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Invited Review **Open Access**

Expanding Genetic Horizons: The Role of MAGIC Populations in Enhancing Plant Breeding Efficiency

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Abstract The burgeoning global population and the concomitant demand for increased agricultural productivity necessitate the exploration of innovative breeding strategies. Multi-parent advanced generation inter-cross (MAGIC) populations have emerged as a pivotal resource in plant breeding, offering a unique amalgamation of genetic diversity and recombination. These populations are derived from multiple founder parents and result in recombinant inbred lines (RILs) that serve as a genetic mosaic, capturing a broad spectrum of genetic variation. The development of MAGIC populations, through either "funnel" or "diallel" cross-designs, ensures a balanced representation of each parent's genome, thereby maximizing the potential for genetic discovery and trait improvement. The application of MAGIC populations has been demonstrated across various crops, including cereals, cowpea, sorghum, tomato, eggplant, rice, and strawberry, highlighting their versatility and potential for enhancing breeding efficiency. Advances in genotyping technologies and specific software development have facilitated the genetic analysis of these complex populations, enabling the identification of quantitative trait loci (QTLs) and the selection of elite breeding material. Furthermore, MAGIC populations are instrumental in dissecting complex traits, such as disease resistance, abiotic stress tolerance, and grain quality, and hold promise for the direct release of new varieties. The integration of MAGIC populations into breeding pipelines, coupled with the potential for inter-specific crosses and the development of populations in non-pure line crops, underscores their transformative role in plant breeding. This review underscores the significance of MAGIC populations in advancing genetic research and breeding, paving the way for the development of improved cultivars to meet future agricultural challenges.

Keywords MAGIC populations; Plant breeding; Genetic diversity; Recombinant inbred lines; Quantitative trait loci; Crop improvement; Genotyping; Genetic analysis; Trait dissection; Cultivar development

1 Introduction

Plant breeding is a critical component of agricultural development, aimed at improving crop yields, resistance to diseases, and adaptation to environmental stresses. However, the complexity of plant genomes and the multifaceted nature of agronomic traits pose significant challenges to breeders. Traditional breeding methods often rely on bi-parental crosses, which can limit the genetic diversity and slow down the breeding process. To overcome these limitations, advanced genetic tools are needed to explore the vast genetic potential within crop species and accelerate the development of improved varieties.

One such advanced tool is the Multi-parent Advanced Generation Inter-Cross (MAGIC) population. MAGIC populations are derived from the intercrossing of multiple founder parents, resulting in a diverse and recombined genetic resource. These populations are characterized by their ability to capture a wide array of genetic variation from several different lines, thus providing a powerful platform for genetic analysis and selection of elite breeding material (Cavanagh et al., 2008; Bandillo et al., 2013; Pascual et al., 2015; Wei and Xu, 2015; Meng et al., 2016; Ongom and Ejeta, 2017; Huynh et al., 2018; Campanelli et al., 2019; Arrones et al., 2020; Mangino et al., 2021). The emergence of MAGIC populations represents a significant step forward in plant breeding, as they combine the genetic contributions of multiple parents and facilitate the mapping of QTLs with greater precision.

The objectives of this review are to provide an overview of the challenges faced in plant breeding and the need for advanced genetic tools like MAGIC populations, to define and discuss the emergence of MAGIC populations and their design, and to explore how these populations can enhance the efficiency of plant breeding programs. By examining the development and application of MAGIC populations across various crop species, this review aims to highlight their potential in unlocking genetic diversity and driving the next wave of crop improvement.

2 Development of MAGIC Populations

2.1 Historical development of MAGIC populations in plant breeding

The concept of MAGIC populations represents a significant evolution in plant breeding methodologies. Historically, plant breeding has relied on bi-parental crosses to combine desirable traits. However, the advent of MAGIC populations has expanded the genetic horizons by incorporating alleles from multiple founder parents into a single population. This approach has been increasingly adopted across various crops, including cereals, legumes, and vegetables, to enhance genetic diversity and improve complex traits (Cavanagh et al., 2008; Bandillo et al., 2013; Meng et al., 2016; Ongom and Ejeta, 2017; Huynh et al., 2018; Campanelli et al., 2019; Arrones et al., 2020; Mangino et al., 2021; Samineni et al., 2021; Singh and Shrivastav, 2023).

2.2 Genetic principles and breeding strategies involved in creating MAGIC populations

MAGIC populations are constructed by intercrossing a number of diverse founder lines, followed by several generations of mating, which can include both structured and random matings. The resulting RILs are a genetic mosaic of the founder genomes, providing a rich resource for genetic analysis and breeding. The development of these populations can follow "funnel" or "diallel" cross-designs, ensuring a balanced representation of each parent's genome (Huynh et al., 2018; Arrones et al., 2020). The use of advanced genotyping technologies, such as genotyping-by-sequencing (GBS), has facilitated the characterization of these complex populations (Bandillo et al., 2013; Ongom and Ejeta, 2017). The genetic makeup of MAGIC populations allows for the fine mapping of QTLs and the identification of novel alleles for trait improvement (Cavanagh et al., 2008; Samineni et al., 2021).

2.3 Comparison with traditional and other contemporary breeding methodologies

Compared to traditional bi-parental crosses, MAGIC populations offer a higher level of recombination and allelic diversity, which is advantageous for dissecting complex traits (Bandillo et al., 2013; Arrones et al., 2020). Unlike other contemporary breeding methods, such as genome-wide association studies (GWAS) that rely on natural populations, MAGIC populations are specifically designed with breeding goals in mind, combining desirable traits from elite breeding lines (Cavanagh et al., 2008). This targeted approach, along with the lack of genetic structure and high phenotypic diversity, makes MAGIC populations a more powerful tool for both gene discovery and the direct enhancement of breeding populations (Meng et al., 2016; Huynh et al., 2018; Campanelli et al., 2019; Mangino et al., 2021; Singh and Shrivastav, 2023). The development of MAGIC populations, despite being resource-intensive, has led to the identification of strong associations and candidate genes for important agronomic traits, thereby contributing to the development of advanced varieties (Mangino et al., 2021; Samineni et al., 2021; Singh and Shrivastav, 2023).

In conclusion, the development of MAGIC populations marks a significant milestone in the history of plant breeding, offering a sophisticated tool for expanding genetic diversity and improving crop traits. The strategic intercrossing of multiple parents and the application of advanced genetic analysis have positioned MAGIC populations as a cornerstone for future breeding efforts aimed at meeting global agricultural demands.

3 Advantages of Using MAGIC Populations

3.1 Enhanced genetic diversity and its impact on breeding

MAGIC populations are a revolutionary step in plant breeding, offering a genetic mosaic derived from multiple founder parents. This results in high genetic and phenotypic diversity, which is essential for the exploitation of plant genetic resources (Arrones et al., 2020). The development of MAGIC populations in crops like cowpea has incorporated a wide array of traits from genetically diverse founders, including resistance to abiotic and biotic stresses, seed quality, and agronomic traits (Huynh et al., 2018). This diversity is a cornerstone for breeding programs aiming to improve crop varieties by combining desirable traits from different lines.

3.2 Improved resolution of QTLs mapping

MAGIC populations have proven to be powerful tools for the dissection of complex traits. The sorghum MAGIC population, for example, has shown that a significant proportion of founder alleles segregate within the population, allowing for high-resolution mapping of QTLs (Ongom and Ejeta, 2017). Similarly, in eggplant, the development of a MAGIC population has enabled the identification of strong associations and candidate genes for anthocyanin pigmentation, a complex quantitative trait (Mangino et al., 2021). The increased recombination events in MAGIC populations, as observed in tomato, lead to a higher resolution in QTL mapping compared to bi-parental populations (Pascual et al., 2015).

3.3 Benefits in terms of breeding cycle time and efficiency

The MAGIC populations are not only valuable for genetic analysis but also for their direct and indirect use in breeding programs. For instance, the rice MAGIC populations have been developed with the purpose of fine mapping QTLs and using the highly recombined lines in breeding programs, thus promising breakthroughs in genetic gain (Bandillo et al., 2013). The MAGIC population in tomato has been used to develop genotypes with important agronomic traits and to perform Participatory Plant Breeding (PPB), demonstrating its utility in breeding cycles (Campanelli et al., 2019). Furthermore, the MAGIC population in winter wheat has captured a significant portion of the allelic diversity available in the breeding gene pool, which is beneficial for carrying out genetic studies for a wide range of economically important traits (Stadlmeier et al., 2018).

In conclusion, MAGIC populations are instrumental in enhancing genetic diversity, improving the resolution of QTL mapping, and increasing the efficiency of breeding programs. These populations are paving the way for the development of new generations of improved crop varieties, which is crucial for meeting the increasing global agricultural demands.

4 Case Studies

4.1 Examples of successful implementation of MAGIC populations in various crops

MAGIC populations have been successfully implemented in various crops, demonstrating their utility in enhancing plant breeding efficiency. For instance, in cowpea (*Vigna unguiculata* L. Walp.), a MAGIC population was developed from eight genetically diverse founder parents, which carried traits for abiotic and biotic stress resistance, seed quality, and agronomic traits. This population resulted in 305 F_8 RILs, each carrying a mosaic of genome blocks from all founders, leading to the identification of QTLs for several parental traits (Figure 1) (Huynh et al., 2018).

The study presented in Figure 1 effectively illustrates the impact of environmental conditions and genetic diversity on the phenotypic expression in cowpeas. By utilizing a MAGIC population, the research showcases a broad spectrum of phenotypic variability, which is crucial for understanding the genetic basis of trait differentiation and for enhancing crop improvement strategies. This approach not only helps in identifying specific traits that can be targeted for genetic improvement but also underscores the importance of considering environmental interactions in breeding programs. The detailed morphological observations under different conditions provide valuable insights into the adaptability and growth dynamics of cowpea, which are essential for developing resilient crop varieties suited to varying climatic conditions.

In sorghum (*Sorghum bicolor* (L.) Moench), the first MAGIC population was created by intercrossing 19 diverse founder lines, followed by 10 generations of random mating. This led to the development of 1 000 immortal MAGIC inbred lines, which were found to be rich in allelic content and highly recombined, making them suitable for gene mapping and marker-assisted breeding (Figure 2) (Ongom and Ejeta, 2017).

The case studied by Ongom and Ejeta (2017) is a significant contribution to the field of plant breeding, particularly in the development of sorghum varieties. The use of a MAGIC population approach combined with genetic male sterility represents an advanced breeding strategy that allows for the integration of a wide range of genetic diversity. This methodology is particularly useful in capturing the extensive genetic variation necessary for improving complex traits such as drought tolerance, pest resistance, and yield stability under varying environmental conditions. By employing genetic male sterility, the researchers have efficiently managed the pollination process, ensuring a higher degree of control over the breeding outcomes. The subsequent cycles of random mating and selfing, followed by the single-seed descent method, have potentially accelerated the attainment of genetic homogeneity while maintaining diversity among the lines. This approach could pave the way for more precise and efficient selection processes in crop improvement programs.

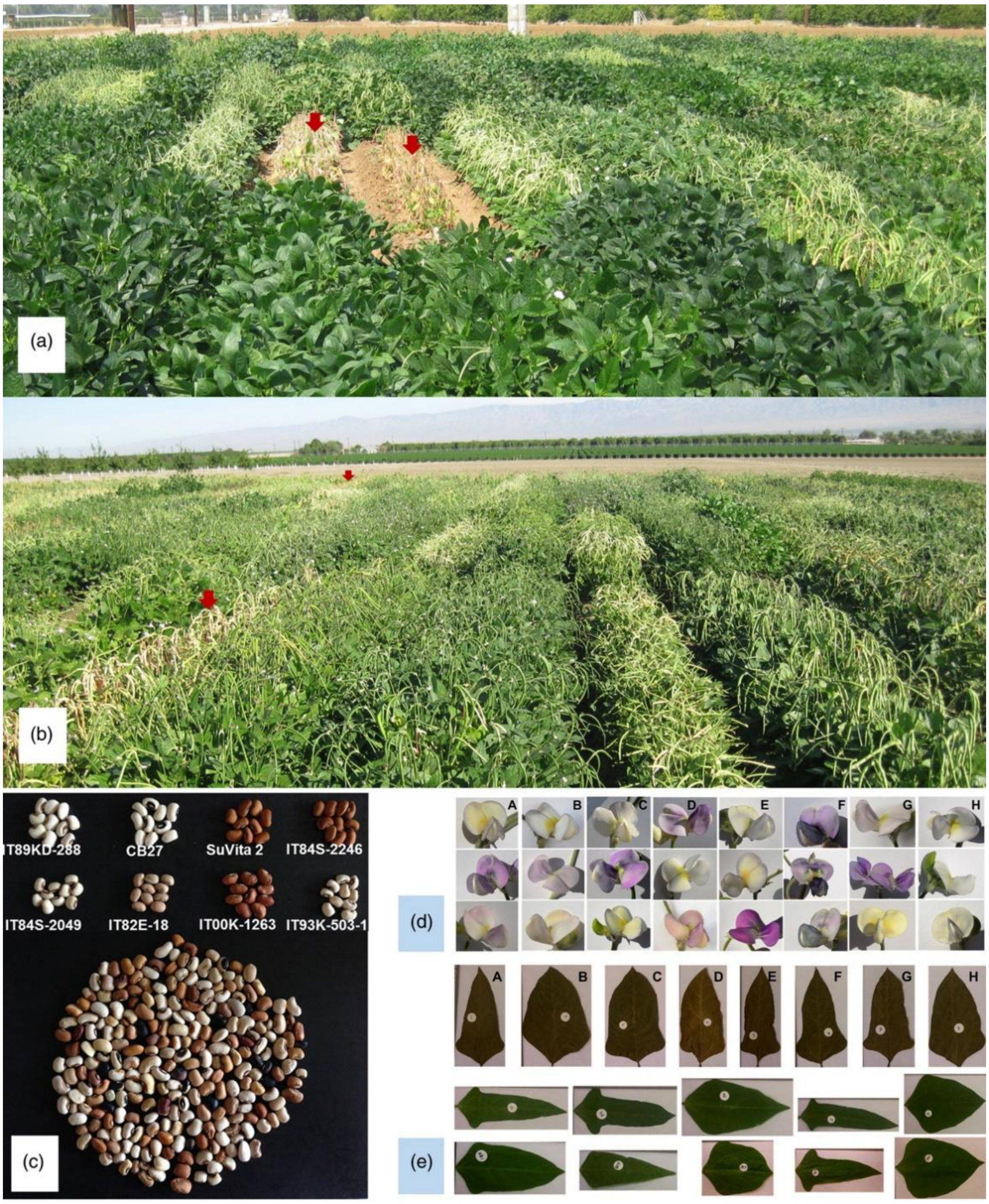

Figure 1 Morphological variation in the cowpea MAGIC population (Adopted from Huynh et al., 2018)

Image caption: Plant appearance at 65 days after planting under (a) long-day conditions at the University of California-Riverside Citrus Experiment Station in 2015 and (b) short-day conditions at the Coachella Valley Agricultural Research Station in 2016, both under full irrigation. (c) Seed appearance, (d) flower color and (e) leaf shape of parents (top panel) and a representation of MAGIC F_8 recombinant inbred lines (RILs) (in the lower part of c, each seed is from a different F_8 RIL). In (a) and (b) red arrows indicate examples of lines that matured earlier than other lines. In (d) and (e) parent codes are: A, IT89KD-288; B, IT84S-2049; C, CB27; D, IT82E-18; E, Suvita-2; F, IT00K-1263; G, IT84S-2246; H, IT93K-503-1 (Adopted from Huynh et al., 2018)

Similarly, a MAGIC population in bread wheat (*Triticum aestivum* L.) called WM-800 was developed by intercrossing eight modern winter wheat cultivars. This population showed significant differences in agronomic traits under contrasting nitrogen fertilization treatments and led to the identification of QTL alleles that improved traits such as grain yield (Figure 3) (Lisker et al., 2022).

This GWAS research represents a significant advance in our understanding of the genetic basis of important agronomic traits in wheat, particularly in relation to nitrogen use. By identifying 240 significant MTAs across 21 wheat chromosomes, the study provides crucial insights into the genetic factors that influence traits such as heading, maturity, plant height, ears per square meter, grain number per ear, thousand grain weight, and grain yield under varying nitrogen levels. This research underscores the complexity of wheat's genetic architecture and highlights the potential for using these findings in breeding programs aimed at improving nitrogen efficiency and overall crop performance. The detailed analysis of haplotypes and singular SNPs offers a valuable resource for plant geneticists and breeders to target specific genetic loci associated with desirable traits, enhancing the precision of breeding strategies and potentially leading to more sustainable agricultural practices.

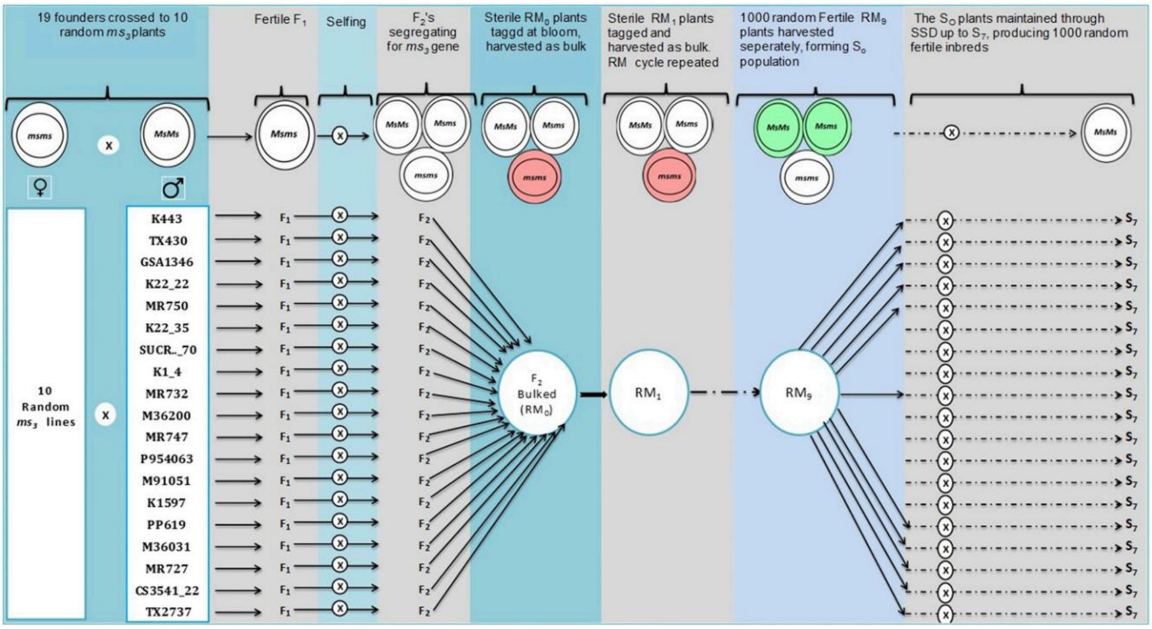

Figure 2 Mating design of the first MAGIC population of sorghum, developed with the aid of genetic male sterility (Adopted from Ongom and Ejeta, 2017)

Image caption: This figure outlines the breeding framework used to create a MAGIC population in sorghum, leveraging male sterility (ms_3). It shows the initial pairwise hybridization among 19 founder parents with 10 randomly chosen sterile plants, followed by nine cycles of random mating (RM_0 to RM_9) and multiple generations of selfing (S_0 to S_7), concluding with the single-seed descent (SSD) method. A total of 1 000 random lines were generated, with a select subset of 200 lines genotyped for further analysis (Adapted from Ongom and Ejeta, 2017)

Another example is the development of a MAGIC population in tomato, which was created by crossing eight founder lines with a wide range of genetic diversity. This population allowed for the mapping of QTLs for fruit weight and the identification of candidate single nucleotide polymorphisms (SNPs) underlying these QTLs (Pascual et al., 2015).

The development of the 8-way MAGIC population as described by Pascual et al. (2015) represents a significant methodological advancement in the field of plant genetics and breeding. By combining genetic material from both large and small fruited varieties, this approach not only enhances the genetic diversity within the breeding population but also increases the chances of capturing novel alleles that could contribute to desirable traits such as fruit size, yield, and resistance to various stresses. The detailed methodology involving initial crosses followed by multiple generations of selfing allows for a comprehensive mixing of genetic backgrounds, which is crucial for the broad applicability of the resultant lines in breeding programs. This strategy exemplifies how complex genetic designs can be effectively used to address both fundamental and applied questions in plant biology, offering substantial potential to accelerate tomato breeding and genetic research.

4.2 Analysis of outcomes and improvements over traditional methods

The outcomes of implementing MAGIC populations in plant breeding have shown several improvements over traditional methods. MAGIC populations combine significant levels of genetic recombination, a lack of genetic structure, and high genetic and phenotypic diversity, which are emerging features over experimental bi-parental and germplasm populations (Arrones et al., 2020). The increased recombination frequencies and the ability to predict haplotype origin in MAGIC populations enhance the precision of QTL mapping and facilitate the identification of causal polymorphisms (Figure 4) (Pascual et al., 2015).

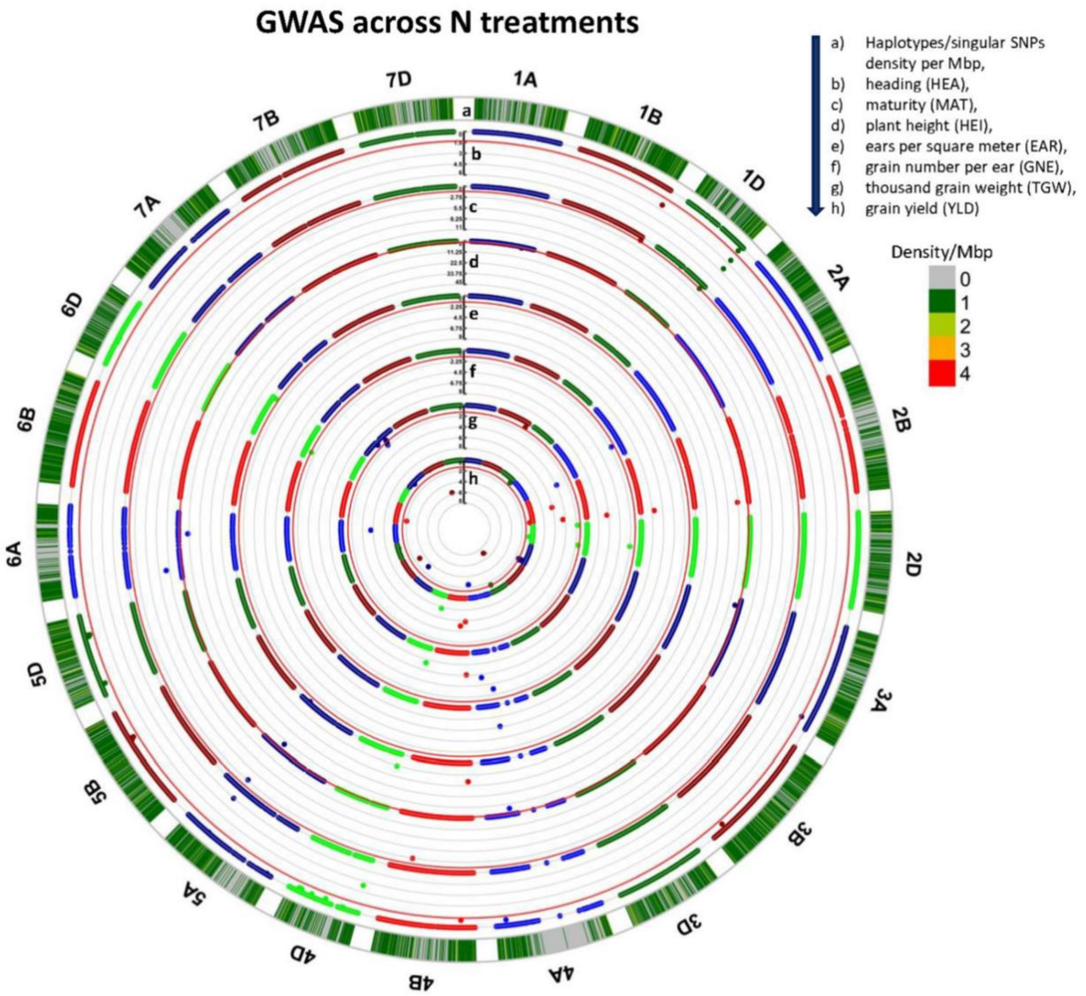

Figure 3 Circular Manhattan plots of genome-wide association scan for seven traits studied in WM-800 across N treatments (Adopted from Lisker et al., 2022)

Image caption: This figure displays the genome-wide association results for seven traits across different nitrogen levels, depicted in circular Manhattan plots (Lisker et al., 2022). Each plot illustrates the -log10 Bonferroni-adjusted p-values (BON_p < 0.05) indicating significant marker-trait associations. The outer circle labels the wheat chromosomes, while circle 'a' shows the density of haplotypes and singular SNPs per megabase. Circles 'b' to 'h' represent the GWAS results for heading, maturity, plant height, ears per square meter, grain number per ear, thousand grain weight, and grain yield, respectively, with the significance threshold highlighted by a red circle at BON_p = 0.05 (Adapted from Lisker et al., 2022)

Moreover, the genetic analysis of complex traits has been facilitated by the development of specific software for MAGIC populations, which can handle their complex genetic constitutions (Arrones et al., 2020). The broad genetic base of MAGIC populations promises breakthroughs in genetic gain, QTL and gene discovery, and the enhancement of breeding populations (Huynh et al., 2018).

The MAGIC breeding approach has also been applied to improve nutrient use efficiency traits in bread wheat, demonstrating the potential to meet the demands of food security through plant breeding (Vats et al., 2015). Additionally, the development of MAGIC populations in crops where pure lines are not available and the establishment of strategies for the straightforward incorporation of MAGIC materials in breeding pipelines are new approaches that have barely been explored (Arrones et al., 2020).

In conclusion, MAGIC populations have proven to be a very powerful tool for the dissection of complex traits and a resource for the selection of recombinant elite breeding material and cultivars, playing a major role in the coming years in allowing for impressive gains in plant breeding (Arrones et al., 2020).

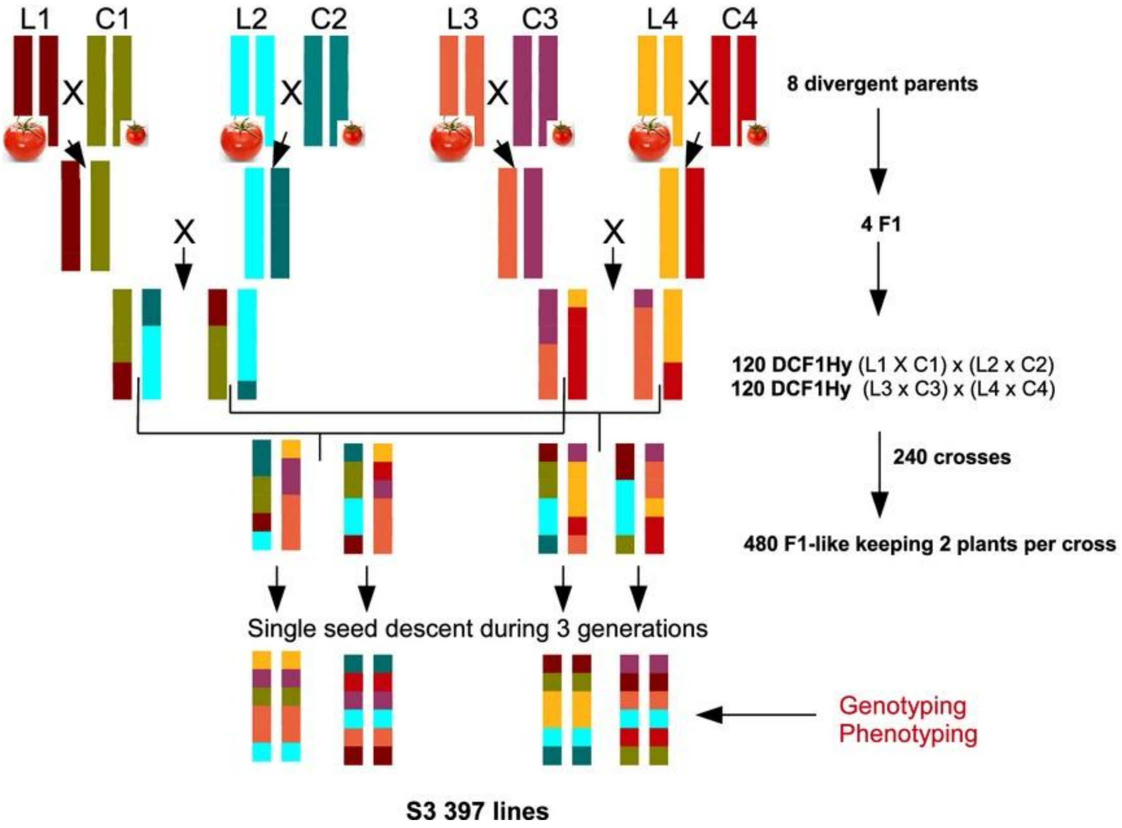

Figure 4 Construction of a tomato 8-way MAGIC population (Adopted from Pascual et al., 2015)

Image caption: This figure illustrates the breeding scheme used to create a diverse tomato MAGIC population, combining large fruited (L1 Levovil, L2 Stupicke PR, L3 LA0147, L4 Ferum) and small fruited (C1 Cervil, C2 Criollo, C3 Plovdiv24A, C4 LA1420) founders. Initial crosses between *S. lycopersicum* and *S. lycopersicum* var. *cerasiforme* lines produced F1 hybrids. Subsequent double crosses and controlled intercrossing of 240 plants led to the creation of 480 F1-like individuals, each incorporating parts of the eight founder genomes. These individuals were further propagated through three selfing generations to establish a collection of 397 MAGIC lines, characterized at the F4-like stage for this study (Adapted from Pascual et al., 2015)

5 Methodological Approaches

5.1 Overview of the techniques used to analyze and exploit MAGIC populations

MAGIC populations represent a significant advancement in plant breeding and genetic analysis. Unlike traditional bi-parental populations, MAGIC populations are derived from multiple founder parents, which increases genetic diversity and improves the relevance of QTLs mapping to breeding programs (Wei and Xu, 2015; Huynh et al., 2018; Arrones et al., 2020). The development of MAGIC populations can be achieved through "funnel" or "diallel" cross-designs (Figure 5), ensuring a balanced representation of each parent's genome in the resulting RILs (Arrones et al., 2020). These populations are characterized by high levels of genetic recombination, absence of genetic structure, and substantial genetic and phenotypic diversity, making them a powerful tool for the dissection of complex traits (Arrones et al., 2020).

The analysis of MAGIC populations involves genotyping and phenotyping the RILs to create a genetic mosaic that reflects the contribution of all founder alleles. This process is confirmed through techniques such as SNP genotyping, which helps in identifying the homozygosity and diversity of agronomic traits across different environments (Huynh et al., 2018). The genetic analysis of these populations allows for the identification of QTLs for various traits, which can lead to genetic gain and the discovery of genes responsible for important agronomic characteristics (Huynh et al., 2018).

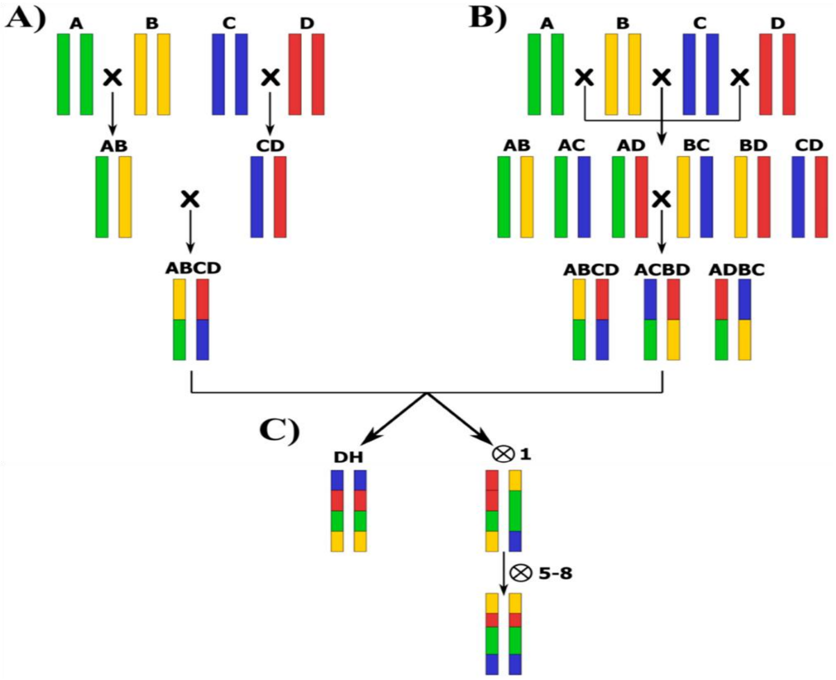

Figure 5 Cross-designs of a 4-way MAGIC population where the founders are A, B, C, and D (Adopted from Arrones et al., 2020)
Image caption: (A) “funnel” design; (B) “diallel” design; and (C) achievement of homozygous individuals by doubled haploids (DH) production, or by several rounds of selfing following the single-seed descent (SSD) method (Adopted from Arrones et al., 2020)

5.2 Statistical models and computational tools employed in genetic studies involving MAGIC populations

The complexity of MAGIC populations requires sophisticated statistical models and computational tools for effective QTL mapping. A random-model approach has been developed to address the challenges posed by multiple founder alleles and the control of genetic background information (Wei and Xu, 2015). In this approach, the founder effects of each locus are treated as random effects following a normal distribution with locus-specific variance, and a polygenic effect is fitted to the model to control the genetic background (Wei and Xu, 2015). This method contrasts with fixed-model approaches and involves scanning the entire genome one locus at a time using likelihood-ratio test statistics, which has been shown to increase statistical power and reduce type I error compared to other methods like composite interval mapping (CIM) and multiparent whole-genome average interval mapping (MPWGAIM) (Wei and Xu, 2015).

Specific software development has also played a crucial role in facilitating the genetic analysis of MAGIC populations. These tools are designed to handle the complex genetic constitutions and to assist in the selection of recombinant elite breeding material (Arrones et al., 2020). The continuous growth in the number of MAGIC populations across different crops underscores the need for and effectiveness of these computational resources in plant breeding and genetic analysis (Arrones et al., 2020).

In summary, the methodological approaches to analyzing and exploiting MAGIC populations involve a combination of strategic cross-designs, advanced genotyping techniques, and the application of robust statistical models and computational tools. These methodologies enable the effective dissection of complex traits and the selection of superior breeding material, promising significant contributions to the future of plant breeding.

6 Challenges and Limitations

6.1 Technical and practical challenges in developing and utilizing MAGIC populations

Developing and utilizing MAGIC populations present several technical and practical challenges. Firstly, the creation of MAGIC populations involves crossing multiple founder lines, which requires careful selection and an understanding of the genetic background and compatibility of each parent. This process can be technically demanding, as it involves multiple generations of crossing and selection to ensure a thorough mixing of the parental genomes.

Additionally, maintaining the genetic diversity within a MAGIC population without inadvertently introducing genetic drift or bottleneck effects demands meticulous breeding management. The high number of recombinations and segregations can also complicate the genetic analysis, making it challenging to trace the inheritance patterns of specific traits.

6.2 Limitations in terms of cost, complexity, and time investment

The cost associated with developing MAGIC populations is significant. The process requires extensive resources not only for the initial setup and breeding cycles but also for the genotyping and phenotyping necessary to analyze the genetic makeup and trait expressions of the resultant populations. Such comprehensive genetic analysis demands sophisticated equipment and substantial bioinformatics support, which may not be readily available in all breeding programs, particularly in less funded or smaller-scale operations.

In terms of complexity, managing a MAGIC population requires advanced knowledge in genetics, statistics, and computational biology. The data generated from these populations are voluminous and complex, necessitating robust statistical models to decipher the genetic architecture of traits. This complexity can be a barrier for institutions without the technical expertise or computational infrastructure to handle large datasets.

The time investment needed to develop and stabilize MAGIC populations is also considerable. Multiple generations are needed to establish a truly mixed population, with each generation requiring careful planning, execution, and analysis. This long timeline can delay the application of findings to practical breeding programs, which may be a significant drawback in rapidly changing agricultural contexts where breeders need to respond quickly to new challenges such as climate change, pest outbreaks, or market demands.

Overall, while MAGIC populations hold great promise for enhancing plant breeding efficiency, the technical, financial, and temporal demands pose substantial challenges that need to be addressed to fully leverage their potential.

7 Future Perspectives

7.1 Potential advancements in MAGIC population technology and methodology

The development of MAGIC populations has been a significant step forward in plant breeding, offering a genetic mosaic of multiple founder parents and combining high levels of genetic recombination with a lack of genetic structure and high genetic and phenotypic diversity (Arrones et al., 2020). Future advancements in MAGIC population technology are likely to focus on optimizing cross-designs such as "funnel" or "diallel" to select appropriate parents and define optimal population sizes. Additionally, the continuous growth in the number of MAGIC populations across various crops suggests that there will be significant improvements in the software tools designed to analyze these complex genetic constitutions (Arrones et al., 2020).

7.2 Integration with other genomic techniques and technologies

MAGIC populations are already proving to be a powerful tool for the dissection of complex traits and the selection of elite breeding material (Arrones et al., 2020). The integration of MAGIC populations with other genomic techniques, such as SNP genotyping, has been demonstrated in the development of a cowpea MAGIC population (Huynh et al., 2018). This integration allows for a more precise identification of QTLs and the verification of loci with major effects on traits like photoperiod sensitivity and seed size (Huynh et al., 2018). As genomic technologies continue to advance, the synergy between MAGIC populations and these technologies will likely lead to breakthroughs in genetic gain, QTL and gene discovery, and the enhancement of breeding populations.

7.3 Prospects for the future of plant breeding with MAGIC populations

The prospects for the future of plant breeding with MAGIC populations are promising. The broad genetic base of MAGIC populations, as seen in the cowpea example, promises to facilitate genetic gain and the discovery of new QTLs and genes (Huynh et al., 2018). Furthermore, the development of MAGIC populations in crops like sorghum, which capture diversity among seed parent gene pools, will likely enrich the seed parent gene pool and improve the precision of QTL mapping (Kumar et al., 2023). The MAGIC approach, which can include the development of inter-specific MAGIC populations and MAGIC-like populations in crops where pure lines are not available, is still in its infancy and holds great potential for the straightforward incorporation of MAGIC materials into breeding pipelines (Arrones et al., 2020). As these populations become more widely used and integrated into breeding programs, they are expected to play a major role in developing new generations of dramatically improved cultivars, thereby contributing to global agricultural production and food security (Arrones et al., 2020).

In conclusion, the future of plant breeding with MAGIC populations is bright, with potential advancements in technology and methodology, integration with other genomic techniques, and the promise of significant contributions to breeding programs worldwide.

8 Concluding Remarks

MAGIC populations have emerged as a significant advancement in plant breeding, offering a suite of benefits that address the need for increased agricultural production and genetic diversity. The key benefits of MAGIC populations include the combination of high levels of genetic recombination, the absence of genetic structure, and the presence of high genetic and phenotypic diversity. These populations are derived from multiple founder parents, resulting in RILs that are genetic mosaics and thus provide a powerful tool for the dissection of complex traits and the selection of elite breeding material.

However, the development and utilization of MAGIC populations are not without challenges. The complexity of their genetic constitution requires significant resources for development, including specific software for genetic analysis (Arrones et al., 2020). Additionally, the creation of these populations is a labor-intensive process that can span many years, as seen in the development of a sorghum MAGIC population which took over 15 years (Ongom and Ejeta, 2017). Despite these challenges, the potential for breeding and the continuous growth in the number of MAGIC populations across different crops demonstrate their value in modern plant breeding.

MAGIC populations stand at the forefront of a transformative era in plant breeding. Their ability to capture a broad genetic base and facilitate the identification of QTLs and causal variants makes them an indispensable resource in the quest for improved crop varieties. The integration of MAGIC populations with advanced genotyping and phenotyping technologies further enhances their utility, allowing for more precise mapping and the potential for direct releases of new varieties.

As the agricultural sector faces the challenges of climate change and a growing global population, MAGIC populations offer a promising avenue for harnessing natural genetic diversity and achieving genetic gains in crop productivity. Their role in breeding programs is likely to expand, as they provide a means to break yield barriers and enhance tolerance to various stresses (Johal et al., 2008).

In conclusion, MAGIC populations are poised to play a pivotal role in the future of plant breeding, enabling the development of cultivars that are not only high-yielding but also resilient and nutritionally enhanced.

Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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