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Trait Association and Genetic Variability Study in Rice MAGIC Lines for Yield Related Traits

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The study was aimed to assess genetic variability and associations between grain yield and morphological traits in 50 multi-parent advanced generation intercross (MAGIC) lines generated by single seed descent utilizing eight diverse parents (to impart tolerance to biotic and abiotic stresses) were utilized in the study along with eight checks at Zonal agricultural and horticultural research station, Navile, Shivamogga during *kharif* 2022. Improvement in grain yield, a quantitative trait is one of the key objective of plant breeders which depends upon the magnitude of genetic variability

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existing in the genetic material utilized in the breeding programme. The analysis of variance revealed the presence of significant differences were found among lines for all traits. Moderate to high genotypic and phenotypic variation, heritability and genetic advance were recorded for plant height, tillers per plant, filled grains per panicle, test weight and grain yield. Correlation analysis revealed positive associations between grain yield and tillers per plant, panicle length, filled grains per panicle, panicle fertility and test weight. These findings emphasize the importance of indirect selection for these traits to improve grain yield in rice. The results suggest that breeders can utilize these traits as selection criteria to enhance grain yield, ultimately contributing to rice yield improvement programs. Our study provides valuable insights for rice breeders to develop high-yielding rice varieties with improved tolerance to biotic and abiotic stresses.

Keywords: MAGIC; GCV; PCV; heritability; genetic advance as per cent of mean.

1. INTRODUCTION

“Rice (*Oryza sativa* L.) is one of the most needed cereal crop and is considered as the staple food for more than 2.7 billion people on a daily basis. Rice imparts more than 50% of regular calories by direct consumption and is planted in about one-tenth of the earth’s arable land” (Niharika et al., 2022). “Globally, rice is being cultivated in 167.10 mha with the production of 782 mt and an average productivity of 4.67 t/ha” (Niharika et al., 2022; Anonymous, 2023). “India has the largest area under rice cultivation and ranks second in production next to China. In 2023-24, the rice area, production and productivity in India is 47.6 mha, 137.83 mt and 4.3 t/ha, respectively” (Anonymous, 2023).

“Grain yield (GY) is a multifaceted attribute that is impacted by an arrangement of genes, the environment in which they develop, and the degree and types of diversity in genotypes” (Sarker & Mian, 2003). “In addition, GY is directly or indirectly interrelated with other agronomic traits such as plant stature, growth spell, panicle length (PL), tiller per plant, loaded grains per panicle, and primary and secondary branches per panicle (Asante et al., 2019; Beena et al., 2021). The primary focus of plant breeders concentrates on picking desirable features in the blend, granting each an economic gain based on GY to generate a preference index” (Saroj et al., 2021).

“Genetic variability and correlation studies are fundamental in crop improvement programs, as they provide insights into the extent of genetic diversity within a population and the relationships among traits of interest. The level of genetic variability within the gene pool directly influences the success of breeding efforts, determining the potential for selecting desirable traits. Correlation analysis further aids in identifying key traits associated with target characteristics, enabling breeders to simultaneously improve multiple attributes, including economic yield. The importance of genetic variability, heritability, and genetic gain for yield and related traits is critical, as it provides the foundation for designing effective breeding programs. To achieve significant genetic gains, breeders are encouraged to adopt strategies that simultaneously utilize both additive and non-additive gene effects” (Rasheed et al., 2023). Therefore, present study was conducted to evaluate genetic variability among rice MAGIC lines and correlation among traits.

2. MATERIALS AND METHODS

The experiment was laid out in a randomized complete block design with two replications during *kharif* 2022 at Zonal agricultural and horticultural research station, Navile, Shivamogga. The MAGIC lines were developed by utilizing eight diverse parents, and in our experiment we have utilized F_7 of this population (Fig. 1). The seedlings of all fifty MAGIC lines and eight checks were raised in the nursery, later twenty-one days old seedlings were transplanted into the main field with single seedling per hill in a row length of ¾ meters with the spacing of 20 cm between rows and 15 cm between plants. The recommended agronomic practices were followed to raise healthy and maintain good crop stand.

Five plants were randomly selected from each line and labelled for recording observations. Mean of the observations recorded on these five plants were considered for statistical analysis. The characters for which observations recorded are as follows; Days to 50 per cent flowering (DFF), days to maturity (DM), plant height (PH), number of tillers per plant (NT), panicle length (PL), number of filled grains per panicle (NFG), panicle fertility (PF), test weight (TW), length/breadth ratio (LB) and grain yield per plant (GY).

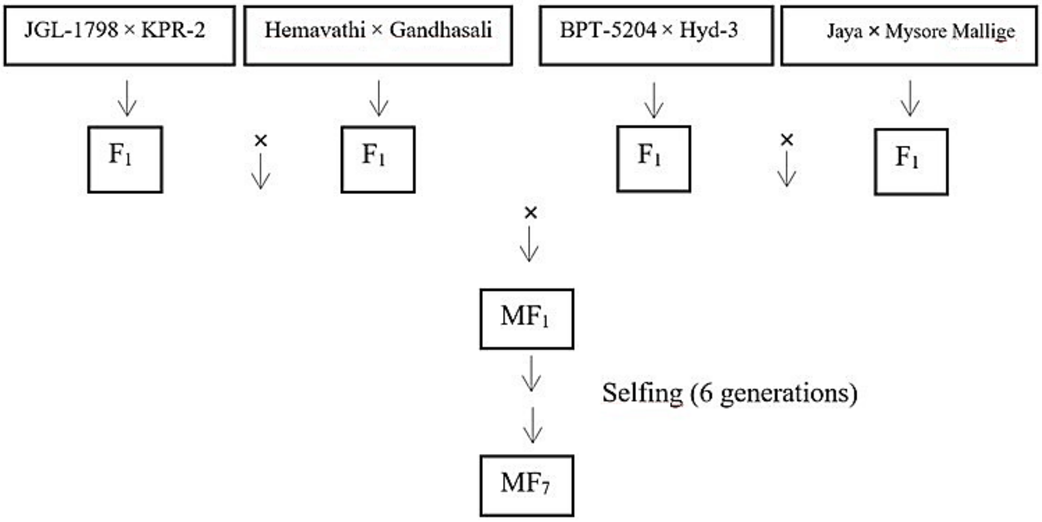

Fig. 1. Flow chart representing the generation of MAGIC lines

2.1 Statistical Analysis

The R-statistic program (R version 4.3.3 – https://www.R-project.org) was utilized to conduct the statistical analysis. The analysis is done based on the following:

2.2 Estimation of Genetic Parameters

The genotypic and phenotypic variances were estimated using the formula given by Weber and Murthy, (1952).

Genotypic variance (σ^2_g) =

$$\frac{MSS\ (genotype) - MSS\ (error)}{Number\ of\ replications}$$

Phenotypic variance (σ^2_p) = σ^2_g + MSS (error)

2.3 Coefficient of Variability

The coefficient of variability both at phenotypic and genotypic levels for all the characters were computed by applying the formula as suggested by Burton and De Vane (1953).

$$CV\ (\%) = \frac{S.D}{\bar{X}} \times 100$$

S.D: standard deviation; $\bar{X}$: grand mean of the character

Phenotypic coefficient of variation (PCV):

$$PCV = \frac{\sigma p}{\bar{X}} \times 100$$

Genotypic coefficient of variation (GCV):

$$GCV = \frac{\sigma g}{\bar{X}} \times 100$$

Where,
$\bar{X}$ = grand mean of the character
σp= phenotypic standard deviation
σg = genotypic standard deviation
PCV and GCV were calcuated as suggested by Shivasubramanian and Menon (1973).

Heritability (h^2) broad sense:

Heritability in broad sense for all the characters was computed by the formula suggested by Lush (1949).

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,
h^2 = heritability
σ^2 g = genotypic variance
σ^2 p = phenotypic variance

Genetic advance as per cent mean (GAM):

The expected GA as *per cent* of mean was estimated according to the formula given by Johanson et al. (1955)

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where,
GA = Genetic advance
$\bar{X}$ = General mean

Correlation coefficients: The correlation coefficients were calculated to determine the degree of association of the characters with yield and also among the different yield components. Both genotypic and phenotypic coefficients of correlation between all pairs of characters were determined by using variance and covariance components as suggested by Al Jibouri (1958).

$$r_{g(x,y)} = \frac{Cov_{g(x,y)}}{\sqrt{\sigma^2_{g(x)} \cdot \sigma^2_{g(y)}}}$$

$$r_{p(x,y)} = \frac{Cov_{p(x,y)}}{\sqrt{\sigma^2_{p(x)} \cdot \sigma^2_{p(y)}}}$$

Where,
r_p and r_g are phenotypic and genotypic correlation coefficients, respectively.
$Cov_{p(x,y)}$ and $Cov_{g(x,y)}$ are phenotypic and genotypic covariance between the characters, x and y.
$\sigma_{p(x)}^2$ and $\sigma_{p(y)}^2$ are the phenotypic variances of the characters x and y.
$\sigma_{g(x)}^2$and $\sigma_{g(y)}^2$ are the genotypic variances of the characters x and y.
The calculated value of r was compared with table r value with (n-2) degree of freedom at 5 and 1 *per cent* level of significance.

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

ANOVA is a tool for plant breeders to categorize variability into known and unknown sources. The prevalence of vast variability among the treatments is emphasized by significant variations among them. MAGIC lines exhibited significant variations for all traits studied except days to 50% flowering, indicating significant amount of variation among the genetic material utilized in the study (Table 1). A diverse genetic pool enables breeders to select and combine favorable alleles, leading to the development of superior rice varieties (2024). “Studies have shown that understanding and utilizing genetic diversity within rice germplasm is critical for effective improvement strategies” (Kimwemwe et al., 2023). “Without sufficient genetic variability, the potential for improvement diminishes, limiting the development of robust crop varieties” (Salgotra & Chauhan, 2023).

3.2 Variability Studies

For developing selection methods, understanding the estimates of variability in terms of yield and its component characteristics is crucial. In order to develop an appropriate breeding method, it is necessary to analyze the heritable and non-heritable components of phenotypic variability. In this context, various morphological characters were studied in 50 MAGIC lines for variability parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (h^2_{bs}), and genetic advance as per cent of mean (GAM). High PCV and moderate GCV were observed for number of filled grains per panicle (21.24% and 14.86%) while moderate PCV and GCV was observed for traits plant height (14.03% and 10.41%), number of tillers per plant (17.02% and 13.43%), test weight (14.57% and 13.07%) and grain yield per plant (21.57% and 18.31%). This indicates the existence of wide genetic base among the MAGIC lines taken under study and possibility of genetic improvement through direct selection for these traits.

In general, the magnitude of GCV was lower when compared to the PCV for almost all characteristics, suggesting that variability was not just attributable to genotype but also the environment. The presence of ample amount of variation reveals the effectiveness of selection (Table 2). The results are in line with findings of Sumanth et al., (2017), Chamar et al., (2021) and Demeke et al., (2021). “The differences between PCV and GCV were very small for PF, LB and TGW, indicating additive gene action for these traits. This observation is consistent with the previous research findings” (Niharika et al., 2022) that reported minimal differences between PCV and GCV for PH, DM, PF, LB and TGW.

Among the traits studied, moderate to high heritability was observed for the traits *viz.,* plant height, number of tillers per plant, panicle length, number of filled grains per panicle, panicle fertility, test weight, length to breadth ratio and grain yield. Similar results were obtained by Edukondalu et al. (2017), Anyaoha et al., (2018) and Bandi et al., (2018). GAM estimates the measure of the genetic gain obtained under selection, which was higher for the traits *viz.,* number of tillers per plant, number of filled grains per panicle, test weight and grain yield. Edukondalu et al., (2017) and Demeke et al., (2022) obtained similar results. In the current investigation, traits viz., plant height, test weight and grain yield exhibited high GAM coupled with high heritability along with moderate to high GCV and PCV indicating that, due to additive gene action the high heritability is exhibited which can be employed in crop improvement program and can implement effective selection process.

Table 1. Analysis of variance for yield and yield attributing traits in rice MAGIC lines

Source of variation	df	DFF	DM	PH	NT	PL	NFG	PF	LB	TW	GY
		Mean sum of squares									
Replications	1	45.94	193.97	344.07	0.01	0.01	2755.35	0.07	0.04	0.59	4.36
Treatment	57	41.81	146.12*	467.80**	20.26**	9.99**	3064.48**	62.11**	0.21**	10.97**	147.99**
Error	57	27.68	82.33	135.77	4.71	4.98	1049.76	19.21	0.03	1.19	23.99
Mean		107.35	134.00	123.82	20.76	24.71	213.55	84.83	3.78	16.92	43.00

**Significant at P = .05, ** Significant at P = .01*

DFF- Days to fifty percent flowering, DM- Days to maturity, PH- Plant height, NT- Number of tillers per panicle, PL- Panicle length, NFG- Number of filled grains per panicle, PF- Panicle Fertility, LB- Length to breadth ratio, TW- Test weight, GY- Grain yield per plant

Table 2. Mean, range and genetic variability parameters for yield and yield attributing traits in rice MAGIC lines

Sl. No.	Traits	Mean	Range		GCV (%)	PCV (%)	h^2_{bs}(%)	GAM (%)
			Minimum	Maximum				
1	**Days to 50% flowering**	107.35	95.00	126.00	2.48	5.49	20.34	2.30
2	**Days to maturity**	134.00	100.00	154.00	4.21	7.98	27.92	4.59
3	**Plant height (cm)**	123.82	76.50	200.00	10.41	14.03	55.01	15.90
4	**Number of tillers /plant**	20.76	12.00	27.80	13.43	17.02	62.27	21.83
5	**Panicle length (cm)**	24.61	17.00	30.67	6.87	10.06	46.67	9.67
6	**Number of filled grains/ panicle**	213.55	129.34	332.67	14.86	21.24	48.97	21.43
7	**Panicle fertility (%)**	84.83	69.06	94.62	5.46	7.52	52.75	8.17
8	**Length/ Breadth ratio**	3.78	3.01	5.03	7.95	9.30	73.02	14.00
9	**Test weight (g)**	16.92	12.75	26.88	13.07	14.57	80.36	24.13
10	**Grain yield/ plant (g)**	43.00	23.75	61.90	18.31	21.57	72.10	32.03

GCV- Genotypic co-efficient of variation, PCV- Penotypic co-efficient of variation, h^2_{bs}- Broad sense heritability, GAM- Genetic advance as percent of mean

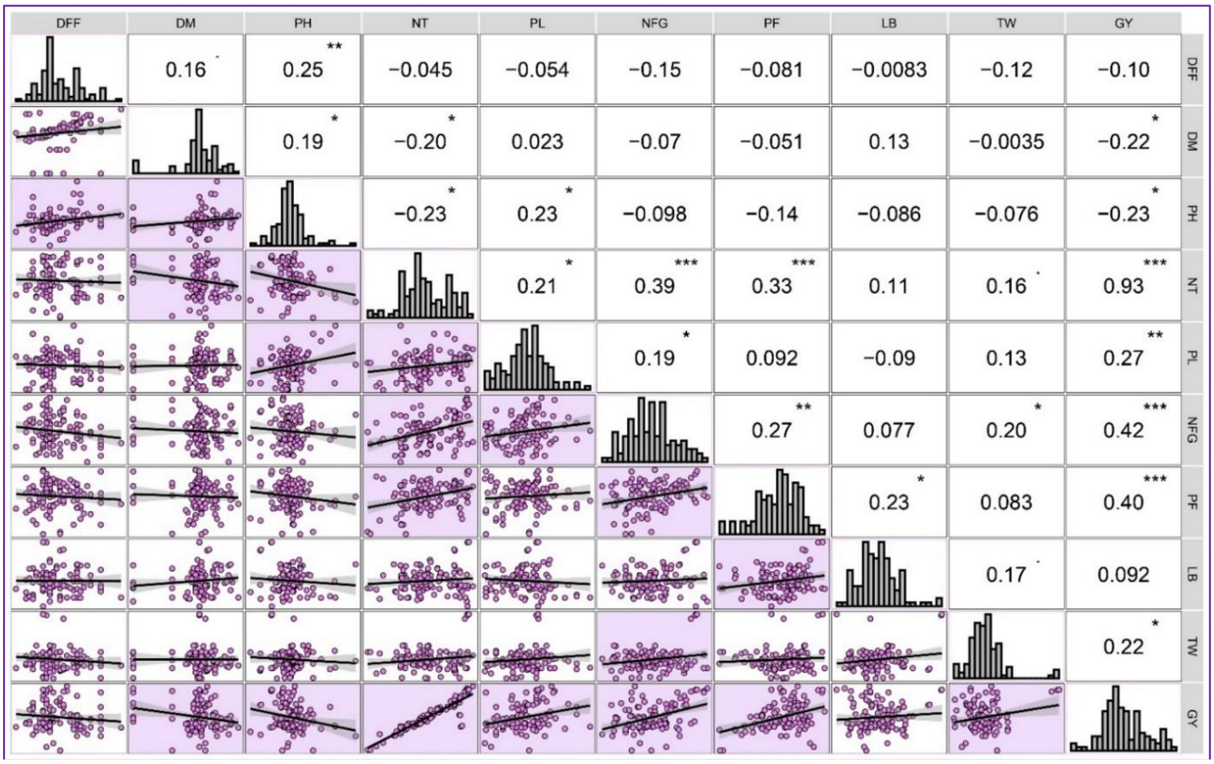

Fig. 2. Trait association between yield and yield attributing traits in rice

Significant at P = .05, ** Significant at P = .01 probability level, * Significant at P = .001 probability level*
DFF- Days to fifty percent flowering, DM- Days to maturity, PH- Plant height, NT- Number of tillers per panicle, PL- Panicle length, NFG- Number of filled grains per panicle, PF- Panicle Fertility, LB- Length to breadth ratio, TW- Test weight, GY- Grain yield per plant

3.3 Correlation Studies

"Correlation establishes the extent of association between yield and its components thus giving an obvious understanding of their association with grain yield. Correlation is a powerful tool to study the association of characters and is therefore very useful to decide selection strategy for improvement of a character without sacrificing gain in the other traits" (Babu et al., 2012). This statistical approach measures the extent and direction of the relationship between two variables, guiding researchers in understanding complex trait interactions. Phenotypic correlations among several traits were analyzed in 50 MAGIC lines to identify key associations beneficial for breeding programs.

Grain yield per plant exhibited significant positive correlation with several yield attributing traits like number of tillers per plant (0.93), panicle length (0.27), number of filled grains per panicle (0.42), panicle fertility (0.40) and test weight (0.22), suggesting indirect selection of these traits would impart yield improvement (Fig. 2). These results were in accordance with Kumar et al., (2022), Dhavaleshvar et al., (2019), Naotia et al., (2021), Katkani et al., (2023). In contrast, significant negative association was shown by plant height with grain yield per plant (-0.23) (Katkani et al., 2023). By understanding these associations, breeders can focus on improving traits that are strongly correlated with yield, even if they are not directly selecting for yield itself. This holistic understanding allows for more balanced selection strategies, leading to the development of rice varieties with optimized yield potential under diverse environmental conditions.

4. CONCLUSION

Genetic variability studies revealed significant differences for all traits examined, showing that these MAGIC lines had enough variability and can be exploited for further improvement. Traits *viz.,* number of tillers per plant, number of filled grains per panicle, plant height and test weight exhibited moderate to high GCV, PCV, heritability and genetic advance as percent of mean indicating sufficient amount of variation which imparts effectiveness of selection. Results revealed that PCV was higher than GCV for all the traits under studied, which could be due to environmental factors for the expression of these characters. Breeders should take this into consideration when setting a breeding programme for yield improvement. Positive association of yield attributing traits *viz.,* panicle length, panicle fertility, number of tillers per plant and number of filled grains per panicle with grain yield per plant can be effectively utilized for indirect selection for yield improvement.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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