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Popular Article

# Utilization of multi-parent populations in the tracing the genetic determinants of quantitative traits

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## Introduction

In the context of climate change and increasing population size it is important to breed high yielding varieties and hybrids harbour resistance against biotic and abiotic stresses. Taking the aid of the plant genetic resources and introgressing these useful loci into the existing leading varieties to overcome some of their drawbacks seems to be an attractive approach. However, the complexity associated with the inheritance of these traits is a major hurdle for trait introgression breeding. It is important to understand the complexity of trait through QTL mapping for the strategical implementation of marker-assisted breeding approaches. Two majorly used approaches to map the loci associated with trait of interest are bi-parental linkage mapping and genome wide association studies (GWAS). Bi-parental mapping utilizes the progeny derived from two parents, while GWAS harnesses the historic recombination in mapping loci using natural populations. Bi-parental mapping have advantages like simple population construction (eg., DH and F<sub>2</sub>), high power of detection QTLs and low linkage disequilibrium decay. However, the limited effective recombination, low genetic diversity and the loci identified are limited to the two genetic backgrounds are the major disadvantages of bi-parental mapping populations. In contrary, GWAS considers historic recombination events and maps loci with higher resolution. The presence of rare variants and inherent population structure reduces the statistical power of mapping (Lipka *et al.*, 2015).

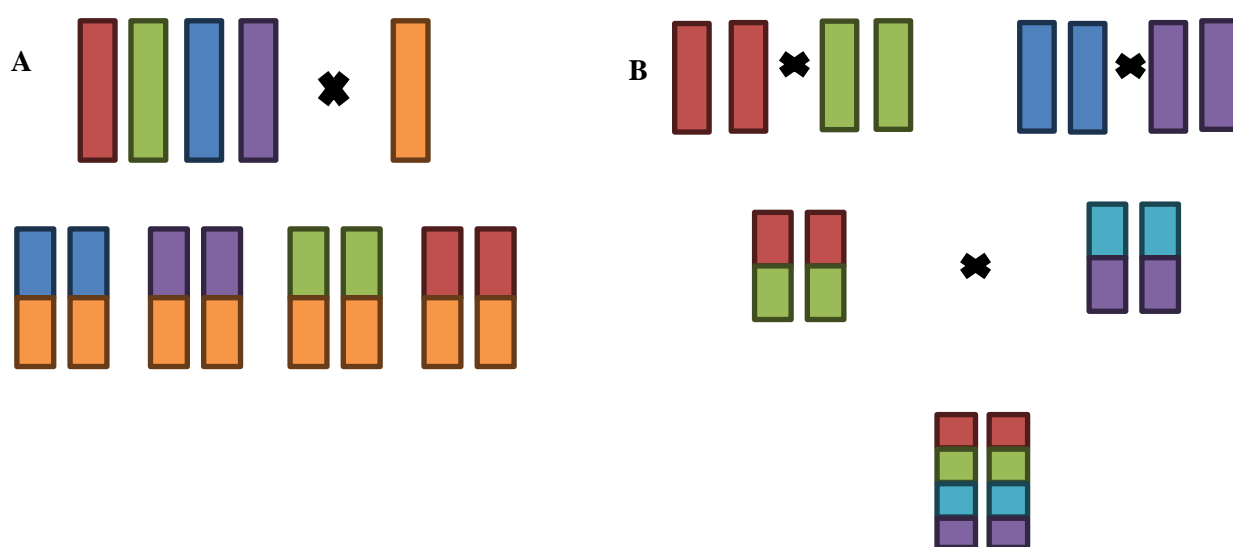
To overcome this drawback, multi-parental populations (MPPs) have been established to detect the loci associated with the traits. These multiparent population include nested association



mapping (NAM) and multi-parent advanced generation intercross (MAGIC) populations (Huang *et al.*, 2015; Cockram and Mackay 2018). Progenies are derived through intercrossing multiple inbred founders in a well-defined manner several times to develop a MAGIC population while, a set of related or unrelated lines are crossed to a common parent in deriving NAM populations. Using genetically diverse parents in developing these populations exploits historic recombination events, increases the allelic richness and deriving the MAGIC and NAM recombinant inbred lines (RILs) through some generations of selfing gives the advantage to map the loci based on recent recombination events.

### Development and application of multi-parental populations:

The basic essentials of deriving the MPPs are identification of true breeding diverse founder lines, derive mapping populations that are analyzed together as a population. The important criteria to be considered while choosing the founder parents is maximizing the genetic diversity. Founders are chosen based on target trait or target environment or targeting diversity to exploit interaction among different traits.



**Fig 1. Schematic representation of development of NAM (A) and MAGIC (B) populations. In NAM a single founder is crossed to a set of genetically diverse lines, while in MAGIC the founder parents are intercrossed in all possible combinations to derive RILs**

To date many studies have been conducted to map loci for simple and complex traits in several crops using NAM and MAGIC populations. For example, three QTLs for grain yield and three for flowering time along with candidate genes have been identified using maize MAGIC population (Dell'Acqua *et al.*, 2015). Similarly, *Xa4* and *Sub1* were identified and validated using rice MAGIC populations (Bandillo *et al.*, 2013).



## Conclusion

These multi-parental populations act as permanent mapping populations for QTL mapping as the QTLs are identified using the genetically diverse founder parents. These are also the tailor-made population for plant breeders as they aid in understanding the complex genome interactions and, historic and recent recombination in mapping QTLs for simple and complex traits.

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