Genetic Variability and Character Association Studies in Diverse Rice (*Oryza sativa* L.) Genotypes for Agro-Morphological Traits in *Terai*Region of West Bengal

ABSTRACT

Aims: The study aims to analyze the genetic variability in diverse rice genotypes and establish correlations with grain yield and its attributes. By identifying and quantifying the genetic elements influencing grain yield and associated traits, the research intends to offer insights for developing high-yielding and resilient rice varieties, ultimately enhancing food security and agricultural sustainability.

Study Design: The experiment was set up in a randomized complete block design (RCBD) with two replications, using a spacing of 20 cm × 15 cm.

Place and Duration ofStudy: The experiment was conducted at the Instructional Farm of Uttar BangaKrishiViswavidyalaya, Pundibari, Coochbehar, West Bengal during the *Kharif(Aman)* season of 2019 and 2020.The duration of the study encompassed the entire *Kharif* seasons of both years.

Methodology: The study evaluated forty-two diverse rice genotypes based on nine agro-morphological traits. The methodology encompassed the utilization of ANOVA to evaluate significant differences in trait means and discern genetic variability among rice genotypes. Central tendency and variability were assessed through the calculation of mean, range, and standard deviation to gain insights into genetic variation. Furthermore, variation among traits was quantified using phenotypic and genotypic coefficient of variation to aid in understanding genetic variability. Heritability in broad sense was estimated to ascertain the genetic contribution to the observed variation, while the identification of traits with potential for improvement was achieved through the analysis of genetic advance as percent of mean. Furthermore, correlation and path coefficient analyses were conducted to comprehend the connections between the agro-morphological traits and grain yield, offering insights into the genetic relationships among the traits and their direct and indirect impacts on grain yield patterns.

Results: The analysis of variance results confirmed the presence of significant differences among the evaluated genotypes. The phenotypic coefficient of variation displayed elevated values, closely associated with the genotypic coefficient of variation for all traits. Both phenotypic and genotypic coefficient of variation values were observed to be low to moderate for all the nine traits. Furthermore, specific traits such as grain breadth, panicles plant^{-1}, and grain L/B ratio exhibited high heritability and high genetic advance percentage of mean, indicating their potential for selection and improvement in breeding programs. Additionally, the correlation study at the genotypic level revealed positive and significant correlations between grain yield plant^{-1}, test weight, and spikelet fertility. Moreover, the path coefficient analysis showed that grain length had the maximum positive direct effect on grain yield plant^{-1}.

Conclusion: In conclusion, the analysis revealed significant genotype variations across multiple traits, indicating potential for targeted breeding improvements. Traits like grain breadth, panicles plant^{-1}, and grain L/B ratio showed promising heritability and genetic advancement, emphasizing their value for selection in breeding programs. Correlation and path coefficient analyses highlighted interrelationships and direct effects on yield, underlining the importance of genetic factors in trait expression.

Keywords: *Correlation; Genetic parameters; PR 121; Rice; Spikelet fertility*

1. INTRODUCTION

Rice (*Oryzasativa* L., 2n=2x=24) belongs to the family *Poaceae* and is believed to be originated in South-East Asia. Rice stands as the single most crucial global food crop, serving as a primary dietary staple for over one-third of the world's population. Remarkably, over 90% of the world's rice production takes place in Asia, the continent where 60% of the Earth's population live (1). Indeed, it is cultivated in more than 100 countries around the world (2). Rice production nearly tripled during the latter half of the previous century. However, there is an urgent need to double rice production by 2050 in order to adequately feed a global population that is expected to surpass nine billion people (3). Globally, India ranks first in terms of rice cultivation area, covering 46.38 million hectares, and second in production, yielding 130.29 million tonnes, with a productivity of 2.809 tonnes per hectare. In the specific context of West Bengal, the area, production, and productivity of rice were reported as 5.60 million hectares, 16.76 million tonnes, and 2.996 tonnes/hectare, respectively (4).

Plant breeders and geneticists are highly interested in the genetic variation found both between and within populations of crop species, as it serves as a significant focal point for improvement (5). Hence, presence of genetic variability in any crop is a fundamental requirement for the selection of superior genotypes over the existing cultivars (6). The success of plant breeding programmes has been reported to be directly proportional to the extent of genetic diversity (7). A brief understanding of genetic diversity is essential for the formulation of future breeding strategies and the development of desired genotypes (8). The need for superior genotypes that can thrive in a variety of conditions has increased due to the rising demand for rice (9 and 10). The magnitude of variation due to heritable component is very important because, it would be a guide for selection of parents for crop improvement (11). Therefore, it is very much important for screening effectiveness and breeding enhancement in yield and its attributing traits.

Genetic parameters like the genotypic coefficient of variation (GCV) and the phenotypic coefficient of variation (PCV) serve as valuable tools for assessing the degree of variability within germplasm (12). Heritability estimates are valuable as they indicate the proportion of variation in a trait that can be inherited by offspring in coming generations. Broad-sense heritability estimates, as discussed by researchers like (13), (14), and (15), provide insight into the relative contributions of genetic and environmental factors to the variation within a population. This information helps breeders in assessing the potential scope for improvement through selective breeding. However, broad-sense heritability, on its own, may not be sufficient for selection based on phenotype, as it is influenced by environmental factors. Therefore, integration of heritability with genetic advance is more reliable and helpful in forecast the genetic gain under selection, as discussed by (16). This approach takes both genetic potential and the expected improvement into consideration. Genetic advance as percentage of mean furnishes valuable information regarding the expected genetic gain obtained through the selection of superior individuals. Therefore, having information on various genetic parameters related to the variability of different economically significant traits is crucial for plant breeders before developing any new variety.

Character association analysis was done to evaluate relationships between traits and it helps in selection of genotypes with desirable economic attributes. Correlation coefficient analysis describe the strength and direction of the linear relationship between two variables but does not provide information about the direction of influence or causality. Path coefficient analysis (17), on the other hand, allows for the assessment of causal relationships by partitioning the total correlations into direct and indirect effects of different traits on grain yield (18). It helps to determine the pathways and the relative contributions of each variable in influencing the dependent variable. Grain yield is a complex, quantitative trait greatly influenced by multiple component traits and environment (19). Therefore, focusing solely on selecting for grain yield may not be satisfying unless consideration of its attributing traits. So, grain yield along with contributing traits should be studied through character association techniques among the traits for yield improvement (20). Thus, positive correlations between yield and yield components are required for effective yield component breeding aimed at increasing grain yield in rice (21). So, it is important for plant breeders to find plant selection criteria, understanding the relationship between yield and related variables is crucial (22 and 23).

2. MATERIALS AND METHODS

2.1 Seed Materials and Field Experiment

The experiment was conducted at the Instructional Farm of Uttar BangaKrishiViswavidyalaya, Pundibari, Coochbehar, West Bengal during the kharif season of 2019-20 and 2020-21. The experiment involved 42 rice genotypes (Table 1), which included both landraces and varieties from two states (West Bengal and Andhra Pradesh) and was laid out in a randomized complete block design (RCBD) with two replications, utilizing a spacing of 20 cm × 15 cm.

The experimentation site was located at an elevation of 43 meters above mean sea level, with geological co-ordinates of 26°19'86'' N latitude and 89°23'53'' E longitude. The recommended package of practices were followed during the crop season to raise a good crop in the main field. Twenty-eight days seedlings were transplanted in the main field. The genotypes were collected from various states with wider adaptability in areas of their recommendation.

Table 1. Details of the rice genotypes used in the experiment

Sl. No.	Name of the Genotype	Sl. No.	Name of the Genotype	Sl. No.	Name of the Genotype
1)	Balam	15)	Zugal	29)	Nonabokra
2)	Baramshall	16)	Kakri	30)	BPT 2295
3)	Baskathi	17)	Kalavati	31)	BPT 5204
4)	Basmati	18)	KaloAush	32)	CR 910
5)	Kharadhan	19)	Kamal	33)	Geetanjali
6)	Chamarmani	20)	Kanakchur	34)	NL 44
7)	Chamatkar	21)	Kerala Sundari	35)	NL 46
8)	Dehradun Gandheswari	22)	KhaliaEulo	36)	NLR 0106
9)	Dudeswar	23)	Kalonunia	37)	NLR 3242
10)	Gopalbhog	24)	Khara	38)	MTU 1061
11)	Indulshall	25)	Lal Badsahbhog	39)	NLR 20084
12)	Jhara	26)	Patnai	40)	NLR 40058
13)	JP 90	27)	SagarSugandhi	41)	NLR 145
14)	JP 120	28)	TulsiMukul	42)	BPT 2411

The observations were documented for nine agro-morphological traits as outlined in the following steps:

a. The inner middle rows of each plot were used to randomly select five competitive plants in both replications.

b. In each replication, data was collected using five tagged plants from each genotype.

Plant Height [PH] (cm) was measured at maturity stage in cm from the base to the tip of last leaf at maturity stage. Panicles plant^{-1} [PPP] were counted, at maturity and average panicles per plant was recorded. By counting the number of spikelets per panicle. Filled grains were counted from five spikelets taken from each plant, and the resulting average was recorded as filled grains spikelet^{-1} [FGPP]. Spikelet fertility (%) [SF] was measured by counting the percentage of filled grain per panicle. Grain length (GL) and grain breath (GB) were measured in millimetre by using Vernier calliper. Grain length: breadth ratio (LBR) was measured in millimetre as ratio between GB and GL. Test weight (g) [TW] was obtained by weighing 1000 number of filled grains in grams. Grain yield plant^{-1} (g) [GYP] was recorded by weighing the total filled grain per plant in grams.

2.2 Statistical Analysis

The mean values were subjected to log transformation prior to statistical analysis to test the significance of variance (ANOVA) as per standard statistical procedure by (24). ANOVA for individual years and combined over Combined over the yearsyears was performed to assess the significance of genotypes across the years separately, between the years and interaction of genotypes with years as suggested by (25) and their significance was tested by referring to the values of 'F' table (26) to compare the significant difference between the genotypes. The treatment means were tested for significance (LSD) at 1% or 5% probability level.

The variability present in the genotypes was estimated by phenotypic and genotypic coefficient of variations using the procedure suggested by (27). Phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) were estimated using the formula suggested by (28) and expressed in percentage. The estimates of PCV and GCV were categorized based on the scale given by (29). Heritability in the broad sense (h2b) was computed using the formula given by (27) and expressed in percentage. The range of heritability, expected genetic gain or genetic advance as percent of mean (GAM) under selection were calculated as suggested by (30). The genotypic correlation coefficients were estimated using the standard procedure suggested by (31). Path coefficient analysis was done as suggested by (32) using the phenotypic as well as genotypic correlation coefficients to determine the direct and indirect effects of yield on grain yield for individual years and Combined over the years data. The residual effect (h) was calculated using the formula (32).

All the statistical analyses were done by using GENRES statistical package (33). RStudio software (34)was used to visualize the distribution and probability density of the datausing *vioplot*package (35) and (36) for violin plot analysis to uncover the best connections among features.

3. RESULTS AND DISCUSSION

3.1 Analysis of variance

The analysis of variance (ANOVA) was used to assess individual years, with a combined over the years analysis conducted for both years and revealed that all the traits were significantly different for each genotype under two different years as well as combined over the years (Table 2). Based on the ANOVA for Combined over the years, significant effect of year is observed for all the traits under the study. At replication within year level, only PPP, TW and GYP traits were significantly different from each other, while none of the other traits were found to be significantly different indicating that their role is negligible in expression of the trait. The genotype × year was highly significant for FGPP, SF, GL, TW and GYP. The reason for wide spectrum and high magnitude of variability in the present study may be due the fact that the studied genotypes were collected and developed in different breeding programmes representing different agro-climatic conditions of the country. These results were in conformity with the earlier findings of (23), (37) and (6).

3.2 Estimation of genetic parameters

The (Table 3) provides the general mean, range, and genetic parameters for the nine traits, while (Figure 1) displays a violin plot illustrating the distribution of the nine yield-attributing traits in rice genotypes. PH was ranged from 63.82 cm (NL 46) to 182.09 cm (Kakri) with grand mean value of 130.47; the highest and lowest ranges for PPP were 6.25 (Nonabokra) and 19.65 (Jhara) respectively, with a grand mean value of 10.56; FGGP varied from 68.00 (Indulshall) to 193.35 (Kakri) with grand mean value of (111.29), 72.20 (Indulshall) and 88.84 (BPT 2295) for SF with grand mean value of 82.38; GL ranging from 4.20 (NLR 0106) to 9.41 (Geetanjali) with grand mean value of 6.15, highest and lowest ranges of GB were 1.38 (NLR 0106) and 3.12 (Jhara) with grand mean value of 2.36; LBR was varied from 1.64 (Kanakchur) to 3.86 (Baskathi) with grand mean value of 2.70; TW varied from 8.38 (Tulsi Mukul) to 22.43 (NLR 3242) with grand mean value of 15.15 and GYP ranged from 11.79 (Tulsi Mukul) to 26.91 (NLR 20084) with grand mean value of 18.75.

The estimation of PCV, GCV, broad-sense heritability (H2), and genetic advance as percent of mean (GAM) has been analyzed for all the genotypes. The GCV values were lower than PCV value, suggesting a minimal environmental effect on the manifestation of the trait for all the traits. The traits displayed low to moderate estimates for both PCV and GCV but none have exhibited high values for either parameter. Similar results are obtained by (38). The traits namely, GB (12.61, 12.76), LBR (11.77, 11.90) and PPP (11.05, 11.14) have recorded medium PCV and GCV values. Similar results were reported for GB by (39), (40) and (41); (39), (42), (43), (44), (45) for PPP and (46) for LBR.

Table 2. ANOVA for grain yield and its attributing traits in 42 genotypes of rice

Year	Sources of variation	d.f.	Mean sum of squares								
			PH	PPP	FGPP	SF	GL	GB	LBR	TW	GYP
1	Replication	1	.001	.004**	.002	.001	.001	.001	.001	0.002**	.001
	Genotype	41	0.032**	0.027**	0.023**	.001**	0.010**	0.009**	0.009**	0.016**	0.023**
	Error	41	.001	.001	.001	.001	.001	.001	.001	.001	.001
2	Replication	1	.001	.001*	.001	.001	.001	.001*	.001	0.003**	.001*
	Genotype	41	0.031**	.028**	.025**	.001**	.011**	0.009**	0.009**	0.015**	0.020**

	Error	41	.001	.001	.001	.001	.001	.001	.001	.001	.001
Combined over the years	Year	1	.001*	0.048*	0.075*	.002*	.002*	0.007*	0.002*	0.103*	0.123**
	Replication within year	2	.001	.003**	.001	.001	.001	.001	.001	0.003***	.001*
	Genotype	41	0.063**	0.055**	0.046**	0.002**	0.021**	0.017**	0.018**	0.031**	0.041**
	Year × Genotype	41	.001	.001	.001*	.001**	.001*	.001	.001	.001**	.001**
	Combined over the years Error	82	.001	.001	.001	.001	.001	.001	.001	.001	.001

* Significant 5% at (*P* = .05) probability level, ** * Significant at 1% (*P* = .01) probability level, d.f. – degree of freedom, PH - Plant height (cm), PPP - Panicles plant-1, FGPP - Filled grains spikelet-1, SF - Spikelet fertility (%), GL - Grain length (mm), GB - Grain breadth (mm), LBR - Grain length: breadth ratio (mm), TW - Test weight (g) and GYP - Grain yield plant-1 (g).

Table 3. Estimates of variability, heritability and genetic advance for yield and its yield attributing traits of rice (Combined over the years)

Traits	Mean	Range		Standard Deviation	GCV	PCV	H^2b	GAM
		Min.	Max.					
PH	130.47(2.10)	63.82(1.80)	181.09(2.26)	0.126	5.99	5.99	99.84	12.33
PPP	10.56(1.05)	6.25(0.86)	19.65(1.31)	0.116	11.05	11.14	98.34	22.57
FGPP	111.29(2.03)	68.00(1.83)	193.35(2.29)	0.108	5.25	5.33	96.74	10.63
SF	82.38(1.92)	72.20(1.86)	88.84(1.95)	0.021	1.14	1.18	92.81	2.26
GL	6.15(0.85)	4.20(0.72)	9.41(1.02)	0.072	8.48	8.49	99.76	17.44
GB	2.36(0.52)	1.38(0.38)	3.12(0.61)	0.065	12.61	12.76	97.53	25.64
LBR	2.70(0.56)	1.64(0.42)	3.86(0.69)	0.068	11.77	11.90	97.34	23.92
TW	15.15(1.20)	8.38(0.97)	22.43(1.37)	0.088	7.30	7.33	99.12	14.97
GYP	18.75(1.26)	11.79(1.07)	26.91(1.43)	0.103	8.03	8.07	98.95	16.45

Values in the parenthesis indicates the log transformed values of the individual traits; The range, standard deviation, GCV, PCV, heritability and the GA as percentage of mean have been calculated with the log transformed values of the traits. (Min.- Minimum, Max.-Maximum, PCV- Phenotypic Coefficient of Variation; GCV- Genotypic Coefficient of Variation), H^2b – Heritability in broad sense , GAM – Genetic advance as percent of mean, PH - Plant height (cm), PPP - Panicles plant-1, FGPP - Filled grains spikelet-1, SF - Spikelet fertility (%), GL - Grain length (mm), GB - Grain breadth (mm), LBR - Grain length: breadth ratio (mm), TW - Test weight (g) and GYP - Grain yield plant-1 (g).

Low values of GCV and PCV were seen in GL (8.48, 8.49), GYP (8.03, 8.07), TW (7.30, 7.33), PH (5.99, 5.99), FGPP (5.25, 5.33), and SF (1.14, 1.18) were recorded low GCV and PCV values. Similar results obtained by (47) for GL; (37) and (48) for GYP; (49), (41) and (50) for PH; (51) for FGPP; (39) and (52) for SF; (53) for TW, and (54) for TW and SF. It indicates that selection may be effective based on these traits with medium PCV and GCV values and their phenotypic expression would be a good indication of genetic potential. A narrow difference in phenotypic and genotypic coefficients of variation was obtained for the aforementioned traits, indicating the least effect of the environment on these traits. Thus, these traits expressed the true genetic potential in varied environments.

The heritability (H2b) estimates (>80%) were recorded for all agro-morphological traits viz. PH (99.84), PPP (98.34), FGPP (96.74), SF (92.81), GL (99.76), GB (97.53), LBR (97.34), TW (99.12) and GYP (98.95), indicating traits are least influenced by environment and selection for improvement is rewarding. Similar findings were reported by (38) for FGPP, SF and TW; (52) and (48) for PH, TW, FGPP, SF and GY while (44) for GL, GB and LBR and (42) for PPP. Therefore, heritability can be utilized as a tool for achieving effective improvements in the abovementioned traits that are undergoing selective breeding practices.

The values of genetic advance as per cent of mean (GAM) showing high (>20%) for GB (25.64), LBR (23.92) and PPP (22.57). Similar results obtained by (40) and (47) for GL and LBR; (42) and (43) for PPP. Moderate GAM (10-20%) obtained for GL (17.44), GYP (16.45), TW (14.97), PH (12.33) and FGPP (10.63) like results of (40) and (46) for GYP; (49) for TW; (47) for GL; (49) for PH, and (55) for FGPP. At last, low GAM (<10%) was revealed by SF (2.26). The similar result obtained by (56), (39), (45), (49) and (57) for SF.

The sole estimate of heritability is limited in its capacity to predict the outcome of selecting the best genotype due to its inclusion of both additive and non-additive gene effects. Nonetheless, high genetic advance consistently arises from the action of additive genes. Consequently, it is important to take both heritability and genetic advance as a percentage of the mean into consideration. It's important to note that high heritability does not ensure a corresponding high genetic advance (30). Therefore, a more effective approach involves combining heritability with genetic advance rather than relying solely on heritability.

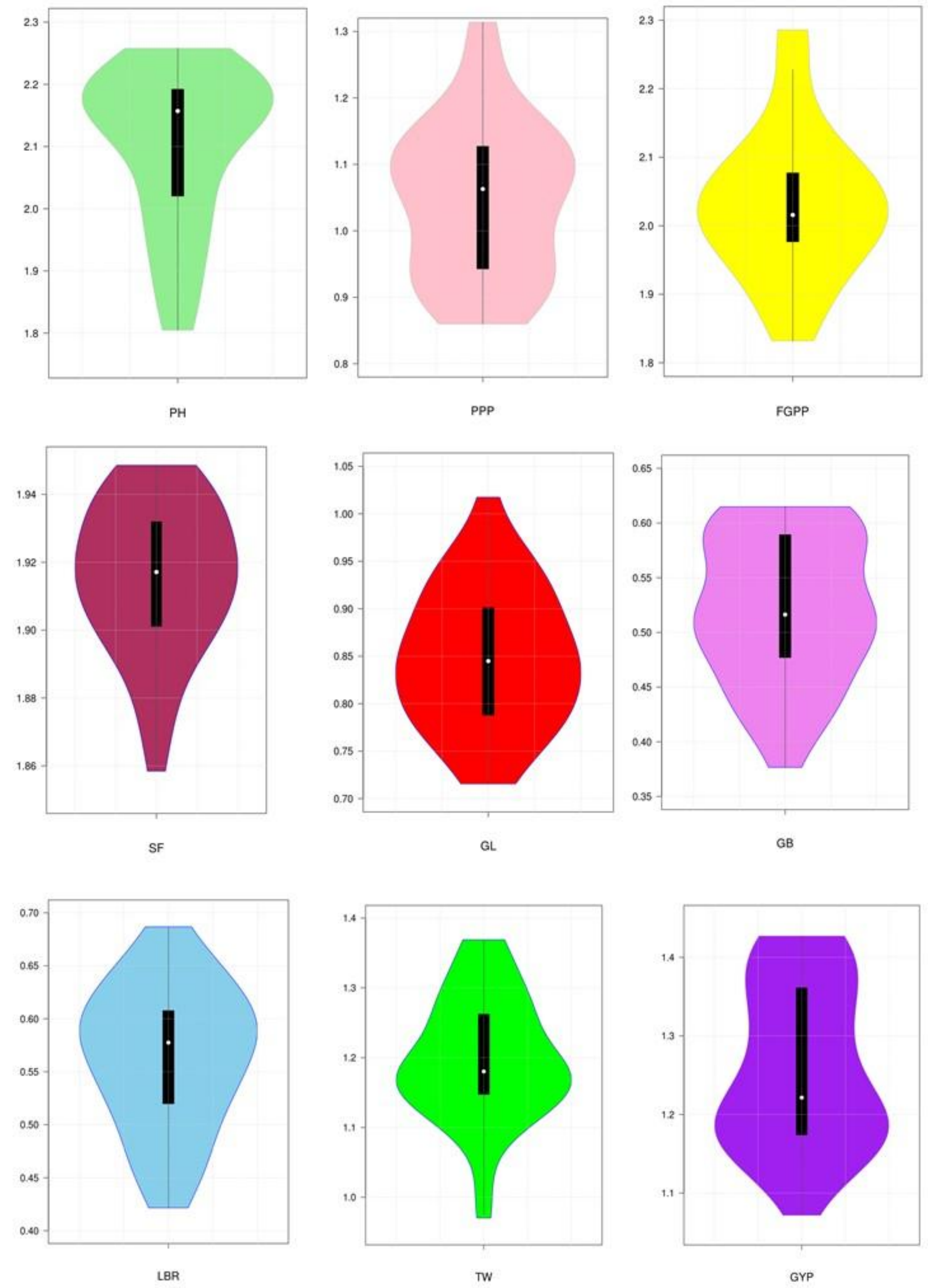

Figure 1. Violin plot for nine yield attributing traits in rice genotypes (combined over the years)

High heritability coupled with high GAM was observed for three traits indicating that traits viz., GB (97.53, 25.64), LBR (97.34, 23.92) and PPP (98.34, 22.57) are governed by additive genes and improvement is effective. Similar kind of results were obtained by (40) and (47) for GB; (49), (40) for LBR; and (58), (59) for PPP. High heritability coupled with moderate GAM was recorded by (49), (50) for PH; (49), (60) for TW; (61) for GL; (46) for GYP and (51) for FGPP. The trait, SF exhibited high heritability along with low genetic advance mean (GAM), signalling non-additive gene action. Consequently, selecting this trait may not lead to significant rewards. Similar result was obtained by (39).

3.3 Correlation coefficient analysis

A complex trait such as yield, which plays a significant role in crop improvement programmes, is intricate and arises from the interplay of various components. Correlation coefficients measure the strength and direction of the relationship between pairs of variables, offering insight into the degree of interrelation between the variables. The genotypic correlation coefficients estimated between GYP and other traits under the study are indicated in Table 4. Grain yield is the outcome of many independent traits, and some of them are highly associated with grain yield. The analysis of the relationship among these traits and association with grain yield is essential to establish selection criteria.

Table 4. Genotypic correlation between yield and its attributing traits in rice (Combined over the years)

Traits	Plant height (cm)	Panicles plant^{-1}	Filled grains panicle^{-1}	Spikelet fertility (%)	Grain length (mm)	Grain breadth (mm)	Grain L/B ratio	Test weight (g)	Grain yield (g plant^{-1})
Plant height (cm)	1.00	0.285*	0.204	-0.277*	0.431**	0.289*	0.098	-0.061	-0.152
Panicles plant^{-1}		1.00	0.197	-0.151	0.123	0.082	0.019	-0.067	-0.040
Filled grains panicle^{-1}			1.00	0.471**	-0.109	-0.171	0.077	0.003	0.225
Spikelet fertility (%)				1.00	-0.323*	-0.282*	0.011	0.139	0.320*
Grain length (mm)					1.00	0.456**	0.429**	0.101	-0.198
Grain breadth (mm)						1.00	-0.607**	0.074	-0.186
Grain L/B ratio							1.00	0.035	0.016
Test weight (g)								1.00	0.622**
Grain yield (g plant^{-1})									1.00

* Significant at (*P*=.05) 5% probability level, ** * Significant at (*P* =.01) 1% probability level

Traits such as TW (0.622) and SF (0.320) had shown significant and positive correlation with GYP. Hence, selection for these traits would help in improving the grain yield in rice crop. Similarly results are obtained by (62), and (63) for TW; and (64) for spikelet fertility. However, none of the character was found to be significantly negative with GYP affecting the expression of the grain yield as reported by (40) and (44). Therefore, traits directly influencing yield should be chosen, and their associations with other traits must be considered simultaneously, as this can have indirect effects on grain yield. The genotypic correlation revealed that PH exhibited a positive and significant correlation with GL, GB and PPP. Similar results were reported earlier by (65) for GL and GB; (66) and (39) for GB; (23) for GL; (67), and (68) for PPP. This indicates that the longer length and breadth grain bearing genotypes were taller genotypes. The character PPP did not show a significant correlation with any trait, but exhibited a positive association with FGPP, indicating genotypes with more number of filled grains are possessed by more number of panicles. The trait PPP showed only positive association with FGPP, indicating that genotypes with number of panicles contains more number of filled grains. FGGP had significant and positive correlation with only spikelet fertility. This result was in similar with (69) as indicates like genotypes which contains more filled grains have higher spikelet fertility. But, there was a significant negative correlation between spikelet fertility (%) and length and breadth of grain. GL had only a significantly positive correlation with GB and LBR as. The results are in agreement with the reports of (46) for GB; (40) and (66) for LBR. SF had negative and significant association with GL and GB like similar results by (70) for GL and GB; and (71) for GL. GB exhibited only negative, significant association with LBR. The results are in agreement with the findings of (40), (66) and (71). TW recorded only significant positive correlation with GY. Similar results are obtained by (54), (72) and (71) for GYP.

The positive and significant association of traits at the genotypic level justifies the influence of genetic factors over phenotypic ones, suggesting the potential for a correlated response to selection.

3.4 Path coefficient analysis

Path Coefficient Analysis is an effective approach for determining both direct and indirect causes of association. It involves a detailed analysis of the specific forces at play in producing a correlation and also evaluates the relative significance of each causal factor. Path coefficient analysis is distinct from simple correlation in that it identifies cause-and-effect relationships, whereas the latter solely measures mutual association without considering causation. The causal (independent) variables were plant height, panicles plant^{-1}, filled grains panicle^{-1},spikelet fertility, grain length, grain breadth, grain L/B ratio, and test weight whereas the outcome (dependent) variable was grain yield plant^{-1}. The table 5 displayed the direct and indirect path coefficients of the nine causal factors on grain yield plant^{-1} using genotypic path coefficient analysis.

Table 5. Direct (diagonal) and indirect (off-diagonal) effects of different yield components in rice (Combined over the years)

Traits	Plant height (cm)	Panicles plant^{-1}	Filled grains panicle^{-1}	Spikelet fertility (%)	Grain length (mm)	Grain breadth (mm)	Grain L/B ratio	Test weight (g)	Correlation with Grain yield (g plant^{-1})
Plant height (cm)	**0.292**	-0.023	-0.004	-0.098	6.057	-4.745	-1.574	-0.057	-0.152
Panicles plant^{-1}	0.083	**-0.082**	-0.004	-0.054	1.731	-1.344	-0.309	-0.062	-0.040
Filled grains panicle^{-1}	0.060	-0.016	**-0.020**	0.168	-1.539	2.803	-1.233	0.003	0.225
Spikelet fertility (%)	-0.081	0.012	-0.010	**0.356**	-4.542	4.630	-0.174	0.129	**0.320****
Grain length (mm)	0.126	-0.010	0.002	-0.115	**14.066**	-7.475	-6.886	0.094	-0.198
Grain breadth (mm)	0.085	-0.007	0.003	-0.100	6.413	**-16.395**	9.746	0.069	-0.186
Grain L/B ratio	0.029	-0.002	-0.002	0.004	6.038	9.960	**-16.043**	0.032	0.016
Test weight (g)	-0.018	0.005	0.000	0.049	1.424	-1.211	-0.558	**0.930**	**0.622****

* Significant at 5% probability level, Residual Effect= 0.59

Genotypic path coefficient analysis revealed traits like GL (14.066), TW (0.930), SF (0.356) and PH (0.292) exhibited direct positive effect with GYP at genotypic level. Therefore, these traits should be viewed as vital selection criteria in all rice improvement programmes, and direct trait selection is recommended for improving yield. These results are in conformity with (73) for TW and SF; (44) for PH and GL; (74) for PH and TW; and (38) for TW. Nevertheless, the positive and significant association of these traits with GYP suggests that indirect effects may be responsible for the correlation. Therefore, it is essential to account for indirect causal factors while selecting the traits for improving yield through these traits. Traits such as GB (-16.395) and LBR (-16.043) recorded direct maximum negative direct effect on grain yield followed by PPP (-0.082) and FGPP (-0.020). These findings are in agreement with (40) for FGPP and LBR, PPP; and (44) for GB.

The residual effect signifies the unexplained variability of the dependent factor, GYP. This moderate value of 0.59 suggests that the traits analyzed in the path coefficient analysis accounted for 40.95% of the variation in GYP. The residual effect on GYP in this study could be attributed to various factors such as other unaccounted traits, environmental influences, and sampling errors that were not included in the investigation.

4 CONCLUSION

Analysis of variance exhibited the presence of significant differences among the rice genotypes for all the traits included in the study. Occurrence of high variability in the genotypes will increase the probability of producing desirable recombinants in successive generations. Phenotypic coefficient of variation was found slightly higher than the genotypic coefficient of variation revealed less influence of environment on the traits under study.

Therefore, response to direct selection may be effective in improving these traits. Selection of traits with high heritability coupled with high genetic advance would help in improving the traits under study such as grain length, length: breadth ratio and panicles plant^{-1}. Based on correlation and path analyses carried out in this study suggests that only two traits viz., TW and SF influenced the GYP more than any one of the traits taken for the study. Therefore, significant emphasis given on these traits to facilitate improvements in rice breeding programmes.

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6 COMPETING INTERESTS

The authors declare that there is no conflict of interest.

7 AUTHOR’S CONTRIBUTION

This work was carried out in collaboration among all authors. 2nd author guided in planning and implementation of research work. 1st author conducted the field experiment as a part of doctoral degree and collected all data and drafting the manuscript also. Their practical involvement guarantees that the implementation matches the intended experiment, leading to trustworthy results. 3rd, 4th, 5thand 6thauthor guided in planning and implementation of research and data analysis.7thand 8thauthorhelped in collectingseed material from West Bengal and Andhra Pradesh.9th author helped in writing review. The collaboration among these authors leads to a unified and comprehensive article that not only conveys the experiment's specifics but also offers significant insights and contributions to the scientific field.

8 DISCLAIMER

The authors have indicated that there are no conflicting interests. The materials used in this study are commonly and frequently utilized in our country and research location. As our objective is to advance knowledge rather than to use these products for litigation purposes, there is no conflict of interest between the authors and the manufacturers of the products. Furthermore, the authors funded the research using their own resources rather than relying on the producing company.

REFERENCES

1. Khush GS. Origin, dispersal, cultivation and variation of rice. Plant molecular biology. 1997; 35: 25-34. http://dx.doi.org/10.1023/A:1005810616885.
2. Muthayya S, Sugimoto JD, Montgomery S, Maberly GF. An overview of global rice production, supply, trade, and consumption. Annals of the New York Academy of Sciences. 2014; 1324(1): 7-14. https://doi.org/10.1111/nyas.12540.
3. Alexandratos N, Bruinsma J. World agriculture towards 2030/2050: the 2012 revision. 2012; ESA Working paper No. 12-03. Rome, FAO. https://www.fao.org/3/ap106e/ap106e.pdf.
4. Government of India. Department of Agriculture Cooperation and Farmers Welfare. Agricultural Statistics at a Glance. Rice: Area, Production and Yield during 2019-20 and 2020-21 in major producing states along with coverage under irrigation [Internet]. New Delhi; The Department; 2022 [cited in 2022]. Available from: https://desagri.gov.in/wp-content/uploads/2023/05/Agricultural-Statistics-at-a-Glance-2022.pdf.
5. Hayward MD, Breese EL. Population structure and variability. In: Hayward MD, Bosemark NO, Romayosa I, editors, Plant Breeding: Principles and Prospects. London: Chapman and Hall; 1993. p. 16-29. http://dx.doi.org/10.1007/978-94-011-1524-7_3.
6. Dhurai SY, Bhati PK. Saroj SK. Studies on genetic variability for yield and quality characters in rice (*Oryzasativa* L.) under integrated fertilizer management. The Bioscan 2014; 9(2): 845-848. https://www.researchgate.net/publication/265473724_STUDIES_ON_GENETIC_VARIABILITY_FOR_YIELD_AND_QUALITY_CHARACTERS_IN_RICE_ORYZA_SATIVA_L_UNDER_INTEGRATED_FERTILIZER_MANAGEMENT.
7. Allard RW (1960) Principles of Plant Breeding. John Wiley and Sons Inc., New York. 485. https://doi.org/10.2134/agronj1962.00021962005400040037x.
8. Luqman T, Qamar ZU, Tabasum A, El-Kallawy WH, Nazir T, Attacha S, Fiaz S, Nadeem MA, Hameed A, Maryum Z, Kimiko I. Genetic characterization of coarse and basmati rice (*Oryza sativa* L.) through microsatellite markers and morpho-agronomic traits. Genetic Resources and Crop Evolution. 2023; 70: 1-4. http://dx.doi.org/10.1007/s10722-023-01620-w.
9. Sarker U, Biswas PS, Prasad B. Mian MA. Correlated response, relative selection efficiency and path analysis in cold tolerant rice. Bangladesh J. Pl. Breed. Genet. 2001; 14(2): 33-6.
10. Thant AA, Zaw H, Kalousova M, Singh RK, Lojka B. Genetic diversity and population structure of Myanmar rice (*Oryza sativa* L.) varieties using DArTseq-based SNP and silicoDArT markers. Plants. 2021; 10(12): 2564.

http://dx.doi.org/10.3390/plants10122564.

11. Dutta P, Dutta PN, Borua PK. Morphological traits as selection indices in rice: A statistical view. Universal Journal of Agricultural Research. 2013; 1(3): 85-96.
12. Idris A. Genetic variability and inter relationship between yield and yield components in some rice genotypes. American Journal of Experimental Agriculture. 2012; 2: 233-239. http://dx.doi.org/10.9734/AJEA/2012/961.
13. Dudley JW, Moll RH. Interpretation and use of estimates of heritability and genetic variances in plant breeding 1. Crop science. 1969; 9(3): 257-262. https://doi.org/10.2135/cropsci1969.0011183X000900030001x.
14. Marwede V, Schierholt A, Möllers C, Becker HC. Genotype× environment interactions and heritability of tocopherol contents in canola. Crop Science. 2004; 44(3): 728-31. https://acsess.onlinelibrary.wiley.com/doi/pdfdirect/10.2135/cropsci2004.7280.
15. Raffi SA, Nath UK. Variability, heritability, genetic advance and relationships of yield and yield contributing characters in dry bean (Phaseolus vulgaris L.). J. Biol. Sci. 2004; 4(2): 157-159. : https://www.cabidigitallibrary.org/doi/full/10.5555/20043200955.
16. Ogunbayo SA, Sié M, Ojo DK, Sanni KA, Akinwale MG, Toulou B, Shittu A, Idehen EO, Popoola AR, Daniel IO, Gregoria GB. Genetic variation and heritability of yield and related traits in promising rice genotypes (*Oryza sativa* L.). J. Plant Breed. Crop Sci. 2014; 6(11): 153-159. https://doi.org/10.5897/JPBCS2014.0457.
17. Wright S. Correlation and causation. Journal of Agricultural Research. 1921; 20: 557-585.
18. Rajarathinam S and Raja VG. Correlation and path analysis in some rice varieties under alkaline stress. Madras Agricultural Journal. 1992; 79(7): 374-378. : https://doi.org/10.29321/MAJ.10.A01769.
19. Moosavi M, Ranjbar G, Zarrini HN, Gilani A. Correlation between morphological and physiological traits and path analysis of grain yield in rice genotypes under Khuzestan. Biol. Forum Int. J. 2015; 7(1): 43-47. https://www.researchgate.net/publication/283054306_Correlation_between_morphological_and_physiological_traits_and_path_analysis_of_grain_yield_in_rice_genotypes_under_Khuzestan_conditions.
20. Oladosu Y, Rafii MY, Magaji U, Abdullah N, Miah G, Chukwu SC, Hussin G, Ramli A, Kareem I. Genotypic and phenotypic relationship among yield components in rice under tropical conditions. BioMed research international. 2018; 2018: 1-10. : https://doi.org/10.1155/2018/8936767.

21. Ogunbayo SA, Sié M, Ojo DK, Sanni KA, Akinwale MG, Toulou B, Shittu A, Idehen EO, Popoola AR, Daniel IO, Gregoria GB. Genetic variation and heritability of yield and related traits in promising rice genotypes (*Oryza sativa* L.). J. Plant Breed. Crop Sci. 2014; 6(11): 153-159. https://doi.org/10.5897/JPBCS2014.0457.
22. Aman J, Bantte K, Alamerew S. Sbhatu DB. Correlation and path coefficient analysis of yield and yield components of quality protein maize (Zea mays L.) hybrids at Jimma, western Ethiopia. International Journal of Agronomy. 2020; 2020: 1-7. https://doi.org/10.1155/2020/9651537.
23. Singh G, Khanna R, Kaur R, Kaur K, Kaur R, Sharma N, Mangat GS. Performance under multi-environment trial for quantitative traits of rice (*Oryza sativa* L.) genotypes in North-West India (Punjab). Ecological Genetics and Genomics. 2023; 1: 28. https://doi.org/10.1016/j.egg.2023.100190.
24. Panse VG, Sukhatme PV. Statistical Methods for Agricultural Workers, 2nd edition, Indian Council of Agricultural Research Publication, New Delhi. 1985.
25. Singh, Chaudhary BD. Biometrical methods in quantitative genetic analysis. In: Biometrical methods in quantitative genetic analysis. 1977.
26. Fisher RA and Yates F. Statistical tables for biological, agricultural and medical research. Oliver and Boyd, London. 1963.
27. Burton GW, Devane EM. Estimating heritability in tall fescue (Festucaarundinaceae). From replicated clonal materials Agron. J. 1953; 45: 78-481.
28. Burton GW. Quantitative Inheritance in Grass. Proc.6th Int. Grassland Cong., 1952 ; 1: 277 – 283.
29. Sivasubramanian S, Madhavamenon P. Genotypic and phenotypic variability in rice. Madras Agricultural Journal. 1973; 60: 1093-1096.
30. Johnson HW, Robinson HF, Comstock R E. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 1955; 47: 314- 318.
31. Miller PA, William C, Robinson HF, Comstock RE. Estimates of genotypic and environmental variances and co-variances in upland cotton and their implications in selection. Agron. J. 1958; 50: 126-131.
32. Dewey DR, Lu KH. A correlation and path coefficient analysis of components of crested wheat grass seed production. Agron. J. 1959; 51: 515-518.
33. Payne RW. Genstat 5 release 3 reference manual. Oxford University Press; 1993.
34. Horton NJ, Kleinman K. Using R and RStudio for data management, statistical analysis, and graphics. CRC Press; 2015.
35. Adler D, Kelly ST, Elliott T, Adamson J (2022). vioplot: violin plot. R package version 0.4.0, https://github.com/TomKellyGenetics/vioplot.

36. Adler D, Kelly ST. vioplot: Violin plot. R package version 0.2, URL http://CRAN. R-project. org/package= vioplot. 2005.
37. Konate AK, Zongo A, Kam H, Sanni A, Audebert A. Genetic variability and correlation analysis of rice (*Oryza sativa* L.) inbred lines based on agro-morphological traits. Afr. J. Agricult. Res. 2016, 11(35): 3340–3346. https://doi.org/10.5897/AJAR2016.11415.
38. Faysal AS, Ali L, Azam MG, Sarker U, Ercisli S, Golokhvast KS, Marc RA (2022) Genetic variability, character association, and path coefficient analysis in transplant Aman rice genotypes. Plants. 11(21): 2952. : https://doi.org/10.3390/plants11212952.
39. Dinesh K, Devi MS, Sreelakshmi C, Paramasiva I. Exploring the genetic diversity for yield and quality traits in indigenous landraces of rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding. 2023; 14(2): 502-10. https://doi.org/10.1007/s12041-018-1023-8.
40. Kondi RK, Kar S, Mandawi NC. Study of genetic parameters, correlation and path analysis for yield and quality characters in fine scented rice genotypes. ORYZA-An International Journal of Rice. 2022; 59(1): 20-30. https://doi.org/10.35709/ory.2022.59.1.3.
41. Roy SC and Shil P. Assessment of genetic heritability in rice breeding lines based on morphological traits and caryopsis ultrastructure. Scientific reports. 2020; 10(1): 7830. https://doi.org/10.1038/s41598-020-63976-8.
42. Keerthiraj B, Biju S. Genetic variability, heritability and genetic advance of yield and lodging-related traits in rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding. 2020; 11(04): 1093-1098. https://doi.org/10.37992/2020.1104.177.
43. Mallimar M, Surendra P, Hanamaratti NG, Jogi M, Sathisha TN, Hundekar R. Genetic variability for yield and yield attributing traits in F3 generation of rice (*Oryza sativa* L.). Research in Environment and Life Sciences. 2015; 9(1): 24-8. https://www.researchgate.net/publication/295074472_Genetic_variability_for_yield_and_yield_attributing_traits_in_F3_generation_of_rice_Oryza_sativa_L.
44. Gudepu S, Chennamadhavuni GR, Katragadda S. Variability and association studies for yield and yield contributing traits in long grain rice (*Oryza sativa* L.) Oryza. 2023; 59(4): 409-417. https://doi.org/10.35709/ory.2022.59.4.3.
45. Shanmugam A, Suresh R, Ramanathan A, Anandhi P, Sassikumar D. Unravelling genetic diversity of South Indian rice landraces based on yield and its components. Electronic Journal of Plant Breeding. 2023; 14(1):160-9. https://doi.org/10.37992/2023.1401.007.
46. Yuvaraja A, Gokulvigneswaran P, Praba SS, Nirubana V. An assessment of early generation genetic variability and correlation for yield and quality traits in rice (*Oryza*

sativa L.). ORYZA-An International Journal of Rice. 2019; 56(4): 411-415. https://doi.org/10.35709/ory.2019.56.4.10.

47. Chacko A, Jayalekshmy VG, Shahiba AM. Studies on PCV, GCV, Heritability, and Genetic Advance in Rice Genotypes for Yield and Yield Components. Int. J. Plant Soil Sci. 2023; 35(16): 324-30. https://doi.org/10.9734/ijpss/2023/v35i163266.
48. Sadimantara GR, Yusuf DN, Febrianti E, Leomo S, Muhidin M. The performance of agronomic traits, genetic variability, and correlation studies for yield and its components in some red rice (*Oryza sativa*) promising lines. Biodiversitas Journal of Biological Diversity. 2021; 22(9): 3994-4001. https://doi.org/10.13057/biodiv/d220947.
49. Kumari S, Sinha S, Satyendra, Kumar V, Singh RS, Kumar A, Kumar RR, Singh S. Estimation of genetic variability, correlation and path analysis in elite rice genotypes (*Oryza sativa* L.). ORYZA-An International Journal on Rice. 2023; 60(1): 125-131. https://doi.org/10.35709/ory.2023.60.1.3.
50. Paul A, Ahmad E, Singh DN, Singh MK. Identification of selection parameters for evaluating superior rice hybrids. ORYZA-An International Journal on Rice. 2018; 55(1): 230-233. https://doi.org/10.5958/2249-5266.2018.00027.9.
51. Islam MA, Raffi SA, Hossain MA, Hasan AK. Analysis of genetic variability, heritability and genetic advance for yield and yield associated traits in some promising advanced lines of rice. Progressive Agriculture. 2015; 26(1): 26-31. https://doi.org/10.3329/pa.v26i1.24511.
52. Kushwaha BK, Gobu R, Lal JP. An assessment of genetic variability for drought tolerance in rice. ORYZA-An International Journal on Rice. 2019; 56(1): 26-32. https://doi.org/10.5958/2249-5266.2019.00004.3.
53. Srihari G, Babu PR, Babu JD, Jayalalitha K and Sreelakshmi C. Characterisation, genetic parameters of variation and correlation studies in Molakolukulu Rice cultivars of Andhra Pradesh, India. Electronic Journal of Plant Breeding. 2023; 14(2): 540-50. https://doi.org/10.37992/2023.1402.059.
54. Nithya N, Beena R, Stephen R, Abida PS, Jayalekshmi VG, Viji MM, Manju RV. Genetic variability, heritability, correlation coefficient and path analysis of morphophysiological and yield related traits of rice under drought stress. Chemical Science Review and Letters. 2020; 9(33): 48-54. https://doi.org/10.37273/chesci.cs142050122.
55. Sahu H, Saxena RR, Verulkar SB. Genetic variability and character association study for different morphological traits and path analysis for grain yield of rice under irrigated and rainfed condition. Electronic Journal of Plant Breeding. 2017; 8(1): 38-45. 10.5958/0975-

928X.2017.00005.9.https://www.ejplantbreeding.org/index.php/EJPB/article/view/890
.

56. Allam CR, Jaiswal HK, Qamar A, Venkateshwarlu C, Reddy YS. Variability, heritability, genetic advance studies in some indigenous genotypes of basmati rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding. 2015; 6(2): 506-511. https://www.ejplantbreeding.org/index.php/EJPB/article/view/858/443
57. Krishnan V, Sivaranjani V, Tamilzharasi M, Anandhan T. Characterization of morpho-phenological traits in the traditional landraces of rice. Electronic Journal of Plant Breeding. 2023; 14(1): 234-45. https://doi.org/10.37992/2023.1401.026.
58. Pandey P, Anurag PJ, Tiwari DK, Yadav SK and Kumar B. Genetic variability, diversity and association of quantitative traits with grain yield in rice (*Oryza sativa* L.). Journal of bio-science. 2009; 17: 77-82. https://doi.org/10.3329/jbs.v17i0.7110.
59. Lavanya K, Suman K, Fiyaz AR, Chiranjeevi M, Surender R, Satya AK, Sudhakar P, Rao LVS. Phenotypic assessment of rice landraces for genetic variability and diversity studies under heat stress. Oryza. 2022; 59(1): 31-38. https://doi.org/10.35709/ory.2022.59.1.4.
60. Tezera M. Variability, Heritability, Genetic advance of introduced upland rice genotypes at Fogera in North Western Ethiopia. Journal of Plant Studies. 2021; 10(2): 30-38. https://doi.org/10.11648/j.cb.20210902.13.
61. Gayathridevi G, Shanthi P, Suresh R, Manonmani S, Geetha S, Sathyabama K, Geetha P. Genetic variability, association and multivariate analysis for yield and yield parameters in rice (*Oryza sativa* L.) landraces. Electronic Journal of Plant Breeding. 2023; 14(3): 991-9. https://doi.org/10.37992/2023.1403.136.
62. Gunasekaran K, Sivakami R, Sabariappan R, Ponnaiah G, Nachimuthu VV, Pandian BA. Assessment of genetic variability, correlation and path coefficient analysis for morphological and quality traits in rice (*Oryza sativa* L.). Agricultural Science Digest-A Research Journal. 2017; 37(4): 251-6. https://doi.org/10.18805/ag.D-4643.
63. Veni BK, Rani NS. Association of grain yield with quality characteristics and other yield components in rice. Oryza. 2006; 43(4): 320-322.
64. Srijan A, Dangi KS, Senguttuvel P, Sundaram RM, Chary DS, Kumar SS. Correlation and path coefficient analysis for grain yield in aerobic rice (*Oryza sativa* L.) genotypes. The Journal of Research PJTSAU. 2018; 46(4): 64-8. https://epubs.icar.org.in/index.php/TJRP/article/view/88821/36350.
65. Sumalatha TV. Morphological and Biochemical Characterization of Aromatic Rice Cultivars (*Oryza sativa* L.) of Wayanad District of Kerala. M.Sc. [Dissertation], Thrissur: Kerala Agricultural University; 2010. Available from: http://14.139.185.57:8080/jspui/bitstream/123456789/8648/1/173026.pdf.

66. Radha T, Kumar PS, Saravanan K, S Suganthi. Genetic Variability, Association and Path Analysis for Grain Yield and Quality traits in Rice (*Oryza sativa* L.) Plant Archives 2019; 19(2): 2522-2526. http://www.plantarchives.org/19-2/2522-2526%20(4911).pdf.
67. Chhangte L, Devi TR. Correlation and path analysis studies in aromatic rice germplasm of North-East region of India. The pharma Innovation Journal. 2019; 8(10):01-4. https://www.thepharmajournal.com/archives/2019/vol8issue10/PartA/8-9-54-597.pdf.
68. Kole PC, Chakraborty NR and Bhat JS. Analysis of variability, correlation and path coefficients in induced mutants of Aromatic non-basmati rice. Tropical Agricultural Research and extension. 2008; 11: 60-64. https://doi.org/10.4038/tare.v11i0.1791.
69. Sabri RS, Rafii MY, Ismail MR, Yusuff O, Chukwu SC, Hasan NA. Assessment of agro-morphologic performance, genetic parameters and clustering pattern of newly developed blast resistant rice lines tested in four environments. Agronomy. 2020; 10(8): 1098. https://doi.org/10.3390/agronomy10081098.
70. Sharma M, Singh AK, Salgotra RK, Sharma BK, Gangurde SS, Bakshi P, Raina M, Kumar B. Assessment of genetic advance and correlation coefficient for yield and yield attributed traits of RIL population in basmati rice (*Oryza sativa* L.). Journal of Pharmacognosy and Phytochemistry. 2021; 10(1): 328-30. https://www.phytojournal.com/archives/2021/vol10issue1/PartE/9-6-354-738.pdf
71. Sharma R, Singh D, Kaushik RP, Pandey DP. Correlation and path analysis for grain yield and its component traits in rice. ORYZA-An International Journal on Rice. 2012; 49(3): 215-218.
72. Umarani E, Hemalatha V, Subbarao LV, Neeraja CN, Suneetha K, Reddy NS. Studies on character association and path coefficient analysis for anaerobic germination traits, yield and its contributing characters in rice (*Oryza sativa* L.). International Journal of Current Microbiology and Applied Sciences. 2019; 8(4): 355-62. https://doi.org/10.20546/ijcmas.2019.804.039.
73. Sudeepthi K, Srinivas TV, Kumar BR, Jyothula DP, Umar SN. Assessment of genetic variability, character association and path analysis for yield and yield component traits in rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding. 2020; 11(01): 144-8. : https://doi.org/10.37992/2020.1101.026.
74. Madhukar P, Raju CS, Vanisree S, Kumar SS. Influence of environment on characters association in rice hybrids and varieties. ORYZA-An International Journal on Rice. 2016; 53(2): 213-22. https://epubs.icar.org.in/index.php/OIJR/article/view/69851/29620.