Original Research Article

Trait Association and Genetic Variability Studies in Rice MAGIC Lines for Yield and Yield Attributes

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ABSTRACT

Aims: Improvement in grain yield, a quantitative trait is one of the key objective of plant breeders which depends upon the magnitude of genetic variability existing in the genetic material utilized in the breeding programme. A set of 50 rice MAGIC lines were utilized to assess the genetic variability and association between grain yield and other morphological traits *viz*, days to fifty per cent flowering, days to maturity, plant height, number of tillers per plant, panicle length, number filled grains per panicle, panicle fertility, length to breadth ratio and test weight.

Study design: The investigation was carried out in a randomized complete block design with two replications.

Place and Duration of Study: Zonal agricultural and horticultural research station, Navile, Shivamogga during *kharif* 2022.

Methodology: 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. Data was recorded and statistical analysis was carried out using R software

Results: The analysis of variance revealed the presence of significant differences among MAGIC lines for all traits studied. Moderate to high genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability coupled with high genetic advance as per cent of mean were recorded for traits, plant height, number of tillers per plant, number of filled grains per panicle, test weight and grain yield per plant. Correlation studies revealed that, grain yield per plant was in positive association with number of tillers per plant, panicle length, number of filled grains per panicle, panicle fertility and test weight.

Conclusion: Our study emphasized the importance of indirect selection of traits *viz.,* number of tillers per plant, panicle length, number of filled grains per panicle, panicle fertility and test weight imparts improvement in grain yield in rice.

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. Globally, rice is being cultivated in 167.10 mha with the production of 782 mt and an average productivity of 4.67 t/ha [1]. 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 was 47.6 mha, 137.83 mt and 4.3 t/ha, respectively~~.~~ [1].

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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 advance 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 [2]. Additionally, the success of crop improvement efforts is largely influenced by the nature and extent of genetic variability within the crop, as it determines the potential for selecting and improving desirable traits [3].Therefore, present study was conducted to evaluate genetic variability and correlation among rice MAGIC lines.

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Commented [NA3]: Repetitive statement (The level of genetic variability within the gene pool directly influences the success of breeding efforts, determining the potential for selecting desirable traits).

Commented [NA4]: Genetic variability among the MAGIC lines and correlation among the traits.

2. MATERIAL 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 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 R-statistic program (R version 4.3.3 – https://www.R-project.org) was utilized to conduct the statistical analysis.The characters for which observations recorded are as follows; Days to 50 per cent flowering, days to maturity, plant height, number of tillers per plant, panicle length, number of filled grains per panicle, panicle fertility, test weight, length/breadth ratio and grain yield per plant.

What lines are used to develop the magic population? Mention briefly about how the population was developed. If the population is referenced from any other literature, please mention that.

It is also essential to mention how each statistical measures like GCV, PCV, H^2, GAM are calculated. Mention formulas.

3. RESULTS AND DISCUSSION (DISCUSSION IS NOT ENOUGH)

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. Studies have shown that understanding and utilizing genetic diversity within rice germplasm is critical for effective improvement strategies [4].Without sufficient genetic variability, the potential for improvement diminishes, limiting the development of robust crop varieties [5].

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}~~ H^2), 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 pla` nt (21.57% and 18.31%). 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. [6], Chamar et al. [7] and Demeke et al. [8].

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. [9], Anyaoha et al. [10] and Bandi et al. [11]. 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. [9] and Demeke et al. [8] 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.

3.1 Correlation studies

Correlation analysis is a vital tool in assessing the interrelationship between traits, offering valuable insights into genetic, physiological, and biochemical linkages. 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.

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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 (Figure 1). These results were in accordance with Kumar et al. [12], Dhavaleshvar et al. [13], Naotia et al. [14], Katkani et al. [15]. In contrast, significant negative association was shown by plant height with grain yield per plant (-0.23) [16]. 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.

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 1% * significant at 5%*

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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}~~H^2*- Broad sense heritability, GAM- Genetic advance as percent of mean*

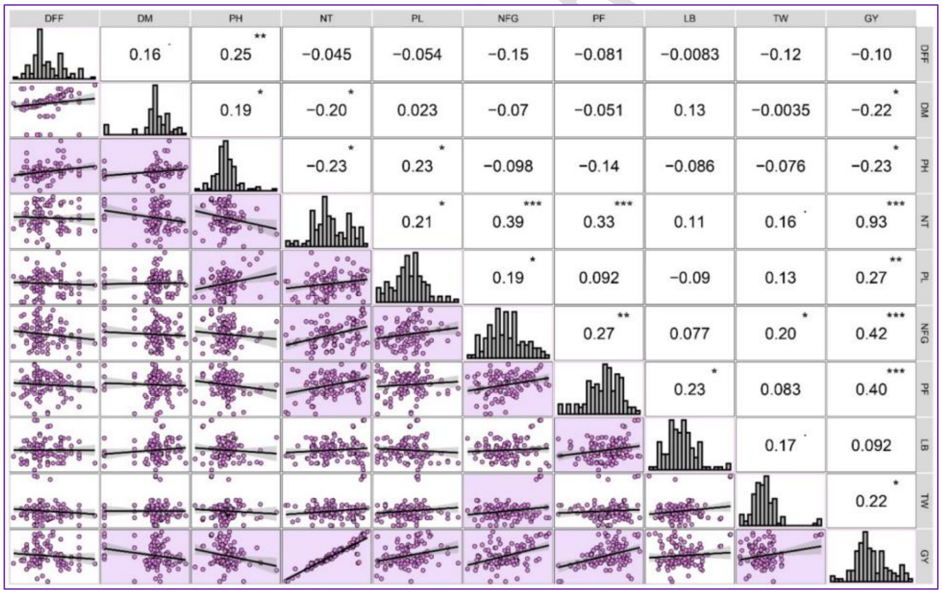

Figure 1: Trait association between yield and yield attributing traits in rice

Significant at P =* ~~0~~*.05, ** Significant at P =* ~~0~~*.01 probability level, * Significant at P =* ~~0~~*.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

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. 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 ~~s~~yield improvement.

HOW DO YOU CORRELATE EACH RESULTS WITH EACHOTHER CONCLUDE THAT WAY? THE CONCLUSION SEEMS LIKE THE RESULT.

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