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Review Article

MULTI-PARENT ADVANCED GENERATION INTERCROSS (MAGIC) POPULATION FOR GENOME MAPPING IN PLANT

MANDAL LINCOLN[1*], VERMA SUNIL KUMAR[2], SASMAL SAUGATA[3], EKKA ANJU RANI[1] AND KATARA JAWAHAR LAL[4] AND KOTASTHANE ANIL S.[1]

[1]Department of Agriculture and Biotechnology, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh 492012, India.
[2]Department of Genetics and Plant Breeding, CARS, Bemetara, IGKV, Raipur, 491335, India
[3]Krishi Vigyan Kendra, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh 492012, India
[4]Department of Plant Biotechnology, National Rice Research Institute, Cuttack, Odisha, 753006, India
*Corresponding Author: Email- lincolndbt@gmail.com

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Abstract- The multiparent advanced generation inter-cross (MAGIC) population is one of a new generation emerging mapping population for plant genetics study. They are generally created by intercrossing multiple founder lines over several generations. The MAGIC populations offer an alternative to traditional linkage or association mapping populations by increasing the precision of quantitative trait loci (QTL) mapping resolution and analysis of gene–trait association by taking the advantages of both historical and synthetic recombination. MAGIC offer great potential both for dissecting genomic structure and for improving breeding populations.

Keywords- MAGIC population, Precise QTLs mapping, Linkage map construction.

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Introduction

Multi-parent populations (MPPs) have emerged as powerful next-generation mapping resources combining diverse genetic founder contributions with high levels of recombination [1-3]. MAGIC population fulfills the major limitations of existing mapping populations [4-6]. The MAGIC population is called a second-generation mapping resource [7]. The Complex Trait Consortium [8] introduced the concept of a multi-parental advanced generation intercross (MAGIC) population using mice. Multi-cross populations were first proposed for plants by Mackay and Powell [1]. The first plant MAGIC population was developed in *Arabidopsis thaliana* [9]. Subsequently, MAGIC populations have been developed in wheat [2, 5, 10-11], chickpea [12], rice [4], sorghum [13], maize [14], barley [15], tomato [16], Strawberry [17] etc.

Genetic properties

The MAGIC populations represent combining of high genetic recombination and diversity. Linkage disequilibrium (LD) patterns depicted the MAGIC population to be highly recombined [5]. Huang, *et al*. [6] demonstrated that a MAGIC population more clearly illustrated the fine-scale mosaics of founder parental genomes and wider genetic and phenotypic variation than populations derived from bi-parental crossing. The characterization of MAGIC maize lines shows that the population is a balanced, evenly differentiated mosaic of the eight founders, with mapping power and resolution strengthened by high minor allele frequencies and a fast decay of linkage disequilibrium [14]. The eight-way population had higher gene diversity in rice [18]. Upland cotton MAGIC population contained abundant genetic diversity [19]. High heritability coupled with high and moderate genetic advance was observed for all the traits studied using MAGIC F_2 segregating populations of Tobacco (*Nicotiana tabacum* L.) [20]. The MAGIC barley population was generated from intercrossing among eight parental lines and thus, offered greater genetic diversity to detect higher-order epistatic interactions [21].

Mating Design and Development of MAGIC population

The MAGIC design concept is similar to that of advanced intercross lines (AILs) proposed by Darvasi and Soller, [22], except that AILs are still derived from a two-parent cross. MAGIC populations are generally created by intercrossing multiple founder lines over several generations. Using multiple founders contributes more allelic diversity than that captured in typical biparental mapping populations. An eight-parent MAGIC population created of winter-sown wheat (*Triticum aestivum* L.) [5]. Three rice (*Oryza sativa* L.) multi-parent advanced generation intercross (MAGIC) populations were developed using eight elite *Indica rice* varieties [18]. Bandillo, *et al*., [4] developed 4 multi-parent MAGIC populations for rice.

Development steps of MAGIC population:

1. Founder selection: Founder lines must be chosen based on genetic and/or phenotypic diversity of elite cultivars, geographical adaptation or material of more diverse origins (worldwide germplasm collections, distant relatives). Use of landraces as founders may introduce greater diversity.
2. Mixing: In the first stage of population development, multiple parents are intercrossed to form a broad genetic base. The inbred founders are paired off and inter-mated, known as a funnel. The result of this stage is a set of lines whose genomes comprised contributions from each of the founders.
3. Advanced intercrossing: The mixed lines from different funnels are randomly and sequentially intercrossed as in the advanced intercross. The main goal of this intercrossing is to increase the number of recombinations in the population.
4. Inbreeding: The individuals resulting from the advanced intercrossing

stage is progressed to create homozygous individuals [6]. The scheme derived for 8-way and 4-way cross population shown [18].

Population size

Valdar, *et al*., [23] compared variations on the first two stages of the collaborative cross (CC) design and bench marked against biparental advanced intercross RILs for a trait with 0.5 heritability. They found that a MAGIC population of size 500 could achieve high power to detect single quantitative trait loci (QTL) explaining 5 % of phenotypic variability.

Advantages and disadvantages

The MAGIC population has three major advantages: (i) more abundant genetic diversity than a biparental population and higher allele balanced frequency than the panels consisting of diverse accessions in association mapping because of controlled allelic inputs from multiple parents (ii) negligible impact from population structure [1, 9, 23] and (iii) increased mapping resolution by taking the advantages of both historical and synthetic recombination. Negligible population structure allows the use of simple association analysis with reduced false positive rate [7, 24]. In MAGIC population, the multiple intermating generations have the added useful effect of introducing more recombinations along the chromosomes within the population, meaning that the chromosome blocks inherited by each individual mapping line are reduced in size compared with those of the parent genomes, thus allowing geneticists to better uncouple the effects of linked genes [25]. The development of MAGIC is a time-consuming process.

Applications of MAGIC populations

1. **Multiline variety**: The 12-parent MAGIC population reported by Li, *et al*. [26] has been used to develop the multiline variety Duo-Ji-Xin 3, which is being commercialized in China [27]. The *indica* MAGIC population developed at IRRI [4] has been explored by IRRI breeders for targeting irrigated and rainfed environments and for direct and indirect use in variety development.
2. **Precise QTLs mapping**: The MAGIC populations serve as permanent mapping populations for precise QTL mapping [4]. Application of the resource MAGIC population for quantitative trait loci mapping using the complex traits plant height and hectolitre weight in wheat [10]. The characterization of the full MAGIC maize population will lead to higher power and definition in QTL mapping and lay the basis for improved understanding of maize phenotypes, heterosis included [14]. MAGIC populations are valuable for QTL identification, 8-way populations being more powerful [18]. Fine-mapping of quantitative trait loci (QTL) in the MAGIC lines [9] and Wheat *Snn1* locus [28].
3. **Linkage map construction**: Utilization of a MAGIC population for the first time for linkage map construction [12]. The linkage map obtained showed an 87% increase in recombination frequencies compared to biparental populations [16]. A high-density MAGIC linkage map has recently been developed in wheat [29].
4. **Genome introgressions:** The MAGIC populations also present opportunities for studying the interactions of genome introgressions and chromosomal recombination [4]. Applications of this resource include interrogation of the wheat genome [10].

Conclusion

The multiparent advanced generation intercross (MAGIC) populations offer an alternative to traditional mapping populations by increasing the precision mapping. The MAGIC populations created by several generations of intercrossing among multiple founder lines leading to greater accumulation of recombination events. MAGIC population contained abundant genetic diversity. MAGIC populations are valuable for multiline variety development, linkage map construction, precise QTLs mapping and fine-mapping of Quantitative Traits, analysis of gene–trait association etc.

Application of review: The major application of the MAGIC population is linkage map construction for fine- mapping of Quantitative Traits in plants.

Review Category: Genome Mapping

Abbreviations: Multiparent advanced generation intercross (MAGIC), Quantitative trait loci (QTL), Recombinant inbred line (RIL), Multi-parent populations (MPPs), Advanced intercross lines (AILs)

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***Research Guide or Chairperson of research: Dr Anil S. Kotasthane**
University: Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh 492012
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References

[1] Mackay I.J. and Powell W. (2007) *Trends Plant Sci*., 12, 53.
[2] Cavanagh C., Morell M., Mackay I. and Powell W. (2008) *Curr. Opin. Plant Biol*., 11, 215–221.
[3] Ongom P.O. and Ejeta G. (2018) *genomes. Genetics*, 8, 331-341.
[4] Bandillo N., Raghavan C., Muyco P.A., Sevilla M.A.L., Lobina I.T., Dilla-Ermita C.J., Tung C.W., McCouch S., Thomson M., Mauleon R., Singh R.K., Gregorio G., Redo~na E. and Leung H. (2013) *Rice*, 6, 11.
[5] Mackay I.J., Bansept-Basler P., Barber T., Bentley A.R., Cockram J., Gosman N., Greenland A.J., Horsnell R., Howells R., O'Sullivan D.M., Rose G.A. and Howell P.J. (2014) *G3: Genes, Genomes, Genet*., 4, 1603–1610.
[6] Huang B.E., Verbyla K.L., Verbyla A.P., Raghavan C., Singh V.K., Gaur P., Leung H., Varshney R.K. and Cavanagh C.R. (2015) *Theor. Appl. Genet*., 128, 999–1017.
[7] Rakshit S., Rakshit A. and Patil J.V. (2012) *J. Genet*., 91, 111–117.
[8] Churchill G.A., Airey D.C., Allayee H., Angel J.M., Attie A.D., Beatty J., Beavis W.D., Belknap J.K., Bennett B., Berrettini W., Bleich A., Bogue M., Broman K.W., Buck K.J., Buckler E., Burmeister M., Chesler E.J., Cheverud J.M., Clapcote S., Cook M.N., Cox R.D., Crabbe J.C., Crusio W.E., Darvasi A., Deschepper C.F., Doerge R.W., Farber C.R., Forejt J., Gaile D., Garlow S.J., Geiger H., Gershenfeld H., Gordon T., Gu J., Gu W., de Haan G., Hayes N.L., Heller C., Himmelbauer H., Hitzemann R., Hunter K., Hsu H.C., Iraqi F.A., Ivandic B., Jacob H.J., Jansen R.C., Jepsen K.J., Johnson D.K., Johnson T.E., Kempermann G., Kendziorski C., Kotb M., Kooy R.F., Llamas B., Lammert F., Lassalle J.M., Lowenstein P.R., Lu L., Lusis A., Manly K.F., Marcucio R., Matthews D., Medrano J.F., Miller D.R., Mittleman G., a Mock B., Mogil J.S., Montagutelli X., Morahan G., Morris D.G., Mott R., Nadeau J.H., Nagase H., Nowakowski R.S., O'Hara B.F., Osadchuk A.V., Page G.P., Paigen B., Paigen K., Palmer A., Pan H.J., Peltonen-Palotie L., Peirce J., Pomp D., Pravenec M., Prows D.R., Qi Z., Reeves R.H., Roder J., Rosen G.D., Schadt E.E., Schalkwyk L.C., Seltzer Z., Shimomura K., Shou S., Sillanpää M.J., Siracusa L.D., Snoeck H.W., Spearow J.L., Svenson K., Tarantino L.M., Threadgill D., Toth L.A., Valdar W., de Villena F.P.M., Warden C., Whatley S., Williams R.W., Wiltshire T., Yi N., Zhang D., Zhang M. and Zou F. (2004) *Nat. Genet*., 36, 1133–1137.
[9] Kover P. X., Valdar W., Trakalo J., Scarcelli N., Ehrenreich I.M., Purugganan M.C., Durrant C. and Mott R. (2009) *PLoS Genet*., 5, e1000551.

[10] Huang B.E., George A.W., Forrest K.L., Kilian A., Hayden M.J., Morell M.K. and Cavanagh C.R. (2012) *Plant Biotechnol. J*., 10,826–839.
[11] Rebetzke G.J., Verbyla A.P., Verbyla K.L., Morell M.K. and Cavanagh C.R. (2014) *Plant Biotechnol J*., 12, 219–230.
[12] Gaur P.M., Jukanti A.K. and Varshney R.K. (2012) *Agronomy*, 2, 199–221.
[13] Higgins R.H., Thurber C.S., Assaranurak I. and Brown P.J. (2014) *G3 (Bethesda)*, 4, 1593–1602.
[14] Dell'Acqua M., Gatti D. and Pea G. (2015) *Genome Biol*., 16, 1–23.
[15] Sannemann W., Huang B.E., Mathew B. and Léon J. (2015) *Mol. Breed*., 35, 1–16.
[16] Pascual L., Desplat N., Huang B.E., Desgroux A., Bruguier L., Bouchet J.P., Le Q.H., Chauchard B., Verschave P. and Causse M. (2015) *Plant Biotechnol. J*., 13, 565–577.
[17] Wada T., Oku K., Nagano S., Isobe S., Suzuki H., Mori M., Takata K., Hirata C., Shimomura K., Tsubone M., Katayama T., Hirashima K., Uchimura Y., Ikegami H., Sueyoshi T., Obu K-i., Hayashida T. and Shibato Y. (2017) *Breeding Science*, 67, 370–381.
[18] Meng L., Guo L., Ponce K., Zhao X. and Ye G. (2016) *The plant genome*, 9(2), 1-14.
[19] Li D.G., Li Z.X., Hu J.S., Lin Z.X. and Li X.F. (2016) *Genetics and Molecular Research*, 15(4), gmr15048759.
[20] Dhavala C.V.N., Papidandla U.M., Ullagaddi C., Thimmegowda G.C. and Gandra S.V.S. (2017) *Not Sci. Biol*., 9(3), 392-396.
[21] Mathew B., Léon J., Sannemann W. and Sillanpää M. J. (2018) *Genetics*, 208, 525–536.
[22] Darvasi A. and Soller M. (1995) *Genetics*, 141, 1199–1207.
[23] Valdar W., Flint J. and Mott R. (2006) *Genetics,* 172, 1783–1797.
[24] Yamamoto E., Iwata H., Tanabata T., Mizobuchi R., Yonemaru J., Yamamoto T. and Yano M. (2014) *BMC Genet*., 15, 50.
[25] Holland J. (2015) *Genome Biol*., 16, 163.
[26] Li Z., Ye G., Yang M.E.I., Liu Z., Lu D., Mao X., Wu Q. and Li X. (2014) *Res. Crops*, 15, 28–37.
[27] Li X.F., Liu Z.X., Lu D.B., Liu Y.Z., Mao X.X., Li Z.X. and Li H.J. (2013) *Euphytica*, 192, 77–86.
[28] Cockram J., Scuderi A., Barber T., Furuki E., Gardner K.A., Gosman N., Kowalczyk R., Phan H.P., Rose G.A., Tan K.C., Oliver R.P. and Mackay I.J. (2015) *G3 genes.genomes.genetics*. 5, 2257-2266.
[29] Gardner K.A., Wittern L.M. and Mackay I.J. (2016) *Plant Biotechnol. J.,* 14, 1406–1417.