



Magic Population in Crop Improvement

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A population that is suitable for linkage mapping of genetic markers is known as mapping population. Generated by crossing two or more genetically diverse lines and handling the progeny in a definite fashion. It is used for determining genetic distances between pairs of genes and map them to specific locations in the genome. Identification of molecular markers that are linked to genes of interest.

Types of Mapping Population

1. Bi-parental mapping population

a) F₂ population:

- Produced by selfing of the F₁ individuals.
- Requires only two generations.
- Best suited for oligogenes.
- Estimates of additive and dominance components.
- Limited recombination the markers identified to be linked with target genes are likely to be located at greater distance.

b) Recombinant inbred lines:

- RILs are a set of homozygous lines, derived from F₂ populations usually by SSD method.
- They have increased recombination events and improved map resolution.
- Additive and additive x additive components (homozygous).
- Most commonly used.

c) Near isogenic lines:

- Pairs of homozygous lines that are identical in genotype, except for a single gene/locus.
- Fine mapping
- Effect of Minor QTL can be studied using these lines.

d) Advanced intercross lines:

- Intermating F₂ population, followed by selfing after which RILs are derived for QTL analysis.
- The additional rounds of intermating reduce the level of LD and increase the precision of QTL location.

Limitations of Bi-parental populations

- These populations mainly depend on the recombination events that take in F₁ generation and not enough time is available to shuffle the genome in small fragments. As a result, the QTL get placed on a large chromosomal region.
- Allows mapping of for only those allelic pairs that are present in two parents i.e, whole genetic variation can't be exploited in such populations.

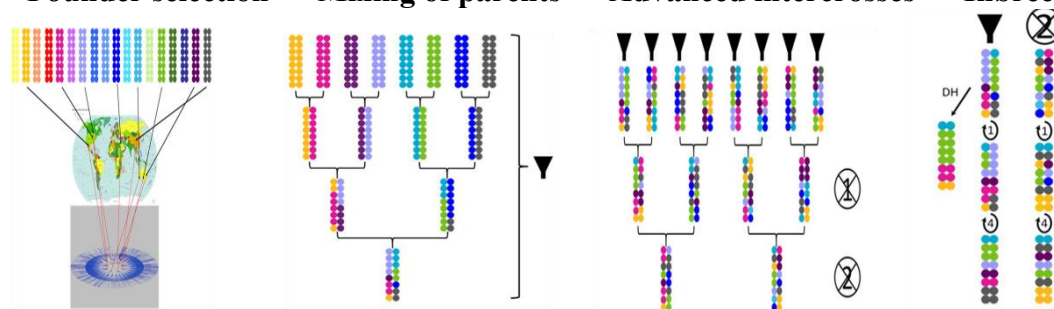
2. Multi-parental mapping population

a) Multi-parent Advanced Generation Intercrosses (MAGIC):

- To overcome the limitations associated with biparental populations, a strategy has been proposed to integrate multiple alleles and to provide increased recombination and mapping resolution.
- MAGIC populations are a collection of RILs produced from a complex cross involving several parental lines.
- These populations are an extension of the AILs proposed by Darvasi and Soller (1995).
- This concept was first used in Mice as “heterogeneous stocks” and later extended to plants by Mackey and Powell (2007), who also proposed the name MAGIC.
- The main objective of developing MAGIC populations is to promote intercrossing and shuffling of the genome.

Steps for development of MAGIC lines

Founder selection → Mixing of parents → Advanced intercrosses → Inbreeding.



Founder selection

- Founders are selected based on the relevance to a breeding program for specific trait based on geographic, genetic and phenotypic diversity.

Consideration of flowering time

Mixing of parents

- Mixing of parents together in predefined patterns, or funnels.
- Broad genetic base.

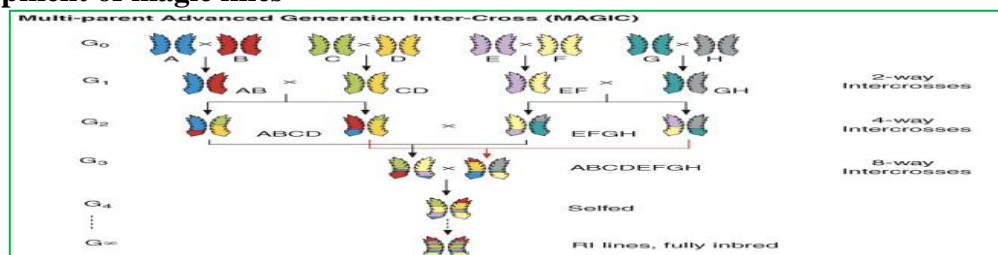
Advanced intercrosses

- Intercrossing of individuals derived from different funnels for additional generations.
- The main goal of this intercrossing is to increase the number of recombinations in the population.
- If n founder lines are taken, they need to be intercrossed for $n/2$ generations till all the founders are combined with equal proportions.

Inbreeding

- Selfing or DH method.
- In general selfing for 6–7 generations is done to obtain MAGIC RILs.
- DH method- faster
- Selfing-additional recombination

Development of magic lines



Importance of the MAGIC population

To compare utility of different types of populations for mapping, Broman (2005) calculated the number of crossovers that accumulate in offspring population in different mapping populations.

- BC or DH populations it is 1.
- 2-way RILs it is 2.
- 4-way RILs it is 3.
- For MAGIC population it is 6.

Thus it clearly shows that, MAGIC population will give maximum number of crossovers.

Advantages of using multi-parent populations

- The genetic diversity of multiple parents, recombined over several generations (level of recombination) generates a genetic resource population with large phenotypic diversity suitable for high-resolution trait mapping.
- Increased recombination in MAGIC populations can lead to novel rearrangements of alleles and greater genotypic diversity.
- From a practical standpoint, a compact genetic resource with moderate population size and a concentration of high-value traits is particularly valuable as a pre-breeding gene pool

Limitations of MAGIC population

- Requires greater initial investment of time for careful selection of founders.
- With increase in founder size the intercrossing cycles also proportionately increases (Handling of many number of crosses)
- Large scale phenotyping – resources may not be available to breeders.
- Show extensive segregation for developmental traits, limiting their use in the analysis of complex traits like yield or drought tolerance.

Application in crop improvement

- Best combinations of genes for important traits development.
- Facilitate the discovery, identification and manipulation of new forms of allelic variability.
- The discovery of new forms of allelic variability.
- It is also possible to study the gene interactions but it is challenging because of different genetic background.
- G X E interactions can be studied well.

Developed 4 multi-parent populations:

- Indica MAGIC (8 indica parents)
- MAGIC plus (8 indica parents with two additional rounds of 8-way F1 inter-crossing)
- Japonica MAGIC (8 japonica parents)
- Global MAGIC (16 parents–8 indica and 8 japonica).

Institutes involved in development of MAGIC populations

For bread wheat- NIAB, for rice IRRI, for sorghum ICRISAT and for cowpea IITA.

Conclusion

- The MAGIC populations serve a dual purpose: permanent mapping populations for precise QTL mapping and for direct and indirect use in variety development.
- These populations also present opportunities for studying the interactions of genome introgressions and chromosomal recombination.

- The MAGIC populations can also be explored to study gene-gene interactions. For instance a QTL may not be effective in a single background (one of the eight parents), but may be effective in the MAGIC populations (a mixed background of the 8 parents).
- Testing the diverse AILs across a wide range of environments will provide a better understanding of the extent of adaptation for these highly recombined MAGIC populations as well as of $G \times E$ interactions.
- Fine mapping of the AILs from the indica MAGIC population can be used to develop trait-specific SNP markers for application in breeding programs.