

## **Multiparent Advanced Generation Intercross Populations**

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### **SUMMARY**

MAGIC populations offer great potential both for dissecting genomic structure and for improving breeding populations & further opportunities for crop improvement due to its complex pedigree structure. The genetic diversity of multiple parents, recombined over several generations, generates a genetic resource population with large phenotypic diversity suitable for high-resolution trait mapping. Those populations where the parents have all been inter-mated, typically termed Multi-parent Advanced Generation Intercrosses (MAGIC). Such populations have already been created in model animals and plants, and are emerging in many crop species. A traditional experimental population captures only a small snapshot of the factors affecting the trait due to the narrow genetic base. Whereas MAGIC populations have ability to mix well-characterized founder genomes in controlled pedigrees, and facilitate the investigation of both the genome itself and its relationship with traits and the environment.

### **INTRODUCTION**

The multiparent advanced generation intercross (MAGIC) populations are a collection of RILs produced from a complex cross/outbred population involving several parental lines. The parental lines may be inbred lines, clones, or individuals selected on the basis of their origin or use. MAGIC populations are developed by intercrossing multiple (typically four, eight or sixteen) parental lines in a balanced funnel crossing scheme. The resulting RILs are highly recombined mosaics of the founder genomes. MAGIC populations are an extension of the AIL proposed by Darvasi and Soller (1995), but differ from them with respect to the involvement of multiple parents in their construction. This concept was first used in mice as “heterogeneous stocks” by Threadgill and Churchill, 2012) and later extended to plants by Mackay and Powell (2007), who also proposed the name MAGIC. They are also similar to the Arabidopsis multi-parent recombinant inbred line (AMPRIL) population described by Huang et al. (2011) which was developed from diallel crossing of eight Arabidopsis accessions from diverse geographical origins. Huang et al. (2015) provide an excellent discussion on various aspects of MAGIC populations, including recent achievements from, and the unique opportunities and advantages offered by the MAGIC populations. MAGIC allows the identification of genes controlling quantitative traits, by crossing different combination of multiple parents. MAGIC combines high diversity with high recombination due to which it gives greater precision in QTL location and greater opportunity to detect more QTL.

### **Objectives**

- MAGIC has the potential to increase the speed and efficiency of breeding.
- It will direct impact on the production of farms as well as the ability to change the way of scientists to identify the genes that control the quality and disease resistance.
- MAGIC population served as source material for extraction and development of breeding lines and varieties.
- Development of variety with several agronomically beneficial traits.
- Variety which can be adopt to several diverse region of the world and suitable for diverse climatic conditions.
- MAGIC populations are bring model shift toward QTL analysis, gene mapping, variety development etc. in plant species.

### **Procedure**

Careful consideration of design prior to initiating population development helps to ensure not only the novelty of a population, but also its ability to answer practical questions of interest. The objectives for the

population need to be clearly defined before embarking on population development. The Following steps are included in development of MAGIC population-

- Founder selection
- Mixing of parents
- Advanced intercrossing
- Inbreeding

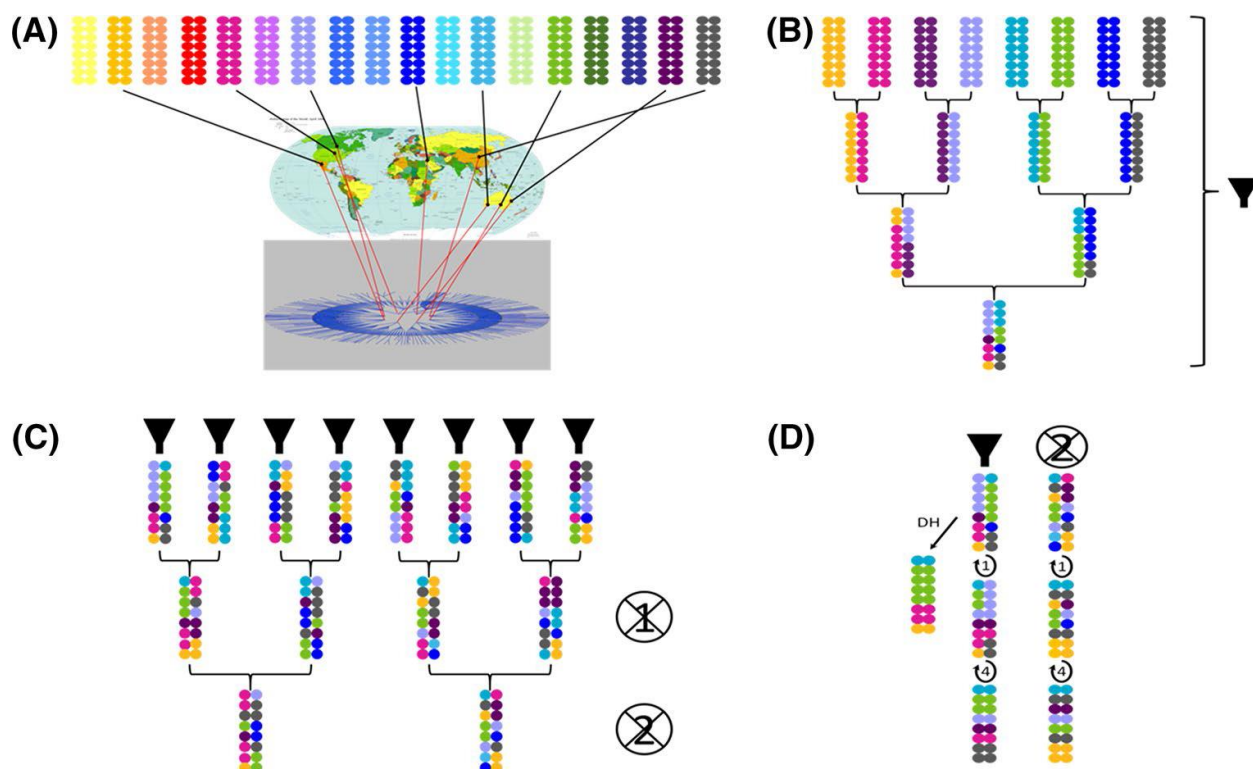


Fig.1: Stages of MAGIC population development design for eight founders **a** selection of founders based on geographic, genetic, phenotypic diversity. The maternal pedigree tree is presented at the *bottom* for an eight-way MAGIC population with each *ring* representing a subsequent generation; **b** mixing of parents together in predefined patterns, or funnels (denoted by *symbol* on right); **c** intercrossing of individuals (generations denoted by *number* within *crossed circle*) derived from different funnels for additional generations; **d** selfing (generations denoted by number within *circular arrow*) or double haploidization of individuals either directly from funnels or after advanced intercrossing to form *inbred lines* (color figure online) [Huang et al., 2015].

**Founder selection:** Prior to initiating population development, founder lines must be chosen (Fig. 1a). This may be based on genetic and/or phenotypic diversity, either in a constrained set of material (e.g., elite cultivars, geographical adaptation) or material of more diverse origins (worldwide germplasm collections, distant relatives). Use of landraces as founders may introduce greater diversity, but simultaneously reduce the generalize ability to the current breeding populations (Huang *et al.*, 2015). In addition to genetic diversity, the phenotypic diversity, such as flowering time in the founders will avoid segregation for undesirable values in the progeny must be carefully managed to produce a resource which is also practical.

**Mixing of parents:** In this stage, the inbred founders are paired off and inter-mated in a prescribed order for each line, known as a funnel. If each recombinant inbred line (RIL) is the product of a  $2^n$  way cross, then the mixing stage will require  $n$  generations. The result of this stage is a set of lines whose genomes comprised contributions from each of the founders. In the population development, multiple parents are intercrossed to form a broad

genetic base (Fig. 1b) inspired by the heterogeneous stock (HS), proposed by McClearn *et al.* (1970) and taken up by Demarest *et al.* (2001).

**Advanced intercrossing:** The main goal of this intercrossing is to increase the number of recombinations in the population. In the second stage (Fig. 1c), the mixed lines from different funnels are randomly and sequentially intercrossed as in the advanced intercross (AIC) proposed by Darvasi and Soller (1995). Yamamoto *et al.* (2014) concluded that at least six cycles of intercrossing were required for large improvements in QTL mapping power.

**Inbreeding:** In the third stage, the individuals resulting from the advanced intercrossing stage are progressed to create homozygous individuals (Fig. 1d). RILs in plants can be created via single seed descent (Bailey 1971) or doubled haploid production (Forster *et al.* 2007). Plants have been self pollinated for five or more generations, so the expected level of heterozygosity in the genome is less than 3 %. In general to develop MAGIC populations a minimum of 8 crop seasons is required to reach at least the S5 generation.

### Genetic analysis of MAGIC population

- **Linkage map construction:** The large number of polymorphic markers across all founders and accumulation of recombination events through many generations. This MAGIC pedigree can be used to achieve dense and high-resolution mapping of the genome. MAGIC population can be seen most clearly in the region around centromeres. The first linkage map from a MAGIC population was constructed in wheat (Huang *et al.*, 2012).
- **QTL mapping approaches:** The use of heterogeneous stocks (HS) improves the power to detect and localize QTL. The large number of parental accessions increases the allelic and phenotypic diversity. The larger number of accumulated recombination events increase the mapping accuracy of the detected QTL compared to an F2 cross. Thus, MAGIC lines occupy an intermediate position between naturally occurring accessions and existing synthetic populations.

### Application of MAGIC population

MAGIC population may be used directly as source materials for the extraction and development of breeding lines and varieties. Development of variety can be possible with several agronomically beneficial traits via MAGIC population. Variety which can adopt to several diverse regions of the world and suitable for diverse climatic conditions. MAGIC population can provide solutions to a range of production constraints (particularly stress tolerance). In MAGIC, high levels of recombination result in low LD and give high mapping resolution. A high density MAGIC linkage map has recently been developed in wheat (Gardner *et al.*, 2016). MAGIC populations have been developed in many plant species including Arabidopsis (Kover *et al.*, 2009), tomato (Pascual *et al.*, 2015), barley (Sannemann *et al.*, 2015), maize (Dell'Acqua *et al.*, 2015), sorghum (Higgins *et al.*, 2014), wheat (Huang *et al.*, 2012; Mackay *et al.*, 2014) and rice (Bandillo *et al.*, 2013). A MAGIC population of over 1,000 MLs would enable assessment of two-way and three way epistatic interactions (Cavanagh *et al.* 2008). Trait mapping in structured MPPs involves the use of statistical models developed based on their theoretical properties. Many models for genetic data analysis have been generated by computer simulation to determine the properties and outcomes of an experimental design. For example, simulation studies in MPPs can be applied to determine the optimal number of founder lines, crosses and the size of the population needed to effectively track the genetic architecture of quantitative traits (Myles *et al.*, 2009). Kover *et al.* (2009) simulated the effects of MPP size on mapping resolution and power for QTL detection determining that QTL detection error rates decreased when population size increased and QTL could be mapped to smaller intervals. MAGIC populations are likely to bring model shift towards QTL analysis, gene mapping, variety development etc. in plant species.

### Advantage of MAGIC population

One of the real advantages of MAGIC for breeding is that new genetic combinations are created from the re-shuffling of the starting varieties. Intercrossed mapping population is created from multiple founder lines. Each generation reduces the extent of linkage disequilibrium (LD), thus allowing QTL to be mapped more accurately. It can be used for extraction of good combination and directly release as a variety. MAGIC has multiple

advantages with existing approaches, as it permits a more precise identification of genes that are responsible for superior quality traits. It facilitates the discovery, identification and manipulation of new forms of allelic variability. The MAGIC population has a large number of individuals and is the product of numerous generations of inter-crossing the original founders or parent plants, scientists are able to more accurately identify the genes of important traits.

### Limitations of MAGIC population

A MAGIC population requires greater initial investment in capability and time than a biparental, careful selection of founders allows its generalize ability to the wider breeding population and ensures relevance as a long term genetic resource panel. It takes more time because of incompatibility between the parents, large scale phenotyping, requirement of more inputs and due to extensive segregation, better marker system is necessary to identify QTLs.

### CONCLUSION

MAGIC population may be used directly as source materials for the extraction and development of breeding lines and varieties. Development of variety can be possible with several agronomically beneficial traits via MAGIC population, which can adapt to several diverse regions of the world and suitable for diverse climatic conditions. The continued enrichment of MAGIC population with open-access phenotypic and genotypic resources will enhance their power as growing genetic toolbox to enhance crop improvement.

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