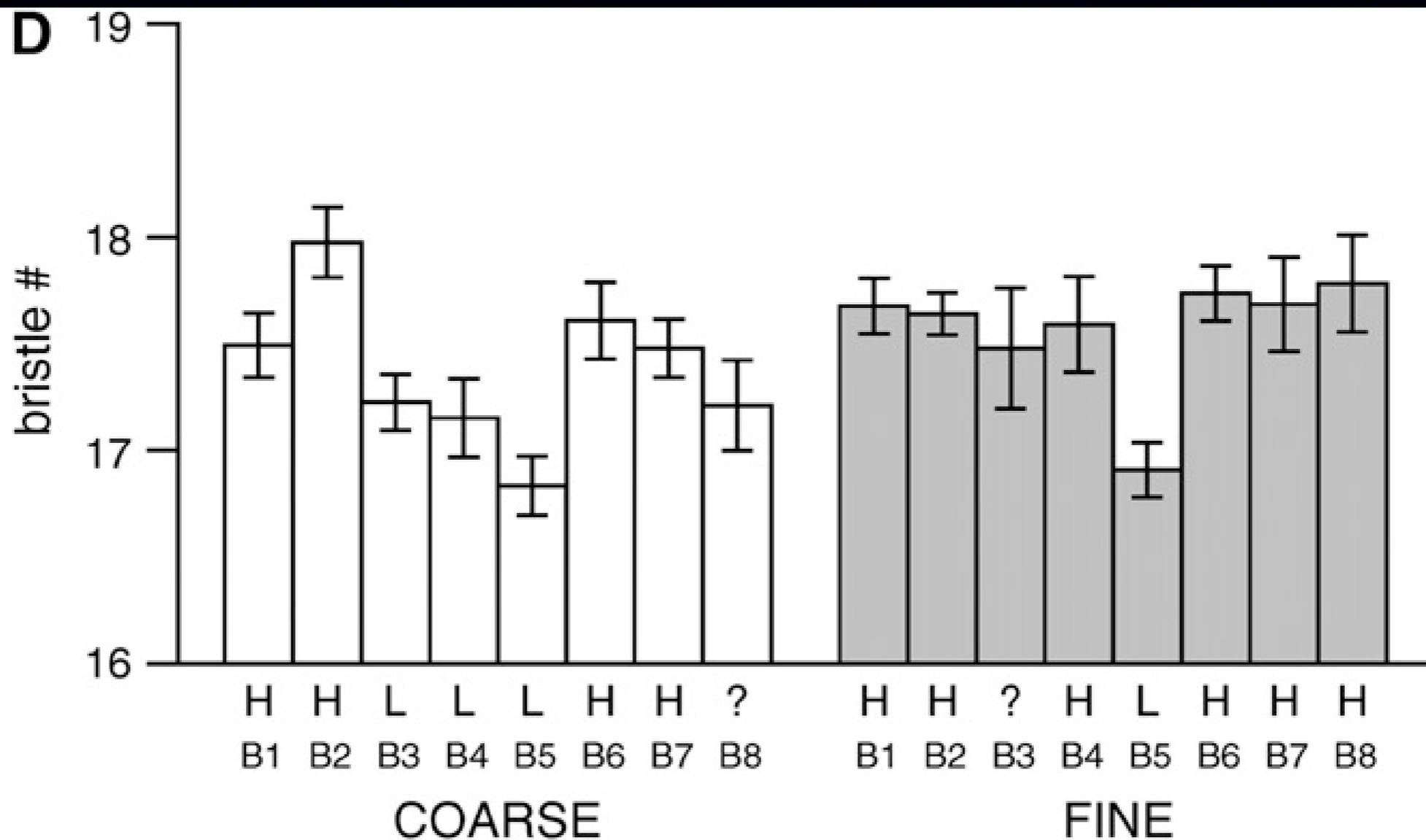
Multiparent Population



Multiparent QTL



Allelic Effects



Deleterious Mutations

- An mutation that reduces fitness or viability (yield)
- Premature stop codons, insertions/deletions, splice site variants
- Amino acid changes
- Cis-acting regulatory factors
- 100s to 1000s per genome in humans

a

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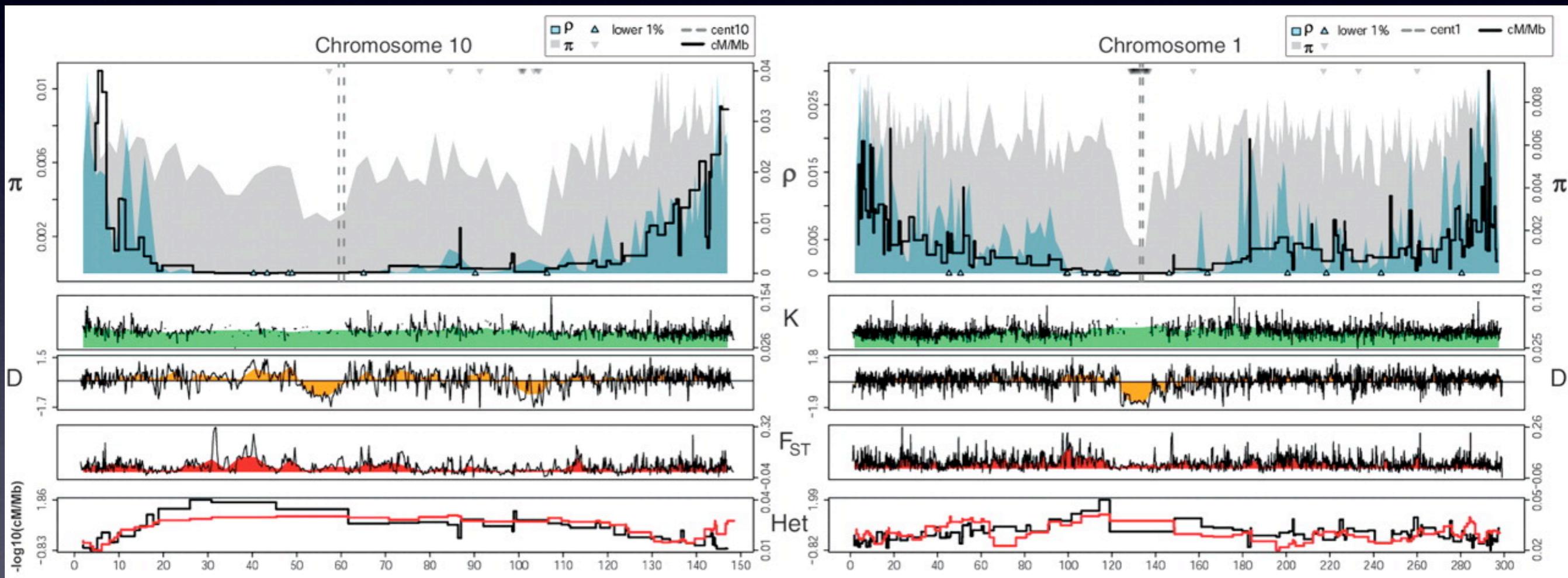
Deleterious Mutations

Rice	. . .	A A C	C A C	C T T	. . .
Brachypodium	. . .	A A C	C A C	C T C	. . .
Sorghum	. . .	A A T	C A T	C T C	. . .
		Asn	His	Leu	
Maize	. . .	A A C	G A T	C T C	. . .
		Asn	Asp	Leu	

Deleterious vs. Lethal

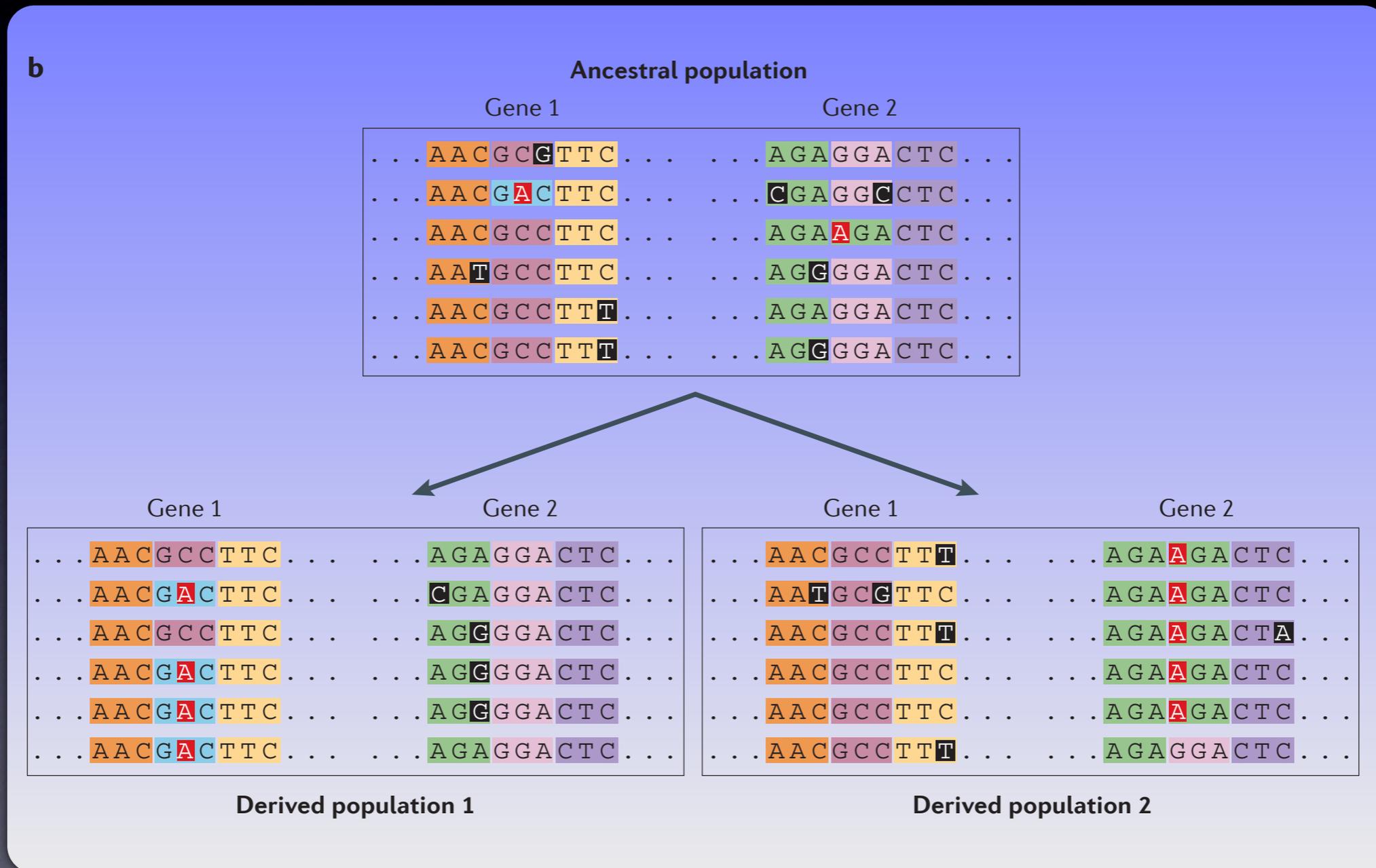
- Lethal mutations - quickly purged upon inbreeding
- Deleterious mutations - modest frequency
 - Can reach higher frequencies due to linkage drag or 'allelic surfing'
 - Harbored in genomic regions with low recombination rate

Recombination Rate



Gore et al. 2009

In Breeding Populations



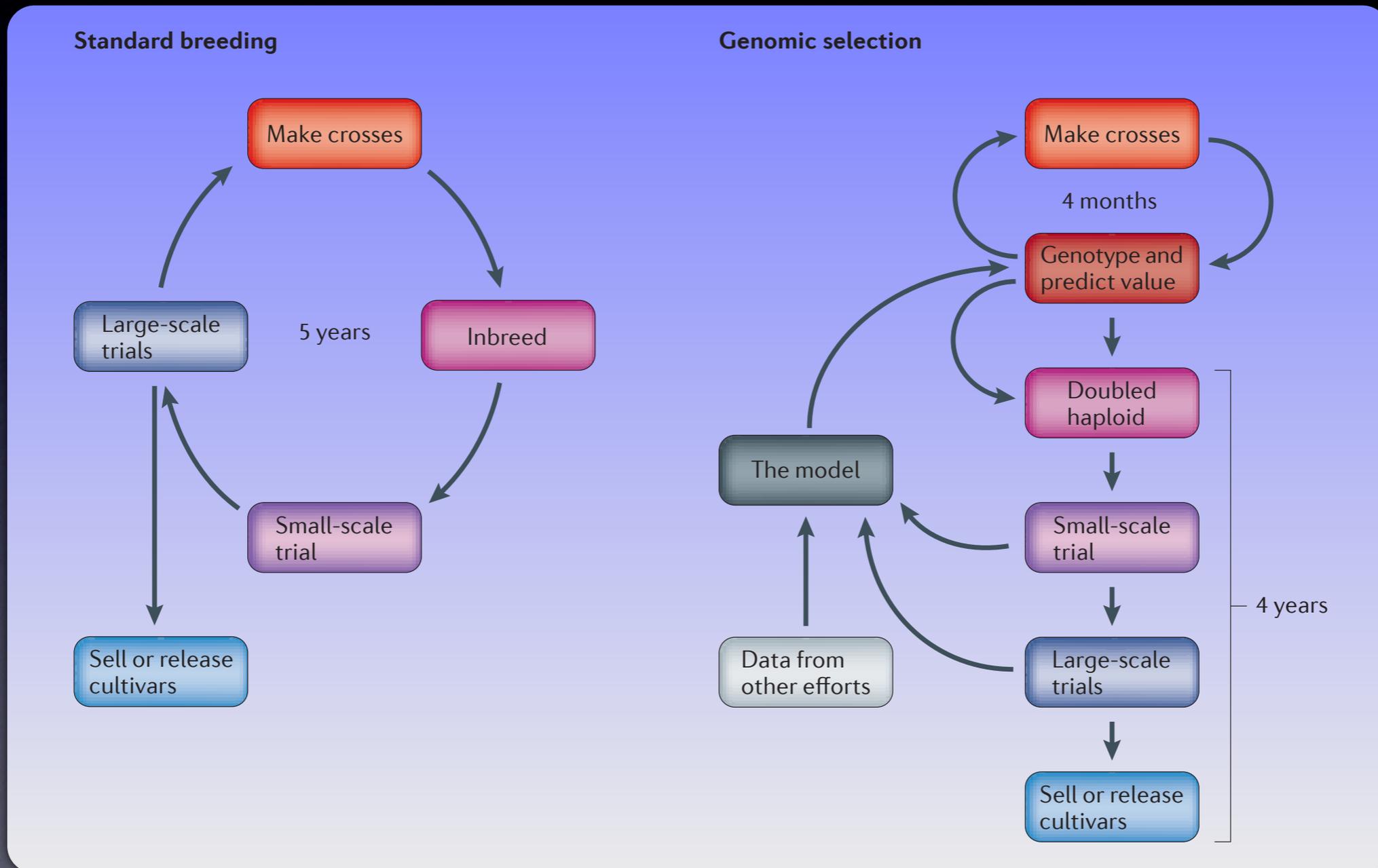
Relevance to Crops

- The potential to purge deleterious mutations is related to population size
 - Many breeding programs have very small effective size
- Biggest diminution in fitness when deleterious mutations are homozygous
 - Barley, soybeans, and wheat...

Applications

- ‘Reverse genomic selection’ against deleterious mutation could improve yield
- Deleterious changes in genes that aren’t directly associated to traits
- Targeted recombination - purge deleterious changes

Genomic Selection

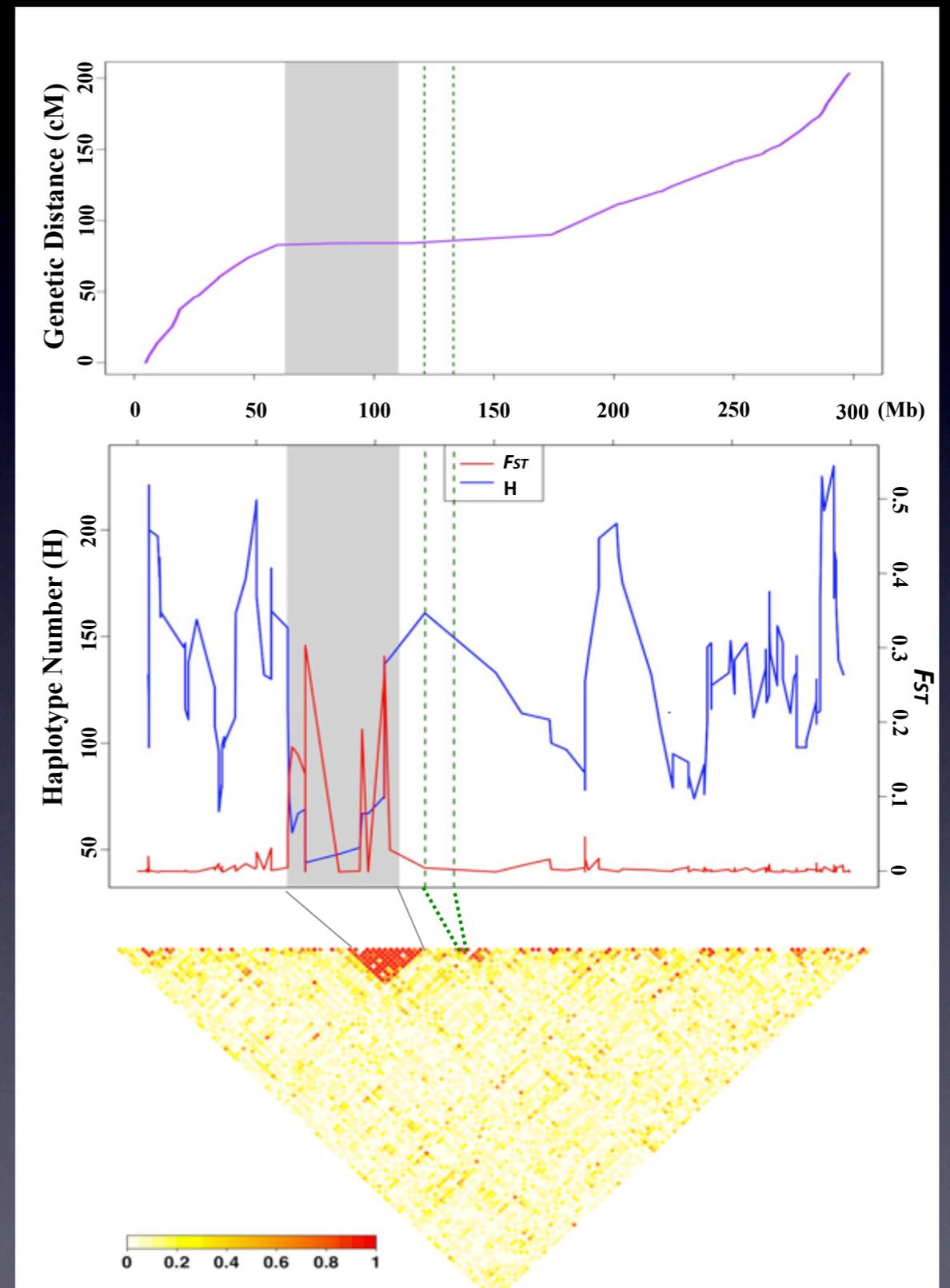


Genome Level Analysis

- Extended linkage disequilibrium in teosinte
- Genetic provenance of climate adapted mutations in barley

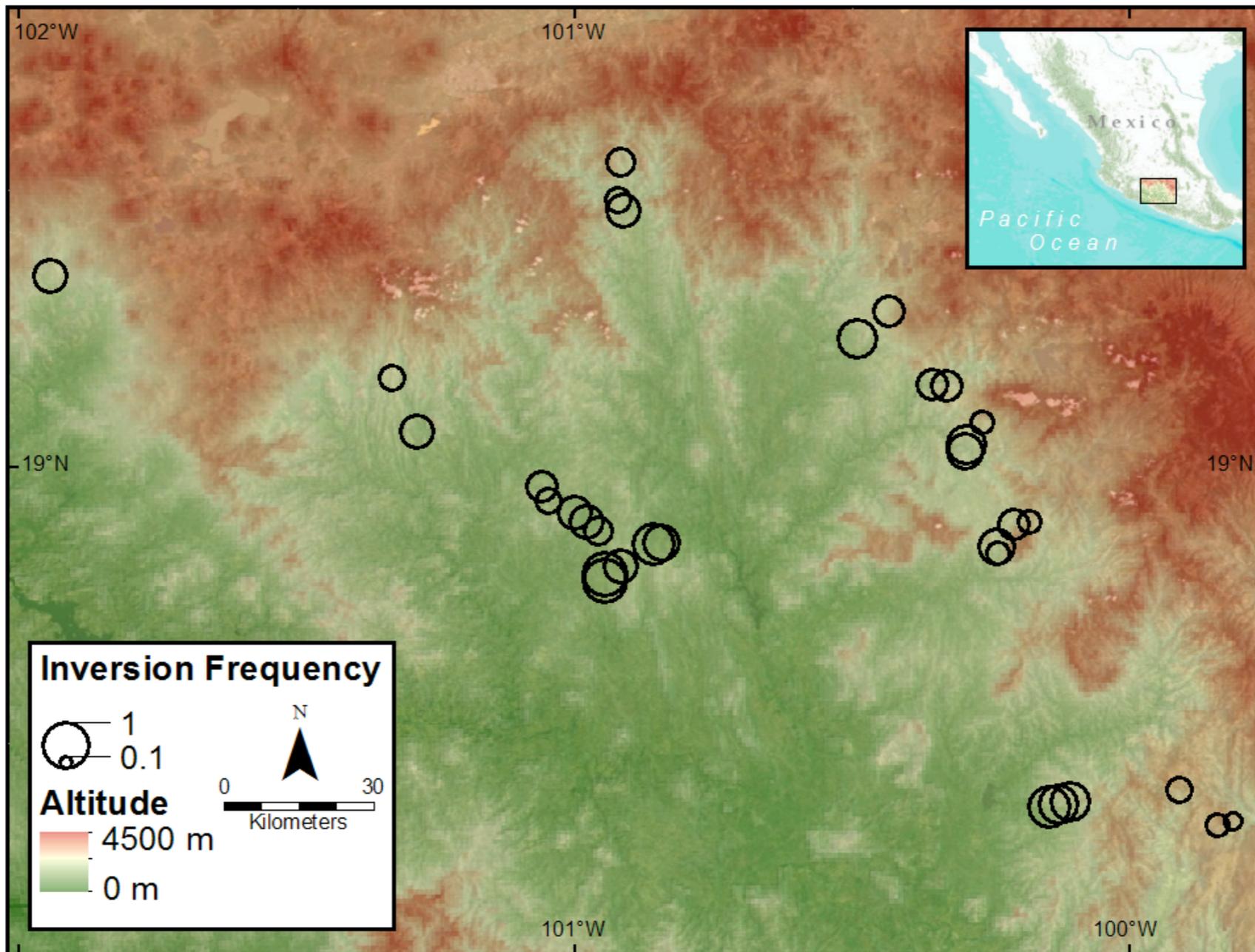
Inversion Evidence

- Decreased recombination rate in inversion region
- Low haplotype numbers for the SNPs inside inversion
- High F_{ST} values for the SNPs inside inversion



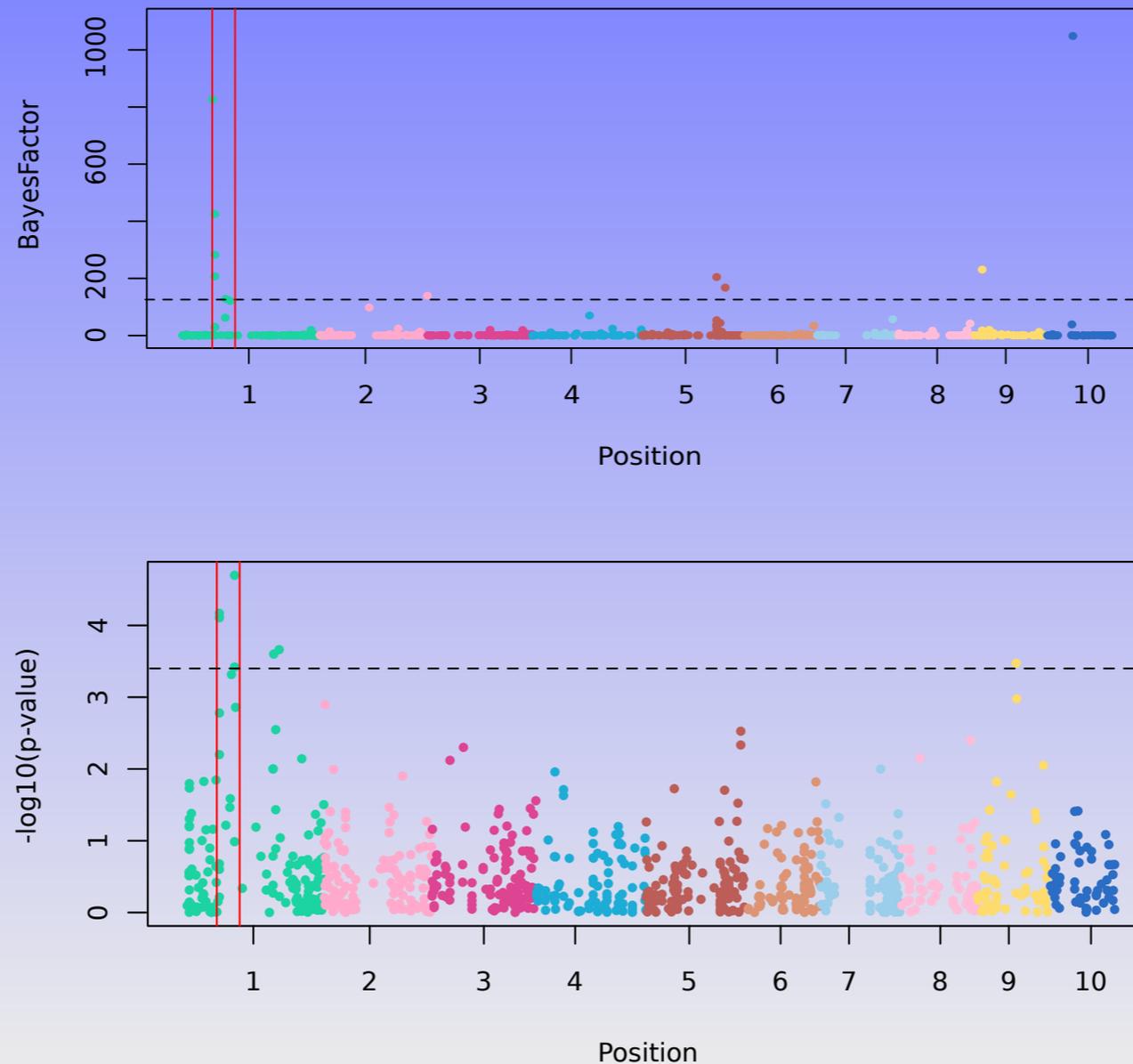
Fang et al. (in review)

Inversion Frequency



Fang et al. (in review)

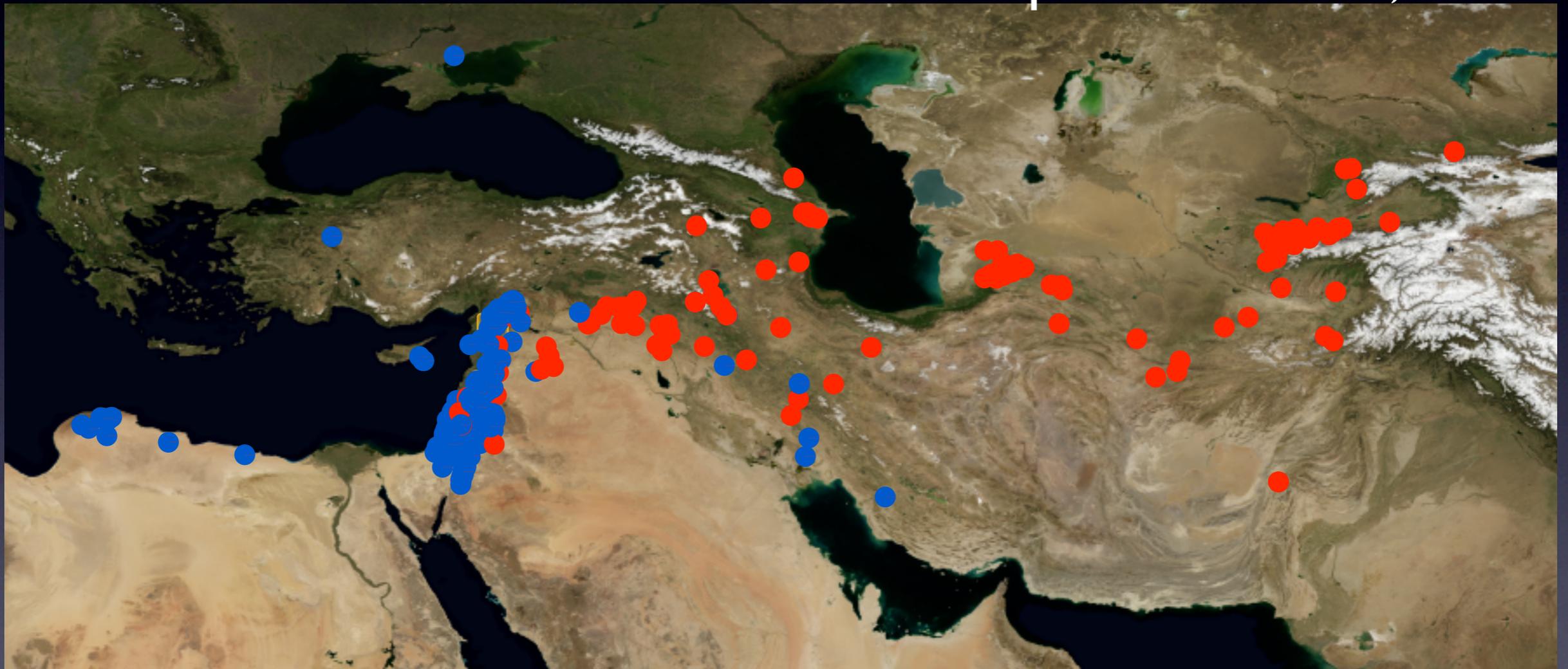
Association - Altitude



Fang et al. (in review)

Wild Barley Diversity Collection

Sample Sizes - 196, 116

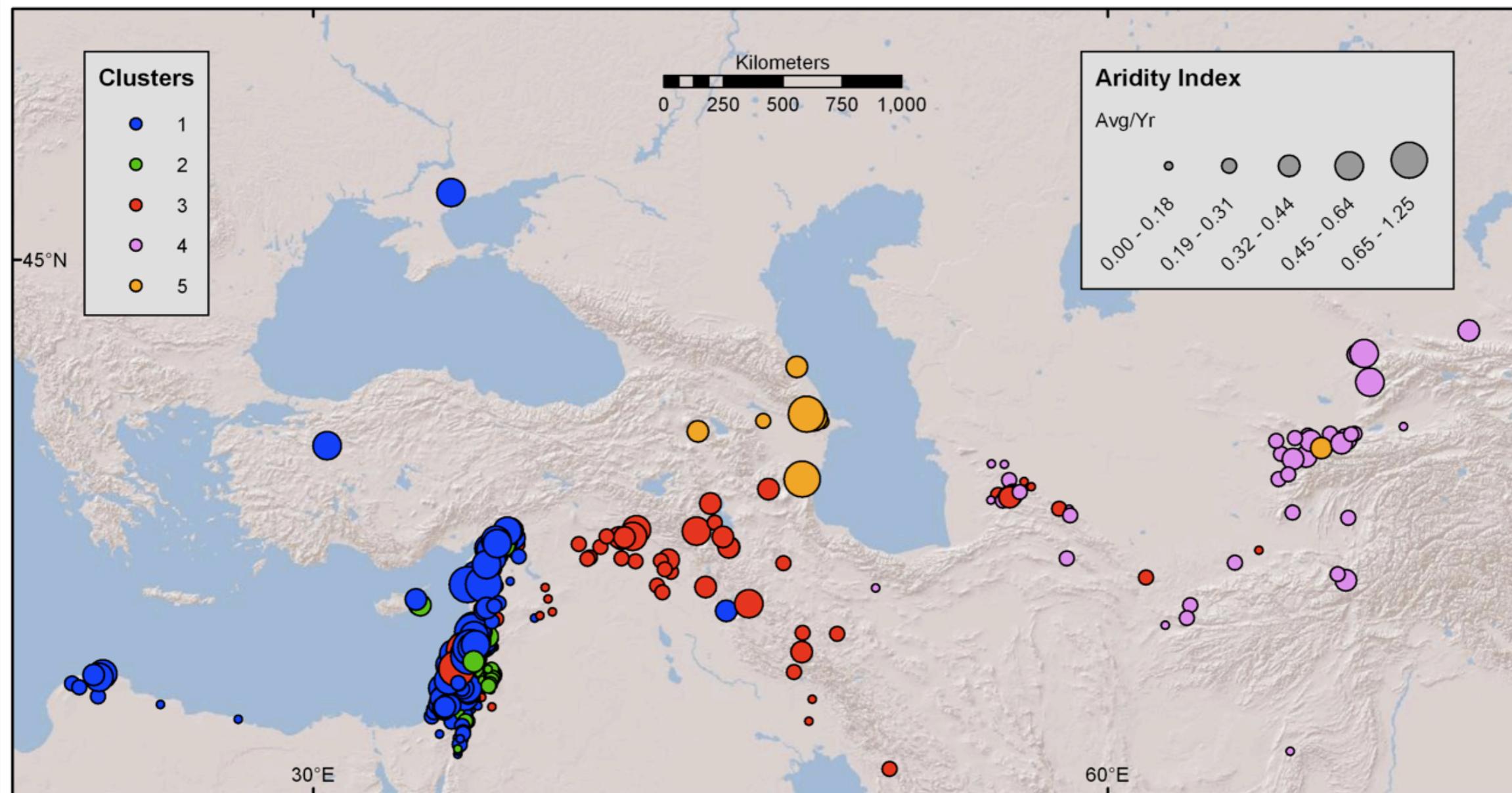


Average
 F_{ST}

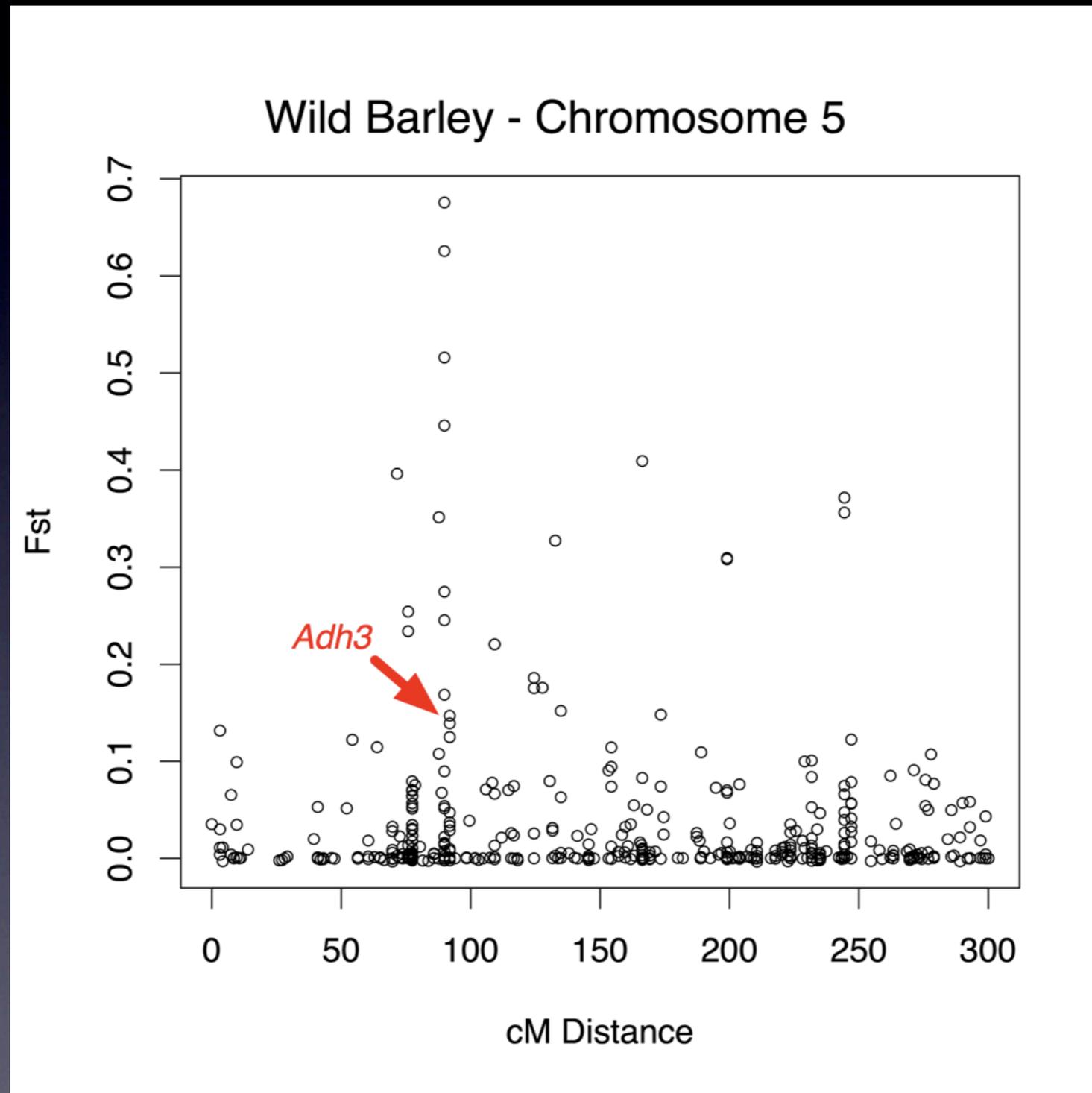
BOPA1
0.09

BOPA2
0.13

Aridity - Western Asia



F_{ST} - Chromosomal



443 SNPs

Opportunities

- Genomics era has just begun
 - Many patterns are easy to find
- SNP metadata 'data about data' is very important
- Latent with information from places we can't visit!

Acknowledgements

- Funding
 - USDA NIFA National Needs Fellowship
 - Soybean genetic load
 - USDA NIFA T-CAP
 - Barley
- Maize Inversions
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United States
Department of
Agriculture

National Institute
of Food and
Agriculture

See: <http://faculty.agronomy.cfans.umn.edu/pmorrell/>

Gene Isolation

