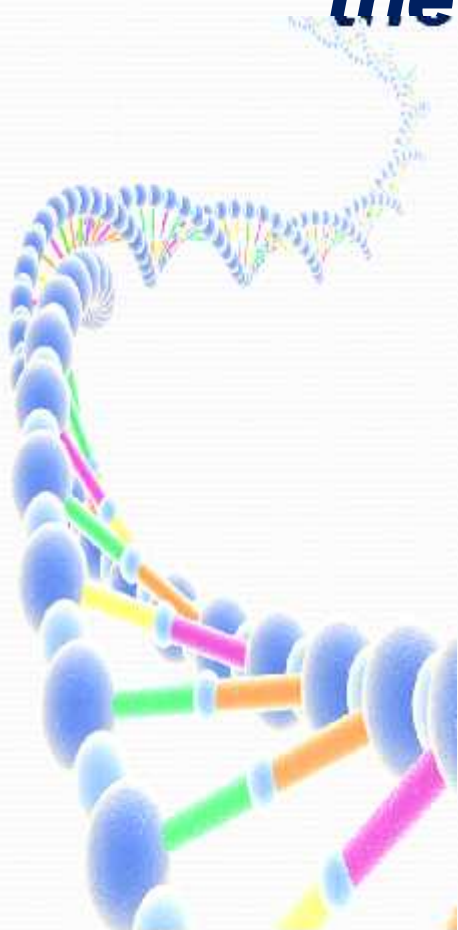


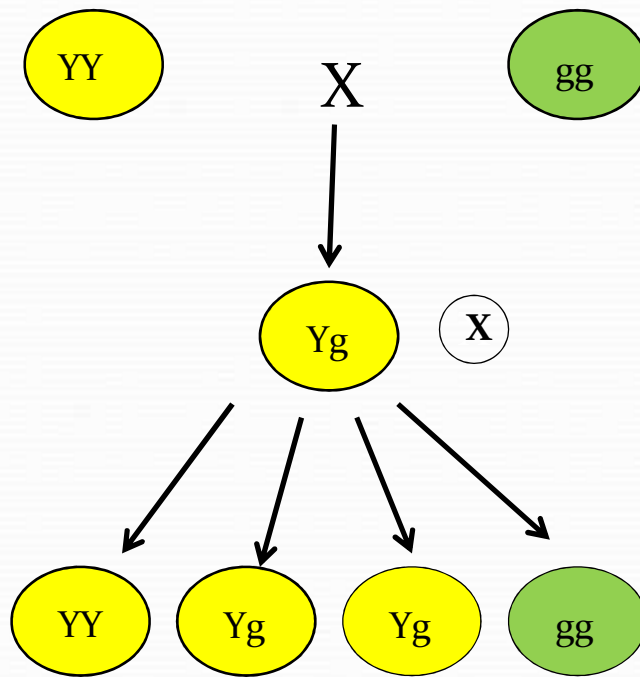
# ***Genetic approaches towards marker-assisted and genomic selection, and the challenges in sweet potato***

Dorcus C. Gemenet

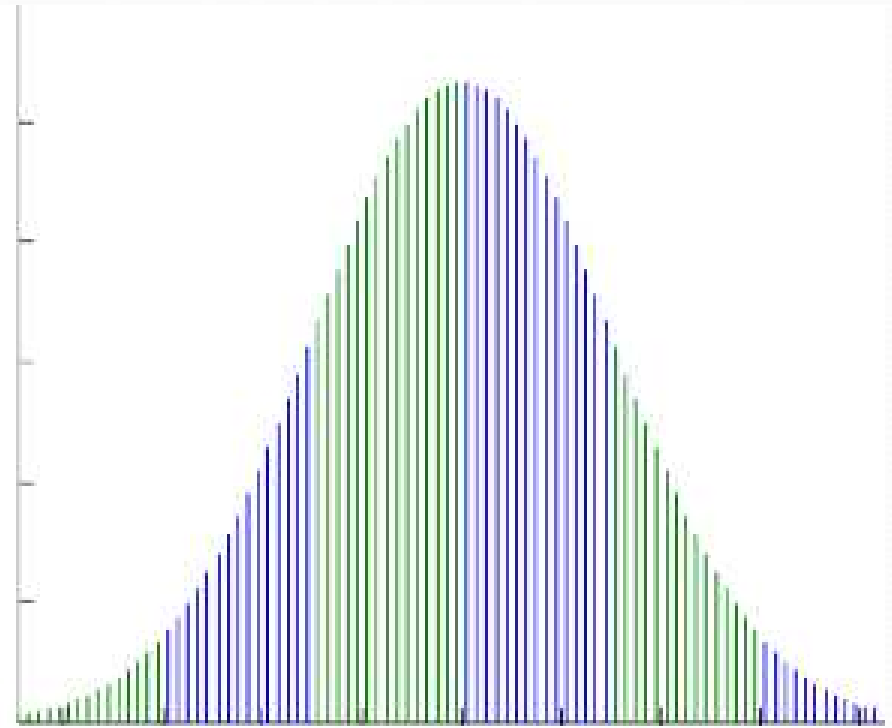
Sweet potato breeders' meeting,  
Uganda, 2<sup>nd</sup>- 5<sup>th</sup> June 2015



# Qualitative vs quantitative traits



Monogenic: diversity at one locus

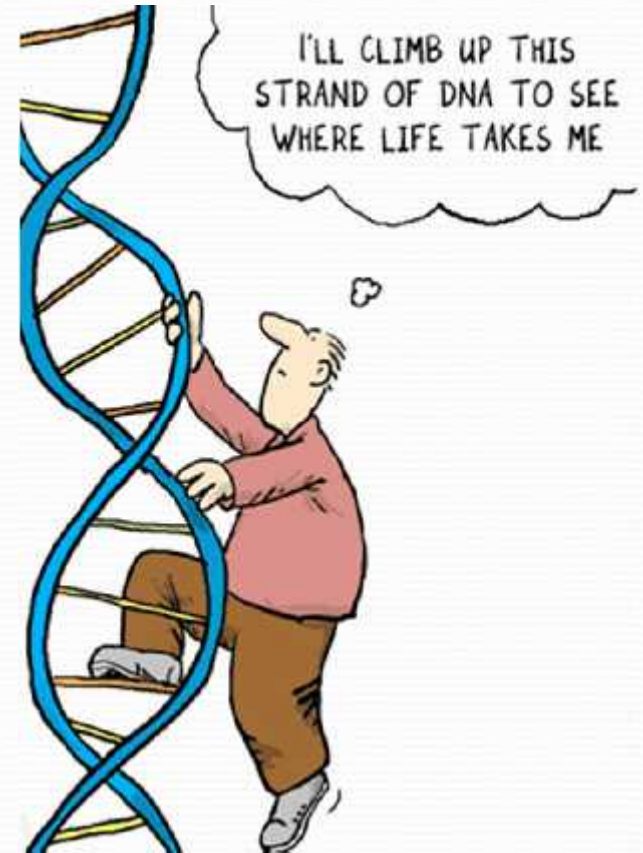


Polygenic trait: diversity at all loci associated with the trait

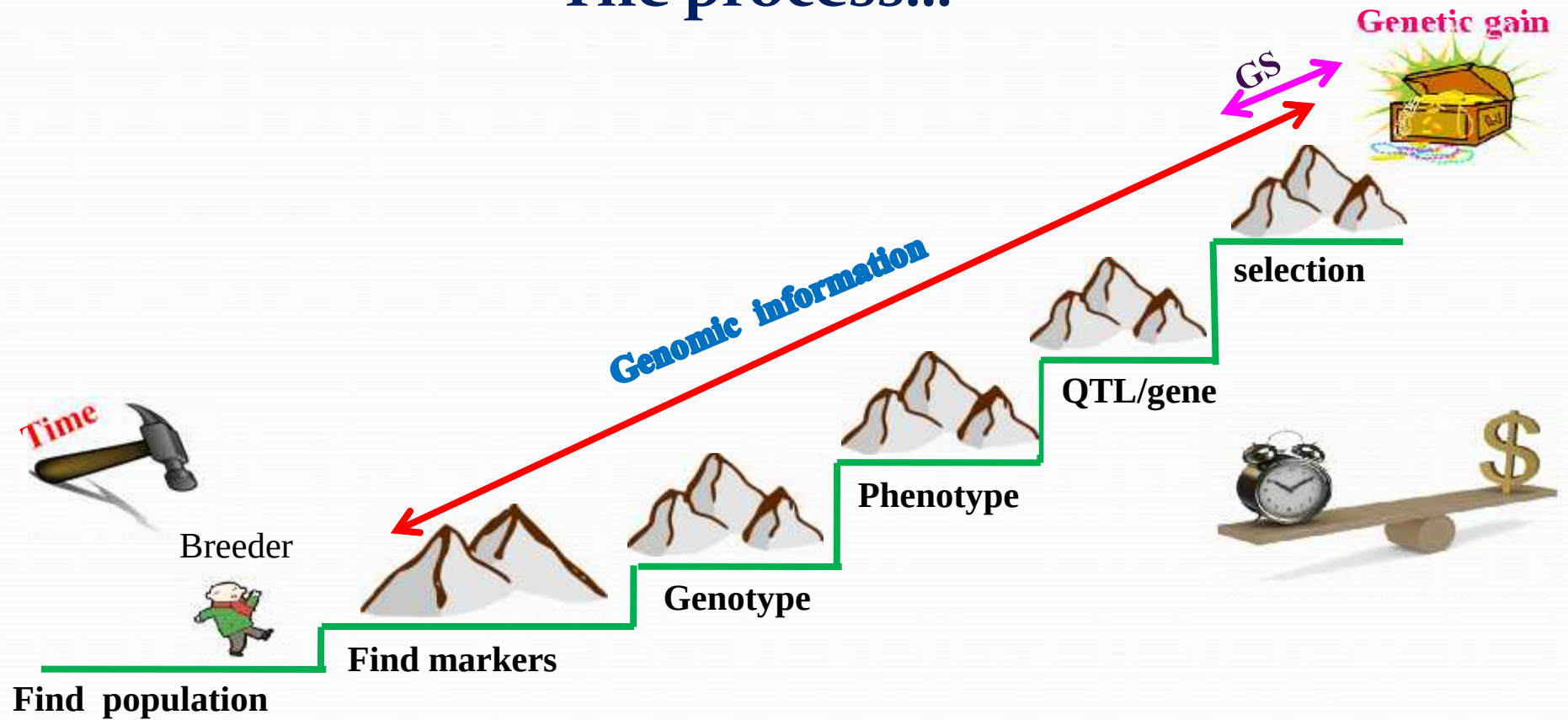
**Most traits of agronomic importance are polygenic**

# Traits of importance in sweet potato

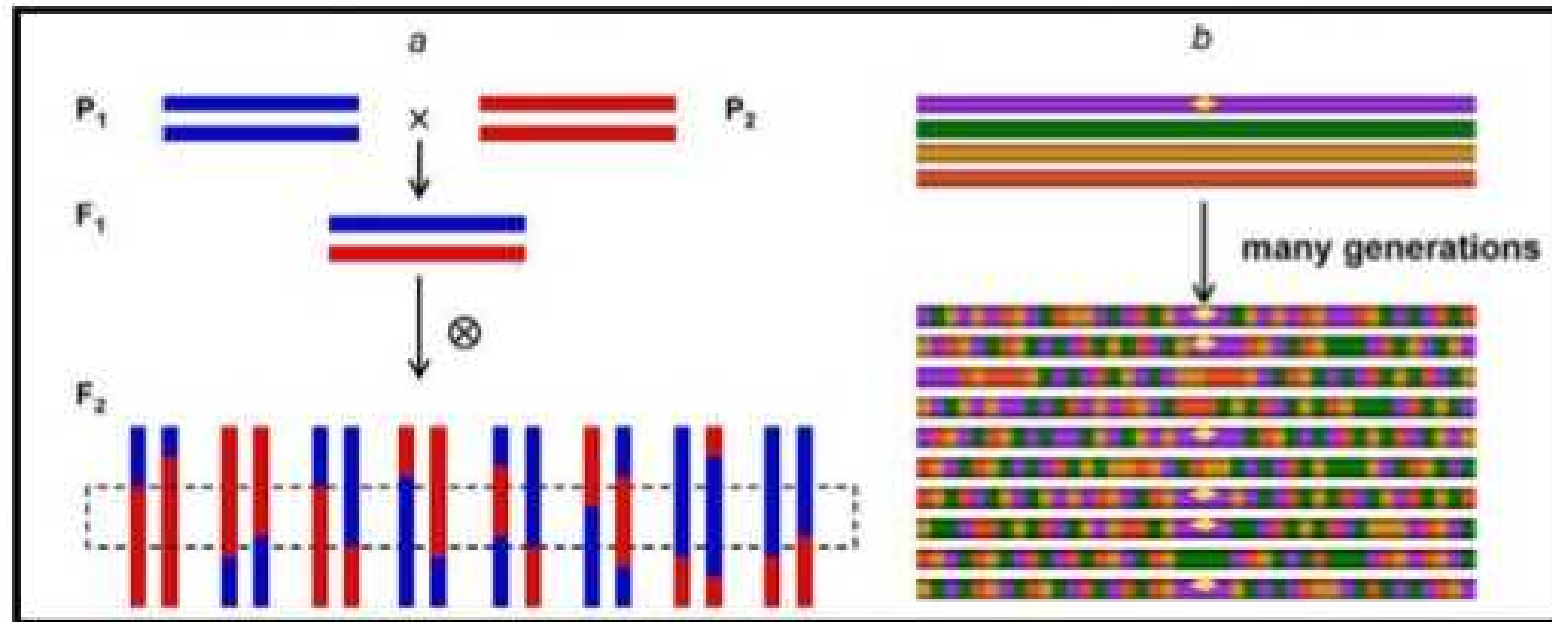
1. Storage root yield
2. Diseases esp. SPVD
3. Pests esp. SPW
4. Drought
5. Quality traits
6. Low soil fertility
7. Dual-purposes
8. Storability



# The process...



# Approaches in QTL dissection



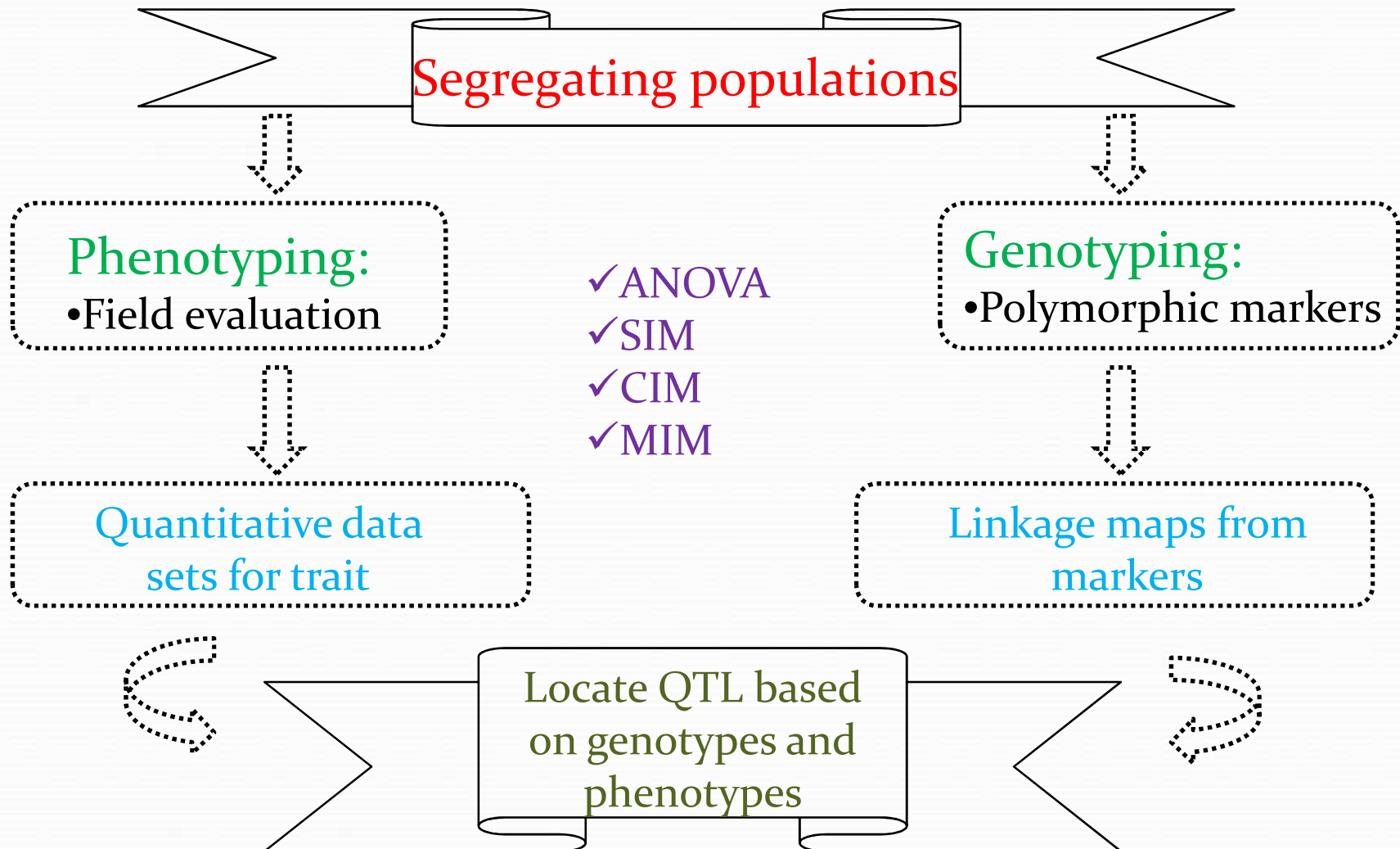
## Linkage mapping

- Recent recombination
- High power
- Moderate marker density
- Low resolution
- Analysis of 2 alleles

## Association mapping

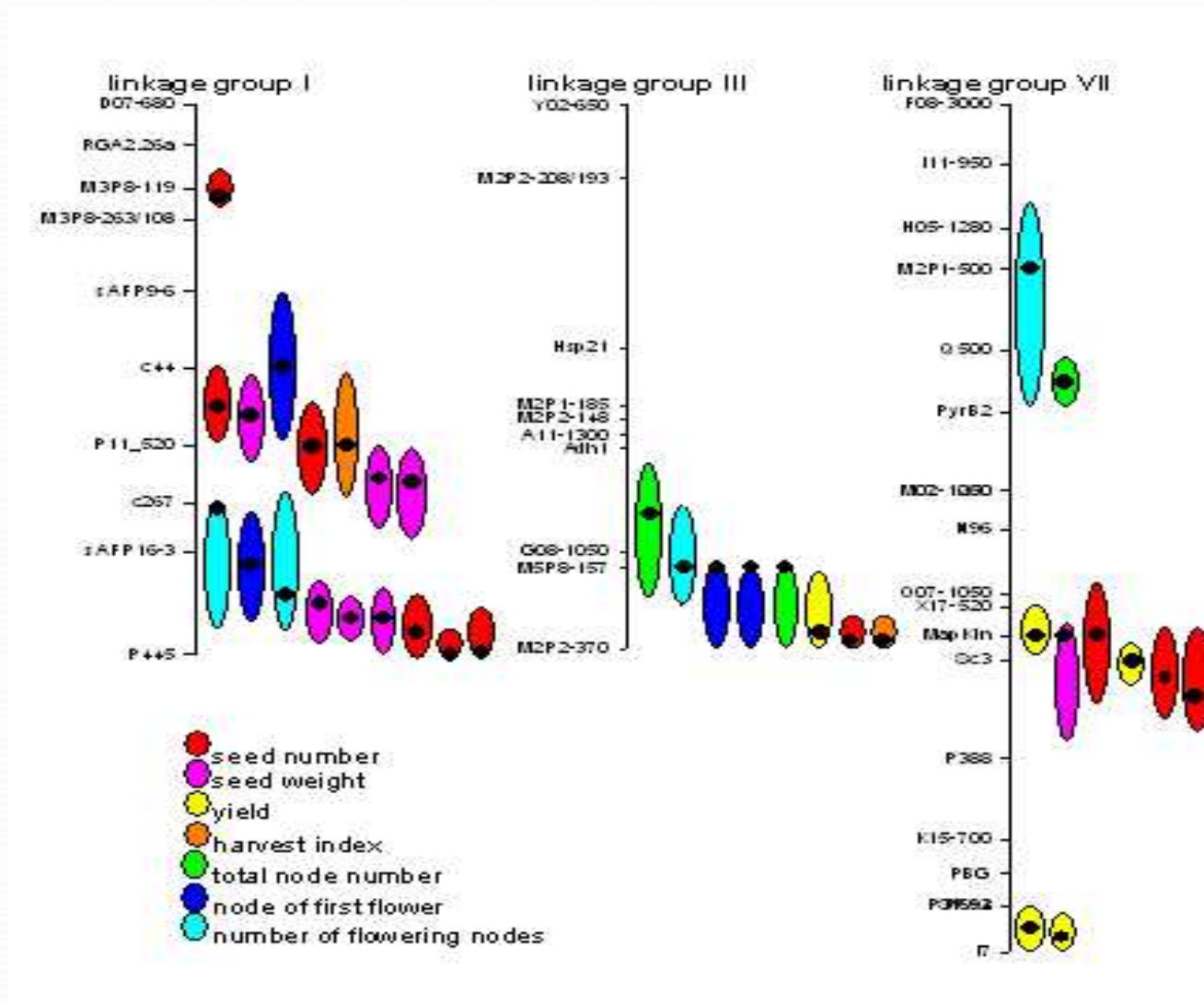
- Historic recombination
- High resolution
- Analysis of many alleles
- High marker density
- Low power

# Dissection of QTL based on linkage mapping



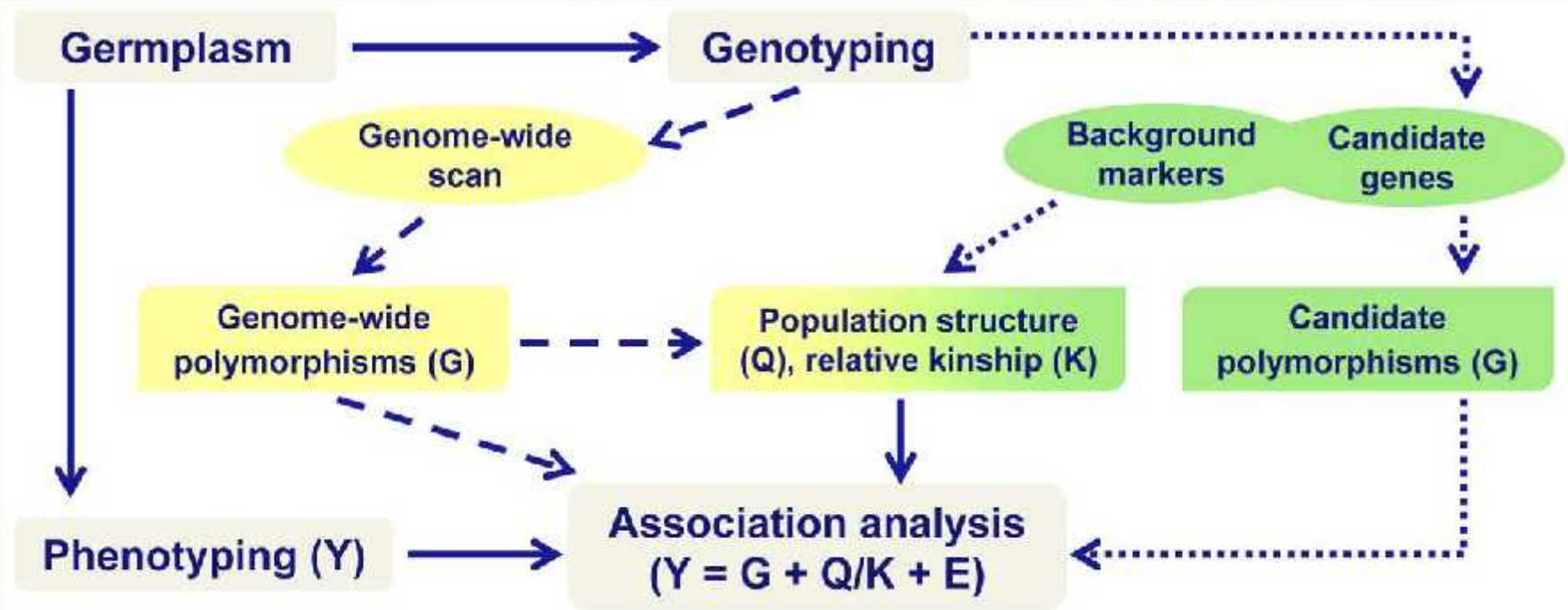


# Example of a QTL map in pea



Timmerman-Vaughan et al. (2005)

# Dissection of QTL based on association mapping



## GWAS

- Large number of markers
- Large number of traits
- No prior information

## CG

- Trait specific
- Low-cost
- Prior information

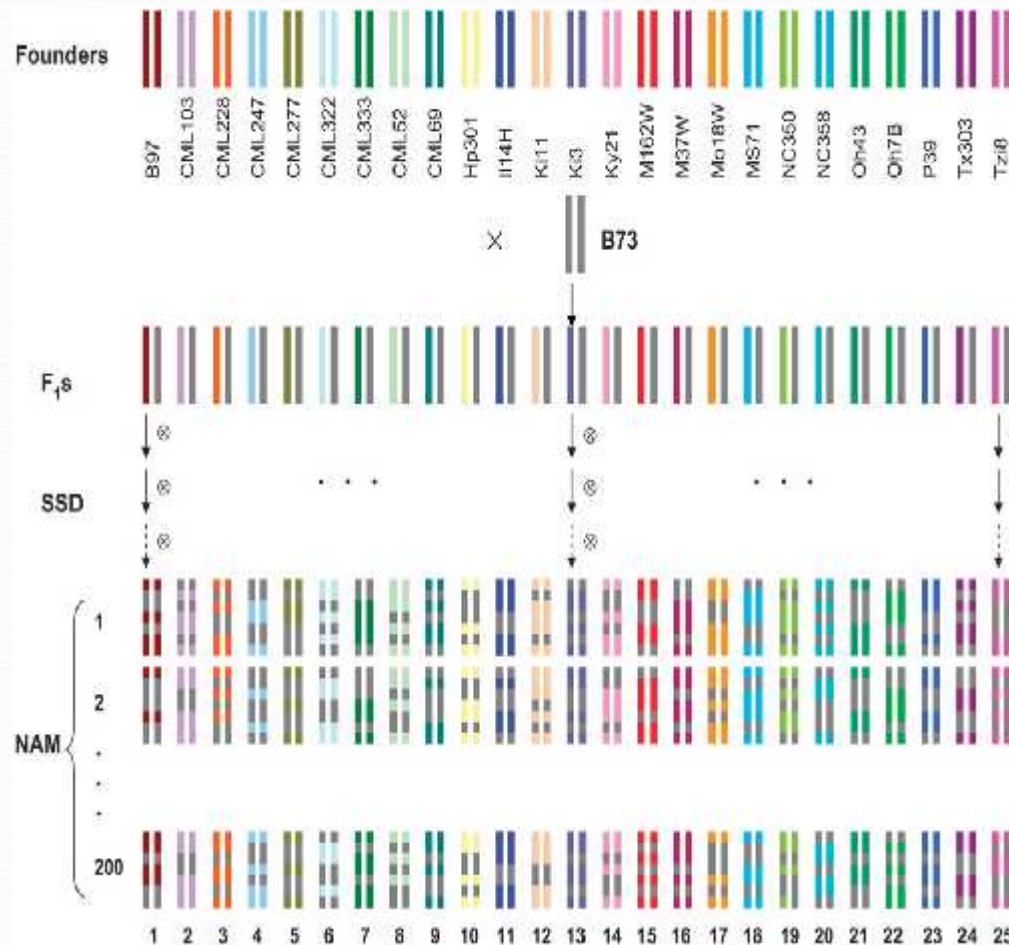
Zhu et al. 2008



# Nested association mapping



Could we  
combine LM and  
AM???



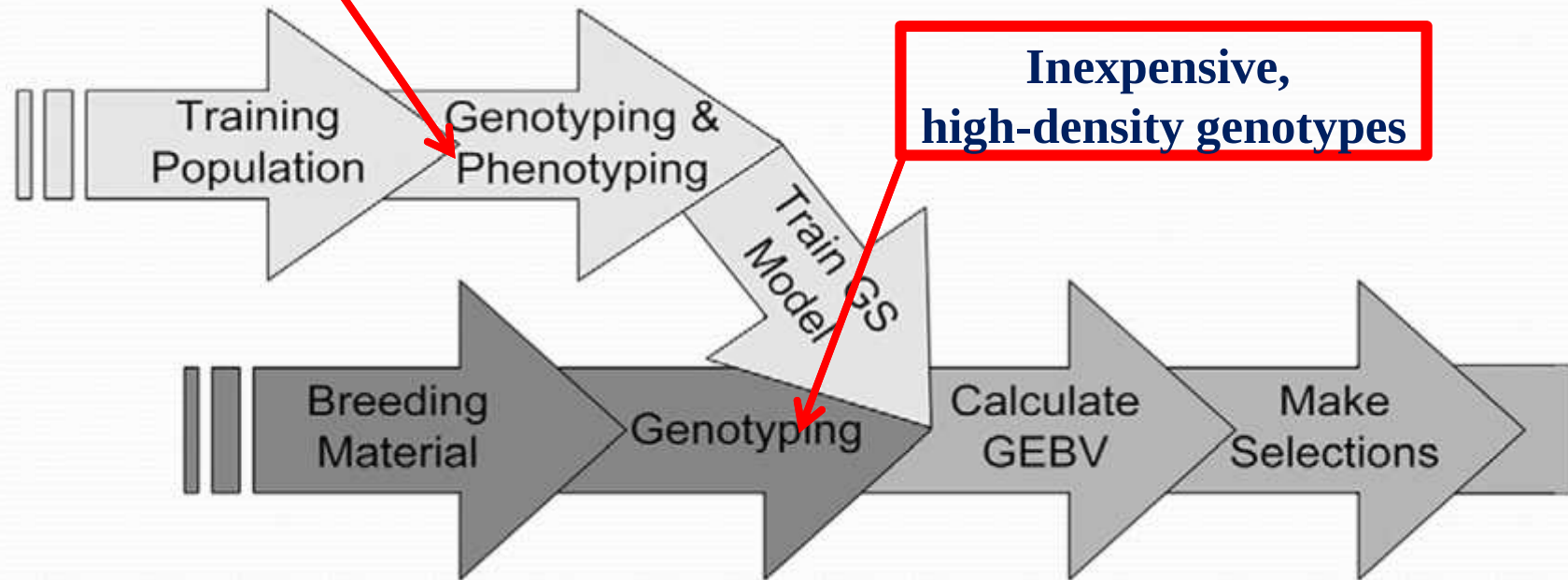
Yu et al. 2008

- Nested Association Mapping**
- Recent and ancient recombination
  - High power
  - High resolution
  - Analysis of many alleles
  - Moderate genetic marker density
  - High projected marker density

# Genomic selection

**Accurate phenotypes**

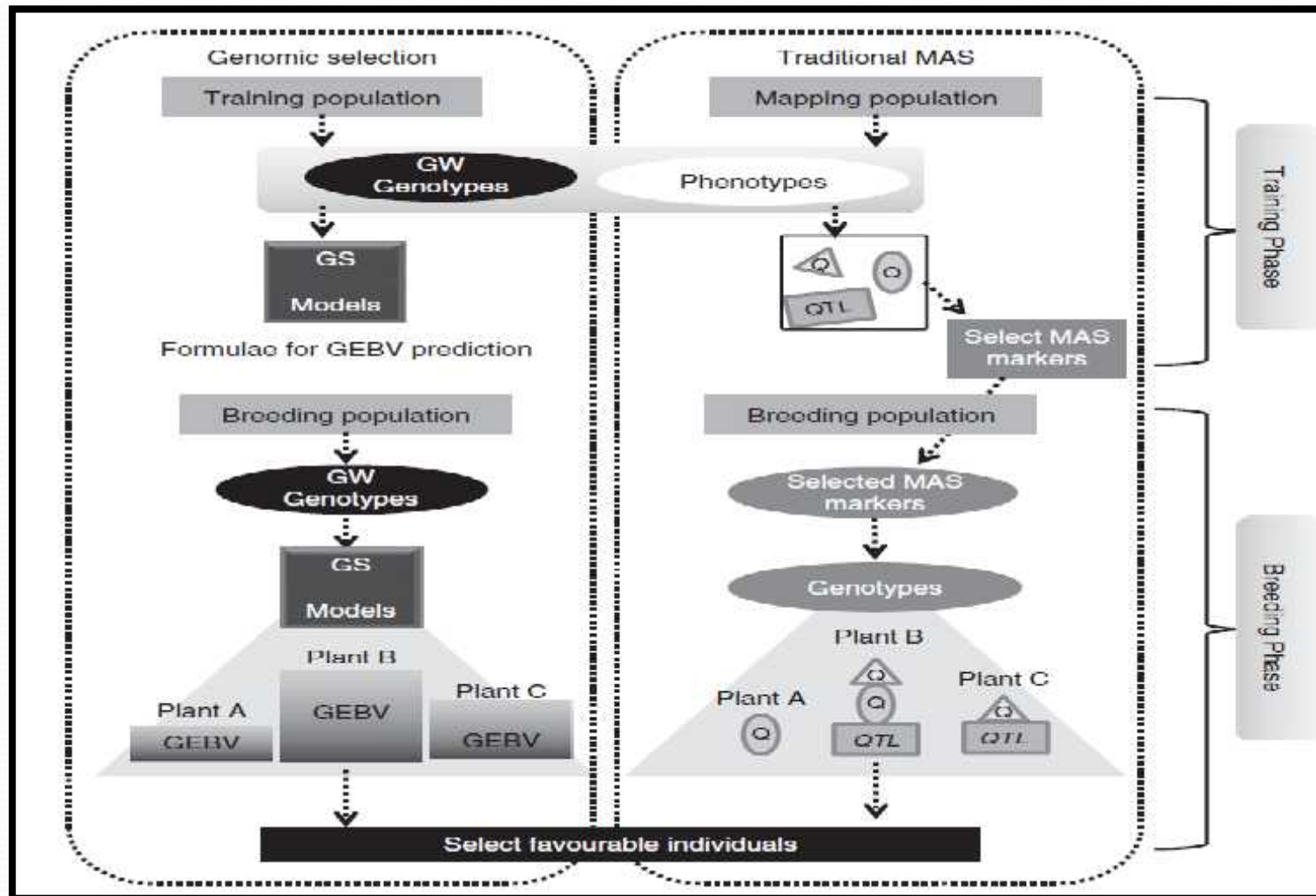
Zhu et al. 2008



- LD between M/QTL (high LD)
- Trait heritability (high)
- Size of training population (high)

- Genetic structure of the trait (Lower no. of QTLs)
- No. of generations after training (Low)

# The two approaches...



Nakaya and Isoke 2012



## Challenges in genetic analysis of sweet potato

- Self-incompatibility, inbreeding depression-no homozygous parents
- Unavailability of good quality sequence information
- Multiple alleles at marker loci and at loci for traits of interest
- Different possibilities of allele dosages across homologous chromosomes
- Large amounts of unobserved marker data based on dominant markers

## Challenges...

- Both bivalent and multivalent pairing during meiosis
- Possibility of preferential pairing of different homologs
- Possibility of different recombination frequencies for different pairs of homologs
- Higher number of possibilities for the linkage phases between markers
- Possibility of double reduction during meiosis



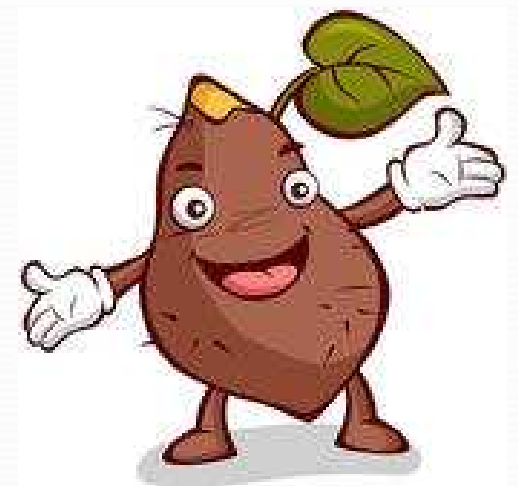
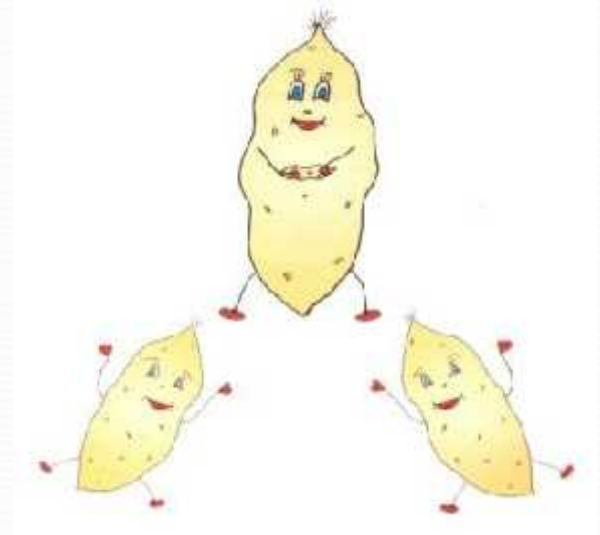


## Challenges...

- Lack of clear distinction in cosegregation due to same homologous chromosome and that due two different homologs that end up together
- Current linkage approaches which put strong emphasis on single-dose loci are not appropriate
- No appropriate software for hexaploids

## Opportunities?







# Genetic Linkage Maps

- Graphical representation of the genome of an organism
- Relative positions of genes, molecular markers and phenotypic markers along a chromosome
- Distances derived from linkage analysis to determine the frequency at which two loci are separated during chromosome recombination



# Applications of Genetic Maps

- Allow localization of genes or quantitative trait loci (QTL)
- Facilitate introgression of desirable genes or QTLs through marker-assisted selection
- Allow comparative evaluation of gene order and function between different species
- Provide a framework for anchoring with physical maps
- First step towards positional or map-based cloning of genes responsible for economically important traits



# Steps in Linkage Mapping

1. Creation of mapping population
2. Detection of polymorphic loci
3. Segregation analysis of single markers
4. Estimation of recombination frequencies
5. Identification of linkage groups
6. Calculation of map distances