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ASSESSMENT OF GENETIC PARAMETERS, CORRELATION AND PATH COEFFICIENT ANALYSIS FOR YIELD AND YIELD COMPONENT TRAITS IN RICE (*ORYZA SATIVA* L.)

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ABSTRACT

The present investigation was carried out with 29 genotypes of rice during *Kharif*, 2022 in Randomized Block Design at Regional Agricultural Research Station (RARS), PJTAU, Warangal, Telangana, to study genetic variability, heritability, genetic advance, correlation and path coefficient analysis for 7 quantitative characters. On the basis of mean performance highest grain yield kg per ha reported in UPLRH 181325 (9479) genotype followed by IRRH-130 (7634), HRI 214 (7425), VNR 288 (7299) and UPLRH 162087 (7277). Analysis of variance revealed significant difference among 29 rice genotypes for all characters indicating the existence of variability. High genotypic and phenotypic (GCV and PCV) coefficient of variations were observed for grain yield kg per ha and number of filled grains per panicle, suggesting that these characters were relatively much influenced by the environment. High heritability coupled with high genetic advance as percent mean for number of filled grains per panicle, 1000 grain weight and Grain yield kg per ha indicating the effectiveness of direct selection for improvement of these traits. Correlation and path-coefficient analysis, concluded that, 1000 grain weight, days to 50% flowering and plant height exhibited maximum positive direct effect on grain yield seems to be primary yield contributing characters and could be relied upon for selection of genotypes to improve genetic yield potential of rice. Hence, utmost importance should be given to these characters during selection for single plant yield improvement.

Keywords: GCV, PCV, Heritability, Genetic Advance, Rice, Correlation, Path Analysis

Introduction

Rice (*Oryza sativa* L.) is the most important food crop and a primary food source for more than one third of the world's population. More than 90 percent of the world's rice is produced and consumed in Asia, which is known as the "rice bowl of the world." Rice feeds more than half the world's population and improving the productivity of this grain is necessary for food security. India has emerged as the world's largest rice producer during 2024–25, with a production of 150.18 million tonnes, accounting for about 28% of global rice production. The crop covers an area of 51.27 million hectares, with an average productivity of 2.93 tonnes per hectare. (Unified Portal for Agricultural Statistics, Department of Agriculture and Farmers Welfare, Ministry of Agriculture and Farmers Welfare, Government of India, 2025). In Telangana, rice is of

prime importance, being cultivated on 4.81 million hectares and producing 17.45 million tonnes with a productivity of 3.63 t/ha annually (Unified Portal for Agricultural Statistics, 2025). To meet the growing demand of human population, rice varieties with higher yield potential and greater yield stability need to be developed (Khush, 2005). To date, majority of the increased yields have come from manipulating traits to meet future demands, which will necessitate the use of novel genetic resources. Many traits have been identified as possessing the potential to improve yield and high expression of these traits has been found in germplasm collections (Chandra Bose *et al.*, 2024).

Significant improvement in rice production and productivity was achieved through the Green Revolution; however, the current yield plateau is restricting further increases in production needed to

meet the demands of the ever-growing population, particularly in developing and underdeveloped countries (Sreelaxmi *et al.*, 2021). Information on heritability, genetic advance, and the extent of genetic variability for grain yield and its component traits in the experimental material would greatly assist breeders in selecting elite genotypes to overcome these yield plateaus in rice. Furthermore, understanding the direct and indirect effects, along with the degree and direction of association between grain yield and its component characters, would also help breeders develop superior varieties through more effective selection strategies. Hence, an attempt was made to estimate the extent of variation in yield-contributing traits among 29 rice genotypes by analyzing genetic parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance, correlation, and path coefficient analysis. These parameters help in formulating suitable selection indices for the improvement of rice.

Materials and Methods

The present investigation was carried out at Regional Agricultural Research Station (RARS), PJTAU, Warangal, Telangana, India during *kharif*, 2022 (July–November) which is located at 18°01'N Latitude, 79°60'E Longitude and at an elevation of 270 m above mean sea level (MSL). Experimental material comprises of 29 rice genotypes (Table 1) which includes varieties and hybrids grown in randomized complete block design with 3 replications. 25 days old seedlings of each genotype was transplanted in 9.6 m² area by adopting spacing of 15 cm × 15 cm between the rows and within the row. Two-three seedlings were planted at each hill. All recommended package of practices and need based plant protection measures were followed to raise a good crop. Data were recorded at maturity on 10 random plants for each entry in each replication for number of productive tillers m⁻², plant height (cm), panicle length (cm) and number of filled grains panicle⁻¹, days to 50% flowering and grain yield kg ha⁻¹ were recorded on whole plot basis, whereas, random sample was used to estimate 1000 grain weight (g) for each genotype in each replication. The mean data after computing for each trait was subjected to analysis of variance (Panse and Sukhatme, 1995), Genotypic and phenotypic co-efficients of variation were computed following the methodology outlined by Burton (1952), while the estimates of heritability and genetic advance were obtained as per the procedures outlined by Burton and Devane (1953), and Johnson *et al.* (1955), respectively. Correlation was worked out using the formulae suggested by Falconer (1964),

while the direct and indirect contribution of various characters to yield were calculated through path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). For statistical analysis software Window Stat Version 9.1 was used.

Results and Discussion

Analysis of variance (ANOVA) for yield and yield attributing traits revealed highly significant mean squares due to genotypes for all traits, indicating the existence of sufficient variation among the genotypes for yield and yield component traits studied (Table 2). Estimates of mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h² broad sense) and genetic advance as percent of mean (GAM) for morphological and yield component traits studied in the current study were depicted in Table 3. Wide range of variation was observed for plant height (96.4-132.1 cm) and number of filled grains per panicle (157.0-334.0) grain yield kg ha⁻¹ (3334.6-9479.3). On the basis of mean performance highest grain yield kg per ha reported in UPLRH 181325 (9479) genotype followed by IRRH-130 (7634), HRI 214 (7425), VNR 288 (7299) and UPLRH 162087 (7277).

Genetic variability parameters

The estimates of phenotypic coefficient of variation for all the characters under study were higher than the estimates of genotypic coefficient of variation. Suggested the presence of high degree of variability and so better scope for the improvement through simple selection. These findings are in agreement with the reports by Rama sai *et al.* (2025), Chandra *et al.* (2022), Devi *et al.* (2022), Nirmaladevi *et al.* (2015). Low PCV and GCV estimates were observed for number of productive tillers m⁻² (5.75% and 2.49%), days to 50% flowering (6.32% and 6.15%), panicle length (6.78% and 6.42%) and plant height (7.72% and 7.67%) indicates narrow genetic base for these traits. Improvement in these characters can be brought about by hybridization or induced mutagenesis to widen genetic base followed by pedigree selection in advanced generations. Similar findings were previously reported by Suraj Kumar *et al.* (2024), Priyanka *et al.* (2023), Chandra *et al.* (2022), Chavan *et al.* (2022), Devi *et al.* (2022) and for days to 50% flowering, panicle length and plant height, Chandra *et al.* (2022) and Singh *et al.* (2020) for number of productive tillers m⁻² and plant height, Umamaheswara *et al.* (2024) for plant height. While high PCV and GCV was manifested by grain yield kg ha⁻¹ (24.78% and 23.05%) and number of filled grains panicle⁻¹ (21.63% and 19.96%) indicating the existence of

sufficient variation among the genotypes for potential yield improvement through selection. Similar findings were previously reported by Singh *et al.* (2024), Chandra Bose *et al.* (2024), Devi *et al.* (2022) and Sreelaxmi *et al.* (2021) for number of filled grains panicle⁻¹ and grain yield kg ha⁻¹ while moderate PCV and GCV estimates was observed for 1000 grain weight (16.41% and 15.84%) this indicates the existence of comparatively moderate variability for this trait, which could be exploited for improvement through selection in advanced generations. Similar findings by Rama Sai *et al.*, (2025), Sai Teja *et al.* (2023), Chavan *et al.* (2022), Chandra *et al.* (2022), Sreelaxmi *et al.* (2021) and Sudeepthi *et al.* (2020).

Heritability and Genetic Advance

Heritability is the measure of transmission of characters from generation to generation and estimates of heritability are helpful to the breeder in selecting superior individuals and successfully utilizing them in breeding programme(s) (Bharathi *et al.*, 2017). Heritability estimates were high for all the traits except number of productive tillers m⁻² (18.7%), Maximum heritability estimates were recorded for plant height (98.8%) followed by days to 50% flowering (94.7%), 1000 grain weight (93.2%), panicle length (89.7%), grain yield kg ha⁻¹ (86.4%) and number of filled grains panicle-1 (85.2%) indicating that heritability observed was due to additive gene effects and therefore selection would be effective in improvement of these traits. These results are in conformity with the findings by Chandra Bose *et al.* (2024), Priyanka *et al.* (2023), Singh *et al.* (2024), Akshay *et al.* (2022) for number of filled grains panicle-1 and plant height, Rama sai *et al.* (2025) for 1000 grain weight, Similarly, high genetic advance as percent of mean was manifested by grain yield kg ha⁻¹ (44.11) followed by number of filled grains panicle-1 (37.96) and 1000 grain weight (31.5), whereas number of productive tillers m⁻² (2.23) manifested low genetic advance as per cent over mean. These findings are in consonance with earlier reports of Chandra Bose *et al.* (2024) and Priyanka *et al.* (2023) for number of productive tillers m⁻²; Chandra Bose *et al.* (2024), Singh *et al.* (2024), Priyanka *et al.* (2023), Nath and Kole (2021) and Sindhura *et al.* (2022) for grain yield/plant, number of filled grains panicle-1 and 1000 grain weight. Based on the results of variability parameters, it may be concluded that number of filled grains per panicle, test weight and Grain yield kg ha⁻¹ exhibited high heritability and high genetic advance as per cent of mean whereas the character test weight manifested moderate PCV and GCV along with high heritability as well as high genetic advance as per cent of mean suggesting the

predominance of additive gene action in the inheritance of these traits. Hence, simple selection will be highly rewarding for improving these characters.

Correlation coefficients

Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in the yield. In the present study, Grain yield exhibited positive and significant correlation with days to 50% flowering (0.3710**, 0.4041**), plant height (0.3172**, 0.3389**) and test weight (0.2409**, 0.2870**) indicating simultaneous improvement of grain yield with improvement of these characters (Tables 4 and 5). Hence, priority should be given to these traits while making selection for improvement of grain yield. These findings are in harmony with earlier findings of Chandra Bose *et al.* (2024) and Priyanka *et al.* (2023), Saketha *et al.* (2023), Kavitha *et al.* (2020), Nath and Kole (2021), for days to 50% flowering, plant height, and 1000 grain weight. The negative non significant correlation with grain yield was reported for panicle length. Further, studies on inter-character association between yield component traits revealed significant and positive correlation of days to 50% flowering with plant height (0.5929**, 0.6138**) and number of productive tillers m⁻² (0.208**, 0.481**) and panicle length (0.2906**, 0.3123**) (Figure 1 & 2). Significant and positive correlations were noticed for plant height with panicle length (0.479**, 0.511**) and test weight (0.3160**, 0.3333**) at both phenotypic and genotypic levels, whereas negative non significant relation with number of filled grains panicle⁻¹ (-0.1746, -0.1817). Plant height recorded positive and significant association with grain yield kg ha⁻¹ (0.317**, 0.338**). This revealed that plant height is an important trait for realizing more yield and tallness is associated with problem of lodging. Plants having sturdy and medium height culms should be preferred. Tejaswini *et al.* (2018) Babu *et al.* (2012), Devi *et al.* (2017) also reported similar findings for days to 50 per cent flowering and plant height. Selection based on the plant height simultaneously improves grain yield per plant. Panicle length manifested significant and positive relationship with test weight (0.2567**, 0.2915**), suggesting that the genotypes with longer panicles had long bold grain resulting in high test weight. These results were in agreement with previous findings of Priyanka *et al.* (2023), Premkumar *et al.* (2016) and Gunasekara *et al.* (2017). In contrast, significant negative association was observed for the traits, namely, number of productive tillers m⁻² at genotypic level with panicle

length; and number of filled grains panicle⁻¹ with 1000 grain weight, probably due to competition for a common possibility such as nutrient supply. Balanced selection therefore needs to be practiced while attempting simultaneous improvement of these traits. Studies by Chandra Bose *et al.* (2024), Herawati *et al.* (2021) Saha *et al.* (2019) revealed similar findings for number of productive tillers m⁻² with panicle length and for number of filled grains panicle⁻¹ with test weight respectively.

Path analysis studies

Path coefficient analysis performs partitioning of correlation coefficient into direct and indirect effects to determine the component characters' relative importance. It provides information about the relationship between yield and its component traits, which can be used to design an adequate selection criterion. Various direct and indirect effects of component traits on grain yield were discussed hereunder and the results are presented in Table 5. Selection based on characters with positive direct effect along with positive correlation with grain yield kg ha⁻¹ are needed to achieve fruitful results for yield improvement in breeding programmes. The results of path coefficient analysis revealed that 1000-grain weight manifested highest positive direct effect (0.6258 and 0.4097) on grain yield kg ha⁻¹ followed by days to 50% flowering (0.6889 and 0.2904), plant height (0.3745 and 0.2160) and number of filled grains panicle⁻¹ (0.2226 and 0.3077) at both genotypic and phenotypic levels (Table 5). The traits, 1000 grain weight, days to 50% flowering and plant height had also recorded significant and positive association with grain yield kg ha⁻¹. High direct effects of these traits therefore appear to be the main factor for their association with grain yield kg ha⁻¹. Hence, the traits should be considered as important selection criteria in

all rice improvement programmes for grain yield and direct selection for these traits is recommended for effective yield improvement. The results are in conformity with the findings of Kalpande *et al.* (2024), Sudeepthi *et al.* (2020), Devi *et al.* (2017), Saha *et al.* (2019) and Nath and Kole (2021) However, panicle length had recorded negative correlation with grain yield kg ha⁻¹ and hence, a restricted simultaneous selection model needs to be followed for improvement of grain yield through the trait by imposing restrictions to nullify the undesirable indirect effects in order to make use of the direct effects (Singh and Chaudhary, 1977). Further, panicle length and number of productive tillers m⁻² had recorded negative direct effects on grain yield kg ha⁻¹. These findings are in agreement with Sudeepthi *et al.* (2020) for panicle length.

Conclusion

High heritability (broad sense) coupled with high genetic advance as percentage of mean was reported for characters like number of filled grains per panicle, 1000 grain weight and grain yield kg per ha indicating additive gene action. PCV values found to be slightly higher than GCV values showing the influence of environment on character expression. High PCV and GCV estimates were recorded for grain yield kg per ha followed by number of filled grains per panicle. Correlation and path coefficient analyses further revealed that characters like 1000 grain weight, days to 50% flowering and plant height exhibited maximum positive direct effect on grain yield seems to be primary yield contributing characters and could be relied upon for selection of genotypes to improve genetic yield potential of rice. Hence, concluded the selection among the traits is preferred to increase the yield of rice per plant.

Table 1: List of 29 rice genotypes used in the study.

S.No.	Name of the Genotype	S.No.	Name of the Genotype
1	KNM 11544	16	HRI-214 (Hybrid)
2	NLR 3684	17	Pusa RH-60 (Hybrid)
3	RCPR 82-IR 14L362	18	UPLRH-162087 (Hybrid)
4	CRU-BCKV-22-35 (14-N22/35-13-4-5-2)	19	US 314 (Hybrid Check)
5	KPS 6251	20	IIRRH-130 (Hybrid)
6	MTU 1363	21	VNR-228 (Hybrid)
7	CR 4060-1318-5-2-2-2-1-5-3-4	22	JKRH-1004 (Hybrid)
8	CO-51(National Check)	23	UPLRH-180842 (Hybrid)
9	RNR 39029	24	PAN-2150 (Hybrid)
10	RTN 1403-7-1-1-2-4	25	WGL 962 (Local Check)
11	CRR 841-IR14L245	26	RP 6613- MSM-65-Bio-36-4-15
12	HKR 2018-39	27	RP 6613--MSM-66-Bio-88-4-15
13	MTU 1153 (Zonal Check)	28	RP 6612-MSM-63-Bio-62-4-15
14	KNM 11505	29	Varalu (RP)
15	UPLRH-181325 (Hybrid)		

Source: ICAR-IIRR, Rajendranagar, Hyderabad supplied seed material as a part of AICRIP trial evaluation during kharif, 2022

Table 2 : Analysis of variance (ANOVA) for 7 characters among 29 genotypes of rice

Character	Mean Sum of Squares		
	Replications (df=2)	Treatments (df=28)	Error (df=56)
Days to 50% flowering	2.77	100.82**	1.83
No. of Productive tillers m ⁻²	861.96	502.12*	296.81
Plant height (cm)	2.98	228.36**	0.93
Panicle length (cm)	0.095	8.899**	0.329
No. of Grains panicle-1	925.75	5962.81**	326.699
1000 grain weight (g)	1.03	45.130**	1.07
Grain yield (Kg ha ⁻¹)	438895.7	5640981.65**	281166.6

*, **significant at 5% and 1% level, respectively

Table 3: Estimates of genetic variability parameters for 7 different characters of rice genotypes

Character	Mean	Range		GCV	PCV	h ² (b) (%)	Genetic advance	Genetic advance as % of mean (5%)
		Minimum	Maximum					
Days to 50% Flowering	93.0	84	101	6.155	6.324	94.7	11.518	12.34
Number of productive tillers m ⁻²	332.0	309	360	2.492	5.757	18.7	7.377	2.23
Plant height (cm)	113.47	96.4	132.13	7.673	7.72	98.8	17.82	15.712
Panicle length (cm)	26.31	22.46	29.20	6.424	6.784	89.7	3.297	12.53
Number of grains panicle-1	217.0	157.0	334.0	19.968	21.634	85.2	82.41	37.965
1000 grain weight (g)	24.18	13.30	31.83	15.84	16.413	93.2	7.619	31.497
Grain yield Kg ha ⁻¹	5802.0	3334.6	9479.3	23.035	24.78	86.4	2559.43	44.109

h² (b)=Heritability in broad sense; GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation

Table 4: Estimates of Genotypic and Phenotypic Correlation coefficients between yield and its related traits in 29 rice genotypes

Character		Days to 50% flowering	Plant height (cm)	Number of productive tillers m ⁻²	Panicle length (cm)	Number of filled grains panicle ⁻¹	1000-grain weight (g)	Grain yield kg ha ⁻¹
Days to 50% flowering	rp	1.000	0.5929**	0.2085*	0.2906**	0.1086	0.1089	0.3710**
	rg	1.000	0.6138**	0.4812**	0.3123**	0.1244	0.1131	0.4041**
Plant height (cm)	rp		1.000	0.1460	0.4791**	-0.0867	0.3162**	0.3172**
	rg		1.000	0.2906**	0.5116**	-0.0972	0.3333**	0.3380**
Number of productive tillers m ⁻²	rp			1.000	-0.1596	-0.0496	0.1543	0.0229
	rg			1.000	-0.3288**	-0.1657	0.2265	0.1061
Panicle length (cm)	rp				1.000	-0.1746	0.2567*	-0.0460
	rg				1.000	-0.1817	0.2915**	-0.0688
Number of filled grains panicle ⁻¹	rp					1.000	-0.5292**	0.1665
	rg					1.000	-0.5814**	0.1826
1000 grain weight (g)	rp						1.000	0.2409*
	rg						1.000	0.2870**
Grain yield kg ha ⁻¹	rp							1.000
	rg							1.000

* Significant at 5% and ** Significant at % levels

Table 5: Direct and indirect effects between yield and yield related traits in 29 rice genotypes at phenotypic and genotypic levels

Character	Corr.	Days to 50% flowering	Plant height (cm)	Number of productive tillers m ⁻²	Panicle length (cm)	Number of filled grains panicle ⁻¹	1000-grain weight (g)	Correlation with grain yield kg ha ⁻¹
Days to 50% flowering	rp	0.2904	0.1722	0.0606	0.0844	0.0315	0.0316	0.3710**
	rg	0.6889	0.4229	0.3315	0.2151	0.0857	0.0779	0.4041**
Plant height (cm)	rp	0.1281	0.2160	0.0315	0.1035	-0.0187	0.0683	0.3172**
	rg	0.2299	0.3745	0.1088	0.1916	-0.0364	0.1248	0.3380**
Number of productive tillers m ⁻²	rp	-0.0348	-0.0244	-0.1670	0.0267	0.0083	-0.0258	0.0229
	rg	-0.3464	-0.2092	-0.7200	0.2368	0.1193	-0.1631	0.1061

Panicle length (cm)	rp	-0.0907	-0.1495	0.0498	-0.3120	0.0545	-0.0801	-0.0460
	rg	-0.2667	-0.4370	0.2809	-0.8542	0.1553	-0.2491	-0.0688
Number of filled grains panicle ⁻¹	rp	0.0334	-0.0267	-0.0153	-0.0537	0.3077	-0.1629	0.1665
	rg	0.0277	-0.0216	-0.0369	-0.0405	0.2226	-0.1294	0.1826
1000 grain weight (g)	rp	0.0446	0.1296	0.0632	0.1052	-0.2168	0.4097	0.2409*
	rg	0.0708	0.2086	0.1418	0.1825	-0.3639	0.6258	0.2870**
Grain yield kg ha ⁻¹	rp	0.3710	0.3172	0.0229	-0.0460	0.1665	0.2409	1.0000
	rg	0.4041	0.3380	0.1061	-0.0688	0.1826	0.2870	1.0000

* Significant at 5% and ** Significant at % levels

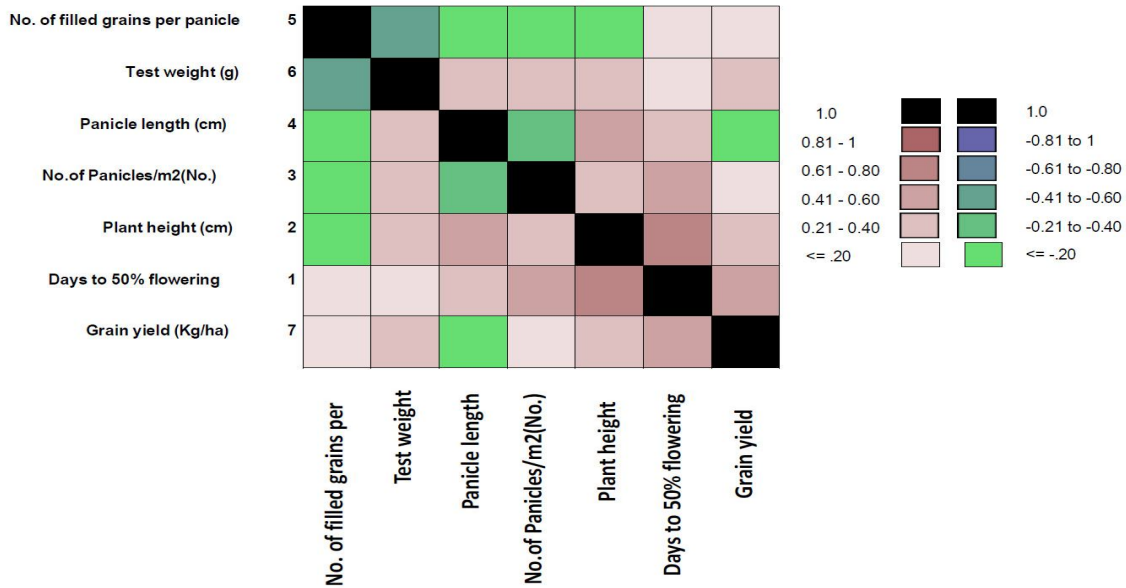


Fig. 1: Genotypic shaded Correlation matrix showing positive and negative relationship between different characters; Black and Red shows positive and negative relationship

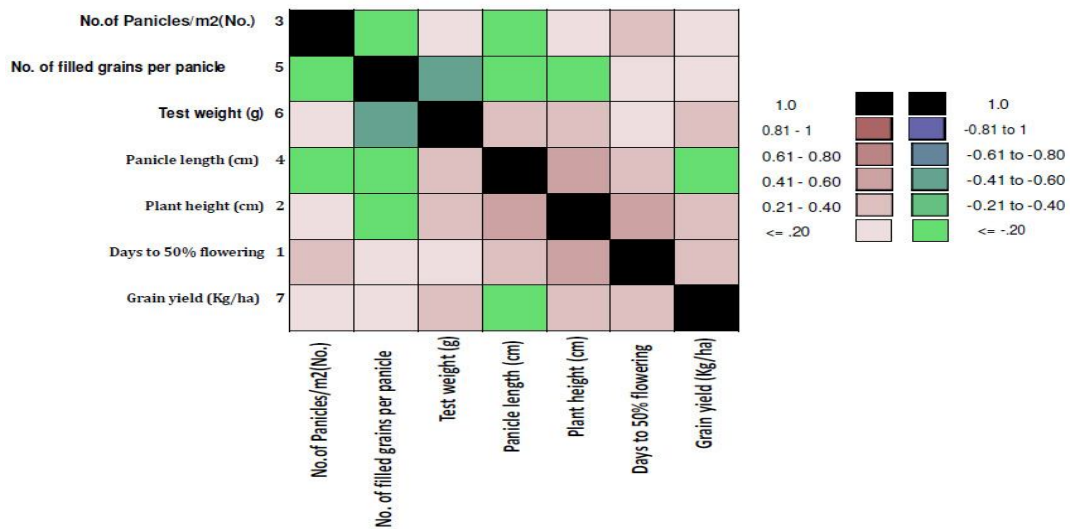


Fig. 2: Phenotypic shaded Correlation matrix showing positive and negative relationship between different characters; Black and Red shows positive and negative relationship

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Conflict of Interest: All authors declare that they have no conflict of interest.

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