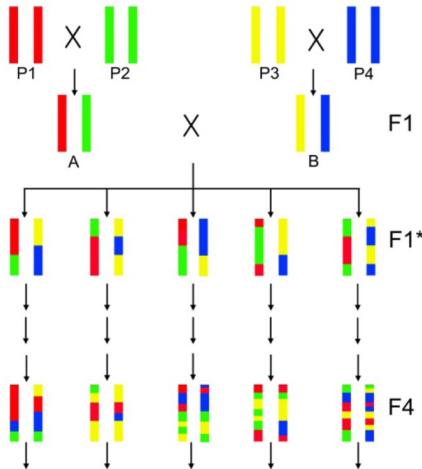


AGR 6322 Advanced Plant Breeding

Fall 2018

QTL mapping and Marker Assisted Selection



Goals for today

Use of molecular markers in Plant Breeding for QTL mapping

QTL mapping and Marker Assisted Selection

- Quantitative genetic approach → population genetic parameters for the traits of interest, such as HERITABILITIES, GENETIC VARIANCES and GENETIC CORRELATIONS.
- These parameters can be estimated using statistical analysis of phenotypic data from pedigrees.
- The genetic architecture: number of genes, effect size and position on the genome are unknown.
- Two types of genetic loci that can be used in breeding
 - 1) Causal Mutation

Difficult to find and validate
 - 2) Marker linked to a QTL

More abundant, but with problems of transference due to linkage phase, allele frequency, gene fixation, etc.

QTL mapping and Marker Assisted Selection

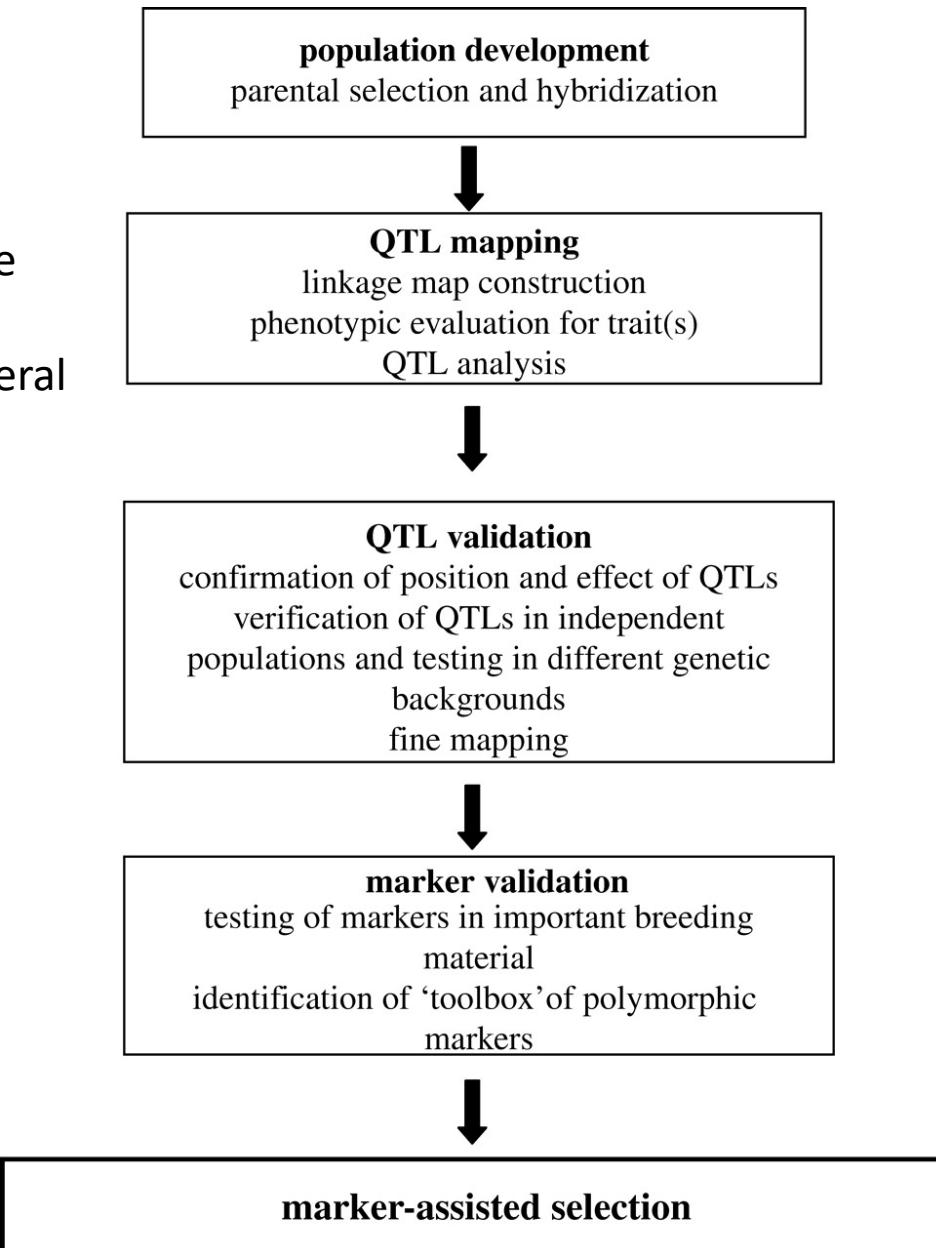
Steps for QTL analysis

Genetic loci or chromosomal regions that contribute to variability in complex quantitative traits, as identified by statistical analysis.

Quantitative traits are typically affected by several genes, and the environment.

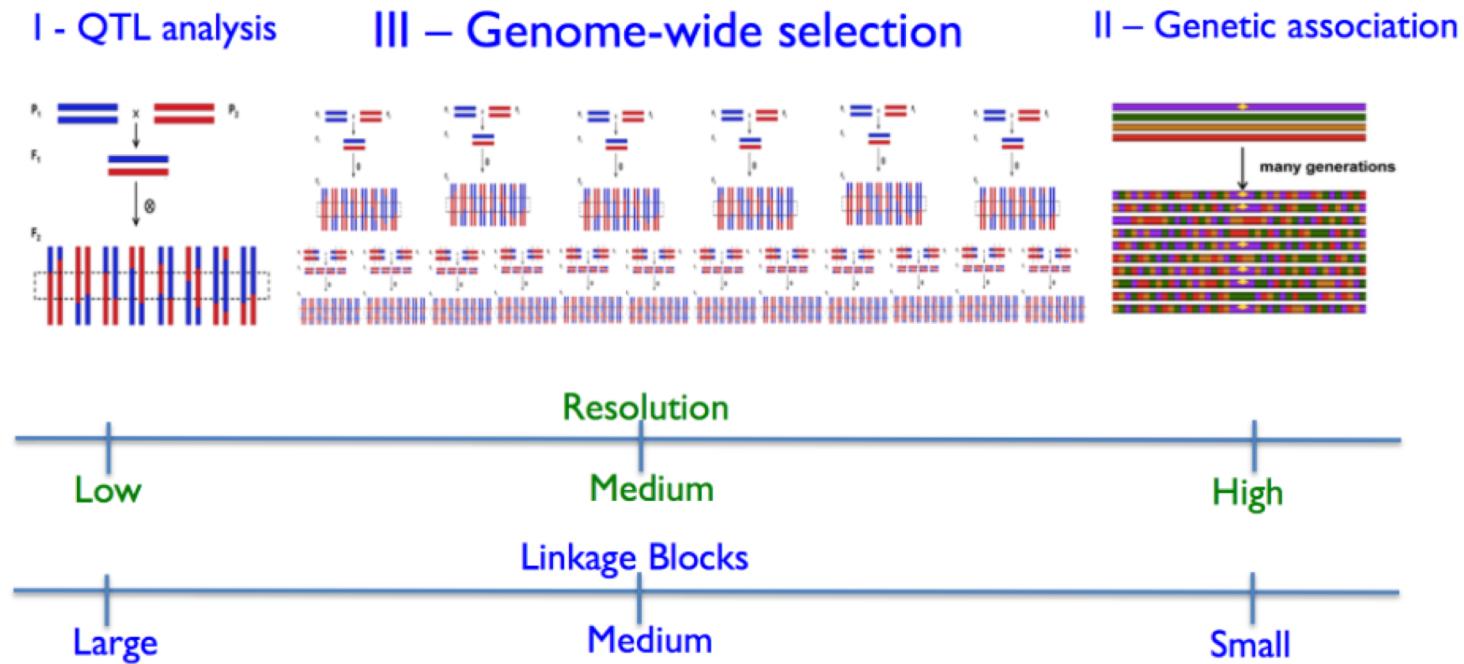
Trait is controlled by many genes

- How many?
- Where are they located in the genome?
- How much variation do they explain for the trait?



QTL mapping and Marker Assisted Selection

QTL analysis, as well as GS and GWAS, depends on LD between markers and genes/QTLs



(Meuwissen et al., 2001)

QTL mapping and Marker Assisted Selection

- Molecular genetics can be used to enhance breeding strategies through **Marker-Assisted Selection (MAS)**

When to use markers in breeding:

- Traits difficult to manage through conventional breeding, expensive or time-consuming
- Traits depending on maturity or environment
- To maintain recessive alleles in backcrossing or to speed up backcrossing
- Pyramiding multiple monogenic traits or several genes for a same trait

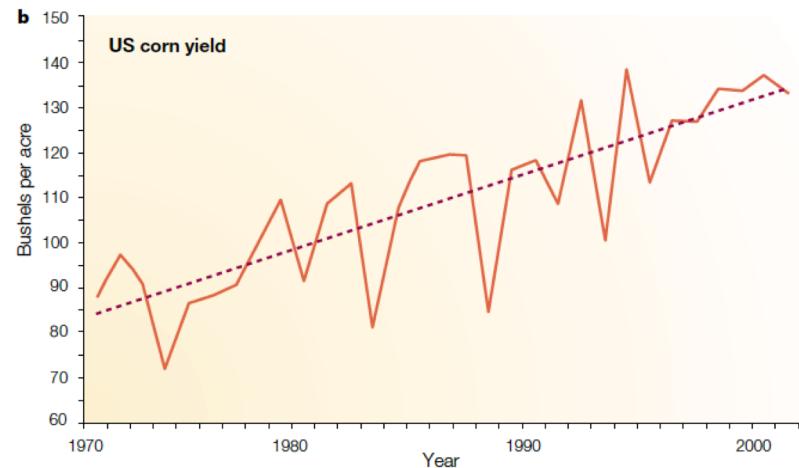
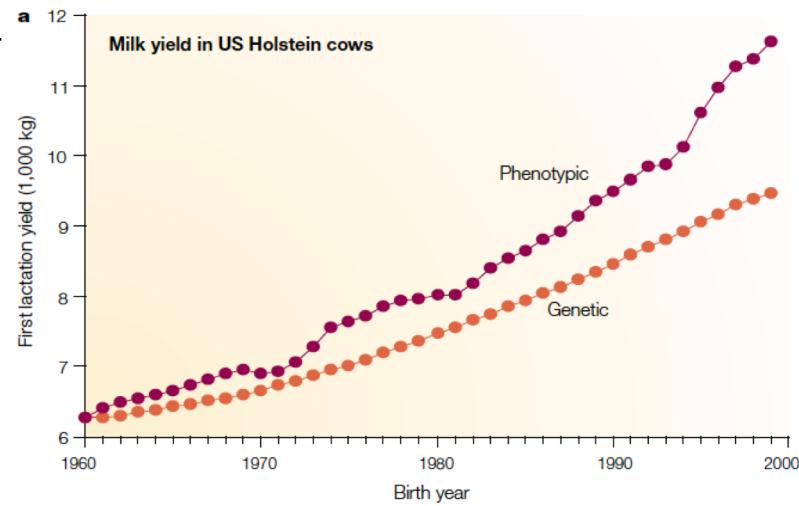
QTL mapping and Marker Assisted Selection

- Markers in Breeding can also help with:
 - Pedigree and fingerprinting (also for protection)
 - Population Structure (STRUCTURE software)
 - Assess diversity of collections and create core-collections
 - Estimation of effective population size (NeEstimator v2 software)
 - Selection using molecular markers (Traditional MAS)
 - Marker-Assisted backcrossing

QTL mapping and Marker Assisted Selection

Genetic improvement through artificial selection

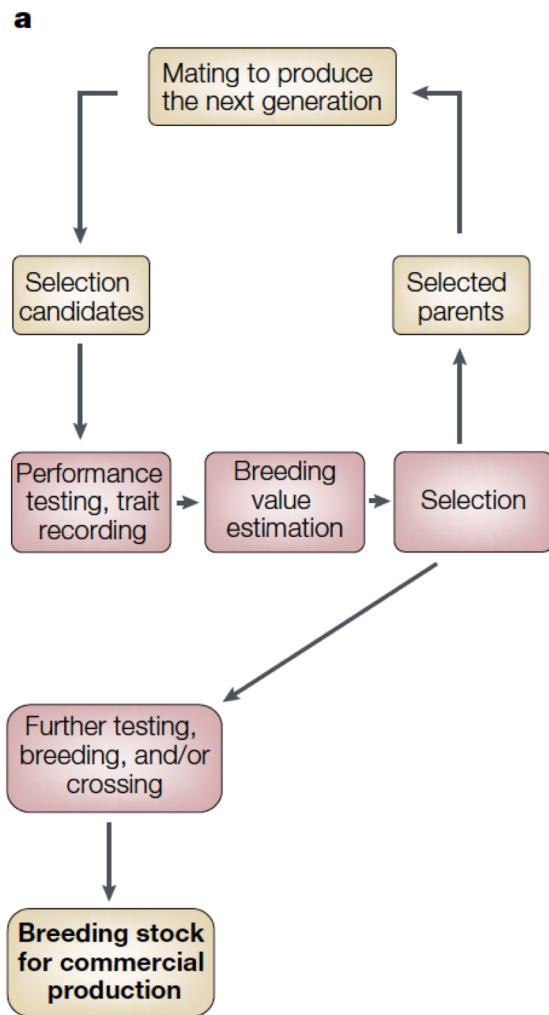
- Complex traits → Polygenic and $P = G+E+G*E$
- Mostly phenotypic selection
- Use of quantitative genetics theory and parameters



Dekkers and Hospital, 2002

QTL mapping and Marker Assisted Selection

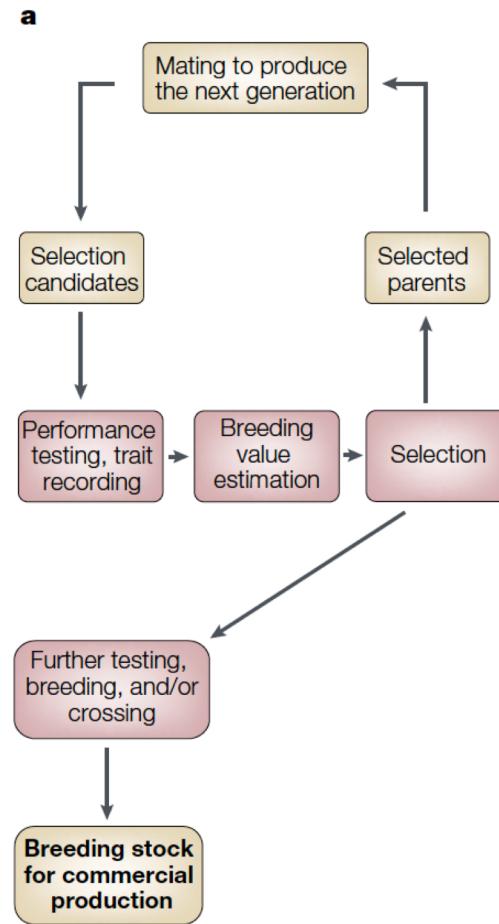
- Recurrent Selection or
- Recurrent Genotypic Selection or
- Genotypic Recurrent Selection
- Use the phenotype and **pedigree** information to **estimate the BV**, thus perform selection base on BV



Dekkers and Hospital, 2002

QTL mapping and Marker Assisted Selection

- Use the phenotype and **pedigree** information to **estimate the BV**, thus perform selection base on BV
- **Pedigree** could be inferred by molecular markers (fingerprinting) or errors in the pedigree can be detected and corrected using markers
- **Estimation of BV** can be performed by using genomic data (*a.k.a* genomic selection)



QTL mapping and Marker Assisted Selection

- Fingerprinting using SSRs is the preferred and straightforward method.
- However, SNPs are more prevalent and can be used at the population level to assign parentage and correct errors in the pedigree.

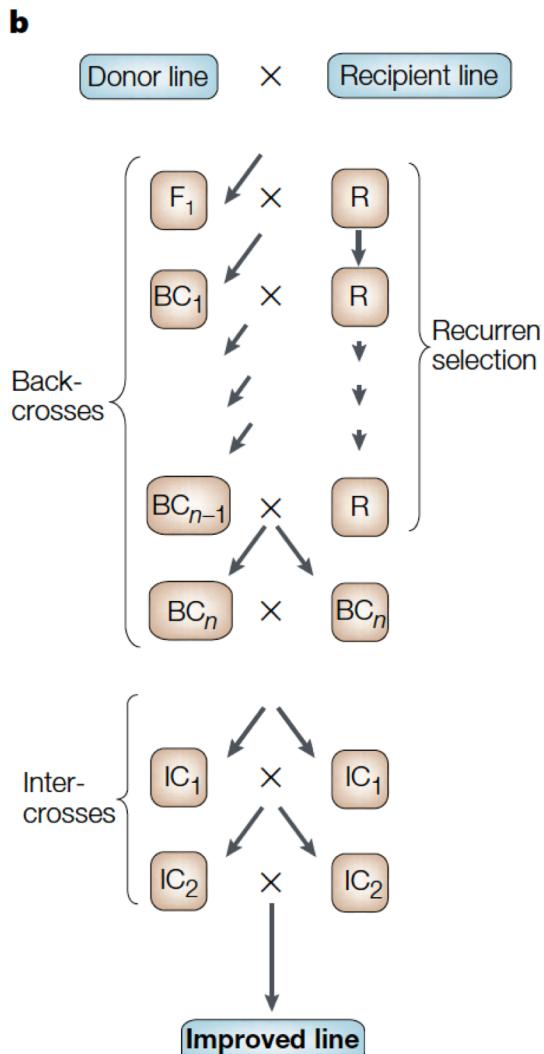
RESEARCH

Genomic Relationship Matrix for Correcting Pedigree Errors in Breeding Populations: Impact on Genetic Parameters and Genomic Selection Accuracy

Patrício R. Munoz, Marcio F. R. Resende Jr., Dudley A. Huber, Tania Quesada, Marcos D. V. Resende,
David B. Neale, Jill L. Wegrzyn, Matias Kirst, and Gary F. Peter*

QTL mapping and Marker Assisted Selection

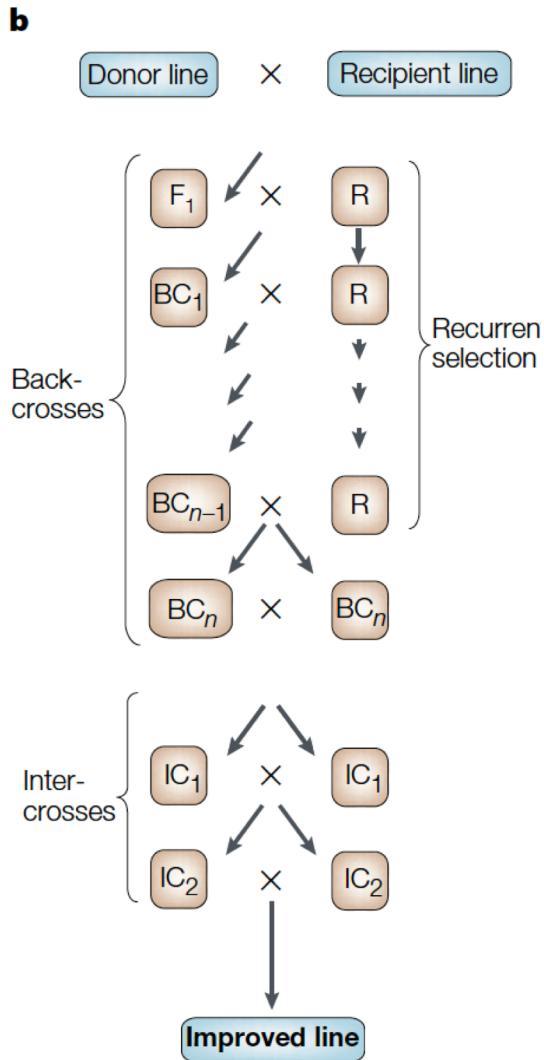
- Introgression strategy
- Donor line – it has a particular characteristics that we want to transfer to the recipient line
- Recipient line – the line (cultivar) of commercial importance
- Progeny is **selected** every generation **based on phenotype**



Dekkers and Hospital, 2002

QTL mapping and Marker Assisted Selection

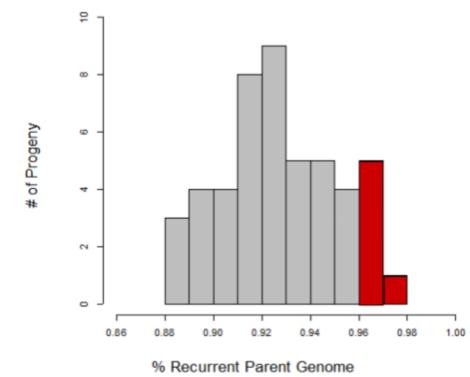
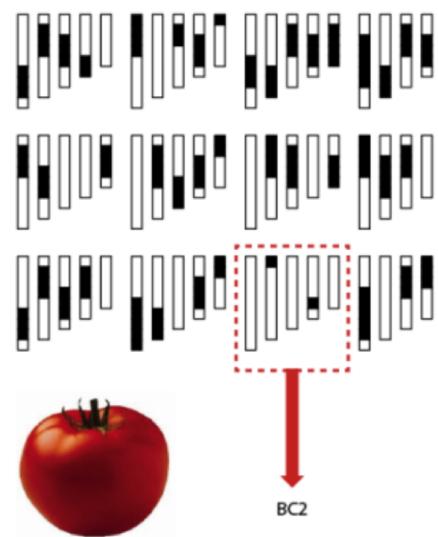
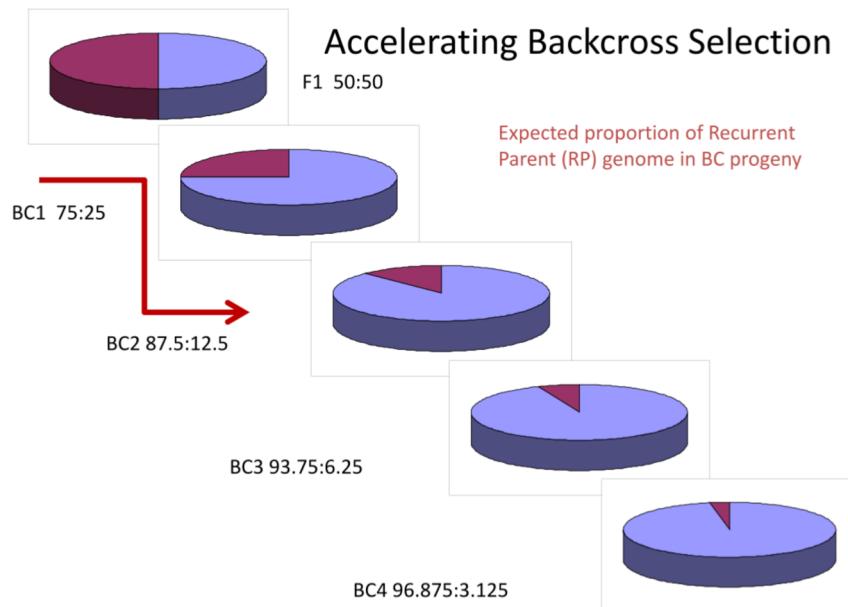
- Progeny is **selected** every generation **based on phenotype**
- **Selection** could be performed based on **Molecular Markers** a procedure known as Marker Assisted Backcrossing



QTL mapping and Marker Assisted Selection

Strategies

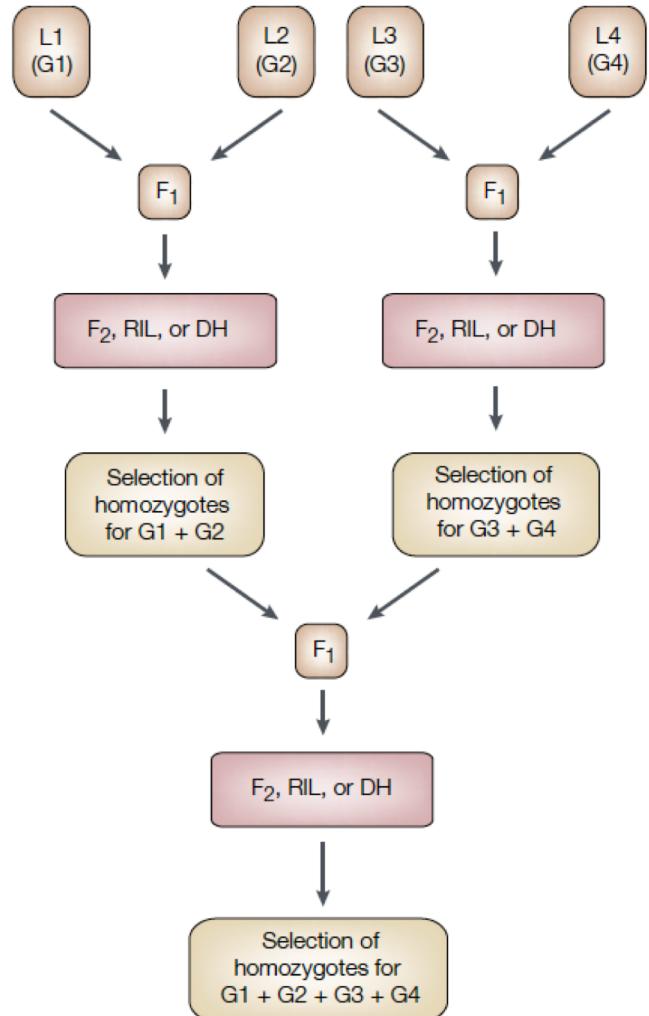
- Background selection
 - ✓ Speed recovery of recurrent parent genome
 - ✓ When is it appropriate/justifiable?
 - Time to phenotype (annual vs perennial crops)
 - Window for genotyping (seed size)



QTL mapping and Marker Assisted Selection

Strategies

- Pyramiding multiple genes

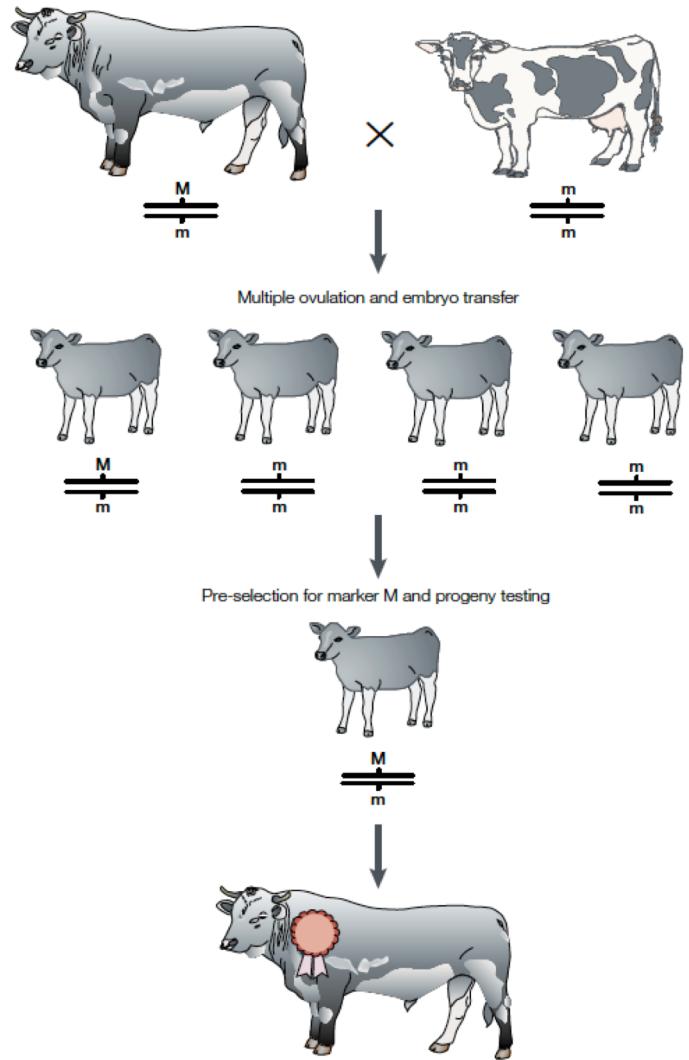


Dekkers and Hospital, 2002

QTL mapping and Marker Assisted Selection

Strategies

Marker-assisted pre-selection for progeny testing



Dekkers and Hospital, 2002

QTL mapping and Marker Assisted Selection

Strategies

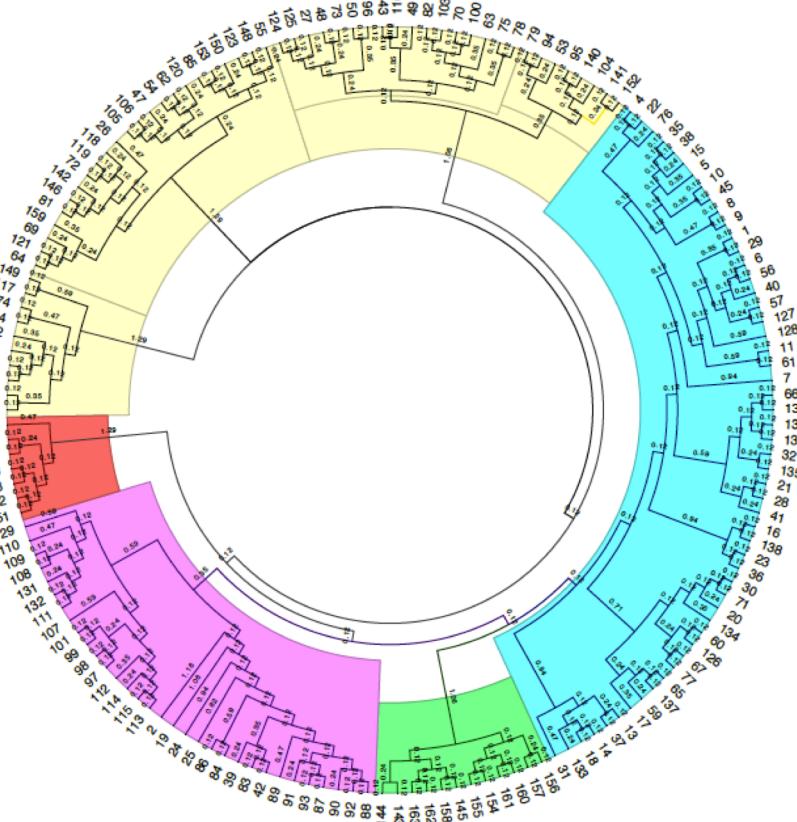
Germplasm conservation, diversity and core-collections

- As breeders we want diversity and variability, but for some species plant collections may be too large to evaluate and use in breeding.
- Use of core collections or mini core collections in breeding provide a way to explore the whole variability using a manageable number of accessions (genotypes/inbred lines/clones).
- A core-collection is a subset of accessions that represent the genetic diversity of a species and its relatives.

QTL mapping and Marker Assisted Selection

Strategies

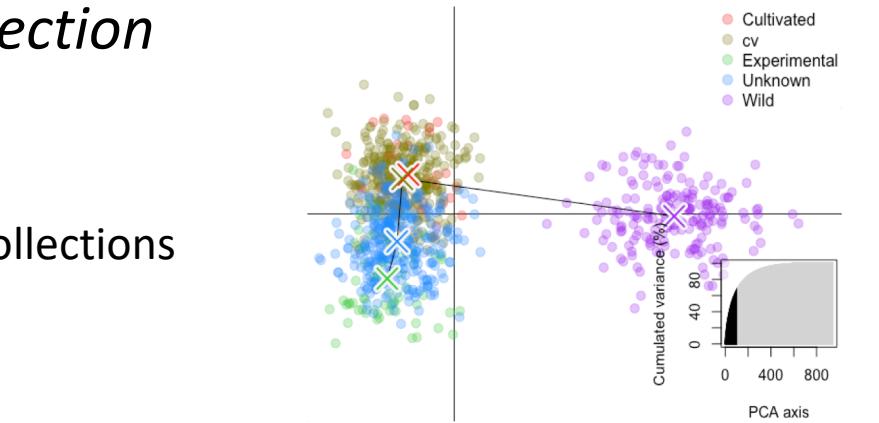
Germplasm conservation, diversity and core-collections



Genetic diversity

vs

Phenotypic diversity



QTL mapping and Marker Assisted Selection

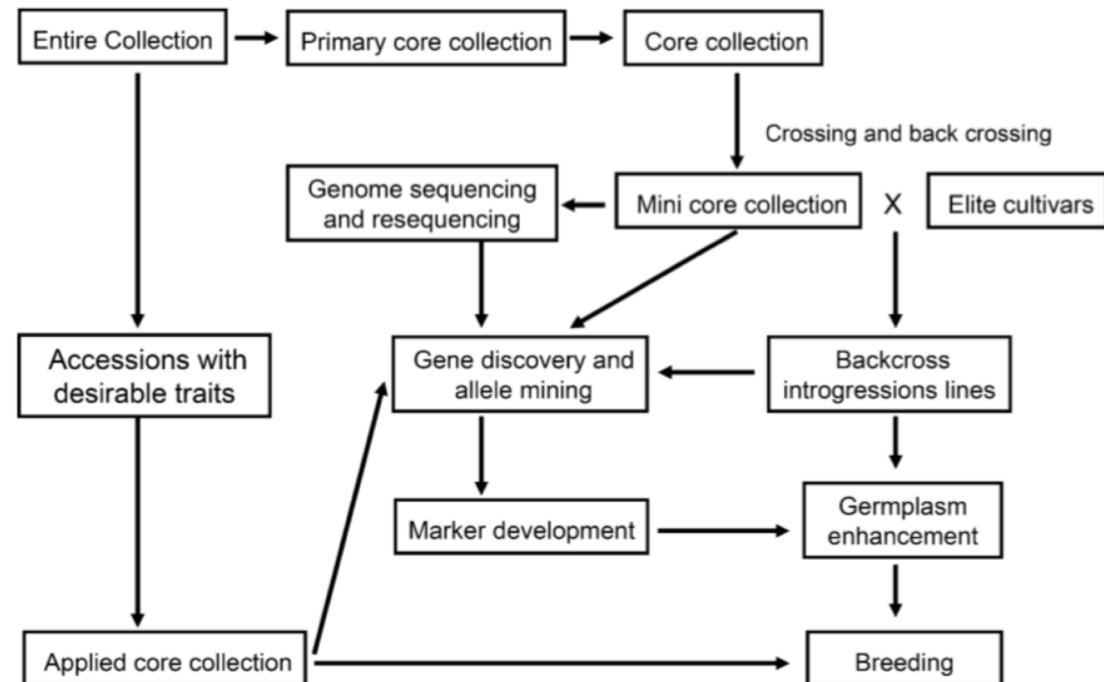
Strategies

Germplasm conservation, diversity and core-collections

Plant Mol Biol (2013) 83:41–50
 DOI 10.1007/s11103-013-0076-6

A platform for soybean molecular breeding: the utilization of core collections for food security

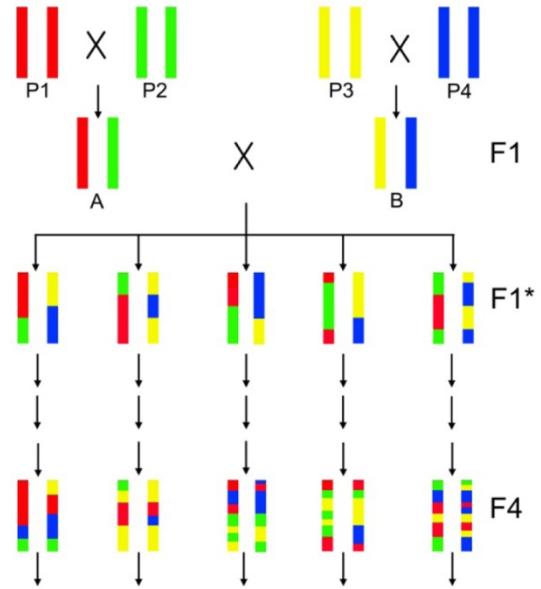
Li-Juan Qiu · Li-Li Xing · Yong Guo ·
Jun Wang · Scott A. Jackson · Ru-Zhen Chang



QTL mapping and Marker Assisted Selection

Considerations for using MAS in breeding

- Type of marker/method for genotyping
 - ✓ Cost per data point
 - ✓ Turn-around
 - ✓ Proximity to genes (LD)
 - ✓ Useful across backgrounds?
- What generation(s) to screen?
- How many individuals?
- Select homozygotes and heterozygotes?
- How to handle multiple loci simultaneously?



QTL mapping and Marker Assisted Selection

Considerations for using MAS in breeding

- The economic aspect will be the determinant of the use of MAS in breeding
- Cost of development (ex: QTL analysis, Association analysis)
- Cost of DNA collection and extraction
- Cost of Genotyping
- Cost of Analysis – bioinformatics

- Cost is offset when phenotyping is expensive
- May be justified to decrease cycle of cultivar development
- Risky when higher genetic gain is expected by investing in MAS

QTL mapping and Marker Assisted Selection

Considerations for using MAS in breeding

REVIEW & INTERPRETATION

Marker-Assisted Selection in Plant Breeding: From Publications to Practice

Yunbi Xu* and Jonathan H. Crouch

- Development of high throughput precision phenotyping systems for QTL mapping,
- Improved understanding of genotype by environment interaction and epistasis,
- Development of publicly available computational tools tailored to the needs of molecular breeding programs

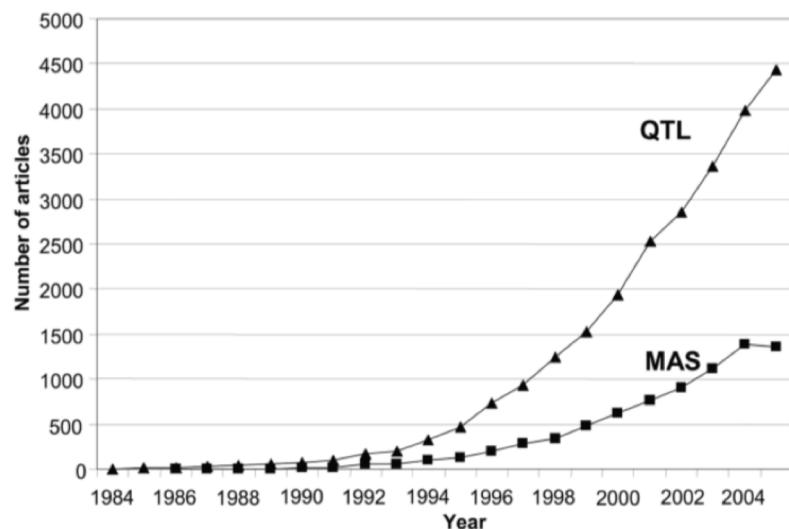


Figure 1. The numbers of articles with the terms *quantitative trait locus* or *quantitative trait loci* (QTL) and *marker-assisted selection* (MAS) by years (1984–2005) from Google Scholar (4 Aug. 2007).

QTL mapping and Marker Assisted Selection

THE USE OF MOLECULAR GENETICS IN THE IMPROVEMENT OF AGRICULTURAL POPULATIONS

Jack C. M. Dekkers* and Frédéric Hospital[#]

Substantial advances have been made in the genetic improvement of agriculturally important animal and plant populations through artificial selection on quantitative traits. Most of this selection has been on the basis of observable phenotype, without knowledge of the genetic architecture of the selected characteristics. However, continuing molecular genetic analysis of traits in animal and plant populations is leading to a better understanding of quantitative trait genetics. The genes and genetic markers that are being discovered can be used to enhance the genetic improvement of breeding stock through marker-assisted selection.

Dekkers and Hospital, 2002

REVIEW

Breeding Technologies to Increase Crop Production in a Changing World

Mark Tester* and Peter Langridge

To feed the several billion people living on this planet, the production of high-quality food must increase with reduced inputs, but this accomplishment will be particularly challenging in the face of global environmental change. Plant breeders need to focus on traits with the greatest potential to increase yield. Hence, new technologies must be developed to accelerate breeding through improving genotyping and phenotyping methods and by increasing the available genetic diversity in breeding germplasm. The most gain will come from delivering these technologies in developing countries, but the technologies will have to be economically accessible and readily disseminated. Crop improvement through breeding brings immense value relative to investment and offers an effective approach to improving food security.

Tester and Langridge, 2010

Editor's Choice Series on the Next Generation of Biotech Crops

Molecular Plant Breeding as the Foundation for 21st Century Crop Improvement¹

Stephen P. Moose* and Rita H. Mumm

Department of Crop Sciences (S.P.M., R.H.M.) and Energy Biosciences Institute (S.P.M.), University of Illinois, Urbana-Champaign, Illinois 61801; and GeneMax Services, Savoy, Illinois 61874 (R.H.M.)

Moose and Mumm, 2008