Review Article

ENCHANTING INSIGHTS AND EXPLORING THE RELEVANCE OF THE MAGIC POPULATION IN ADVANCING CEREAL CROP IMPROVEMENT

ABSTRACT

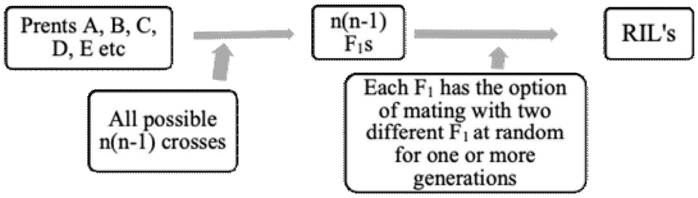
MAGIC populations are portrayed as inbred recombinant sets that were created by inter-crossing certain numerous parents. However it takes a lot of work to produce MAGIC populations but Its more effective approach for detecting QTL's (Quantitative Trait Loci) when we involves MAGIC populations. The availability of more genetic variety in the germplasms due to various founder lines is one of the main benefits of employing a MAGIC population. In order to identify QTL's for crop improvement under biotic and abiotic stress conditions, MAGIC populations were developed for the *indica* and *japonica* rice cultivars as well as MAGIC plus and Global MAGIC populations. Also the employment of MAGIC populations for the improvement of rice grain size also improves the yield and quality aspects of rice. Utilization of rice MAGIC plus populations for the improvement of nutrient profile of rice which is prime important in the biofortification program of rice as a goal of united nations. Where the utilization of association mapping and MAGIC populations in maize crop for improving saccharification efficiency results in higher biofuel production. Various institutes and universities are involved in production of MAGIC populations in respective specialised crops.

Keywords: *GWAS, MAGIC, MPP, NIL, QTL Mapping, RIL*

1. INTRODUCTION

RILs from complicated hybrid/outcross populations made up of various parental strains are known as Multiparent Advanced Generation Inter-cross Populations (MAGIC). A parent line can be an inbred line, a clone, or an individual selected for origin or use. MAGIC populations are an extension of the AIL proposed by Darvasi and Soller, 1995 AIL are created by randomly mating two inbred strains together for a number of generations. MAGIC populations are an extension of AIL, although they differ from AIL in that numerous parents were involved in their development. the name MAG This is done in order to create a complicated cross with several, usually eight, paternal lines and to separate RIL's from the cross. (Singh B.D., 2015)

Plant breeding is crucial to ensuring global food security. Broadening the genetic basis and improving genetic gain of commercially significant crops are vital to support the rising food demand (Ray *et al*. 2012; Zaw *et al*. 2019). Several founders are repeatedly inter-crossed (usually four, eight, or sixteen times) to create MAGIC populations, which are then selfed for subsequent generations to create recombinant inbred lineages (RILs). The gathering of genetic material and the insertion of several alleles in a precisely prescribed order enable this. This creates very varied genotypes for high-resolution mapping and contains uncommon alleles from each founder. (Cavanagh *et al*. 2013; Huang *et al*. 2015)



Picture 1: Three or more RILs, called MAGIC lines, isolated from each cross MAGIC lines from all the crosses together constitute the MAGIC population (Scarcelli *et al*., 2007)

MAGIC involves repeatedly mating several inbred ancestors, fusing the genetic makeup of all the ancestors into a single line. Four separate single crosses are created by crossing eight parental lines in pairs. To create two double crosses, these single crossings are crossed in pairs. Eight paternal complicated crossings are created once two double crosses are finally mated. In order to produce the necessary number of RILs, which together make up the MAGIC population, this complicated cross is processed in accordance with the SSD technique. RILs are a group of homozygous lines (with the same allele) created by mating two inbred strains repeatedly, either with siblings or with oneself, to form a new inbred line whose genome is a composite of its parents. (Huang *et al.,* 2011)

Having the capacity to construct experimental populations is a huge benefit for scientists studying plant and animal genetics. These populations enable investigations of the genome itself and its interactions with characteristics and the environment, as well as the inclusion of well-characterized founder genomes into controlled pedigrees. To find the parts of the genome that impact the characteristic, traditional experimental populations blend the genomes of two parents with divergent phenotypes. Due to the limited genetic diversity in each of these populations, only those genomic regions that differ between the two founders can be detected, and all alleles are highly prevalent in the population. As a result, each population only provides a partial picture of the factors influencing the trait. (Huang *et al.,* 2015)

An alternative to association mapping is sampling people at a distance to provide a panoramic view of the entire population. Thus, although it covers much more diversity, very large samples are required to have sufficient power to detect regions of interest in the genome, which can make it difficult to detect rare and important alleles. Due to the shortcomings of previous designs, a new class of complicated experimental designs has been developed that is, in terms of power, variety, and resolution, intermediate to biparental and association mapping designs. Prior to breeding inbred lines, multi-parent Advanced Generation Inter-Crosses (MAGIC) inter-mating multiple inbred founders results in a heterogeneous population whose genomes are fine-scale mosaics of contributions from all founders. Similar to biparental populations, which have fewer founders, this population has relatively high allele frequencies but substantially higher polymorphism variety. Although while a MAGIC population involves more initial effort and time than a biparental population, thorough founder selection allows for generalizability to a larger breeding population and assures that the population will be useful as a long-term genetic resource panel. (Huang *et al.,* 2015)

1.1 Quantitative Trait Loci (QTL) and QTL mapping

Quantitative trait locus commonly known as QTL, has been defined in various ways by different scientists. QTL may be defined as a region or locus on the chromosome containing alleles that differently affect the expression if quantitative trait (or) QTL is a region of DNA which is associated with the expression of quantitative trait. The characteristics of QTL includes:

1. QTL is polymorphic site (locus) on the chromosome which control the expression of quantitative trait.
2. The presence of QTL is acquired from genetic mapping.
3. Ten or more QTL can influence on single trait.
4. Variation in quantitative trait depends on the number of traits that are governing the trait.
5. Alleles controlling the expression of quantitative trait maybe present on one chromosome or different chromosomes.

QTL Mapping, also known as Gene Mapping, is a method for locating the genes in charge of a certain trait's expression. It refers to the location of the genes that are in charge of producing quantitative qualities. A sophisticated laboratory, skilled personnel, mapping populations (F_2, Backcross populations, Double Haploids), molecular markers (RFLP, AFLP, SSR, SNP, CAPS), and mapping methodologies are required for QTL mapping (single marker regression, simple interval mapping, composite interval mapping, multiple interval mapping, Bayesian interval mapping). (Singh P., 2015)

1.2 Multi-parent populations (MPPs)

Biparental populations resulting from crossing two inbred lines have been the standard design for crop genetic mapping. Two-parent populations have three main advantages.

- Relatively easy to configure. F2 populations (F1 self-pollination/international hybrids) require only two generations, and approximately six generations of inbreeding are required in self-pollinated species to create a genome-fixed recombinant inbred line (RIL).
- High ability to detect QTL because all allele frequencies are generally close to the optimal value of 50%. Low resolution of non-equilibrium linkages within chromosomes.

Per chromosomal arm, there are often just one or two recombinants (RIL inbreeding adds only about one observable recombinant per arm). In other words, QTL mapping only needs a small number of genotypic markers. However, the bi-parent population has two major drawbacks. Low genetic diversity due to poor mapping accuracy due to the limited efficient recombination that occurs during population development and a genetic bottleneck caused by the selection of two founders. This can limit the number of QTL captured. This is because no more than two alleles segregate at a single locus. Consequently, two-generation experimental mapping populations were developed about 10 years ago to address these issues, initially using additional breeding generations from both parents, but eventually mating multiple parents. (Arrones, *et al.,* 2020)

The Advanced Inter-Cross (AIC) design was the first to take into account the restricted genetic recombination in biparental populations. Nested Association Mapping (NAM) and Multi-Parent Advanced Generation Inter-Cross (MAGIC) populations are now the two most used MPP techniques for plants. A repeated founder line and a number of alternate founders are crossed repeatedly to create the NAM population. An improved interparental line (AIL) is a fixed population that serves as a permanent resource generated by MAGIC and is similar to a recombinant inbreeding (RI) population obtained from a two-parent cross. AILs are generated by random and sequential breeding of populations originally derived from the cross of two inbred lines. (Darvasi and Soller, 1995)

A repeated founder line and a number of alternate founders are crossed repeatedly to create the NAM population. A NAM can be viewed as a collection of adoptive parent cohorts connected by a common adoptive parent. As a result, they make sense conceptually to those who are used to working with populations who have two parents. Increased genetic recombination is essentially only recorded by an increase in the number of lines tested, as is the case in a two-parent population, whereas NAM catches more genetic diversity. The design of MAGIC, however, is more intricate. In some aspects, MAGIC is an extension of AIC, but before self-pollination to produce an inbred line, they were crossed for a few of generations. MAGIC populations often result from a basic funnel breeding process with 4, 8, or 16 parents. (Fig. 1) (Scott, *et.al*., 2020)

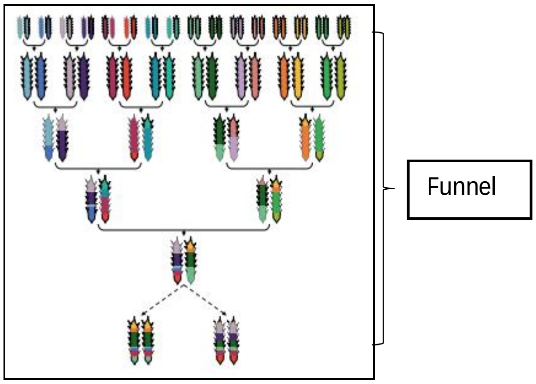


Figure 1: Funnel

(Source: Scott, *et al*., 2020)

1.3 Recombinant Inbred Lines (RIL)

Recombinant inbred lines are inbred lines that result from a cross between two pure inbred lines or inbred lines. By continuously self-pollinating F_2 individuals, RILs are produced. For creating recombinant inbred lines, the single seed descent (SSD) approach is typically utilised. RILs primary characteristics are: RIL's are created by repeatedly self-pollinating F_2 individuals. Single seed descent, pedigree, and backcross procedures are also employed to create RIL's. Since RIL's mix alleles from two distinct inbreds or pure lines, they are known as recombinant inbred lines. The homozygosity is achieved by selling repeatedly over multiple generations. RIL's are utilised for mapping important genes and QTL's, as well as for creating genetic or linkage maps. Whole sib-crosses can be used to create recombinant inbred lines when self-pollination is not possible. (Singh P., 2014)

Depending on the design, prolonged crossovers can be used to build up more extended crossover occurrences to boost mapping resolution. To develop recombinant lines that are genetically stable, lines are finally inbred. (Pollard, 2012)

1.4 Near Isogenic Lines (NIL)

Lines with single locus difference arc referred to isogenic lines or isolines. Near isogonic lines refer to a group of lines which are genetically identical except at one or few loci. The development of NIL's consists of following main steps are;

- The donor and recurrent parents arc crossed and the trait is selected for in F_1 if it is dominant.
- If the trait is recessive, the F_1 is selfed and the trait is selected in F_2 generation where it segregates.
- The selected F_1 plants (dominant) or F_2 plants (recessive) arc backcrossed to recurrent parent.
- Progeny with trait of interest are again selected and these selected plants back-crossed to recurrent parent.
- The backcrossing is repeated for 7 or 8 times.
- The result are NIL's which are identical to recurrent parent at all loci except for one or few loci or except for the region surrounding the gene under selection. (Singh P., 2014)

1.5 Doubled Haploids (DH)

Doubled haploids are individuals or plants which are produced from haploids through chromosome doubling. The colchicine is used for doubling of chromosomes. Thus doubled haploids have two sets of chromosomes identical to the haploid plant. The main features of doubled haploids are given below:

- Doubled haploids are useful in gene mapping or constructing genetic maps.
- Doubled haploids are used for rapid development of pure lines and fixation of heterosis.
- Doubled haploids are useful in the identification of mutant alleles in a population.
- Doubled haploids are produced from haploids.
- Doubled haploids have two identical sets of haploid parent line. (Singh P., 2014)

1.6 Objectives of MAGIC Populations

The Advanced Generation Interparental Crossing (MAGIC) technique with multiple parents has been developed to study numerous alleles and give enhanced recombination resolution and mapping. Facilitating mating and genomic shuffle is a key objective of MAGIC population growth. The following advantages are provided by several parent groups:

a) Based on the choice of parents utilised to create the multi-parent crosses, more specific features from each of the parents may be examined.

b) Greater levels of recombination result in improved accuracy and resolution for QTL detection. (Cavanagh *et al.* 2008)

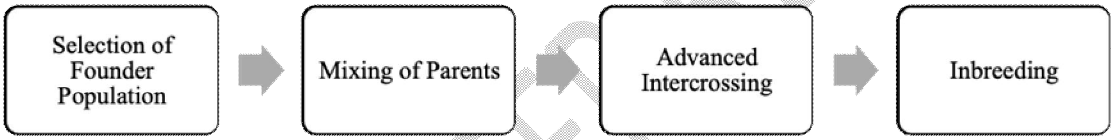
More genetic variety in the germplasm due to several founder strains is one of the main benefits of employing multiparent populations. The population's variety of allelic and cytoplasmic connections increases with the number of basal lineages. As a result, multiparent populations with more intricate allelic recombination are produced, which may be employed for both fundamental and practical plant research. (Rakshit *et al*. 2012)

1.7 Next-generation sequencing technology for MAGIC populations

Agricultural genetics has advanced far more quickly after Sanger sequencing gave way to the advent of next-generation sequencing technology. To date, genome-wide association analyses (GWAS) and QTL mapping have been used to identify informative alleles. The assembly of freshly created reference genomes of all founder lineages is made easier in MAGIC populations because to the use of next-generation sequencing (NGS) technology. Assays for sequencing and bioinformatics that enable the production of genomic assemblies will be made easier as a result. (Mascher *et al*. 2017)

2 Steps for the Development of MAGIC Population

For the production of MAGIC populations there are four main steps: they are



- **a) Selection of Founder Population:** Building of founder populations is the primary step in creating magic population as the required gene pool is carefully selected from the available. The source of founder population includes use of land races. The basis for the creating founder population is by genetic diversity, phenotypic diversity, and geographical diversity.
- **b) Mixing of Parents:** Multiple parents that selected are intercrossed with each other to form broad genetic base. Mixing of parents together in pre-defined manner and then intermated. These innate founders, who mate and interbreed, are called funnels. Result of this step is set of lines whose genomes comprised contributed from each founder.
- **c) Advanced Intercrossing:** Lines that are produced by this crossing are called Advanced Intercross Lines (AIL). it was first proposed by Darvasi and Soller in 1995. Advanced intercrossing is crossing between two inbred lines. Each generation is mated sequentially and randomly. Selection is phenotypic for further reduction in the frequency of deleterious alleles from donor. Mixing lines from different funnels intersect randomly and sequentially, as in an extension cross. The main goal is to get the increased number of recombinants in a population.
- **d) Inbreeding:** The development of homozygous individuals. Self-pollination of individuals directly in the funnel or after extended mating with the formation of inbred lines. Recombinant Inbred Lines (RIL's) in plants can be created by Single Seed Descent (SSD) or Double Haploid (DH). The multiple generations of selfing also introduces additional recombination. (Arrones, *et al.,* 2020)

3. Application of MAGIC Populations

3.1 Rice

Bandillo *et al*., 2013 established the Multi-parent Advanced Generation Inter-Cross populations (MAGIC) in rice and talks about possible uses for mapping quantitative trait loci (QTLs) and for rice varietal development. With 1328 single seed origin (SSD) strains, the *Indica* MAGIC population is the most developed MAGIC population to date. A subset of this population (200 lines) was genotyped at the S4 SSD stage using genotyping by sequencing techniques and assessed for a variety of phenotypes, including crop traits, salinity and flood tolerance, blast and fire blight resistance, and other features. For each quality, a phenotype was assigned. A number of well-known important genes and QTL's were discovered using genome-wide association mapping, including Sub1 related with waterlogging tolerance and *Xa*4 and *Xa*5 connected with fire blight resistance. Also, the results of the genome-wide association study (GWAS) revealed possibly new loci linked to crucial features for rice enhancement. (Fig. 2)

It was intended to develop at least 2,000 inbred lines by inter-crossing of 8 *indica* parents for the *indica* MAGIC population and 8 *japonica* parents for the japonica MAGIC population in order to capture the greatest genotypic diversity. As the experiment advanced, an *indica* population known as the MAGIC plus population was created. This population underwent two more cycles of inter-crossing to increase recombination. To improve total variety, they finally crossed the *indica* and *japonica* basis populations. Because to its inclusion of the internationally produced indica and japonica rice ecotypes, this population was given the name "global MAGIC" population. (Bandillo *et al*., 2013)

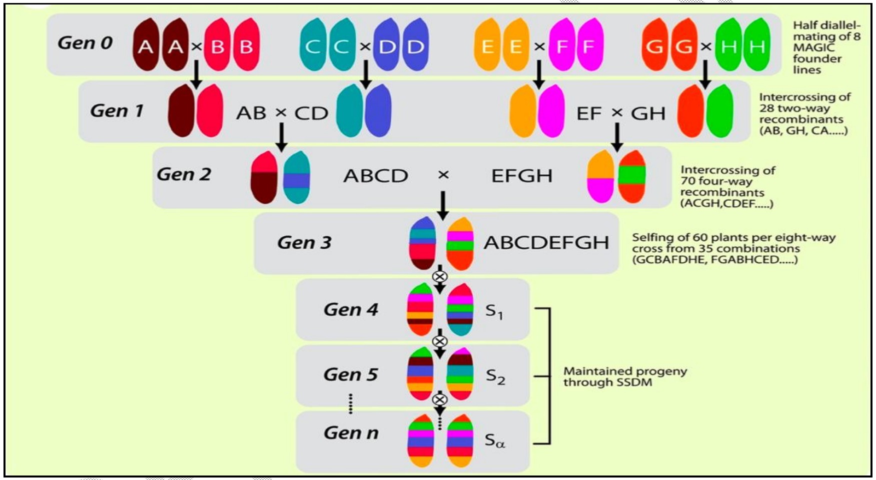


Figure 2: Development of the *indica* MAGIC population and the same scheme was used to develop the *japonica* MAGIC population (Source: Bandillo *et al*., 2013)

The *Indica* MAGIC population consists of 2000 lines developed by Single Seed Origin (SSD), of which 1328 are now S7 and the remaining lines follow as they mature later. In comparison to the indica MAGIC population, the japonica MAGIC population is modest and only has 500 lineages at the S5 stage. The strain will initially undergo a productivity test in Korea and will be appropriate for temperate areas. Because to additional crossover cycles, the MAGIC plus population is presently at stage S4 and may be more useful. Comparing this population to the indica MAGIC population, more recombination is anticipated. The question of whether the additional two rounds of inter-crossing boosted recombination levels sufficiently to permit direct fine-mapping of QTLs using the MAGIC population is one that will hopefully be addressed. Global MAGIC is an effort to integrate the traits of gene pools from Japan and India that have adapted to various conditions. The 16 genomes that make up the global MAGIC population not only offer a potential source of new variation, but they also offer important data for examining the relative contributions of the two rice ecotypes and the degree of recombination. (Fig. 3) (Bandillo *et al*., 2013)

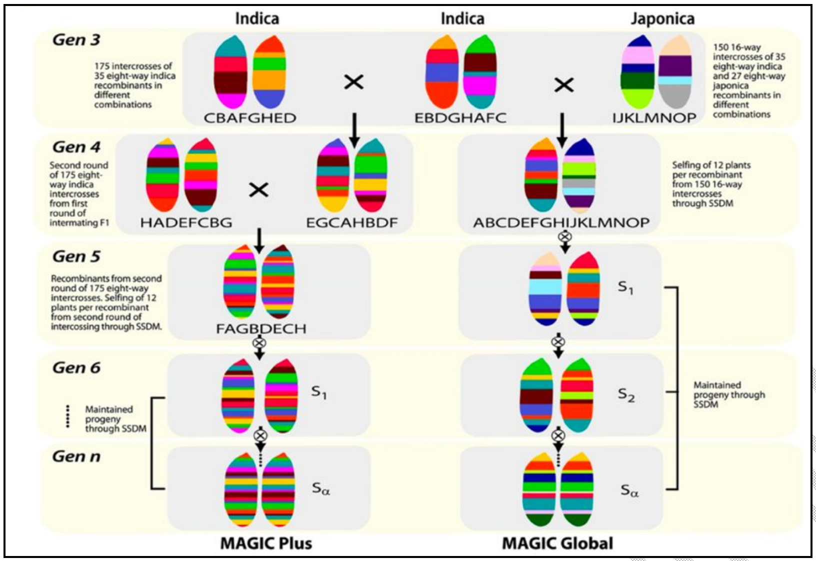
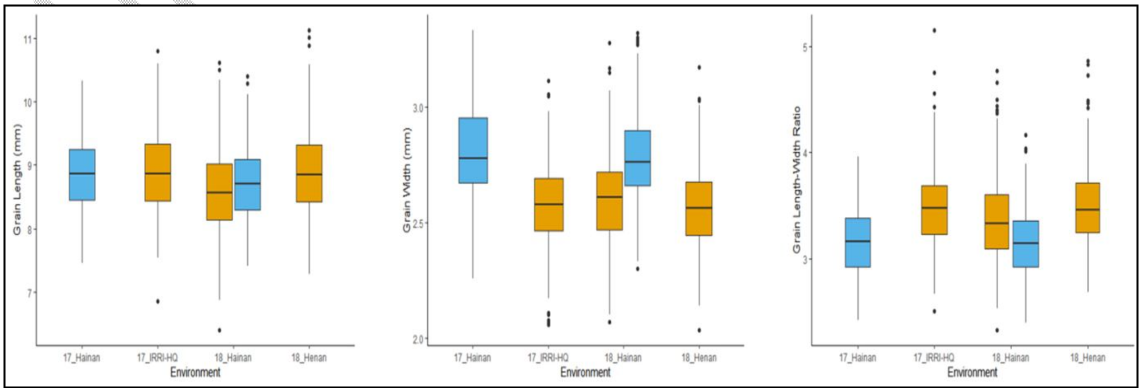


Figure 3: MAGIC Plus and Global MAGIC Population Development. (Source: Bandillo *et al.*, 2013)*[Where A, B, C, D, E, F, G, and H represent the eight index parents. I, J, K, L, M, N, O and P represent the 8 parents of japonica ; SSDM—single-seed descent; S—self-pollination.]*

In MAGIC rice populations with more than 1316 RIL's, the matching interval averaged ~700 kb. (Raghavan *et al*. 2017). The foundation of a rice MAGIC population made up of founders with varying levels of resistance to temperature stressors also relies on multi-environment experiment analysis. (Leung *et al*. 2015). Li *et al.* (2013, 2014) report that new varieties of rice bred using RILs from MAGIC populations have been introduced in China. The MAGIC RIL, IR 95099:7-B-2-10-10-2, is slated for release as a varietal in southern Vietnam based on its maturation date, yield, and grain quality. Other rice MAGIC populations created at the International Rice Research Institute (IRRI) have also been employed, which were assessed in trials at the "Cuu Long Delta Rice Research Institute", Cần Thơ, Vietnam. (Scott, *et al*., 2020)

Ponce *et al*., 2020 Considering that one of the important agronomic qualities resulting from unintentional selection pressure during rice production is grain size. Unintentional selection for seeds that could survive even with deeper soil cultivation led to an increase in grain size as an early adaptive response to rice farming. (Purugganan and Fuller, 2009)

Grain size is one of the main agronomic traits produced by accidental selection pressure during rice cultivation. Rice developed an early adaptive response that resulted in bigger grain size due to unintentional selection for seeds that could endure even with deeper soil tillage. (Fig. 4) (Ponce *et al*., 2020)



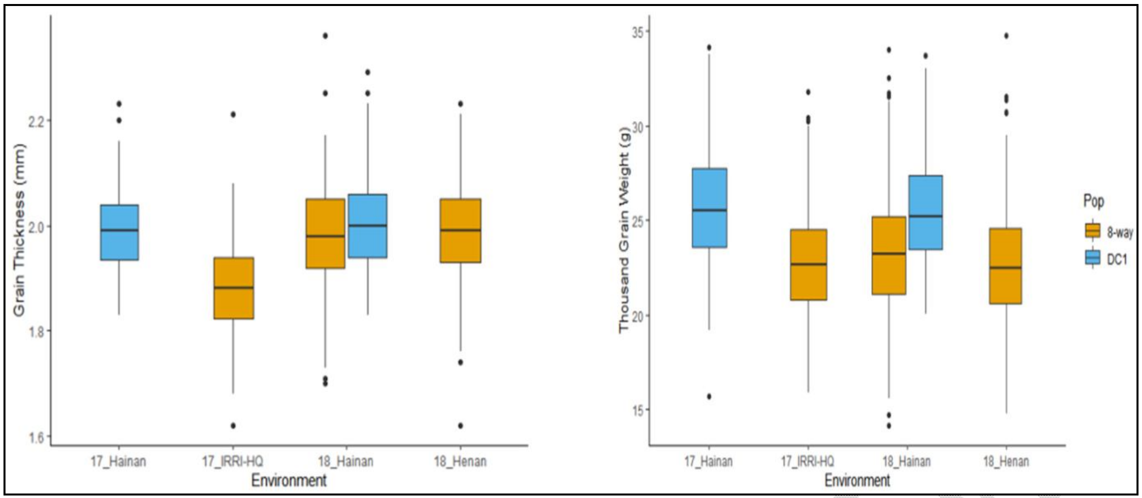
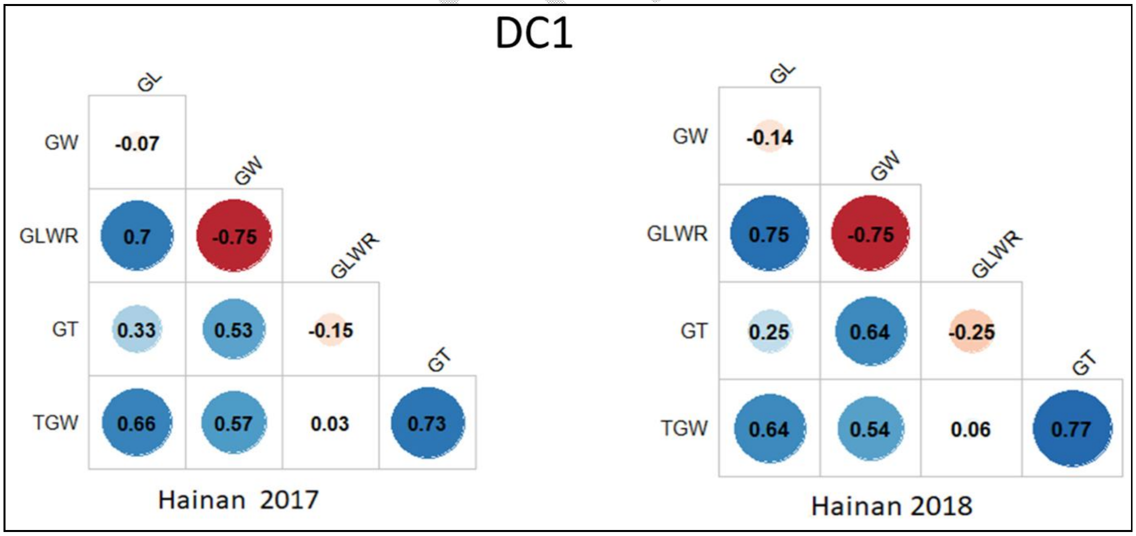


Figure 4 : Boxplots of five particle size related characteristics of MAGIC populations in different environments. (Source: Ponce *et al*., 2020)

The associations between TGW and GL, GW and GT in both groups were favourable throughout a range of contexts, from mild (0.39) to strong (0.80). For DC1 in Hainan in 2017, GT was inversely linked with GLWR, and for BIM in Hainan in 2018, correlations ranged from -0.15 to -0.29. In contrast, both in community settings and in other situations, the correlations between GT, GL, and GW were weak to moderately favourable (Fig. 4). With values ranging from 0.70 to 0.75, the correlation between GLWR and GL was consistently strong throughout all trials. For GLWR and GW, there was a high negative correlation (-0.75) identified in the Hainan 2017 and Hainan 2018 trials, while for BIM, there was a moderate (-0.49) to strong (-0.71) association reported in the Hainan 2018 and IRRI 2017 trials, respectively. (Figure 5) (Ponce et.al., 2020)


DC1

	GL	GW	GLWR	GT
GW	-0.07			
GLWR	0.7	-0.75		
GT	0.33	0.53	-0.15	
TGW	0.66	0.57	0.03	0.73

Hainan 2017

	GL	GW	GLWR	GT
GW	-0.14			
GLWR	0.75	-0.75		
GT	0.25	0.64	-0.25	
TGW	0.64	0.54	0.06	0.77

Hainan 2018

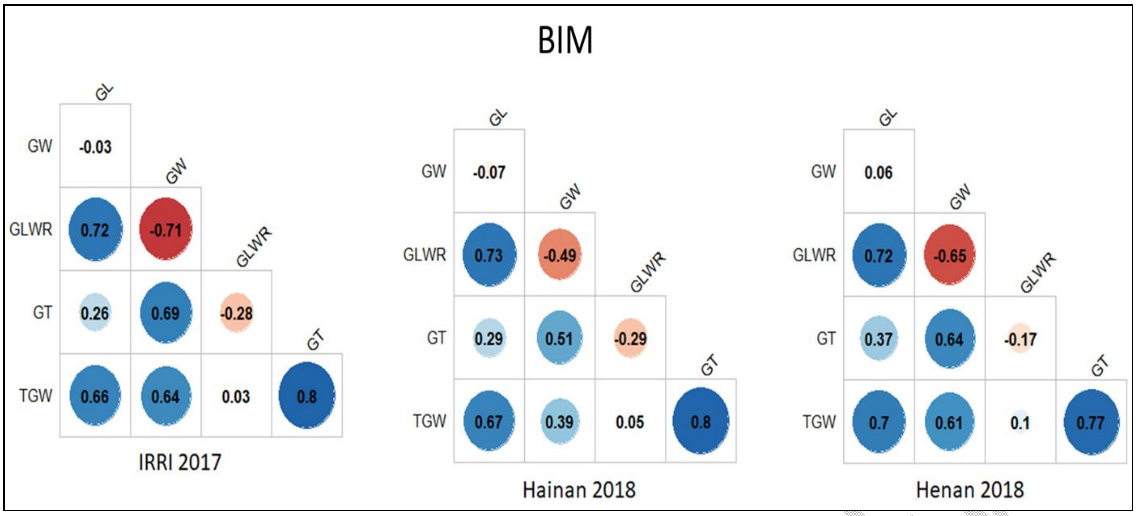


Figure 5: Property correlations for five particle size-related properties in DC1 and BIM populations tested in different environments. (Source: Ponce *et al*., 2020)

In recent years, several genes associated to grain size have been discovered and cloned; nevertheless, the molecular functions of these genes and how they interact with other signalling pathways continue to baffle researchers. The current work provided more insight into the genetic structure of rice grain size based on MAGIC populations evaluated in three environments. Since grain length-associated tendencies exhibit phenotypic plasticity, it is essential to identify QTLs with genetic historical independence and environmental stability. The impact of these genes and their practical variants may be verified using techniques like gene editing and transferred DNA insertion mutant monitoring. Furthermore, it should be noted that populations resulting from multi-parental crosses have a wider range of phenotypic and allelic traits than traditional biparental populations and experience fewer confounding effects in terms of population structure and genetic relatedness than natural populations. The results of the study demonstrate that the BIM population was typically superior to the DC1 population. (Ponce *et al*., 2020)

Descalsota *et al*., 2018 concluded that Over 2 billion individuals experience micronutrient deficiencies, particularly children and pregnant and lactating mothers. Recently, the United Nations (UN) declared that one of the Sustainable Development Goals to be accomplished by 2035 is treating micronutrient deficiencies. Many organisations throughout the world have made significant efforts to treat micronutrient deficiencies through fortification, biofortification, and preventative supplementation (Dalmiya and Schultink, 2003). The most crucial micronutrients for human nutrition and health are iron (Fe) and zinc (Zn). Zn is a crucial cofactor for a number of crucial enzymes involved in metabolic processes. (Frassinetti *et al*., 2006; Roohani *et al*., 2013; Sadeghzadeh, 2013)

By using conventional breeding techniques, several high-Zn rice varieties have been successfully created and released for cultivation; however, this process is slow because high grain Zn has a complex genetic makeup, there aren't any field-based phenotyping tools or tightly linked markers, and there are significant genotype and environmental interactions (Gande *et al*., 2014; Zhang *et al*., 2014). In order to generate superior rice varieties acceptable for farmers, it will be helpful to accurately stack many genes and QTLs by understanding the molecular basis of all these complicated features. To map the QTL/genes of different phenotypes in rice, genome-wide association studies (GWAS) and biparental mapping were also used (Collard and Mackill, 2008; Norton *et al.*, 2014; Zhang *et al*., 2014; Nawaz *et al*., 2015). For Fe, Zn, and other mineral element particles, GWAS was able to pinpoint QTLs. (Norton *et al*., 2010).

Multiparent admixture populations of advanced generation inter-cross (MAGIC) have gained popularity as a genetic resource recently for mapping and creating breeding lines with a variety of desirable features (Kover *et al*., 2009; Bandillo *et al*., 2013; Meng, *et al*., 2016). The MAGIC population lacks any discernible population structure and has a rather wide genetic background, which poses a serious obstacle to linkage mapping with diversity panels. Higher degrees of recombination have led to improved levels of mapping resolution in enhanced MAGIC Plus populations with intermediate interactions of extra generations. In order to facilitate high-resolution QTL analysis and gene identification for both basic and complicated trait mapping, MAGIC Plus rice lines can be a potent genetic resource. (Bandillo *et al*., 2013).

In the study, loci for disease resistance, grain micronutrients (Fe and Zn), yield, and characteristics associated with yield were mapped using the MAGIC Plus population created at IRRI. Initially, the goal was

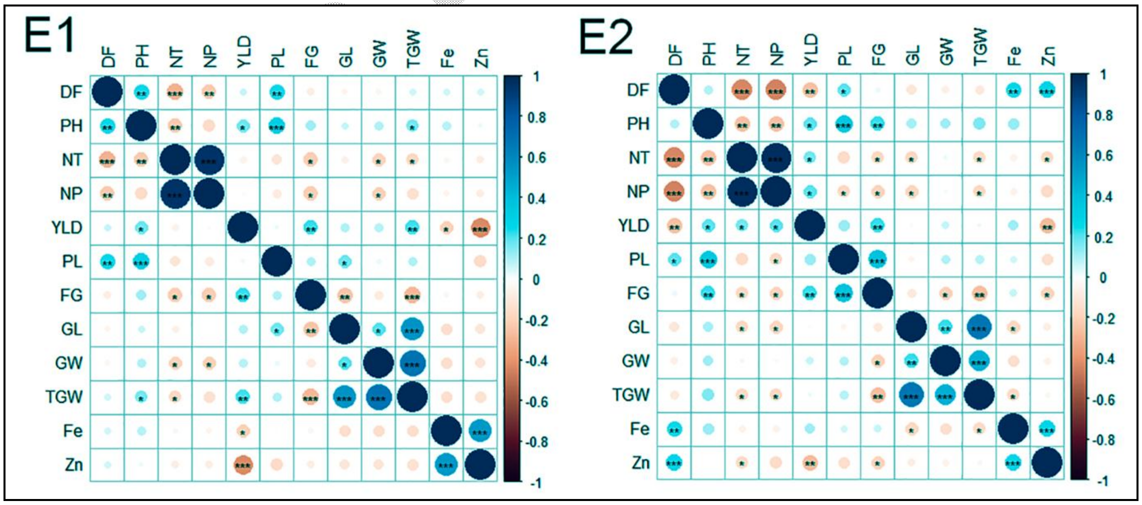
(a) To assess the usefulness of the MAGIC Plus population for the identification of QTLs associated with significant agronomic, biofortification, and disease resistance attributes.

(b) Identifies the MAGIC Plus line as having both strong agronomic characteristics and high grain zinc content.

(c) Identifies QTL and SNP markers that may be integrated into breeding for bio enhancement and disease resistance.

(d) Identifies potential genes linked to significant quantitative trait loci (QTL) for disease resistance, bio-enhancement characteristics, and agronomic features. (Descalsota *et al*., 2018)

In two locations, the Robert Zeigler test station of the International Rice Research Institute (IRRI), Los Baños (LB), Laguna, and the Philippine Rice Research Institute (PhilRice), Munoz (MU), Nueva Ecija, the MAGIC Plus line was assessed throughout the 2015 dry season (DS) and 2015 wet season (WS). The LB exam featured all 144 things, but the MU test only included 142 items. These four settings were given the designations E1 (LB-DS), E2 (LB-WS), E3 (MU-DS), and E4 (MU-WS). (Descalsota *et al*., 2018).



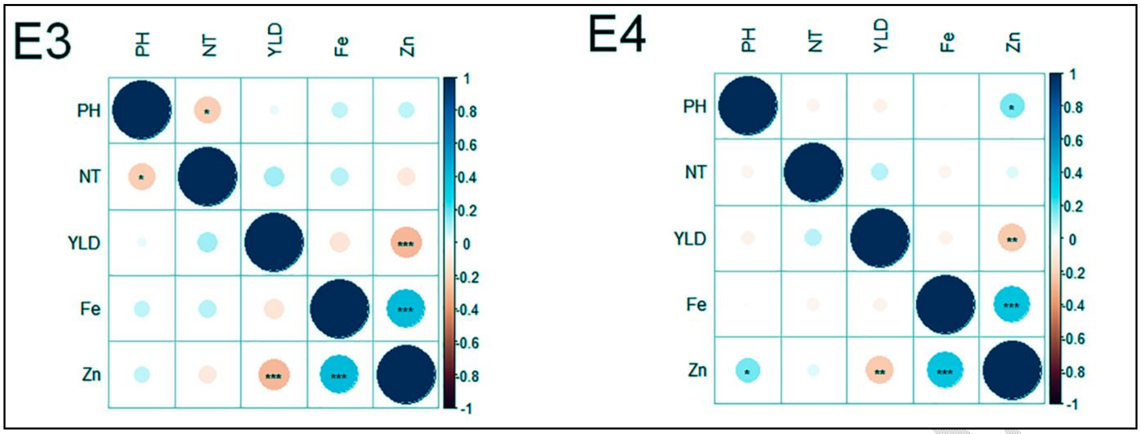


Figure 6: Correlation between agronomic and biofortification properties of the MAGIC Plus population was evaluated in four media. (Source: Descalsota *et al.*, 2018)

Where DF, days to 50% flowering; PH, plant height (cm); NT, number of tillers; NP, number of panicles; PL, panicle length (cm); GL, grain length (mm); GW, grain width (mm); FG, number of filled grains; TGW, thousand grain weight (g); YLD, grain yield (Kg/ha); Fe, iron (ppm); Zn, zinc (ppm); E, denotes environments in which MAGIC Plus population was evaluated; E1: IRRI, LosBanos, Laguna during 2015 DS; E2: IRRI, Los Banos, Laguna during 2015 WS; E3:Phil Rice, Munoz, Nueva Ecija during 2015 DS; E4: Phil Rice, Munoz, Nueva Ecija during 2015WS; The test of significance were indicated as ∗∗∗p < 0.001, ∗∗p < 0.01, ∗p < 0.05. The blue color shows the positive association and red colour indicates the negative association and the intensity of the colour indicates degree of association. (Descalsota *et al*., 2018)

A total of 14,242 SNP markers, with an average density of 30.1 kb, were employed for population structure analysis according to the genetic analysis of the MAGIC Plus population. The findings showed that there was no substantial population structure, with the variance of log probability increasing from K = 1 to K = 10 and the greatest 1K of just 70.3 being recorded at K = 2 (Figure 5). The findings of association studies using kinship, with and without each person's involvement in a cluster, that were compared.

Table 1: Linkage Disequilibrium in the MAGIC Plus Population

Distance (kb)	r^2 ($p < 0.05$)	Significant LD pairs	Marker pairs in complete LD	Marker pairs in complete LD (%)
0–5	0.796	12,440	8,153	65.54
>5–100	0.619	65,140	23,507	36.09
>100–250	0.506	84,254	15,808	18.76
>250–500	0.421	120,362	12,390	10.29
>500–750	0.350	108,080	6,011	5.56
>750–1000	0.318	95,907	3,138	3.27
>1000–1500	0.280	164,489	4,970	3.02
>1500–2000	0.230	141,971	2,601	1.83
>2000–2500	0.200	115,415	1,488	1.29
>2500–5000	0.167	393,990	3,476	0.88
>5000–7500	0.133	232,003	233	0.10
>7500	0.075	623,818	7	0.00

Total		**2,157,869**	**81,782**	
LD- linkage disequilibrium; kb- kilo bases; r^2 - Co-efficient of determination.				

(Source: Descalsota *et al.,* 2018)

In the linkage disequilibrium (LD) analysis performed on the MAGIC Plus population, only 2,157,869 (21.29%) of 9,843,868 marker pairs showed significant ($P < 0.05$) LD. Changes in the r^2 values of significant intrachromosomal marker pairs were observed in groups with different physical distances (Table 1). Average LD was high ($r^2 = 0.796$) dropped to 50% around 400 kb over short distances (<5 kb). Fading was robust but still showed significant residual LD ($r^2>0.2$) at 2.0 Mb. A high proportion of marker pairs in overall LD could be observed in the short-distance group, whereas in overall LD, marker pairs in the long-distance group (>7.5MB) (Descalsota *et al.*, 2018).

Ogawa, *et al*., 2021 Assuming that the initial MAGIC population was created from Arabidopsis accession 19 and examined at the founder haplotype level (Kover *et al*., 2009). Four japonica and four indica cultivars with high grain yield and biomass in Japan were used to create the Japan-MAGIC (JAM) rice population, and the genomic proportions of the eight founders were similar in all lines. The JAM population has a wider range of phenotypes than a set of four biparental RILs made up of the same number of mothers and fathers (8). In the individual JAM traces, information on more than 10,000 single-nucleotide polymorphisms have already been collected and converted into haplotype records. The evaluation of haplotype findings on relevant symptoms and genome-wide affiliation study (GWAS) are hence appropriate uses for the JAM traces. These traces were used for further genetic analysis and high-throughput phenotyping. (Ogawa, *et al*., 2018a, Ogawa, *et al*., 2018b).

The 165 JAM lines' haplotypes were compared to those in the Arabidopsis MAGIC population. (Kover *et al*., 2009), from genotyping-by-sequencing analysis of the 13 603 SNPs and the sequencing data of the eight founders. Shoot biomass in JAM lines is associated with VF during the vegetative stage. The low correlations, however, suggest that VF reflects more than just biomass. On this issue, it is thought that the haplotype technique was successful in determining the correlations for the four typical VF QTLs. The outcome suggests that VF affects shoot biomass at the QTL level. Shoot biomass was a weaker trait than VF, and the four VF QTLs were repeatable, making VF an ideal candidate for DNA marker-assisted breeding. VF is a useful and efficient trait for high-throughput phenotyping in the field for breeding, according to the data. (Ogawa, *et al*., 2021)

3.2 MAIZE

López-Malvar, *et al.,* 2021 Maize has been proposed as a model for comprehending the complicated cell wall architecture and to enhance crop breeding techniques in bioenergy grasses due to its potential to produce a significant source of lignocellulosic biomass. The greatest readily accessible lignocellulosic feedstock is maize stover, the leftover grain after harvesting. (Vermerris, *et al*. 2007, Dhugga, 2007). Maize stover is a source of lignocellulosic biomass, which is made up of 14.9% lignin, 33.1% hemicellulose, and 39.4% cellulose. 2008; Pauly et al. The process of turning lignocellulosic biomass into ethanol involves three steps.:

I. Pre-treatment step
II. Saccharification, the hydrolytic breakdown of carbohydrates into their individual sugar monomers, and
III. Free sugars are finally fermented into ethanol. (Mosier, *et al*., 2005)

After a dilute acid/hot pre-treatment, sugar release was measured in the research by Lorenzana *et al.* (2010). The semi-cellulose part of the biomass is hydrolyzed using strong acids in this approach, which leads to more effective enzymatic hydrolysis. (Marcotullio *et al*., 2010), While in the Penning et al. (2014) investigation, samples were heated to 180 °C and then exposed to a steam explosion.

The MAGIC population was created from eight inbred lines of temperate maize with various genetic backgrounds, and the eight founders all lack hard stem material in their lineages. Because breeders should expect new inbred lines from this MAGIC population to exhibit significant heterosis when mated to inbred lines from the heterozygous Stiff Stalk group, these lines may be of practical relevance to breeders. (Butrón, *et al.,* 2019)

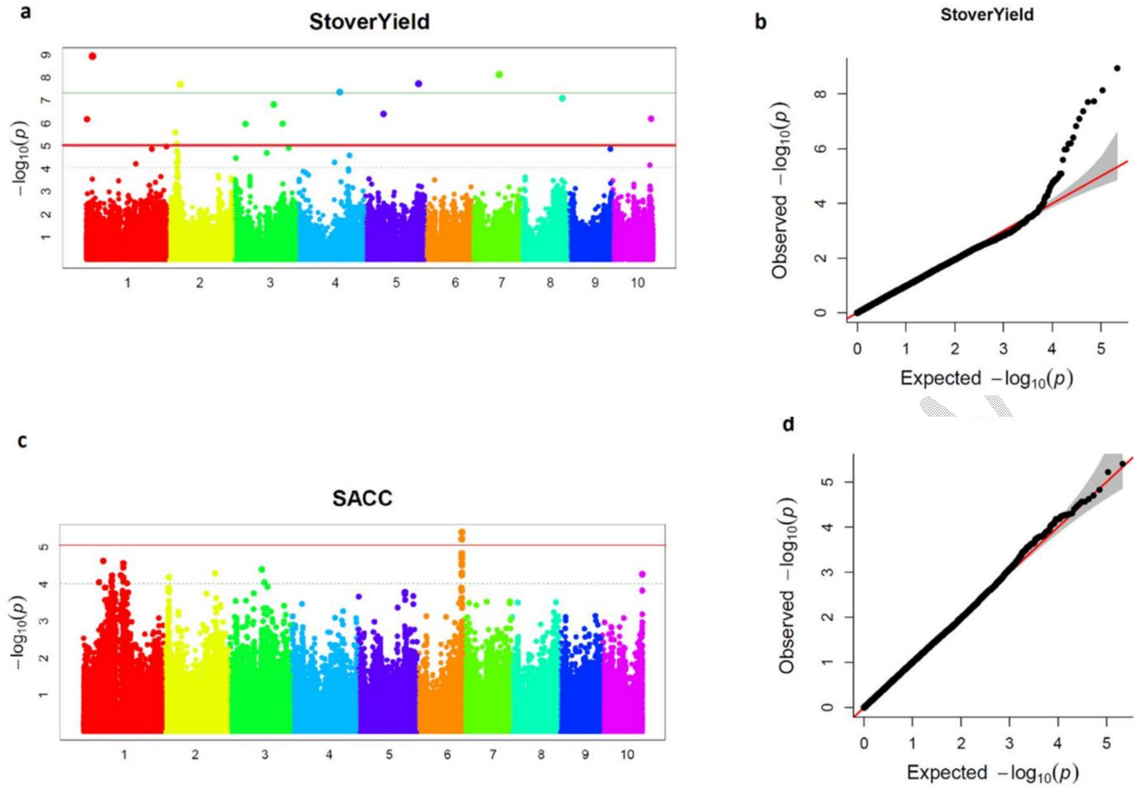


Figure 7: GWAS analysis of saccharification efficiency and stover yield in a maize MAGIC population (López-Malvar, *et al.,* 2021)

Where the picture 'a' shows Manhattan plot of Stover Yield using GWAS mixed linear model. Single-nucleotide polymorphisms (SNPs) above the horizontal red line exceeded the Bonferroni's modification approach's p value criteria. Picture 'b' (graphical representation) shows Quantile–quantile (represented as Q-Q) plot of stover yield using mixed linear model of GWAS. Picture 'c' shows the Manhattan plot of saccharification efficiency (SACC) for the GWAS mixed linear model. The p value threshold achieved using the modified Bonferroni technique was exceeded by single-nucleotide polymorphisms (SNPs) above the red horizontal line. Thereby picture 'd' shows Q-Q plot of SACC using GWAS mixed linear model. (Fig. 7) (López-Malvar, *et al*., 2021)

Eight founders and a selection of 408 RILs from the MAGIC population were assessed for stover production and the efficacy of saccharifying maize stover following an alkaline pre-treatment. The analyses of variance revealed that while variations between founder inbreds were not significant for saccharification efficiency, they were for stover yield. Agronomic data also revealed substantial differences between founders and RILs for plant height, days to silking, and anthesis. In this MAGIC population, association mapping enables us to identify genetic areas that are directly connected to variables that affect the end usage of maize. The development of plant materials for increased biofuel yields will be aided by genomic or phenotypic selection in conjunction with marker selection employing markers situated in these locations. The feasibility of second-generation biofuels can be improved by optimization, according to this study. (López-Malvar, *et al.,* 2021)

Jiménez-Galindo *et al*. 2019 given that In light of the fact that corn borers are a significant global pest of maize; in particular, *Sesamia nonagrioides* Lefèbvre, often known as the Mediterranean corn borer (MCB), causes significant losses in Southern Europe. To boost the effectiveness and longevity of the resistance against corn borers, transgenic techniques can be used with selection techniques. Biparental populations with limited resolution or association inbred panels with low power to detect uncommon variants were used in earlier investigations of the genetic variables influencing

MCB resistance. It has created a Multi-parent Advanced Generation Inter-crosses (MAGIC) population to study the genetic factors influencing MCB resistance in great detail.

Several low impact single nucleotide polymorphisms (SNPs) were found to be connected to MCB resistance to stalk tunnelling. In three smaller sections (at 150, 155, and 165 Mb in chromosome 6) that closely overlap with regions linked to cell wall composition, we divided a broad region related to stalk tunnelling in many investigations. Despite the poor co-localization of important areas amongst characteristics, we also found regions linked to agronomic and kernel resistance traits. This suggests that simultaneous enhancement of resistance and agronomic qualities may be achievable. Therefore The growing mapping population enabled a more detailed analysis of the genetics underlying maize resistance to corn borers and the reliable identification of candidate genes based on functional data. (Jiménez-Galindo, *et al.,* 2019)

4. Institutes Involved in Magic Population Development

1. Bread wheat- National Institute for Applied Botany (NIAB), Cambridge, United Kingdom (U.K.)
2. Durum wheat- University of Bologna, Italy.
3. Rice- International Rice Research Institute, Philippines.
4. Oats- Institute of Biological, Environmental and Rural Sciences, U.K.
5. Sorghum- ICRISAT, Hyderabad, India.
6. Cowpea- IITA, Nigeria.

5. CONCLUSION

The MAGIC population is described as a set of recombinant inbreds resulting from crossing several selected parents. The production of MAGIC populations requires considerable effort. The MAGIC population is a powerful tool for detecting quantitative trait loci (QTLs). A major advantage of using MAGIC populations is that greater genetic diversity exists in the germplasm due to different founder lineages. Develop MAGIC plus and Global MAGIC populations of indica and japonica rice cultivars using MAGIC populations to perform QTL mapping to improve yield under biotic and abiotic stresses. In addition, improving rice grain size using the MAGIC population also improves rice yield and quality aspects. The use of MAGIC plus rice populations to improve the nutritional profile of the most important rice in the rice biofortification program, a goal of the United Nations. Using MAGIC association and population mapping in maize crops to improve saccharification efficiency increases biofuel production. Various institutions and universities are involved in producing MAGIC populations for each specialized crop.

6. FUTURE PROSPECTS OF MAGIC POPULATION IN PLANT BREEDING

The future prospects of MAGIC are promising. MAGIC has the potential to generate a diverse population of recombinant inbred lines that capture a large amount of genetic variation from the parental strains, which can be used for genetic mapping and crop improvement. As genomic technologies continue to advance, the ability to identify and characterize genetic variation within MAGIC populations will improve, allowing for more accurate trait mapping and prediction. Furthermore, as we continue to face environmental challenges such as climate change and increasing food demand, the need for crops with improved yield, disease resistance, and stress tolerance will increase, and MAGIC can play a significant role in generating new crop varieties with more economical traits maintaining efficiency in resource utilization.

REFERENCE

1. Arrones, A., Vilanova, S., Plazas, M., Mangino, G., Pascual, L., Díez, M. J., Gramazio, P. (2020). The dawn of the age of multi-parent MAGIC populations in plant breeding: novel powerful next-generation resources for genetic analysis and selection of recombinant elite material. *Biology,* **9(8)***,* 229.
2. Bandillo, N., Raghavan, C., Muyco, P. A., Sevilla, M. A., Lobina, I. T., Dilla-Ermita, C. J., 2013. Multi-parent advanced generation inter-cross (MAGIC) populations in rice: progress and potential for genetics research and breeding. *Rice* **6***:*11.
3. Butrón, A., Santiago, R., Cao, A., Samayoa, L. F., Malvar, R. A. (2019). QTLs for resistance to fusarium ear rot in a multiparent advanced generation intercross (MAGIC) maize population. *Plant disease,* **103(5)**, 897-904.
4. Cavanagh, C., Morell, M., Mackay, I., Powell, W. (2008). From mutations to MAGIC: resources for gene discovery, validation and delivery in crop plants. *Current opinion in plant biology,* **11(2)**, 215-221.
5. Cavanagh, C. R., Chao, S., Wang, S., Huang, B. E., Stephen, S., Kiani, S., Akhunov, E. (2013). Genome-wide comparative diversity uncovers multiple targets of selection for improvement in hexaploid wheat landraces and cultivars. *Proceedings of the national academy of sciences,* **110(20)***,* 8057-8062.
6. Chahal G.S., Gosal S.S. (2018). Principles and procedures of Plant Breeding- Biotechnological and Conventional Approaches . *Narosa Publishing House Pvt. Ltd.* (ISBN: 978-81-7319-374-3)
7. Collard, B. C., and Mackill, D. J. (2008). Marker-assisted selection: an approach for precision plant breeding in the twenty-first century. *Philos. Trans. R. Soc. Lond B Biol. Sci.* **363**, 557–572. doi: 10.1098/rstb.2007.2170
8. Dalmiya, N., Schultink, W. (2003). Combating hidden hunger: the role of international agencies. *Food and nutrition bulletin*, **24(4)**, S69-S77.
9. Darvasi A, Soller M (1995) Advanced Intercross Lines, an experimental population. *Genetics* **141:**1199–1207.
10. Descalsota, G. I. L., Swamy, B. M., Zaw, H., Inabangan-Asilo, M. A., Amparado, A., Mauleon, R., Reinke, R. (2018). Genome-wide association mapping in a rice MAGIC plus population detects QTLs and genes useful for biofortification. *Frontiers in plant science*, **9**, 1347.
11. Dhugga K.S. (2007). Maize biomass yield and composition for biofuels. *Crop Sci*. **47**, 2211–2227.
12. Frassinetti, S., Bronzetti, G. L., Caltavuturo, L., Cini, M., Della Croce, C. (2006). The role of zinc in life: a review. *Journal of environmental pathology, toxicology and oncology,* **25(3).**
13. Gande, N. K., Kundur, P. J., Soman, R., Ambati, R., Ashwathanarayana, R., Bekele, B. D., Shashidhar, H. E. (2014). Identification of putative candidate gene markers for grain zinc content using recombinant inbred lines (RIL) population of IRRI38 X Jeerigesanna. *African Journal of Biotechnology,* **13(5).**
14. Huang, X., Paulo, M. J., Boer, M., Effgen, S., Keizer, P., Koornneef, M., Van Eeuwijk, F. A. (2011). Analysis of natural allelic variation in Arabidopsis using a multiparent recombinant inbred line population. *Proceedings of the National Academy of Sciences*, **108(11)**, 4488-4493.
15. Huang, B. E., Verbyla, K. L., Verbyla, A. P., Raghavan, C., Singh, V. K., Gaur, P., Cavanagh, C. R. (2015). MAGIC populations in crops: current status and future prospects. *Theoretical and Applied Genetics*, **128**, 999-1017.
16. Jiménez-Galindo, J. C., Malvar, R. A., Butrón, A., Santiago, R., Samayoa, L. F., Caicedo, M., Ordás, B. (2019). Mapping of resistance to corn borers in a MAGIC population of maize. *BMC plant biology,* **19**, 1-17.
17. Kover P.X., Valdar W., Trakalo J., Scarcelli N., Ehrenreich I.M., Purugganan M.D., Durrant C., Mott R. 2009. A multiparent advanced gen- eration inter-cross to fine-map quantitative traits in Arabidopsis thaliana. *PLoS Genetics* **5**, e1000551.
18. Kover, P. X., Valdar, W., Trakalo, J., Scarcelli, N., Ehrenreich, I. M., Purugganan, M. D., (2009). A multiparent advanced generation inter-cross to fine- map quantitative traits in Arabidopsis thaliana. *PLoS Genet.* **5**:e1000551. doi: 10.1371/journal.pgen.1000551
19. Leung H, Raghavan C, Zhou B, Oliva R, Choi I.R., Lacorte V. (2015). Allele mining and enhanced genetic recombination for rice breeding. *Rice* **8**: 1–11.

20. López-Malvar, A., Butron, A., Malvar, R. A., Mc. Queen-Mason, S. J., Faas, L., Gómez, L. D., Santiago, R. (2021). Association mapping for maize stover yield and saccharification efficiency using a multiparent advanced generation intercross (MAGIC) population. *Scientific reports,* **11(1)**, 3425.
21. Lorenzana, R.E., Lewis, M.F., Jung, H.J.G. Bernardo, R. (2010). Quantitative trait loci and trait correlations for maize stover cell wall composition and glucose release for cellulosic ethanol. *Crop Sci*. **50**, 541–555
22. Marcotullio, G. De Jong, W. (2010)..Chloride ions enhance furfural formation from d-xylose in dilute aqueous acidic solutions. *Green Chem*. **12**, 1739–1746
23. Mascher, M., Gundlach, H., Himmelbach, A., Beier, S., Twardziok, S. O., Wicker, T., Stein, N. (2017). A chromosome conformation capture ordered sequence of the barley genome. *Nature,* **544**, 427-433.
24. Meng, L., Zhao, X., Ponce, K., Ye, G., Leung, H. (2016). QTL mapping for agronomic traits using multi-parent advanced generation inter-cross (MAGIC) populations derived from diverse elite indica rice lines. *Field Crops Res.* **189,** 19–42. doi: 10.1016/j.fcr.2016.02.004
25. Mosier, N., Wyman, C., Dale, B., Elander, R., Lee, Y. Y., Holtzapple, M., Ladisch, M. (2005). Features of promising technologies for pre-treatment of lignocellulosic biomass. *Bioresource technology,* **96(6),** 673-686.
26. Nawaz, Z., Kakar, K. U., Li, X. B., Li, S., Zhang, B., Shou, H. X., Shu, Q. Y. (2015). Genome-wide association mapping of quantitative trait loci (QTLs) for contents of eight elements in brown rice (*Oryza sativa* L.). *Journal of agricultural and food chemistry,* **63(36),** 8008-8016.
27. Norton, G. J., Deacon, C. M., Xiong, L., Huang, S., Meharg, A. A., and Price, A. H. (2010). Genetic mapping of the rice ionome in leaves and grain: identification of QTLs for 17 elements including arsenic, cadmium, iron and selenium. *Plant Soil.* **329**, 139–153. doi: 10.1007/s11104-009- 0141-8
28. Norton, G. J., Douglas, A., Lahner, B., Yakubova, E., Guerinot, M. L., Pinson, S. R., Price, A. H. (2014). Genome wide association mapping of grain arsenic, copper, molybdenum and zinc in rice (*Oryza sativa* L.) grown at four international field sites. *PLoS One,* **9(2)***,* e89685.
29. Ogawa D, Nonoue Y, Tsunematsu H, Kanno N, Yamamoto T, Yonemaru JI. 2018a. Discovery of QTL alleles for grain shape in the Japan- MAGIC rice population using haplotype information. *G3 8*, 3559–3565.
30. Ogawa D, Yamamoto E, Ohtani T, Kanno N, Tsunematsu H, Nonoue Y, Yano M, Yamamoto T, Yonemaru JI. 2018b. Haplotype-based allele mining in the Japan-MAGIC rice population. *Scientific Reports* **8,** 4379.
31. Ogawa, D., Sakamoto, T., Tsunematsu, H., Kanno, N., Nonoue, Y., Yonemaru, J. I. (2021). Haplotype analysis from unmanned aerial vehicle imagery of rice MAGIC population for the trait dissection of biomass and plant architecture. *Journal of Experimental Botany,* ***72(7)***, 2371-2382.
32. Pauly M., Keegstra, K. (2008). Cell-wall carbohydrates and their modification as a resource for biofuels. *Plant Journal* **54**, 559–568.
33. Penning, B. W., Sykes, R. W., Babcock, N. C., Dugard, C. K., Held, M. A., Klimek, J. F., Carpita, N. C. (2014). Genetic determinants for enzymatic digestion of lignocellulosic biomass are independent of those for lignin abundance in a maize recombinant inbred population. *Plant Physiology,* **165(4)**, 1475-1487.
34. Phundhan Singh. (2014). Plant Breeding (Molecular and New Approches). *Kalyani Publishers* (ISBN: 978-93-272-4738-1)
35. Phundhan Singh. (2015). Molecular Plant Breeding. *Kalyani Publishers* (ISBN: 978-93-272-5787-8)
36. Pollard, D. A. (2012). Design and construction of recombinant inbred lines. Quantitative Trait Loci (QTL) Methods and Protocols, 31-39.
37. Ponce, K., Zhang, Y., Guo, L., Leng, Y., Ye, G. (2020). Genome-wide association study of grain size traits in indica rice multiparent advanced generation intercross (MAGIC) population. *Frontiers in Plant Science,* **11**, 395.
38. Purugganan, M. D., and Fuller, D. Q. (2009). The nature of selection during plant domestication. *Nature* **457**, 843–848. doi: 10.1038/nature07895

39. Raghavan, C., Mauleon, R., Lacorte, V., Jubay, M., Zaw, H., Bonifacio, J., Leung, H. (2017). Approaches in characterizing genetic structure and mapping in a rice multi-parental population. G3: Genes, Genomes, *Genetics,* **7(6)**, 1721-1730.
40. Rakshit S, Rakshit A, Patil JV (2012) Multiparent intercross populations in analysis of quantitative traits. *Journal of Genetics* **91**:111–117.
41. Ray, D. K., Ramankutty, N., Mueller, N. D., West, P. C., Foley, J. A. (2012). Recent patterns of crop yield growth and stagnation. *Nature communications*, **3(1)**, 1293.
42. Roohani, N., Hurrell, R., Kelishadi, R., & Schulin, R. (2013). Zinc and its importance for human health: An integrative review. Journal of research in medical sciences: *the official journal of Isfahan University of Medical Sciences,* **18(2),** 144.
43. Sadeghzadeh, B. (2013). A review of zinc nutrition and plant breeding. *Journal of soil science and plant nutrition,* **13(4)**, 905-927.
44. Scarcelli, N., Cheverud, J. M., Schaal, B. A., Kover, P. X. (2007). Antagonistic pleiotropic effects reduce the potential adaptive value of the FRIGIDA locus. *Proceedings of the National Academy of Sciences,* **104(43)**, 16986-16991.
45. Scott, M. F., Ladejobi, O., Amer, S., Bentley, A. R., Biernaskie, J., Boden, S. A., Mott, R. (2020). Multi-parent populations in crops: a toolbox integrating genomics and genetic mapping with breeding. *Heredity,* **125(6)**, 396-416.
46. Singh, B. D., Singh, A. K. (2015). Marker-assisted plant breeding: principles and practices. *Springer*.(ISBN: ISBN 978-81-322-2316-0)
47. Vermerris W. Saballos, A., Ejeta, G., Mosier, N. S., Ladisch, M. R., & Carpita, N. C. (2007). Molecular breeding to enhance ethanol production from corn and sorghum stover. *Crop Science*, **47**, S-142.
48. Zaw H, Raghavan C, Pocsedio A., 2019. Exploring genetic architecture of grain yield and quality traits in a 16-way indica by japonica rice MAGIC global population. *Sci Rep* **9**:19605.
49. Zhang, M., Pinson, S. R., Tarpley, L., Huang, X. Y., Lahner, B., Yakubova, E., 2014. Mapping and validation of quantitative trait loci associated with concentrations of 16 elements in unmilled rice grain. *Theor. Appl. Genet*. **127**, 137–165. doi: 10.1007/s00122-013-2207-5.

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