Multi Parental Crop Breeding – Improving Crop **Yield and Stress Tolerance**

Abstract

Multi Parental Populations (MPPs) transformative tools in plant breeding, offering enhanced genetic diversity and mapping Pattambi, Kerala Agricultural precision compared to biparental populations. Key designs, such as Nested Association Mapping (NAM) and Multi Parent Advanced Asish I Edakkalathur Generation Intercrosses (MAGIC), allow for the dissection of complex traits like yield, stress tolerance, adaptation, etc. NAM population involves a common founder parent crossed with diverse donor lines, combining linkage mapping and genome-wide association mapping (GWAS) to detect rare QTLs with improved resolution. MAGIC populations, created through systemic crossing of multiple founders, produce highly recombined, diverse genotypes, enabling precise trait mapping and insights into allelic interactions. Both approaches integrate advanced genotyping, phenotyping, and statistical analysis, utilizing tools like SNP arrays and next-generation sequencing comprehensive for trait evaluations. While NAM populations are simpler and flexible in development, MAGIC populations provide superior haplotype diversity and resolution but are resource intensive. MPPs are particularly advantageous for analysing polygenic traits and enhancing genomic selection strategies. By bridging genetic diversity and mapping efficiency, MPPs contribute significantly to sustainable improvement, addressing global crop challenges in agriculture. This review underscores their role in advancing resilient and high-yielding crop breeding programs.

Authors

are Roshni Vijayan

RARS-Central Zone, University

College of Agriculture, Vellanikkara, Kerala Agricultural University

Jyothilekshmi S

ORARS, Kayamkulam, Kerala Agricultural University

I. INTRODUCTION

Any effective breeding needs a proper understanding of the genetics of the target traits. The crosses made from the desired parents bring in mixing and recombining the genomes of the parents enabling the genetic dissection of the targeted trait, and with the range of variability achieved, it can be utilized to perform selection. In biparental populations like the F2s, backcrosses (BC) and Recombinant Inbred Lines (RILs) are utilized for the identification of QTLs using the linkage analysis. The bi-parental populations are relatively simple in construction when compared to Multi Parental Populations (MPPs). The major drawbacks of the biparental populations like low mapping resolutions and the QTLs can be identified from two segregating individuals alone. In general, MPPs are treated as a tool midway between classical linkage analysis and association mapping. It combines both the approaches of association mapping and GWAS.

II. TYPES OF MULTI-PARENTAL POPULATION (MPPS)

Even though several designs are available for the development of the multiparent populations. The major multi-parental populations developed in crops are Nested association mapping (NAM) populations and multi-parent advanced generation intercross (MAGIC) populations. NAM was first developed in maize by Yu *et al.*, (2008) whereas the potential of MAGIC populations in crops was first articulated by MacKay and Powell (2007).

III. METHOD OF DEVELOPMENT OF MULTI-PARENTAL POPULATIONS

Nested Association Mapping (NAM) and Multi-parent Advanced Generation Intercrosses (MAGIC) are the major multi-parental populations. In this section, we may discuss the development of these populations.

Nested Association Mapping (NAM)

NAM is set of biparental mapping populations connected by a common parent. In NAM, various biparental mapping populations like Recombinant Inbred Lines (RILs), Near Isogenic Lines (NILs), and Doubled Haploids (DHs) are developed using a set of inbred parents. Consider parents A, B, C, D, and E used for the development of the NAM population. Biparental crosses made in this case are AxB, AxC, AxD, and AxE. Thus one parent is common in all biparental crosses and the other parent is different in each cross. The common parent used in all crosses is known as the 'common founder parent' and the differing parents are called 'donor founder parents'. A common founder parent will be usually an elite and widely adopted cultivar. Examples of common founder parents include B 73 in maize (Yu *et al.*, 2008), Rasmusson in barley (Nice *et al.*, 2016; Kumar *et al.*, 2016), IR 64 in rice (Fragoso *et al.*, 2017; Kumar *et al.*, 2022), RTx430 in sorghum (Bouchet *et al.*, 2017), and Avocet-YrA in wheat (Ren *et al.*, 2017). Donor founder parents are selected to increase genetic diversity in the mapping population. Thus, diverse germplasm resources differing in pedigree, morphological, agronomic, and biochemical characters could be employed as donor founder parents. Another method for the selection of donor founder parents is the inclusion of different donors concerned with the trait of interest. Often genetically diverse donor founder parents are selected from a large germplasm employing genotyping with molecular markers like SNPs. The number of donor founder parents may vary from four to fifty or even more.

Biparental crosses are forwarded in subsequent generations either as RILs, NILs, or DHs. Seeds of the above immortal homozygous lines generated from different biparental crosses are mixed in equal quantities to make the NAM population. NAM developed from RILs of different crosses is termed as RIL-NAM. Thus, based on the method of advancement of bi- parental crosses, NAM populations are classified as RIL-NAM, NIL-NAM, and DH-NAM. RIL-NAM is preferred when common parent and donor parents are cultivars. Here biparental crosses are forwarded to RILs through the Single Seed Descent (SSD) method. NIL-NAM developed when donor parents are wild type. In NIL-NAM, biparental crosses are backcrossed to a common parent and then advanced through selfing. When a back cross is employed for the advancement of bi-parental crosses, the resultant NAM is referred to as BC-NAM (Back Cross NAM) and AB-NAM (Advanced Back Cross NAM). DH-NAM is employed in crops where doubled haploid production protocols are ready. This method provides the fastest method for the development of the NAM population. Whatever the method used for generation advancement, care should be taken to mix an equal quantity of homozygous sub-populations generated from each biparental cross. Hence, the NAM population is a mosaic of donor genes in the background of a common founder parental genome. In other words, the resultant population could be described as different gene association combinations distributed or nested in the common founder genome.

NAM population was raised in appropriate statistical designs like RBD (Randomized block design) or ABD (Augmented block design) and morphologically characterized using high through-put phenotyping methods.

For the precise phenotypic evaluation, trials are repeated over seasons and locations. The next step is high throughput genotyping (HTG) using



Figure 1: Flow-Diagram of NAM

SNP-based assays or next-generation sequencing (NGS) technologies like whole genome sequencing (WGS), Genotyping-by-sequencing (GBS), transcriptome sequencing, etc. The further step is the statistical analysis of high throughput phenotyping and genotyping data. Analysis in biparental mapping population deals with two alleles with individual allele frequencies close to 0.50. NAM population deals with multiple families and multiple alleles that necessitate appropriate statistical tools for analysis. Joint linkage analysis, NAM-GWAS, and Combined linkage analysis-linkage disequilibrium mapping approach are the commonly used statistical approaches in NAM. A combination of phenotyping, genotyping, and transcriptome data provide marker-QTL close association as well as spatial and temporal gene expression patterns.

The mating design for developing the NAM population is furnished in Figure 1. Important steps in NAM could be summarized as

- 1. Selection of common founder parent and donor founder parents
- 2. Making biparental cross combinations

- 3. Advancing biparental crosses with a suitable generation advancement scheme
- 4. High through-put phenotyping and genotyping
- 5. Statistical analysis

Biparental mapping has high QTL detection power but has only low resolution. This is because we are dealing with alternate forms of alleles with reduced recombination events in bi-parental mapping. So, the decay of linkage disequilibrium (LD) is low. Association mapping provides better QTL resolution power as it utilizes historically derived LD accumulated over several generations. But genetic similarities inside the population which are often described as population structure may lead to false QTL detection. Further, rare QTLs may go unnoticed. NAM utilizes historically derived LD present in founder parents and recombination-derived LD raised due to generation advancement. As the number of donor parents increases, the historically derived LD component available in the population increases. When the population size and number of generation advancement increases, recombination-derived LD increases. NAM combines the recombination derived LD present in biparental mapping populations with historically derived LD available in association mapping. In this way, NAM combines high power of QTL detection present in biparental mapping with high QTL resolution capacity of association mapping. NAM identifies higher number of QTLs than biparental mapping with high resolution equivalent to association mapping. The chance of finding a rare QTL is higher in NAM than in association mapping as the NAM population increases the frequency of rare QTL present in one or few parents to a higher detectable level in the final population (Ladejobi et al., 2016; Scott et al., 2020; Gireesh et al., 2021).

MAGIC Population

The MAGIC population is an immortal population in which multiple parents are aligned to different bi-parental crosses and crosses are forwarded as advanced intercrosses followed by selfing to generate inbreds. In the magic population, homozygous founder lines in sets of 4, 8, 16, or more will be crossed in a specific pattern to generate a mosaic genome of all parental types. Founder lines selected should be genetically divergent and may be cultivars, landraces or any germplasm resource that permits inter-crossing among them. The resultant population should be genetically divergent enough to exercise mapping. When we develop trait-specific MAGIC populations, founder lines differing for the particular trait of interest will be included.

Once a set of founder lines are selected, they will be crossed in a specific pattern to generate an outbred population. This process of planned crossing of inbred founder lines among themselves and subsequent crossing of resultant hybrids is termed as mixing. A specific crossing scheme adopted for mixing is known as a funnel. The funnel could be explained as a specific scheme for crossing inbred founder lines to generate single cross hybrids and subsequent crossing of single cross hybrids to generate double cross hybrids and so on to generate a combined genotype with all alleles from all founder lines converged into it. The purpose of mixing is to generate such a combined genotype and it is achieved by funnel scheme. Here inbred founder lines are crossed in the first step to generate single cross hybrids. Single cross hybrids crossed in specific patterns to generate double cross hybrids. In the next step, double-cross hybrids crossed together. The combined genotype will comprise alleles of all founder lines. The funnel could be grouped as a single funnel crossing scheme or multiple funnel crossing scheme (Figure 2a). In a single funnel crossing scheme, a particular parent will be used only once in a particular mixing generation. So chances of inbreeding and reciprocal crosses will be avoided in this scheme. Single funnel crossing scheme manages to generate a combined mosaic genome having a contribution from all founder lines in the lowest number of crosses. The multiple funnel crossing scheme is characterized by the use of a founder parent more than once in a particular mixing generation. Here a founder parent crossed with all other founder lines to generate single cross hybrids in the first mixing cycle. In the multiple funnel crossing scheme, suppose 'n' is the number of founder lines, number of single cross hybrids generated in the first mixing cycle will be n(n-1)/2, if reciprocal crosses are not carried out. Thus the number of single cross hybrids generated is equal to half diallel crosses. Consider a mixing scheme with four founder lines A, B, C, and D. Single cross hybrids generated in multiple funnel crossing schemes are AxB. AxC, AxD, BxC, BxD, and CxD. In the next mixing cycle, when the crossing of single-cross hybrids is carried out, inbreeding is evident in the crosses (AxB) x (AxC) and (AxB) x (AxD). Instead, in a single funnel crossing scheme, the first mixing cycle involves the production of single cross hybrids AxC and BxD and in the next mixing cycle, the double cross is made as (AxC) x (BxD) so that inbreeding chances are ruled out (Ladejobi et al., 2016; Scott et al., 2020). Allowing reciprocal crosses in the multiple funnel crossing scheme further increases the number of crosses and level of inbreeding in successive mixing cycles. Multiple funnel schemes with reciprocal crosses will be able to counter variations arising due to maternal effects and segregation distortion. In most of the funnel schemes, care will be taken to avoid inbreeding. From this section, it is evident that multiple funnel crossing increases cost and demands higher resources in the mixing phase. Irrespective of the funnel scheme, crossing

between single-cross hybrids and further crosses involves crosses among heterozygous individuals. Hence it is always better to keep optimum population size and replications to avoid allele loss and to prevent allele distortion in the population.



Figure 2: Mixing Population of the Figure Represent in Two Parts (a) Single funnels crossing scheme involving eight parents (b) First mixing phase of multiple funnel crossing scheme involving eight parents parents

In the next step, combined genotypes generated from funnels in the mixing step are allowed to intercross randomly to increase the number of recombinations among founder genomes. Six cycles of intercross are considered to be optimum to get QTLs with high- resolution power. Above random inter-mating cycles are known as advanced intercrossing. Inbreeding follows advanced intercrossing. Heterozygous combined genotypes arising from recombination events are made into homozygous genotypes such as RILs or DHs. Five rounds of selfing are considered to be optimum to reach a satisfactory level of homozygosity. The resultant inbred genotypes will be highly mixed mosaics of individual founder genomes (Huang *et al.*, 2015).

In the light of above discussion, steps in the development of the magic population could be summarized as

- 1. Selection of founder lines
- 2. Mixing using the proper funnel scheme

- 3. Advanced intercrossing
- 4. Inbreeding
- 5. High through-put phenotyping and genotyping
- 6. Statistical analysis

More number of founder lines in the MAGIC population breaks the genetic bottleneck experienced in biparental mapping populations raised from only two parents. Mixing of more founder lines contributes to the historically derived LD to the population. The presence of more number of parents increases the chance of detecting more number of QTL. Still, more number of founder lines impart difficulties in crossing in the mixing phase and random mating in the advanced intercrossing phase. Besides practical difficulties, several founder lines increase the cost. At the same time, a smaller number of founder lines lead to inbreeding and subsequently to assortative mating in mixing and intercrossing phases causing the development of population structure. Population structure existing in mapping population panel is a disadvantage in association studies like GWAS. Population structure in the mapping population leads to false positives in QTL detection. In the MAGIC population, population structure gets destructed through random matings carried out in advanced intercrosses. The higher number of random mating and subsequent repeated selfing leads to a greater number of recombination which promotes chances of LD decay. Thus recombination-derived LD will be enriched in the MAGIC population leading to higher resolution of QTLs (Arrones et al., 2020).

Similar to NAM, the MAGIC population can detect rare alleles as the final mapping population theoretically comprises all alleles from all founder lines with equal proportions. It can find out a greater number of QTLs, tag QTLs with high resolution, and evaluate allelic interactions and gene introgression as in NAM. Understanding cytoplasmic inheritance interactions of QTLs is an added advantage of the MAGIC population through multiple funnel crossing schemes. Compared to NAM, haplotype diversity is higher in the MAGIC population. This is because fifty percent of the haplotype in the NAM population is contributed by a common founder parent whereas the haplotype in the MAGIC population is a mosaic from all founder lines. More number of donor lines could be added to NAM as and when required whereas such an option of subsequent adding of founder lines is not possible in the MAGIC population. RILs developed from the MAGIC population provide better chances of imparting superior genotypes for use in further breeding programmes. Higher costs and prolonged development phase are the disadvantages of the MAGIC population. Further, care should be taken to keep optimum population size and replications in each generation of mixing and intercross phases to avoid loss of alleles from the population. Optimum population size is influenced by allelic diversity, ploidy level, and genome size.

QTL Analysis Using Multi Parent Population

Multiparent population plays a major role in the identification of complex traits as it combines various trait loci which is essential for crop improvement. Nested association mapping (NAM) and Multiparent advanced generation intercross (MAGIC) are the popular MPP designs that are commonly used in different crops. The genomic regions corresponding to phenotypic variations of a trait are Quantitative trait loci and these loci can be mapped using

MPPs QTL analysis using MPP is extremely useful for mapping genomic regions associated with traits such as yield, biotic and abiotic stress tolerance, and other qualitative traits also. Since phenotype is the interaction between genotype and environment QTLs are developed which can analyze GXE interaction and for environment-influenced traits MPP-ME (Multi Parent Population in Multiple Environment) QTL analysis needs to be worked out for finding out the significance of environment. Genetic variation in MPP-ME can occur at two different levels viz. between genotypes and between environments. As the genetic structure of MPP is from mostly known parental lineage it is comparatively less complex compared to the GWAS population (Navarro *et al.*, 2022).

Approaches in QTL Analysis Using MPP

1. Nested Association Mapping (NAM)

NAM population is developed by crossing multiple parents with a common elite reference parent thereby developing many recombinant inbred lines (RILs). Various statistical models are designed for QTL analysis in the NAM population. In comparison with the biparental segregating population NAM population has the added advantage of higher mapping resolution and has the power to dissect the genetic association of complex traits (Suhong *et al.*, 2021). Since several different parents are crossed with a well-established elite line the population size will be larger and its evaluation will be tedious and space consuming. Generally, evaluation of the NAM population will be carried out at different environmental conditions and hence NAM multi-environment QTL mapping is used as a tool for its analysis. It is essential to have a statistical model for estimating the genetic variance and covariance across and between environments.

Three different approaches are being used in QTL analysis using NAM 1) Joint linkage analysis 2) NAM GWAS 3) Combined linkage analysis and linkage disequilibrium mapping approach. In joint linkage analysis, two different methods are employed for analysis viz. Joint Composite Interval Mapping (JCIM) and Joint Inclusive Composite Interval Mapping (JICIM). In these approaches' variation due to more than two alleles per locus can be identified in comparison to individual family analysis (Ogut *et al.*, 2015). In NAM - GWAS (Genome-wide association studies) rare alleles that are difficult to be identified in natural populations can be detected. In the third approach of combined linkage analysis and linkage disequilibrium mapping, complex traits can be mapped by estimating linkage and linkage disequilibrium between markers.

One of the models used for QTL analysis is the one-stage factor analytic linear mixed model (FALMM) as suggested by Beeck et al., 2010. It takes into account the covariance of the GXE effects across and between environments and the GXE effect can be partitioned into additive and non-additive if the pedigree data is also included (Oakey et al. 2007). FALMM - NAM MET (Multi-environment trial) data is much more beneficial in QTL mapping in crops. Genetic analysis of the NAM population is enabled with joint linkage association analysis. In the study conducted by Fei et al., (2022) JLM (Joint Linkage Mapping) method was used to perform a comprehensive genetic analysis of KRN (Kernel Row Number) in the maize NAM1 population composed of 12 BC1F4/BC2F4 families. Further verification of mapping results was ensured with two different methods to map QTL. In the first method of using Separate linkage mapping (SLM), separate genetic linkage maps of 12 subpopulations were constructed, ranging in length from 993 to 2,093 cM. The genetic map could obtain a number of QTLs associated with KRN in maize and the SLM OTLs overlapped with five consensus OTLs identified by JLM method. In the second method of using GWAS a number of SNPs associated with KRN were identified and 6 SNPs related to KRN were found to be located within four consensus QTLs from the JLM method.

Crop	Founder	Particulars	Reference
	Lines		
Barley	26	25 wild barley crossed with elite	Maurer et al.,
		barley cultivar	2015
	5	4 wild barley crossed with a	Liller <i>et al.</i> ,
		referencecultivar	2017

Nested association mapping (NAM) multiparent populations

Maize	26	25 inbred lines crossed with the	Tian <i>et al.</i> ,
		reference line	2011, Chia et
			al., 2012, Li et
			al., 2015
	12	11 inbred lines crossed with the	Li et al., 2015
		reference line	
	6	Teosinte lines consisting of 4	Chen et al.,
		parviglumis inbreds and 1 mexicana	2019
		teosinte inbred line crossed and the	
		same was backcrossed to a maize	
		inbred line	
Bread wheat	11	One US spring wheat and 9 Kenyan	Bajgain <i>et al.</i> ,
		spring wheats crossed against a	2016
		Canadian spring wheat	
	29	Spring wheat landraces (25) and	Jordan <i>et al.</i> ,
		cultivars (3) crossed to a broadly	2018
		adapted cultivar	
Rice	11	Japonica lines (10) crossed to elite	Fragoso et al.,
		indica reference line	2017
Soybean	41	40 elite accessions crossed to high-	Xavier et al.,
-		yielding cultivar	2018

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2. Multi-Parent Advanced Generation Inter-Cross (MAGIC)

MAGIC design is more complex compared to NAM as it consists of a number of parents ranging from 4-20 in several crops studied. MAGIC line inherits more number of alleles from the parental populations. Correlation between various traits with different genetic bases can be identified with the help of the MAGIC population. QTL affecting plasticity of response to stresses like water, salinity, and heat stress was revealed from the MAGIC population developed (Diouf *et al.* 2020). Since in MPP several parents are being used the population ultimately developed consists of several genes pyramided together and one such example is noted in the Bio-MAGIC population developed at IRRI, which consisted of multiple genes for three major diseases/pest of rice viz. blast, bacterial blight and brown plant hopper without utilizing backcrossing (Leung *et al.* 2015). Similarly, cotton alleles having a direct effect on fiber quality were identified from MAGIC RILs by Thyssen *et al.*, 2019.

The most commonly used methods of QTL mapping in MAGIC are Composite Interval mapping (CIM) which was actually developed for biparental population and also other methods like MCQTL Jourjon *et al.*,2005), R/qtl (Broman *et al.*,2003), R happy (Mott *et al.*,2000) and R/mp Map (Huang and George,2011) in

which CIM can be performed. In the MCQTL method, QTL analysis in multicross design can be performed and R/qtl is a redesigned version of R software for analysis in multi-parent populations. It can be used for the construction of genetic maps and can be used for identification of genotypic errors.

Table 1: Multi-Parent Advanced Generation I	Intercross (MAGIC) Multiparent
Populations	

Crop	Founder	Particulars	Reference
_	Lines		
Barley	8	German land races(7) and modern variety(1) crossed	Sannemann <i>et al.,</i> 2015
Bread wheat	8	Australian elite spring wheat cultivars(3), spring wheat cultivars (4), and Chinese winter wheat (1), crossed in 313 funnels followed by 0, 2 or 3 generations of intercrossing	Shah <i>et al.</i> , 2019
Cotton	11	10 cultivars and one landrace crossed in 50 pairs	Islam <i>et al.</i> , 2016, Naoumkina <i>et al.</i> , 2019
Cowpea	8	US cultivar (1) and sub-Saharan (7) crossed in 6 funnels	Huynh et al., 2018
Rice	8	Indica varieties (8) crossed in 35 funnels	Bandillo <i>et al.</i> , 2013, Raghavan <i>et</i> <i>al.</i> , 2017
	8	Indica cultivars (4) and japonica cultivars (4) crossed in 2 funnels	Ogawa et al., 2018
Sorghum	29	Male-sterile lines (10) crossed with 19 lines chosen for agronomic traits in random mating pattern	Ongom and Ejeta 2018
Tomato	8	<i>S.lycopersicum</i> (4) and <i>S. lycopersicum var. cerasiforme</i> (4) have diverse lines crossed in 1 funnel	Causse <i>et al.</i> , 2013, Pascual <i>et</i> <i>al.</i> , 2015

Table 2: Nested Association Mapping	g (NAM) Mapped Traits in C	rops
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QTL Mapped Traits	Crop	Reference
Flowering time	Maize	Buckler et al., 2009
Seed weight	Groundnut	Gangurde et al., 2020
Carbon and Nitrogen	Maize	Zhang <i>et al.</i> , 2015
metabolism		

Table 3: Multi Parent Advanced Generation Inter-Cross (MAGIC) Mapped
Traits in Various Crops

QTL Mapped Traits	Crop	Reference	
Fruit weight	Tomato	Pascual et al., 2015	
Plant height	Sorghum	Ongom and Ej et al., 2018	
Yield and yield-related	Rice		
traits plant		D_{assal} at πL_{ass}^{-} 2018	
Plant height		Descaisota <i>ei ui., 2</i> 018	
Bacterial leaf blight			
Heading date		Meng, Guo et al., 2016	
Grain quality		Zaw et al., 2019	
Grain length and width		Ponce <i>et al.</i> , 2020	
Flower colour and seed	Cowpea	Huynh et al., 2018	
characteristic			
SnTox 1 and SnTox3	Bread wheat	Cockram et al., 2015; Downie et	
sensitivity		<i>al.</i> , 2018	

IV. CONCLUSION

MPPs have a greater advantage of the development of higher diversity compared to the biparental populations. A time-consuming process of developing the population but with a higher level of flexibility the founders used made this an ideal population with a wider genetic base. The MPPs, especially NAM and MAGIC can be specifically utilised for the identification of the QTLs from the promising lines developed from these populations. For polygenic characters as well as the selection criteria with multiple characters, genomic selection in MPPs is a highly rewarding as well as promising strategy.

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Questions Multi Parent Crop Breeding

- 1. Example of a multi-parental population
 - a. NIL
 - b. RIL
 - c. Magic
 - d. DH
- 2. Example of an immortal population
 - a. RIL
 - b. DH
 - c. Magic
 - d. all the above
- 3. NAM utilizes
 - a. historic derived LD
 - b. recombination derived LD
 - c. both a & b
 - d. None
- 4. If reciprocal differences are present, it is always advised to go for scheme for mixing in magic population
 - a. Single Funnel Crossing Scheme
 - b. Multiple Funnel Crossing Scheme
 - c. DH Production
 - d. RIL Scheme
- 5. Statement I: False positives in QTL detection is a disadvantage in GWAS Reason: Population structure in GWAS leads to false positives in QTL detection

Statement II: There is less chance of false positives in QTL detection in magic population

Reason: Population structure get destroyed in magic population due to random matings carried out in advanced intercrosses

a. Both statements and their reasons are correct

- b. Both statements and their reasons are wrong
- c. Both statements are correct but both reasons are wrong
- d. Both statements are wrong but both reasons are correct

Short Answer Questions

- 1. Differentiate types of founder parents in NAM? What is the basis of selection of these founder parents?
- 2. What are the different types of NAM populations and how they are developed?
- 3. How NAM utilizes different types of LD?
- 4. What are the advantages of magic population over biparental mapping populations and association mapping?
- 5. What are the applications of multi-parental mapping populations?
- 6. What are the steps involved in the development of magic population?
- 7. Why NAM population is called so?
- 8. What are the different approaches used in QTL analysis using NAM?
- 9. Describe the commonly used method of QTL mapping in MAGIC population?
- 10. Briefly describe the different mapping population used for QTL analysis
- 11. Compare the advantages and disadvantages of using NAM and MAGIC for QTL analysis