Molecular breeding: Challenges and perspectives

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Definition

In molecular or marker-assisted breeding (MB), DNA markers are used as a substitute for phenotypic selection and to accelerate the release of improved cultivars.

<u>Marker-assisted selection (MAS)</u>. Selection of individuals with specific alleles for traits controlled by a limited number of loci (up to 6-8).

<u>Marker-assisted backcrossing (MABC)</u>. Transfer of a limited number of loci (e.g. transgene, disese resistance loci, etc.) from one genetic backgrond to another.

<u>Marker-assisted recurrent selection (MARS)</u>. The identification and selection of several genomic regions (up to 20 or even more) for complex traits within a single population.

Critical factors for the success of molecular breeding

Germplasm

- Elite vs. non-elite
- Wild relatives
- Structure

Phenotyping

- Identify key traits
- Stress management

- High-throughput level
- Cost-effectiveness
- Informatics
- Data management

Breeding

- Choice of MB strategy
- Breeders fluent with MB
- Stakeholders involvement
- Seed industry for delivery

MAS and conventional breeding are not mutually exclusive; instead, they are complementary under most breeding schemes (Ribaut et al., COPB 2010).

From gene/QTL discovery to cultivar release

Gene/QTL discovery

- Linkage mappping
- Association mapping
- QTL x Env. x Manag.

Gene/QTL characterization

- Validation of best alleles
- BC in different backgrounds
- Isogenization

Gene/QTL cloning

- Fine mapping
- Positional cloning
- Candidate approach

Marker-assisted breeding

- Cost-effectiveness
- High-throughput

Perfect marker for MAS
GM approach
EcoTILLING
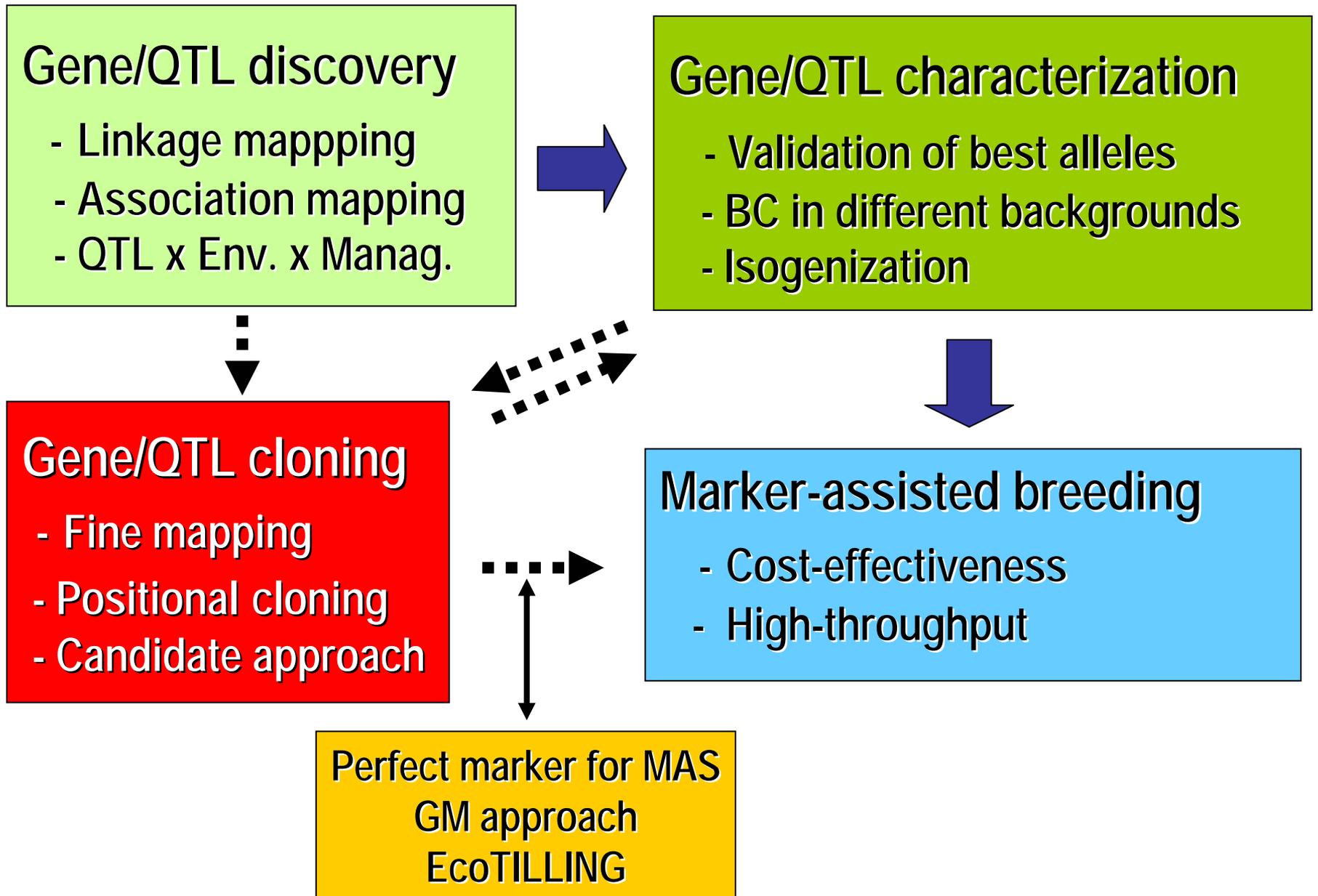
Issues for using molecular breeding in crop improvement

- Cost of each single data point

- Availability and complexity of molecular platforms

- Reliability of marker profiling and scoring (SSR vs. SNP)

- Degree of polymorphism

- Availability of equipment

- Availability of technical expertise

- Integration with breeding programs

MAS is preferable to conventional breeding when:

- Phenotypic screening is particularly expensive or laborious (e.g. root traits, osmotic adjustment, disease resistance, etc.)

- Phenotyping is possible only after flowering

- Linked marker is co-dominant and target gene is dominant

- Strong influence of environment (low heritability)

- Pyramiding multiple resistance genes

- Marker profiles can be obtined from seeds

Marker-assisted backcrossing (MABC)

Susceptible line X **Resistant line**

2-3 cycles of MABC

Gene/QTL
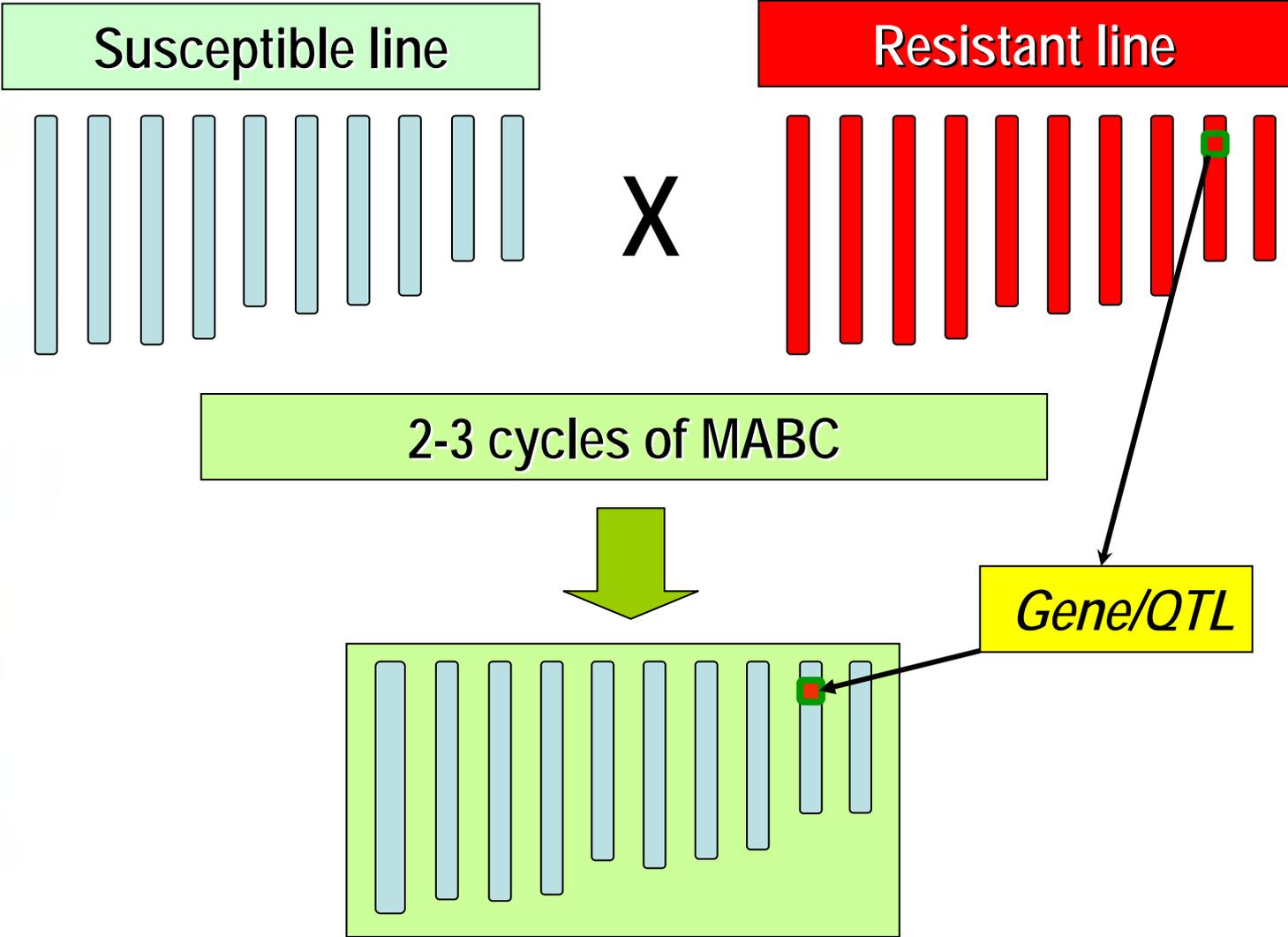
Los Angeles Times April 13, 2008

QTLs
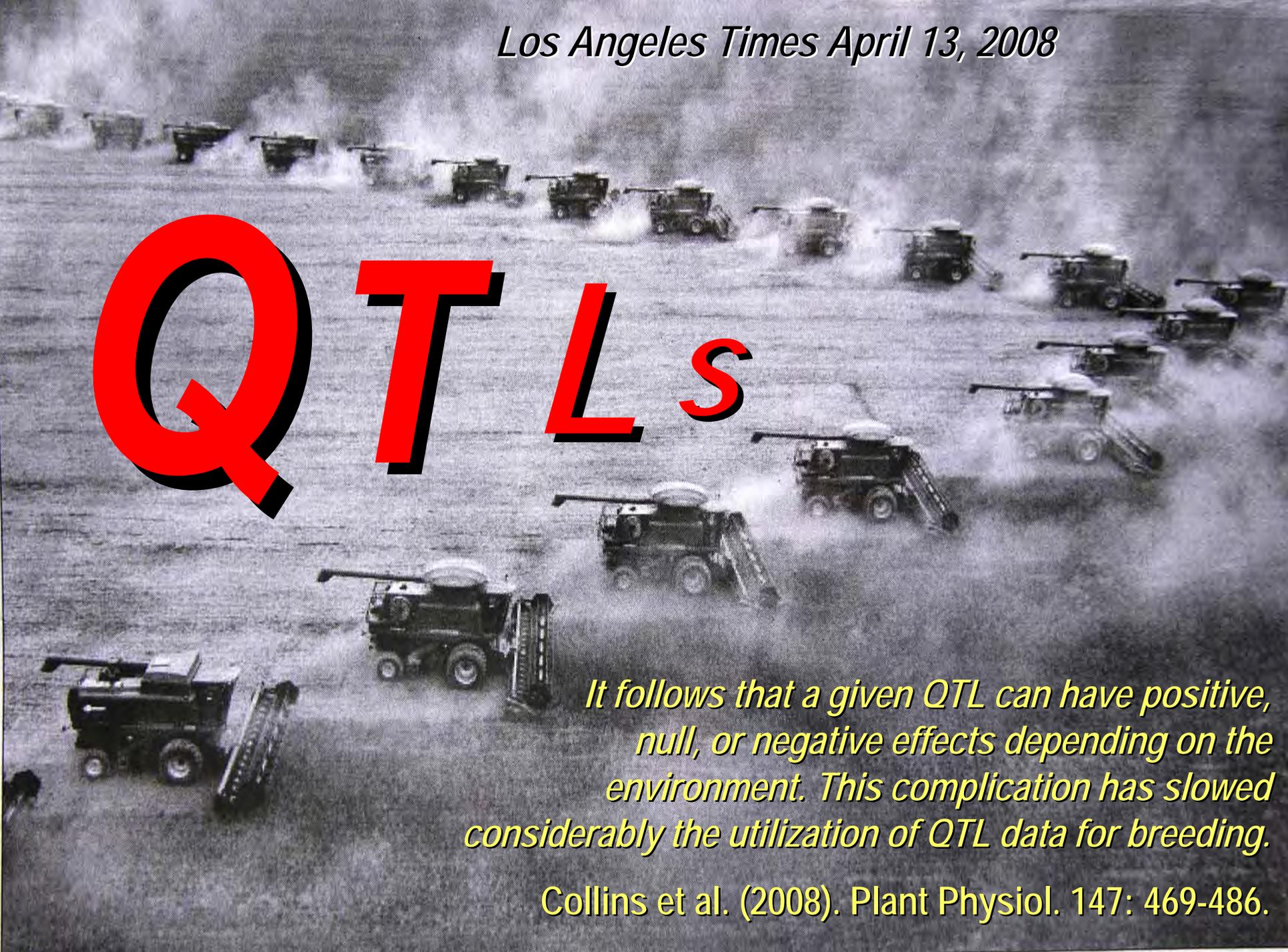
It follows that a given QTL can have positive, null, or negative effects depending on the environment. This complication has slowed considerably the utilization of QTL data for breeding.

Collins et al. (2008). Plant Physiol. 147: 469-486.
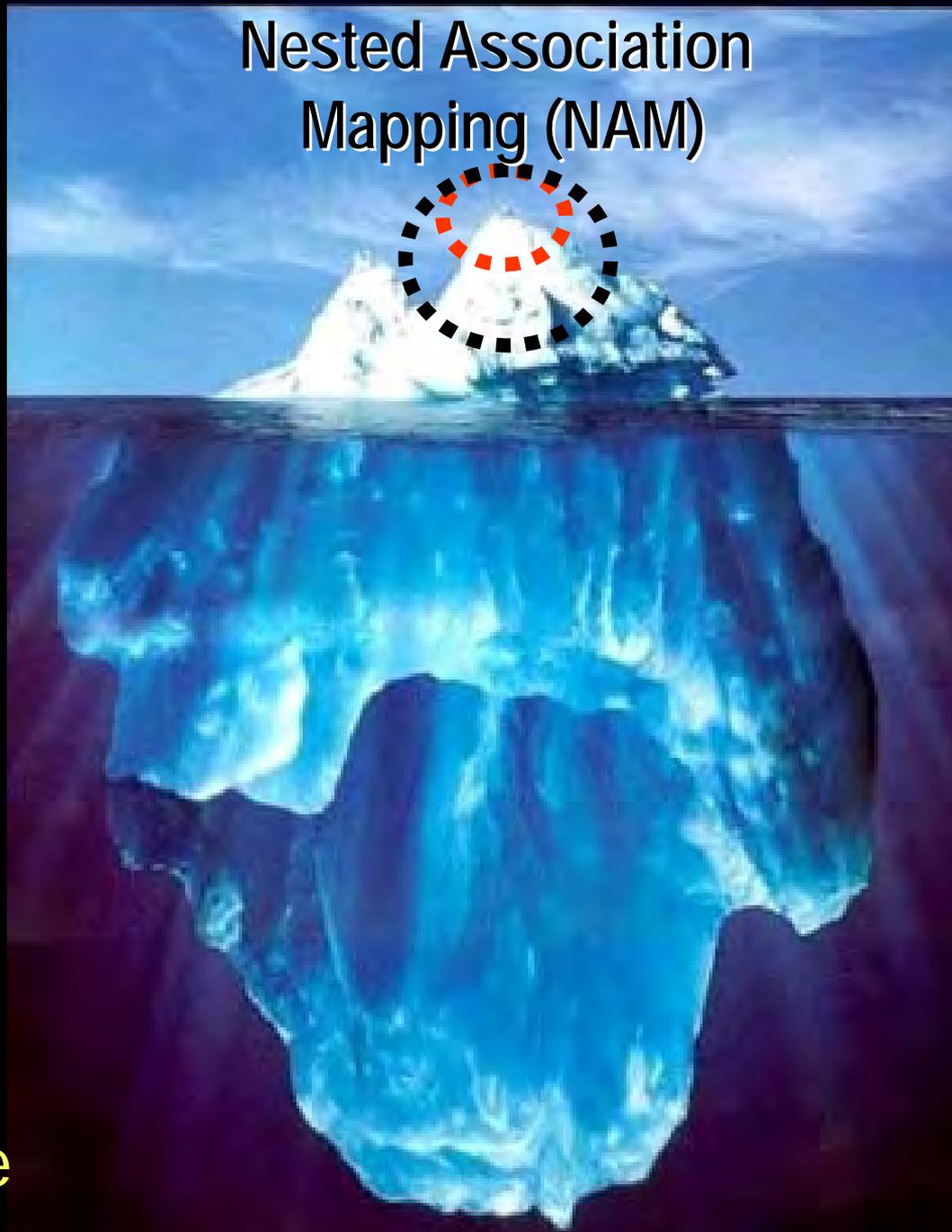
Genome-wide selection

Genome wide selection (GWS) was first suggested in animal breeding (Meuwissen, 2001)

GWS focuses exclusively on prediction of performance based on as many loci as possible (unlimited number)

GWS avoids QTL mapping altogether

- In GWS, the joint effects of all markers are fitted as random effects in a linear model

- Trait values are predicted from a weighed index calculated for each marker

Genome-wide selection

- Simulation studies have shown that across different numbers of QTLs (from 20 up to 100) and levels of h^2, responses to GWS were 18 to 43% larger than MARS (Bernardo and Yu, 2007)

- GWS was found more useful with complex traits and low h^2

- GWS focuses on the genetic improvement of quantitative traits rather than on understanding their genetic basis

- GWS and QTL discovery are not mutually exclusive.

...looking ahead...

Future challenges in molecular breeding

- Developing high-density SNP platforms in target crops

- Platforms to further reduce the cost of SNP profiling

- Multiparental populations for a "breeding-by-design" approach

- Optimize MARS and GWS procedures

- Identifying genes/QTLs for yield potential and stability

- Identifying high-yielding, stable genotypes (low G x E x M)

- Integration of modeling (es. QTL effects)

- Closer collaboration with breeders in DCs

- Training of breeders to integrate MB in their programs

Tying it all together

- On a case-by-case basis, develop appropriate breeding strategies for the improvement of multiple traits
  - Genetic dissection of the developmental and functional correlation between multiple traits, including yield and yield stability
  - Understanding of genetic networks for correlated traits
  - Construction of selection indices across traits

- Delivering improved germplasm and new cultivars will require a close collaboration and an effective coordination among all the relevant stakeholders.

- Only an appropriate engagement of the breeders and seed companies in target areas will allow the above to materialize and tangibly impact crops yield and yield quality.