Genetic Variability, Correlation and Path Analysis of Yield and its Attributing Traits in Rice (*Oryza sativa* L.)

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Authors' contributions

This work was carried out in collaboration between both authors. Author HB designed the study, performed the statistical analysis, wrote the protocol, and final draft of the manuscript. Author TN prepared the first draft of the manuscript and managed the literature searches. Both authors read and approved the final manuscript.

Original Research Article

ABSTRACT

Genetic variability in a species is a crucial aspect that determines its adaptability, resilience and potentiality for improvement. The present study was aimed to estimate variability, correlation and path coefficients of fifteen rice accessions from Kerala Agricultural University for grain yield and its attributing traits. PCV was found to be higher than GCV for all the characters studied. High PCV and GCV values were recorded for the traits like flag leaf length, leaf area, number of filled grains per panicle, fertility percentage and single plant yield indicating that direct selection can be

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employed for the improvement of these traits. High heritability coupled with high genetic advance was shown by the traits plant height, flag leaf length, flag leaf width, leaf area, number of filled grains per panicle, total grains per panicle and single plant yield. Hence direct selection will be highly effective for improvement of these traits. Single plant yield showed significant positive correlation with days to 50% flowering, number of filled grains per panicle, total number of grains per panicle and harvest index at phenotypic level and with harvest index at genotypic level. Path analysis has ascertained that there exist direct and indirect effects for all the independent traits studied. Positive direct effects on single plant yield at genotypic level was shown by the traits number of panicles, panicle length, 1000 grain weight, leaf area, grain length, kernel breadth and harvest index. The characters like days to 50% flowering, plant height, number of tillers, flag leaf length, flag leaf width, total number of grains per panicle, 1000 grain weight, kernel length, kernel breadth and L/B ratio had significant positive direct effects at phenotypic level. The results have shown that the accessions studied can be used for further selection for crop improvement programmes. The interactions between the contributing traits are so complex that a balanced method of selection is to be practised for their improvement.

1. INTRODUCTION

Rice (*Oryza sativa* L.), a self-pollinated cereal crop belonging to Poaceae family (2n=2x=24) holds immense significance for millions of individuals globally, especially in developing nations, and serves as the keystone of nourishment in the Asia-Pacific Region. Out of all the nations cultivating rice globally, India is the largest producer of rice accounting for an area 46.38 million hectare with a production of 130.29 million tonnes and productivity of 2,809 kg ha^{-1} during 2021-2022 [1]. Rice can be grown in extensive agroclimatic regions from mountainous land to below sea level areas like Kuttanad in Kerala. In Kerala rice occupies an area of 0.20 million hectare with a production of 6.3 lakh tonnes and an average productivity of 3105 kgha^{-1} [2]. Even though the production and productivity is increasing compared to previous years, the demand for rice is expected to grow, driven by population growth, economic development, and changing dietary patterns, particularly in regions where rice is a staple food. Variability within rice species is a crucial aspect that influences its adaptability, resilience, and potentiality for improvement. Understanding the extent of genetic variation and its heritable aspects for economically significant traits within a population, holds immense value for plant breeders in shaping their breeding approaches.

Analysis of variance encompasses a range of statistical models and estimation techniques utilized to explore differences among means. It not only estimates variances but also provides the basis of test of significance. Phenotypic variance arises from a combination of genetic and environmental influences, whereas genetic variance arises exclusively from genetic factors. Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) offer insights into the extent of variability within a population. This information aids in directing genetic heterogeneity towards desired traits through appropriate selection criteria. Additionally, estimates of parameters like heritability and genetic advance assist plant breeders in identifying superior genotypes within a genetically diverse population. High heritability suggests that phenotype closely mirrors genotype, indicating minimal environmental influence on trait expression. This emphasizes the significant role of the genetic components in trait expression, providing information on the inheritance degree from parents to progeny. However, heritability estimates alone may not fully reveal the underlying gene action or the genetic progress resulting from selection. Effective selection strategies rely on the merits of various attributes, including genetic advance. Genetic advance refers to the improvement in the mean genotypic value of selected plants over the parental population. While heritability estimates gauge the relative efficacy of selection based on phenotypic expression, genetic advance offers a more beneficial tool for predicting the actual value of selection. On the other hand, the relationship of yield with other characters is also having great significance while formulating any selection program for crop improvement. Correlation studies measures the degree and direction of relationship between different variables [3]. The selection based on grain yield alone in rice without considering the

component characters is not effective since grain yield is a dependent character influenced by several other independent characters. Here, the knowledge of path analysis facilitates indirect selection for the genetic improvement of grain yield. In path coefficient analysis, the total correlation coefficient is partitioned into direct and indirect effects of component variables. Keeping these aspects in view, the present study has been conducted to estimate the variability parameters, correlation and path coefficient analysis for grain yield and its attributing traits in fifteen rice accessions with the aim of better parental selection.

2. MATERIALS AND METHODS

A study on fifteen rice (*Oryza sativa* L.) genotypes was conducted at M. S. Swaminathan Rice Research Station, Kerala Agricultural University, Moncompu, Alappuzha, Kerala during Kharif, 2023. The experiment area is geographically located at 9° 26' 15.8" N latitude and 76° 25' 42.3"E longitude. The list of genotypes which includes seven released varieties and eight prerelease cultures from Kerala Agricultural University is presented in Table 1.

The genotypes were raised in a Randomized Block Design with three replications. A spacing of 20 cm between rows and 15 cm between plants was followed with a plot size of 11 m².

Observations on days to 50% flowering (DFF, %), plant height (PH, cm), number of tillers (TN), number of panicles (PN), flag leaf length (LL, cm), flag leaf width (LW, cm), leaf area (LA, cm²), panicle length (PL, cm), number of filled grains per panicle (FG), number of chaffy grains per panicle (CG), total number of grains per panicle (TG), 1000 grain weight (1000 GW, g), grain length (GL, cm), grain breadth (GB, cm), kernel length (KL, cm), kernel breadth (KB, cm), L/B Ratio, fertility percentage (FP, %), single plant yield (SPY, g) and harvest index (HI) were recorded. The following computations were done using the R studio software [4].

2.1 Analysis of Variance (ANOVA) & Coefficient of Variation

Analysis of variance (ANOVA), as described by Panse and Sukhatme [5]. was conducted for all biometric traits to compare the different genotypes and to estimate variance components. The analysis of variance furnishes estimates of phenotypic and genotypic variances, which are utilized to compute their respective coefficients of variation. The phenotypic and genotypic coefficients of variation were calculated as outlined by Burton [6]. Categorization of the range of variation was followed as reported by Sivasubramanian and Menon [7] as low (< 10%), moderate (10-20%) and high (> 20%).

Table 1. List of genotypes in the study

Sl No.	Genotype	Variety/ Prerelease culture
1	Uma (MO 16)	Varieties
2	Jyothi (PTB 39)	
3	Prathyasa (MO 21)	
4	Makom (MO 9)	
5	Shreyas (MO 22)	
6	Pournami (MO 23)	
7	KAU Manu Rathna	
8	KAUM 236-1-2-1-1-1	Prerelease cultures
9	KAUM 238-1-1-1-1-1	
10	KAUM 240-1-3-2-2-2	
11	KAUM 242-4-2-1-1-1	
12	KAUM 250-1-1-1-1-1	
13	KAUM 255-1-2-1-1-1-1	
14	KAUM 259-5-3-1-1-1	
15	KAUM 261-1-3-1-1-1-1	

2.2 Heritability & Genetic Advance

Heritability in broad sense was calculated as per the formula suggested by Allard [8]. As suggested by Johnson et al. [9] the range of heritability estimates in broad sense were categorized as low (<30%), moderate (30-60%) and high (> 60%). From the heritability estimates the genetic advance was estimated by the formula outlined by Burton [6]. For visualizing the relative utility of genetic advance among the characters, genetic advance as per cent of mean was also estimated using the formula suggested by Govidaswamy et al. [10]. The range of genetic advance as per cent of mean was classified according to Johnson et al. [9] as low (<10%), moderate (10-20%) and high (> 20%).

2.3 Correlation Analysis

Correlation analysis is a statistical tool employed to ascertain the magnitude and direction of the relationship between two or more variables. This encompasses various correlations, including genotypic and phenotypic correlation coefficients, determined through the formula given by Falconer [11].

2.4 Path Co-efficient Analysis

Path coefficient analysis is a standardized partial regression coefficient which splits the correlation coefficient in to the measures of direct and indirect effects as applied by Dewey and Lu [12]. The direct and indirect effects were classified based on range given by Lenka and Mishra [13]. It was categorised as very high (>1), high (0.30-0.99), moderate (0.20-0.29), low (0.10-0.19) and negligible (<0.09).

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance (ANOVA) & Coefficient of Variation

The analysis of variance of the characters under study (Table 2) has shown that there exists significant variation among the genotypes. The mean sum of squares of the genotypes was highly significant for all the traits except number of chaffy grains per panicle. The range, mean, variance, coefficient of variation, heritability (broad sense), genetic advance and genetic advance as percentage of mean of the various characters under study are presented in Table 3. Highest range of values was shown by the character total grains per panicle followed by

filled grains per panicle and plant height. This indicates that there exists maximum variation for these traits for the genotypes studied. Similar results were reported by Lakshmi et al. [14]. Days to 50 % flowering showed a range from 89 to 114 days with a mean of 106.64. The genotypes studied showed high variability for all the characters. The phenotypic variance ($\sigma^2 p$) was higher than genotypic variance ($\sigma^2 g$) in all the characters studied. This indicates that there exists an influence of environment on the expression of the yield contributing traits studied. Plant height showed variation with comparable $\sigma^2 p$ and $\sigma^2 g$ values which is in accordance with Singh et al., [15]. Panicle length also showed comparable $\sigma^2 p$ and $\sigma^2 g$ values. The phenotypic expression of the characters filled grains per panicle, total number of grains per panicle and fertility percentage was highly influenced by the environment which is evident from the comparatively higher $\sigma^2 p$ compared to $\sigma^2 g$. Singh et al., [15] had reported a significant environmental effect on the expressivity of spikelet fertility.

Phenotypic coefficient of variation (PCV) was also found to be higher than genotypic coefficient of variation (GCV) as represented in Table 3 and Fig. 1. The results were in concurrence with Nithya et al. [16], Sudeepthi et al. [17], Bhargava et al [18] Dey et al. [19]. Manivelan et al. [20] Naik et al. [21] Gayathridevi et al. [22] Priyanga et al. [23] and Singh et al. [15]. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was low for the characters viz., days to 50% flowering, panicle length, 1000 grain weight, grain length, grain breadth, kernel length, kernel breadth and fertility percentage. This suggests that the scope for improvement for these traits in the genotypes is very low. Similar results for days to 50% flowering, was reported by Sudeepthi et al. [17] Bhargava et al [18] and Manivelan et al. [20] Naik et al. [21] for kernel length, and kernel breadth by Manivelan et al. [20] for panicle length by Sudeepthi et al. [17] Manivelan et al. [20] and Priyanga et al. [23] and for 1000 grain weight by Bhargava et al [18]. The characters plant height, number of tillers, number of panicles, flag leaf width and L/B ratio recorded moderate PCV and GCV values. Similar results for the traits were reported by Manivelan et al. [20] Naik et al. [21] reported moderate values for plant height, number of tillers as well as flag leaf width. Moderate PCV and GCV values were recorded for plant height by Sudeepthi et al. [17] and Bhargava et al [18]. Among the characters

studied, the variation between PCV and GCV was the least for plant height. These conclusions are in accordance with the findings of Singh et al. [15]. Number of chaffy grains per panicle and total number of grains per panicle recorded moderate GCV values with high PCV whereas harvest index recorded low GCV and moderate PCV values. This indicates that the expression of these characters was influenced by environment and direct selection for these traits will not be effective. These results are in partial concurrence with the results obtained by Dey et al. [19]. Higher PCV and GCV values were observed for the traits like flag leaf length, leaf area, number of filled grains per panicle, fertility percentage and single plant yield which shows minor environmental effect on trait expression. This indicates that the phenotypic expression of these characters is directly influenced by the genotype and hence direct selection can be practiced for its improvement. Gayathridevi et al. [22] reported

that the character filled grains per panicle showed high PCV and GCV. Similar result for grain yield per plant was reported by Nithya et al. [16] Bhargava et al [18] Dey et al. [19] Naik et al. [21], Gayathridevi et al. [22] Priyanga et al. [23] and Singh et al. [15]. This suggests that there exists ample scope in the improvement of the trait single plant yield.

Yadav et al., [24] has suggested that the traits with closer PCV and GCV values are more reliable as they are less influenced by environment and can be used for future breeding programmes. In the present study the traits days to 50% flowering, plant height, flag leaf length, leaf area, panicle length, 1000 grain weight, grain length, grain breadth, kernel length, kernel breadth, L/B ratio, harvest index and single plant yield showed closer PCV and GCV values suggesting that these traits can be used for further improvement.

Table 2. Analysis of variance of the characters under study

Source	Mean Sum of Squares		
	Replication	Genotype	Error
df	2	14	28
Characters under study			
DFF (%)	1.622	146.308***	0.741
PH (cm)	65.72	670.47***	5.24
TN	0.5136	3.9404***	0.8897
PN	0.2936	3.7914**	1.1593
LL (cm)	2.219	131.5***	1.659
LW (cm)	0.021236	0.138602***	0.003597
LA (cm2)	10.38	331.22***	5.83
PL (cm)	0.0545	13.0672***	0.4694
FG	187.54	1133.87***	103.2
CG	7.509	48.771	32.594
TG	179.87	1039.24***	179.72
1000 GW (g)	0.1016	12.5959***	0.3539
GL (cm)	0.04345	0.54965***	0.04002
GB (cm)	0.020482	0.149583***	0.007394
KL (cm)	0.00114	0.44915***	0.01799
KB (cm)	0.001336	0.050580***	0.005086
L/B Ratio	0.000719	0.160426***	0.009045
FP (%)	11.916	57.858**	19.932
HI	0.0009266	0.0036034***	0.0004366
SPY (g)	0.5334	16.7182***	0.6067

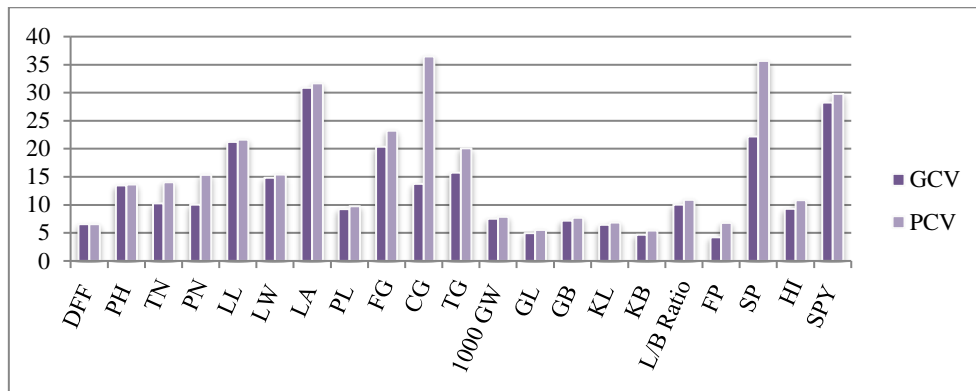*'***' - significant at 0.001 '**' - significant at 0.01*

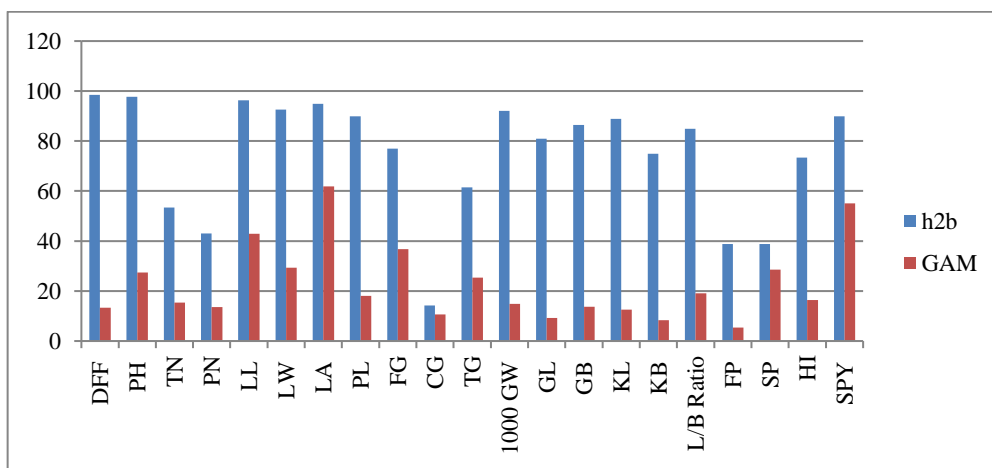**Fig. 1. Genotypic and Phenotypic Coefficient of Variation of the Characters Studied**

Fig. 2. Broad sense heritability and genetic advance as percentage of mean of the characters studied
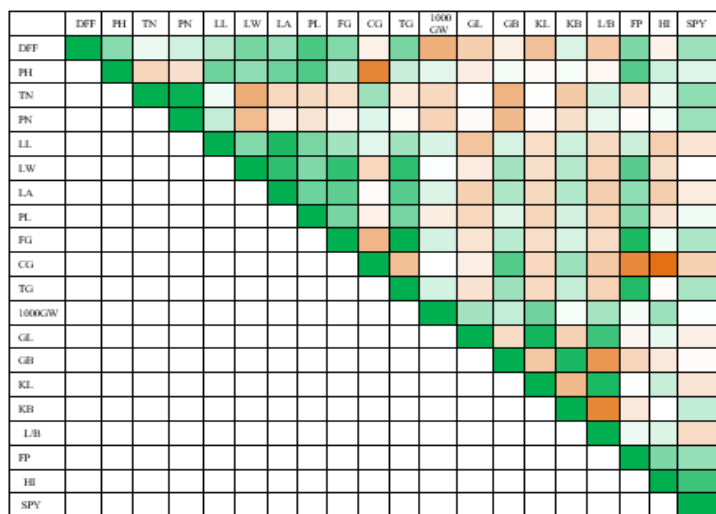

Fig. 3. Correlogram of the genotypic correlation coefficient of the characters studied

Table 3. Range, Mean, Variance, Coefficient of Variation, Heritability (broad sense), Genetic Advance and Genetic Advance as percentage of Mean of the characters under study

Character	Range		Grand Mean	Variance			Coefficient of variation			h_2b (Broad Sense)	Genetic Advance (GA)	Genetic Advance as percentage of mean (GAM)
	Maximum	Minimum		Environ (σ^2e)	Genotypic (σ^2g)	Phenotypic (σ^2p)	ECV	GCV	PCV			
DFF (%)	114.00	89.00	106.64	0.74	48.52	49.26	0.81	6.53	6.58	98.5	14.24	13.35
PH (cm)	145.20	84.40	110.45	5.24	221.75	226.98	2.07	13.48	13.64	97.69	30.32	27.45
TN	12.60	7.00	9.84	0.89	1.02	1.91	9.59	10.25	14.04	53.34	1.52	15.42
PN	12.60	6.60	9.32	1.16	0.88	2.04	11.56	10.05	15.32	43.08	1.27	13.59
LL (cm)	44.00	16.60	30.97	1.66	43.28	44.94	4.16	21.24	21.64	96.31	13.30	42.94
LW (cm)	1.90	1.10	1.43	0.00	0.05	0.05	4.19	14.81	15.39	92.59	0.42	29.36
LA (cm2)	55.86	13.70	33.77	5.83	108.46	114.29	7.15	30.84	31.65	94.9	20.90	61.88
PL (cm)	27.00	17.60	22.13	0.47	4.20	4.67	3.10	9.26	9.76	89.95	4.00	18.09
FG	132.50	63.10	91.02	103.20	343.55	446.76	11.16	20.36	23.22	76.9	33.48	36.79
CG	38.00	8.60	16.90	32.59	5.39	37.99	33.78	13.74	36.47	14.2	1.80	10.66
TG	149.20	79.00	107.61	179.72	286.51	466.23	12.46	15.73	20.07	61.45	27.33	25.40
1000 GW (g)	31.60	23.20	26.83	0.35	4.08	4.43	2.22	7.53	7.85	92.02	3.99	14.88
GL (cm)	8.94	7.20	8.28	0.04	0.17	0.21	2.42	4.98	5.53	80.94	0.76	9.23
GB (cm)	3.53	2.61	3.04	0.01	0.05	0.05	2.83	7.16	7.70	86.5	0.42	13.72
KL (cm)	6.77	5.15	5.88	0.02	0.14	0.16	2.28	6.45	6.84	88.87	0.74	12.52
KB (cm)	2.84	2.38	2.64	0.01	0.02	0.02	2.70	4.67	5.40	74.88	0.22	8.32
L/B Ratio	2.82	1.88	2.24	0.01	0.05	0.06	4.25	10.05	10.91	84.87	0.43	19.07
FP (%)	92.92	67.01	83.99	19.93	12.64	32.57	5.32	4.23	6.79	38.81	4.56	5.43
HI	0.42	0.26	0.36	0.05	0.00	0.00	5.84	9.27	10.83	73.33	0.06	16.35
SPY (g)	12.38	3.81	8.21	0.61	5.37	5.98	9.49	28.22	29.77	89.85	4.53	55.11

Table 4. Genotypic correlation coefficient of yield and the contributing traits

	DFF	PH	TN	PN	LL	LW	LA	PL	FG	CG	TG	1000GW	GL	GB	KL	KB	L/B	FP	HI	SPY
DFF	1 **	0.4628	0.084	0.1871	0.2977	0.5348 *	0.427	0.7021 **	0.4967	-0.0955	0.5332 *	-0.5355 *	-0.3297	-0.114	-0.4141	0.1499	-0.3548	0.5107	-0.0844	0.3937
PH		1 **	-0.2762	-0.2121	0.5705 *	0.443	0.5768 *	0.6939 **	0.3128	-0.8188 **	0.2176	0.1173	-0.1173	0.0429	-0.0303	0.0363	-0.0463	0.6732 **	0.1962	0.1334
TN			1 **	0.9775 **	0.0626	-0.452	-0.0931	-0.1727	-0.0628	0.1305	-0.1533	-0.2612	-0.0075	-0.5085	-0.3529	0.1783	-0.2503	-0.016	0.0425	0.3911
PN				1 **	0.2387	-0.452	-0.0931	-0.1727	-0.0628	0.1305	-0.0391	-0.2951	-0.0305	-0.4634	-0.0276	-0.2125	0.0964	-0.016	0.0425	0.3911
LL					1 **	0.4931	0.8972 **	0.5281 *	0.3639	0.1143	0.3774	0.1608	-0.3946	0.165 NS	-0.2209	0.1961	-0.2461	0.2078	-0.3227	-0.1692
LW						1 **	0.8204 **	0.5041	0.8063 **	-0.2593 S	0.8261 **	0.0213	-0.127	0.3569	-0.2132	0.2953	-0.2964	0.6588 **	-0.2143	0.0026
LA							1 **	0.5745 *	0.6362 *	-0.0251	0.6555 **	0.1452	-0.3155	0.3182	-0.2546	0.3066	-0.3265	0.4406	-0.3297	-0.1237
PL								1 **	0.5357 *	-0.0951	0.5412 *	-0.1238	-0.2589	0.1332	-0.2698	0.1776	-0.2798	0.4905	-0.172	0.0571
FG									1 **	-0.4886	0.9997 **	0.1719	-0.1872	0.2719	-0.2191	0.1589	-0.2371	0.8939 **	0.0621	0.3241
CG										1 **	-0.431	0.0022	-0.1074	0.6804 **	-0.2619	0.3871	-0.3643	-0.8006 **	-0.9651 **	-0.3157
TG											1 **	0.1752	-0.1908	0.3845	-0.25	0.2363	-0.2964	0.8635 **	-0.0243	0.3437
1000GW												1 **	0.3642	0.2354	0.5637 *	0.0357	0.3565	0.0431	0.389	0.0187
GL													1 **	-0.2402	0.9259 **	-0.2986	0.7643 **	-0.0572	0.096	-0.1045
GB														1 **	-0.3718	0.9008 **	-0.699 **	-0.2793	-0.145	-0.0223
KL															1 **	-0.4655	0.8953 **	0.0132	0.2242	-0.1705
KB																1 **	-0.8107 **	-0.1465	0	0.2451
L/B																	1 **	0.0729	0.1463	-0.2384
FP																		1 **	0.5112	0.416
HI																			1 **	0.7646 **
SPY																				1 **

Table 5. Phenotypic correlation coefficient of yield and the contributing traits

	DFF	PH	TN	PN	LL	LW	LA	PL	FG	CG	TG	1000GW	GL	GB	KL	KB	L/B	FP	HI	SPY
DFF	1 **	0.4477 **	0.0608	0.1165	0.2962 *	0.5101 **	0.4182 **	0.6548 **	0.4164 **	-0.087	0.3833 **	-0.5051 **	-0.2979 *	-0.1014	-0.3679 *	0.1052	-0.3012 *	0.3528 *	-0.0693	0.3727 *
PH		1 **	-0.1683	-0.1188	0.5471 **	0.4268 **	0.555 **	0.6336 **	0.2885	-0.2883	0.193	0.1157	-0.1063	0.0408	-0.0289	0.0316	-0.0427	0.4091 **	0.1664	0.1315
TN			1 **	0.9045 **	0.044	-0.3575 *	-0.1694	-0.152	-0.1397	0.1311	-0.0853	-0.1151	-0.0597	-0.3493 *	-.0007	-0.2051	0.1117	-0.142	-0.0646	0.2681
PN				1 **	0.1399	-0.23	-0.0391	-0.0905	-0.0415	0.1278	0.009	-0.0744	-0.0925	-0.2573	-0.0193	-0.1195	0.0542	-0.0926	-0.127	0.2194
LL					1 **	0.4823 **	0.892 **	0.4973 **	0.311 *	0.038	0.291	0.1441	-0.332 *	0.1536	-0.1986	0.138	-0.2056	0.1303	-0.2706	-0.1666
LW						1 **	0.8186 **	0.4928 **	0.7176 **	-0.0478	0.6832 **	0.0125	-0.1177	0.286	-0.1767	0.2208	-0.2378	0.3736 *	-0.1827	0.0012
LA							1 **	0.5464 **	0.5628 **	0.0101	0.5339 **	0.1304	-0.2653	0.2785	-0.2186	0.226	-0.2671	0.261	-0.2798	-0.1218
PL								1 **	0.46 **	0.0086	0.4336 **	-0.117	-0.2096	0.0754	-0.2537	0.1395	-0.2504	0.2641	-0.1848	0.0385
FG									1 **	-0.066	0.9532 **	0.1328	-0.1502	0.1967 NS	-0.2058	0.1935	-0.2442	0.5305 **	0.0615	0.3093 *
CG										1 **	0.2232	-0.0229	-0.0781	0.1767	-0.1613	0.2814	-0.2453	-0.8673 **	-0.3244 *	-0.126
TG											1 **	0.1115	-0.1532	0.23	-0.241	0.2595	-0.2998 *	0.2706	-0.0194	0.2938*
1000GW												1 **	0.3213 *	0.265	0.5013 **	0.0438	0.2945 *	-0.0026	0.0328	0.0145
GL													1 **	-0.2102	0.8161 **	-0.2756	0.6726 **	-0.1257	-0.0969	-0.113
GB														1 **	-0.3257 *	0.7543 **	-0.6142 **	-0.1257	-0.0969	-0.0151
KL															1 **	-0.4442 **	0.8822 **	0.0379	0.1487	-0.1464
KB																1 **	-0.8123 **	-0.1879	0.0469	0.1971
L/B																	1 **	0.1127	0.0749	-0.2041
FP																		1 **	0.3021 *	0.2772
HI																			1 **	0.6472 **
SPY																				1 **

Table 6. Genotypic path analysis showing direct and indirect effects of the contributing traits on yield

	DFF	PH	TN	PN	LL	LW	LA	PL	FG	CG	TG	1000GW	GL	GB	KL	KB	L/B	FP	HI
DFF	**0.0047**	-0.1279	-0.0032	1.0586	-0.0449	0.0222	0.1496	0.1850	-0.2600	0.0341	0.3490	-0.1097	-0.1098	0.0288	1.9136	0.4637	-2.1776	-0.2302	-0.0542
PH	0.0022	**-0.2763**	0.0104	-1.2002	-0.0860	0.0184	0.2021	0.1829	-0.1638	0.2927	0.1424	0.0240	-0.0391	-0.0108	0.1398	0.1123	-0.2841	-0.3035	0.1261
TN	0.0004	0.0763	**-0.0377**	5.5308	-0.0094	-0.0232	-0.0934	-0.0644	0.1095	-0.1405	-0.1003	-0.0535	-0.0025	0.1283	0.0295	-1.0921	1.0947	0.0072	0.0598
PN	0.0009	0.0586	-0.0369	**5.6580**	-0.0360	-0.0188	-0.0326	-0.0455	0.0329	-0.0467	-0.0256	-0.0605	-0.0102	0.1169	0.1276	-0.6575	0.5919	0.0072	0.0272
LL	0.0014	-0.1576	-0.0024	1.3507	**-0.1508**	0.0205	0.3144	0.1392	-0.1905	-0.0409	0.2470	0.0330	-0.1314	-0.0416	1.0210	0.6069	-1.5108	-0.0937	-0.2074
LW	0.0025	-0.1224	0.0210	-2.5577	-0.0743	**0.0416**	0.2875	0.1328	-0.4221	0.0927	0.5408	0.0044	-0.0423	-0.0900	0.9850	0.9144	-1.8201	-0.2970	-0.1380
LA	0.0020	-0.1594	0.0101	-0.5268	-0.1353	0.0341	**0.3504**	0.1514	-0.3330	0.0090	0.4291	0.0298	-0.1051	-0.0803	1.1764	0.9488	-2.0042	-0.1986	-0.2119
PL	0.0033	-0.1917	0.0092	-0.9771	-0.0796	0.0210	0.2013	**0.2635**	-0.2804	0.0340	0.3543	-0.0254	-0.0862	-0.0336	1.2470	0.5497	-1.7178	-0.2211	-0.1106
FG	0.0023	-0.0864	0.0079	-0.3552	-0.0549	0.0335	0.2229	0.1412	**-0.5234**	0.1746	0.6543	0.0352	-0.0624	-0.0686	1.0125	0.4915	-1.4555	-0.4030	0.0399
CG	-0.0005	0.2262	-0.0148	0.7385	-0.0172	-0.0108	-0.0088	-0.0251	0.2557	**-0.3574**	-0.2821	0.0005	-0.0358	-0.1717	1.2103	1.1979	-2.2361	0.3609	-0.6205
TG	0.0025	-0.0601	0.0058	-0.2211	-0.0569	0.0343	0.2297	0.1426	-0.5233	0.1540	**0.6546**	0.0359	-0.0636	-0.0970	1.1555	0.7311	-1.8196	-0.3893	-0.0156
1000GW	-0.0025	-0.0324	0.0099	-1.6697	-0.0242	0.0009	0.0509	-0.0326	-0.0900	-0.0008	0.1147	**0.2049**	0.1213	-0.0594	-2.6053	0.1105	2.1882	-0.0194	0.2501
GL	-0.0016	0.0324	0.0192	-0.1725	0.0595	-0.0053	-0.1106	-0.0682	0.0980	-0.1405	-0.1249	-0.0535	**0.3331**	0.0606	-4.2791	-0.9236	4.6911	0.0258	0.0619
GB	-0.0005	-0.0119	0.0192	-2.6219	-0.0249	0.0148	0.1115	0.0351	-0.1423	-0.2432	0.2516	0.0482	-0.0800	**-0.2523**	1.7184	2.7872	-4.2899	0.1259	-0.0936
KL	-0.0020	0.0084	0.0002	-0.1562	0.0333	-0.0089	-0.0892	-0.0711	0.1147	0.0936	-0.1637	0.1155	0.3084	0.0938	**-4.6214**	-1.4403	5.4960	-0.0059	0.1440
KB	0.0007	-0.0100	0.0133	-1.2024	-0.0296	0.0123	0.1075	0.0468	-0.0832	-0.1384	0.1547	0.0073	-0.0994	-0.2273	2.1514	**3.0938**	-4.9778	0.0661	0.0000
L/B	-0.0017	0.0128	-0.0067	0.5456	0.0371	-0.0123	-0.1144	-0.0738	0.1241	0.1302	-0.1940	0.0731	0.2546	0.1763	-4.1379	-2.5090	**6.1381**	-0.0329	0.0942
FP	0.0024	-0.1860	0.0094	-0.0906	-0.0313	0.0274	0.1544	0.1293	-0.4679	0.2862	0.5652	0.0088	-0.0190	0.0705	-0.0609	-0.4533	0.4477	**-0.4508**	0.3286
HI	-0.0004	-0.0541	-0.0035	0.2393	0.0486	-0.0089	-0.1153	-0.0453	-0.0324	0.3443	-0.0159	0.0796	0.0320	0.0367	-1.0334	0.0000	0.8980	-0.2300	**0.6380**

Residual effect: -0.0139

Table 7. Phenotypic path analysis showing direct and indirect effects of the contributing traits on yield

|	DFF	PH	TN	PN	LL	LW	LA	PL	FG	CG	TG	1000GW	GL	GB	KL	KB	L/B	FP	HI
DFF	**0.3723**	0.2405	0.0126	-0.7067	0.5349	0.6669	-1.5307	-0.1234	-0.4123	0.0998	0.6618	-0.2842	0.0764	0.0283	-0.0845	0.0311	0.0462	-0.2267	0.0294
PH	0.1667	**0.5371**	-0.0349	0.7206	0.9880	0.5579	-2.0314	-0.1194	-0.2857	0.3309	0.3332	0.0651	0.0272	-0.0114	-0.0066	0.0094	0.0066	-0.2629	-0.0699
TN	0.0227	-0.0904	**0.2072**	-5.4855	0.0795	-0.4683	0.6200	0.0286	0.1383	-0.1503	-0.1473	-0.0648	0.0154	0.0973	0.0004	-0.0618	-0.0169	0.0912	0.0236
PN	0.0434	-0.0638	0.1873	**-6.0642**	0.2526	-0.3034	0.1431	0.0171	0.0411	-0.1467	0.0157	-0.0417	0.0239	0.0716	-0.0044	-0.0350	-0.0084	0.0595	0.0533
LL	0.1103	0.2939	0.0091	-0.8486	**1.8058**	0.6310	-3.2649	-0.0937	-0.3079	-0.0436	0.5024	0.0811	0.0851	-0.0427	-0.0456	0.0410	0.0315	-0.0837	0.1134
LW	0.1898	0.2291	-0.0742	1.4073	0.8713	**1.3186**	-2.9959	-0.0930	-0.7105	0.0549	1.1796	0.0073	0.0305	-0.0809	-0.0415	0.0661	0.0371	-0.2400	0.0493
LA	0.1557	0.2981	-0.0351	0.2372	1.6108	1.0705	**-3.6602**	-0.1030	-0.5572	-0.0116	0.9218	0.0734	0.0680	-0.0775	-0.0502	0.0670	0.0410	-0.1677	0.1179
PL	0.2438	0.3403	-0.0315	0.5490	0.8980	0.6452	-1.9999	**-0.1884**	-0.4554	-0.0099	0.7486	-0.0658	0.0539	-0.0209	-0.0584	0.0414	0.0384	-0.1697	0.0754
FG	0.1550	0.1550	-0.0289	0.2517	0.5616	0.9385	-2.0599	-0.0867	**-0.9901**	0.0757	1.6457	0.0747	0.0385	-0.0547	-0.0473	0.0573	0.0375	-0.3409	-0.0257
CG	-0.0324	-0.1549	0.0271	-0.7752	0.0686	-0.0625	-0.0370	-0.0016	0.0654	**-1.1476**	0.3854	-0.0129	0.0201	-0.0492	-0.0371	0.0834	0.0376	0.5573	0.1357
TG	0.1427	0.1037	-0.0177	-0.0552	0.5255	0.8935	-1.9542	-0.0817	-0.9438	-0.2562	**1.7265**	0.0627	0.0393	-0.0640	-0.0553	0.0768	0.0460	-0.1739	0.0080
1000GW	-0.1880	0.0621	-0.0239	0.4501	0.2602	0.0169	-0.4773	0.0220	-0.1315	0.0263	0.1925	**0.5627**	-0.0824	-0.0739	0.1153	0.0099	-0.0466	-0.0281	-0.1238
GL	-0.1109	-0.0571	-0.0125	0.5660	-0.5997	-0.1554	0.9707	0.0396	0.1488	0.0899	-0.2645	0.1808	**-0.2564**	0.0597	0.1882	-0.0818	-0.1029	0.0017	0.0000
GB	-0.0378	0.0219	-0.0724	1.5614	0.2774	0.3802	-1.0194	-0.0142	-0.1947	-0.2028	0.3973	0.1495	0.0550	**-0.2792**	-0.0756	0.2223	0.0940	0.0808	0.0464
KL	-0.1369	-0.0155	0.0004	0.7158	-0.3585	-0.2361	0.8005	0.0479	0.2038	0.1852	-0.4159	0.2824	-0.2101	0.0916	**0.2301**	-0.1346	-0.1345	-0.0244	-0.0810
KB	0.0391	0.0170	-0.0432	0.7158	0.2496	0.2915	-0.8265	-0.0263	-0.1914	-0.3228	0.4473	0.0187	0.0707	-0.2085	-0.1042	**0.2922**	0.1236	0.1201	0.0000
L/B	-0.1122	-0.0229	0.0228	-0.3312	-0.3711	-0.3162	0.9784	0.0472	0.2418	0.2816	-0.5176	0.1709	-0.1720	0.1705	0.2014	-0.2389	**-0.1521**	-0.0725	-0.0446
FP	0.1313	0.2197	-0.0294	0.5617	0.2353	0.4885	-0.9553	-0.0498	-0.5253	0.4672	0.0246	0.0007		0.0350	0.0087	-0.0554	-0.0173	**-0.6426**	-0.1275
HI	-0.0260	0.0893	-0.0116	0.7680	-0.4868	-0.1532	1.0256	0.0338	-0.0605	0.3702	-0.0330	0.1656	0.0000	0.0307	0.0442	0.0000	-0.0162	-0.1948	**-0.2805**

Residual effect: 0.1288
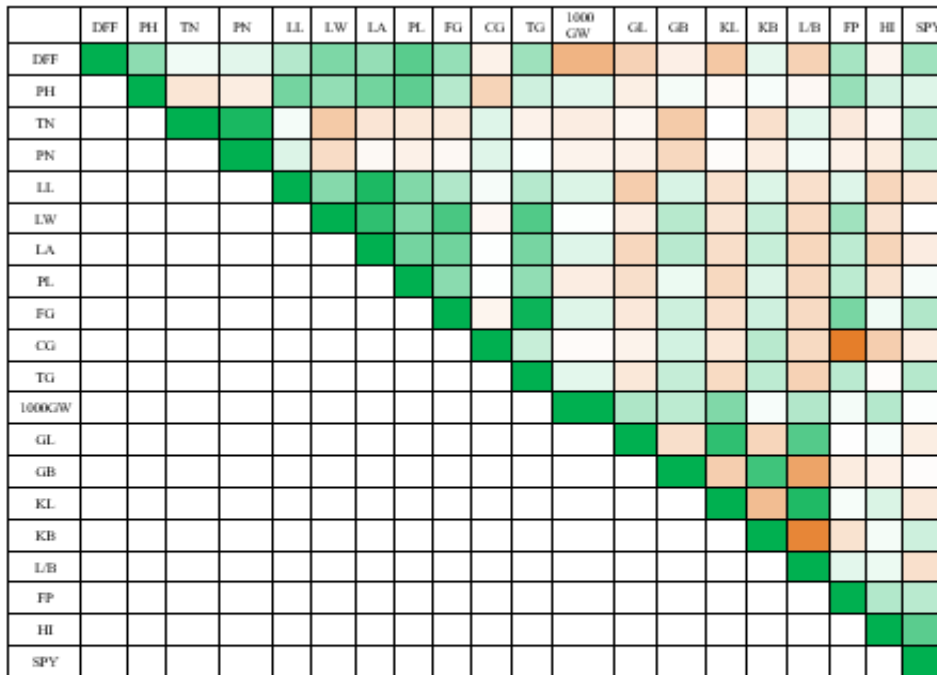
Fig. 4. Correlogram of the phenotypic correlation coefficient of the characters studied

3.2 Heritability and Genetic Advance

Heritability indicates that the character is governed by the genotypic action and is not that affected by environment. Days to 50 % flowering recorded the highest h²b value (98.5 %) with moderate GA and GAM. Plant height also showed high h²b with highest GA and high GAM. Similar findings were reported by Sudeepthi et al. [17] The characters number of tillers and number of panicles exhibited low h²b, GA and GAM, indicating that the selection for these traits will not be effective. For panicle length h²b value was high (89.95) with low GA (4.0) and moderate GAM (18.09) values. Similar results were recorded by Singh et al. [15]. All the leaf characters recorded high h²b. Number of filled grains per panicle and total number of grains per panicle showed moderate h²b whereas number of chaffy grains per panicle showed very low broad sense heritability. The grain characters showed high h²b with low to moderate GAM. Harvest index showed moderate h²b and GAM.

The character single plant yield recorded high broad sense heritability as well as GAM. These results are in concurrence with Mandal et al. [25] and Singh et al. [15].

High heritability and high genetic advance together will help us to identify the characters where direct selection can be applied for selecting the best genotypes. According to Panse and Sukhatme [26] additive gene action is the reason for high genetic advance. Hence the traits plant height, flag leaf length, flag leaf width, leaf area, number of filled grains per panicle, total grains per panicle and single plant yield with high heritability (>60 %) and high genetic advance (>20%) can be used for identifying the best genotypes. Similar reports of high heritability and genetic advance for traits plant height, flag leaf length, flag leaf width, number of filled grains per panicle, total number of grains per panicle and single plant yield was reported by Naik et al. [21] plant height, flag leaf length, flag leaf width, total number of grains per panicle and single

plant yield by Lakshmi et al. [14] plant height, total number of grains per panicle and single plant yield by Sudeepthi et al. [17] and Bhargava et al [18] for plant height and single plant yield by Nithya et al. [16] and Priyanga et al. [23] for total number of grains per panicle and single plant yield by Dey et al. [19] and for single plant yield by Gayathridevi et al. [22]. High heritability coupled with moderate genetic advance was recorded in the traits like days to 50% flowering, panicle length, 1000 grain weight, grain breadth, kernel length, L/B ratio, fertility percentage and harvest index indicating both additive and non-additive gene action in the expression of the characters. This was in concurrence with the results obtained by Bhargava et al [18] for panicle length, fertility percentage and 1000 grain weight; Gayathridevi et al. [22] for days to 50% flowering; Lakshmi et al. [14] for panicle length; Manivelan et al. [20] for days to 50% flowering, panicle length, kernel length and L/B ratio; Nithya et al. [16] for 1000 grain weight and fertility percentage; Priyanga et al. [23] for panicle length and Sudeepthi et al. [17] for days to 50% flowering, panicle length and fertility percentage. Burton [27] has suggested that to ascertain the efficiency of selection we must consider genetic variability along with heritability and genetic advance. In our present study the traits flag leaf length, leaf area, number of filled grains per panicle and single plant yield showed high values for GCV, PCV, h^2b and GAM. This suggests that these traits can be improved by selection as the major player for their expression is additive gene action.

3.3 Correlation Analysis

Yield of rice is directly and indirectly contributed by various traits. As all these traits are interacting each other and with the environment, study of their interrelationships also is very important in selecting the ideal genotypes. Genotypic and phenotypic correlation analysis helps in understanding the association of the traits with each other. Days to 50% flowering showed significant positive correlation with flag leaf width, panicle length and total number of grains per panicle and negative correlation with 1000 grain weight at genotypic and phenotypic levels. Days to 50% flowering showed significant positive correlation at phenotypic level with plant height, flag leaf length, leaf area, number of filled grains per panicle, fertility percentage and single plant yield and negative correlation with grain length, kernel length and L/B ratio. Similar results for days to 50% flowering and panicle length was

reported by Sudeepthi et al. [17] and Manivelan et al. [20] and days to 50% flowering with total grains per panicle was reported by Sudeepthi et al. [17] Plant height showed significant positive genotypic and phenotypic correlations with flag leaf length, leaf area, panicle length and fertility percentage. It also showed significant negative correlation with chaffy grains per panicle at genotypic level and positive correlation with flag leaf width at phenotypic level. Sudeepthi et al. [17] Bhargava et al [18] and Singh et al. [15] reported similar results for plant height and panicle length. Gayathridevi et al. [22] reported significant correlations of plant height with flag leaf length.

Significant positive correlations at both genotypic and phenotypic levels were observed between number of tillers and number of panicles. This was in concurrence with the results of Sudeepthi et al. [17] Manivelan et al. [20] and Rezek et al. [28] Number of tillers showed significant negative correlation with flag leaf width at both levels and with grain breadth at phenotypic level. There was a significant positive genotypic and phenotypic correlation of flag leaf length with leaf area. Flag leaf length showed positive correlations with flag leaf width, panicle length, number of filled grains per panicle and negative correlation with grain length at phenotypic level. Significant positive correlations were recorded between flag leaf width and leaf area, number of filled grains per panicle, total number of grains per panicle and fertility percentage at both levels. At phenotypic level flag leaf width was significantly correlated with panicle length. Leaf area showed positive phenotypic and genotypic correlations with panicle length, number of filled grains per panicle and total number of grains per panicle whereas panicle length showed correlations with number of filled grains per panicle and total number of grains per panicle which was significant at both levels.

Number of filled grains per panicle was positively correlated with total number of grains per panicle and fertility percentage at both phenotypic and genotypic levels and with single plant yield at phenotypic level. Number of chaffy grains per panicle showed significant negative correlations with fertility percentage and harvest index at genotypic and phenotypic levels. The trait also showed a positive correlation with grain breadth. There was a significant positive correlation between total number of grains per panicle and fertility percentage at genotypic level and with single plant yield at phenotypic level. Total

number of grains per panicle showed significant negative phenotypic correlation with L/B ratio. Panicle length and total number of grains per panicle as well as total number of grains and fertility percentage was significantly correlated in the studies of Sudeepthi et al. [17] and Bhargava et al [18]. Total number of grains per panicle had significant positive correlations with leaf area and fertility percentage as reported by Singh et al. [15] and with filled grains per panicle as per the studies of Gayathridevi et al. [22].

1000 grain weight showed significant positive phenotypic correlation with grain length, kernel length, L/B ratio and harvest index whereas significant genotypic correlation was shown only with kernel length. Significant positive genotypic correlations were recorded by grain length with kernel length and L/B ratio and by grain breadth with kernel breadth. The trait grain breadth showed significant negative correlations with L/B ratio at genotypic and phenotypic levels and with kernel length at phenotypic level. Kernel length was positively correlated with L/B ratio and it was significant. At phenotypic level kernel length showed a significant negative correlation with kernel breadth. The correlation between kernel breadth and L/B ratio was negative and significant at both levels. The traits fertility percentage and harvest index was positively correlated at the phenotypic level and their effects were significant. Harvest index and single plant yield was positively correlated significantly at both genotypic and phenotypic levels.

Single plant yield was significantly correlated to days to 50 % flowering, number of filled grains per panicle, total number of grains per panicle and harvest index at phenotypic level and with harvest index only at genotypic level. The result for total number of grains per panicle was in concurrence with the results of Rezek et al. [28] Single plant yield recorded non-significant positive associations with days to 50% flowering, plant height, number of tillers, number of panicles, flag leaf length, leaf area, panicle length, number of filled grains per panicle, total number of grains per panicle, 1000 grain weight and fertility percentage at genotypic level. Non-significant association of yield with number of tillers was reported by Nithya et al. [16]. Similar results for number of tillers, number of panicles and panicle length was also reported by Priyanga et al. [23] Positive associations were noted for single plant yield with days to 50 % flowering, plant height, panicle length, number of tillers, leaf area, number of grains per panicle and number

of filled grains per panicle by Naik et al. [21]. The interactions between the contributing traits studied are so complex that a balanced method of selection for these characters is to be followed.

3.4 Path Analysis

Path coefficient analysis is carried out to identify the direct and indirect effect of the characters. Path coefficient divides the correlation coefficients of the yield contributing characters on the dependent variable *i.e.,* yield into direct and indirect effects. This is important for estimating the degree and direction of association thereby employing suitable methods of selection. The results of the path analysis have shown that there exist direct and indirect effects for all the independent traits studied. The direct effects of the traits number of panicles, kernel breadth and L/B ratio was very high and positive at the genotypic level. The highest direct effect was recorded by number of panicles followed by kernel breadth. Kernel length also showed very high direct effects in a negative direction. Total number of grains per panicle, leaf area, grain length and harvest index showed high positive direct effects whereas number of filled grains per panicle, number of chaffy grains per panicle and fertility percentage showed high negative direct effects. Direct effects were moderate for plant height, panicle length, 1000 grain weight and grain breadth and low for leaf length. The effects of days to 50% flowering, number of tillers and leaf width were found to be negligible at the genotypic level. The phenotypic path coefficients were very high for the flag leaf length, flag leaf width, total number of grains per panicle in the forward direction whereas for number of panicles, leaf area, number of filled grains per panicle and number of chaffy grains per panicle in the reverse direction. The highest direct effect at phenotypic level was shown by flag leaf length. High direct effects at the phenotypic level were shown by days to 50% flowering, plant height, 1000 grain weight and fertility percentage. The direct phenotypic effect was moderate for the traits number of tillers, grain length, grain breadth, kernel length, kernel breadth and harvest index. Panicle length and L/B ratio recorded low direct effects at phenotypic level. Similar result for number of panicles and fertility percentage was obtained by Bhargava et al. [18].

Genotypic path analysis has revealed very high positive indirect effects for number of panicles

through number of tillers and flag leaf length, kernel length through days to 50% flowering, leaf area, panicle length, number of filled grains per panicle, total number of grains per panicle, number of chaffy grains per panicle, grain breadth and kernel breadth, kernel breadth through number of chaffy grains per panicle, L/B ratio through number of tillers, 1000 grain weight, grain length and kernel length. Very high positive indirect effects was recorded by number of panicles through flag leaf width and grain breadth, flag leaf length through leaf area, flag leaf width through leaf area and total number of grains per panicle through flag leaf width and number of filled grains per panicle on phenotypic path analysis. Priyanga et al. [23] reported similar results for number of tillers and panicle length.

A critical analysis of the results shows that the traits number of panicles, panicle length, 1000 grain weight, leaf area, grain length, kernel breadth and harvest index exerted positive direct effects on grain yield at genotypic level. The analysis of phenotypic path coefficients reveals that the days to 50% flowering, plant height, number of tillers, flag leaf length, flag leaf width, total number of grains per panicle, 1000 grain weight, kernel length, kernel breadth and L/B ratio are the traits with significant positive direct effects. Gayathridevi et al. [22] have reported similar results for number of tillers and total grains per panicle. A closer evaluation of the indirect effects of contributing traits studied has shown that all the traits showed high or very high indirect effects on single plant yield through one or the other trait revealing the importance of employing them in efficient methods of selection.

4. CONCLUSION

The present study for assessing and partitioning the genetic variability has revealed that the genotypes showed variation for all the characters studied. High PCV, GCV along with high heritability and genetic advance was recorded for the traits, total number of grains per panicle, number of filled grains per panicle, flag leaf length, leaf area and single plant yield- asserting the importance of these traits in selection. Significant positive correlations was obtained for the traits days to 50% flowering, number of filled grains per panicle, total grains per panicle and harvest index with single plant yield. The characters days to 50% flowering, plant height, number of tillers, number of panicles, flag leaf length, flag leaf width, leaf area, panicle length,

total grains per panicle, 1000 grain weight, grain length, grain breadth, kernel length, kernel breadth, L/B ratio and harvest index showed positive direct effects at either phenotypic or genotypic level. For selecting the best genotypes, the characters studied are to be prioritized based on the overall results. The traits like number of panicles, panicle length, flag leaf length, leaf area, total number of grains per panicle, number of filled grains per panicle, 1000 grain weight, and harvest index are to be given weightage in selection for grain yield. Thus it is revealed that the genotypes studied can be used for further selection for grain yield for utilizing in rice breeding programmes.

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 manuscripts.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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