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Research Article

Genetic variability, association and multivariate analysis for yield and yield parameters in rice (*Oryza sativa* L.) landraces

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Abstract
The present experiment was undertaken to study the variability, trait association and principle component analysis among eighteen characters in 53 rice genotypes including landraces and cultivars. Higher estimates of GCV and PCV coupled with high heritability and GAM were observed for a number of filled grains per panicle followed by a number of spikelets per panicle and single plant yield indicated that these traits could be utilised for selection in rice improvement. Study of association of yield attributing traits revealed that the single plant yield had a significant positive association with the total number of spikelets per plant, number of filled grains per plant and number of primary branches per plant and had a significant negative association with the length of the primary branches. Hence, direct selection of positively associated characters can improve the grain yield and increased primary branch length reduces the number of primary and secondary branches that might lead to a reduction in yield. Path coefficient analysis showed that the number of spikelets per panicle, primary branches per plant and length of secondary branches had a positive direct effect on yield. Therefore, giving weightage during selection to the above the mentioned traits could improve the yield and yield attributes. The principal component analysis showed that out of 18 traits studied, only eight principal components (PCs) had Eigen values greater than 1.00 and accounted for approximately 80.18% of the total cumulative variability. Single plant yield, number of fertile spikelets and total number of spikelets per plant and number of tillers showed maximum vector length confirming that the maximum contribution to the total diversity and the genotypes with the above characters could be utilized as donors to improve the yield and its attributing traits in future breeding programme.

Keywords: Rice, land races, germplasm, PCV, GCV, heritability, GAM, correlation, path analysis, principal component analysis

INTRODUCTION

Over half of the world's population depends on rice for both food and livelihood. Rice is a highly self-pollinated crop in the genus *Oryza* and belongs to the family *Poaceae*. It is the second- ranked cereal crop in the world, cultivated in around 164.19 million hectares with production of 756 million tonnes and its average productivity is 4.6 tonnes/ hectare (2023, Statista.com). In India, it is cultivated in around 43.77 million hectares with a production of 169.14

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million tonnes, the average productivity is 3.86 tonnes/ha (2023, Statista.com). and the country ranks second next to China in production. Due to the increasing population and quick urbanization, expanding the rice farming area beyond a limit is very difficult. Additionally, productivity growth is the only way to increase rice production. To increase grain yield and shatter yield ceilings, numerous breeding techniques are used (Peng, 2003). Direct selection is not very effective as grain yield is a complex characteristic regulated by polygenes that have greater environmental influence. Any crop improvement effort must prioritize genetic diversity in the germplasm since it is the only way to integrate beneficial alleles and produce the desired recombination (Hasan *et al.,* 2020). Hence, it is more important to understand the species' variability, the nature of character relationships and the role of various characteristics in increasing rice production through breeding programme (Khan *et al.,* 2020).

Rice production can be increased by indirectly selecting plants with greater magnitude of yield-attributing traits (Shanthi *et al*., 2011). To improve complicated trait like grain yield in rice, it is highly essential to understand how other attributing traits interact with one another and helps to increase grain production. One of the requirements for directing efficient selection is knowing the degree of relationship between yield and yield contributing factors through correlation studies (Singh *et al.,* 2018). The correlation coefficient identifies only negative or positive relationships between traits but does not show the relative contribution of the traits in selection; thus, the path coefficient analysis has an important role in determining the nature of intra and inter-relation (direct or indirect) of other contributing characters with grain yield (Wright, 1921). Hence correlation can be partitioned into direct and indirect effects through path analysis. Therefore, the correlation coefficient along with path effects is logical as it clearly shows the true nature of association among the traits under study.
Since yield is a challenging attribute that depends on several variables and the environment. To determine and reduce the number of characteristics for efficient selection, a method known as principal component analysis (PCA) has been used. It is a basic technique utilized in contemporary data analysis since it is a simple to comprehend non-parametric strategy for obtaining important features from a complicated set of data (Tiwari *et al*., 2022). By keeping all the above in mind this experiment was carried out to know the variability, heritability, GAM, the positive and negative influence of different traits on grain, the interconnection between different traits along with the classification of genotypes by taking more characters into account and the relationship between them to identify the appropriate selection criteria and breeding method for yield improvement.

MATERIALS AND METHODS

A set of 53 rice genotypes including 50 landraces and three cultivars were evaluated during *Rabi* 2022-23 at the Department of Rice, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore and the genotype list is enclosed in **Table 1**. The selected genotypes were sown in the raised bed and transplanted into the main field 27 days after sowing with a spacing of 20 x 20 cm in randomized block design (RBD) with three replicates and a single seedling per hill was maintained. All the package of practices were followed for the good establishment and growth of the crop. Observations were recorded on five randomly selected plants in each replication and in each genotype for morphological characters *viz.,* plant height (cm), leaf length (cm), leaf width (cm), days to 50 % flowering (DFF), number of tillers/plant, panicle length (cm), total number of spikelets/plant, number of filled grain/plant, number of primary branches/plant, number of secondary branches/plant, length of primary branches (cm), length of secondary branches (cm), test weight (g), grain length (cm), grain width (cm), decorticated grain length (cm), decorticated grain width (cm), single plant yield (g). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated according to the method Burton (1952) and the estimates for variability were treated as per the categorization proposed by Sivasubramanian and Madhavamenon, 1973. The broad sense heritability (h^2) was calculated according to Lush (1940) and the genetic advance as percent of the mean (GAM) estimates as per Johnson *et al.* (1955). The linear association between two variables X and Y was estimated by using Karl Pearson's Coefficient of correlation (rxy) based on the variance and covariance of the variables. To test the significance of correlation coefficient, t-test was used by comparing the calculated t value with the tabulated t value at α level of significance with (n-2) degrees of freedom (Snedecor and Cochron, 1956) and the path coefficient was estimated as suggested by Dewey and Lu (1959) and principal component analysis were calculated using R var 4.3.1 software

RESULT AND DISCUSSION

The detailed knowledge of variability, heritability, magnitude and direction of the relationship between yield and its attributes along with principal component analysis forms the foundation for the effective selection of the traits in crop plants. Identification of the key traits that can be used for crop improvement through various breeding techniques is extremely important. The analysis of variance (ANOVA) demonstrated that the genotypes used in this study were significantly different for all the characters (**Table 2**).

The variability analysis revealed that the PCV was slightly higher than GCV for all the traits (**Table 3**) studied this might be due to the influence of the environment. This result was also confirmed by the findings of Lakshmi *et al.*(2022). The PCV and GCV were higher in the following traits *viz*., single plant yield (30.87, 30.72), total number of spikelets (48.2, 48.1) and fertile spikelets per plant (53.6, 53.46), total number of primary(31.72, 29.54) and

Table 1. List of 53 rice genotypes used in this study

S.NO.	GENOTYPES	S.NO.	GENOTYPES
1.	AARKADU KICHILI	28.	KOTHAMALLI SAMBA
2.	ARA SAMBA	29.	KUZHIYADICHAN
3.	ARIYAN RED	30.	MANGAM SAMBA
4.	ARB 59	31.	MATTA KURUVAI
5.	ARB 64	32.	NOOTRI PATHU
6.	CB-07-701-252	33.	PANAMARASAMBA
7.	CHINTHAMANI	34.	PONKAMBI SAMBA
8.	HALADICHUDI	35.	POKKALI
9.	IDLY	36.	RH2-SM-1-2-1
10.	IG 18(EC 728892- 117880)	37.	RPHP 103
11.	IG 24(EC 728751- 117718)	38.	RPHP 104
12.	IG 26(IC 0590943- 121899)	39.	RPHP 106
13.	IG 35(EC 728858- 117843)	40.	RPHP 129
14.	IG 51(EC 728772- 117742)	41.	RPHP 48
15.	IG 52(EC 728756- 117723)	42.	RPHP 80
16.	IG 72(EC 728650- 117587)	43.	RPHP 93
17.	IG 75(EC 728587- 117420)	44.	SEMBALA
18.	IR 83294-66-2-2-3-2	45.	SHENMOLAGAI
19.	JEEVAN SAMBA	46.	SORNA KURUVAI
20.	KAPPIKAR SELECTION	47.	THILLAINAYAGAM
21.	KARHIGAI SAMBA	48.	THOOYAMALLI
22.	KARTHI SAMBA	49.	VADAKATHI SAMBA
23.	KARUNGAN	50.	VALASAMUDON
24.	KARUTHAKAR	51.	CO51
25.	KAVUNI	52.	CO52
26.	KODAI	53.	CR1009
27.	KOOLAVALI		

Table 2. Analysis of variance for eighteen different quantitative traits of 53 rice genotypes

Source of variation	df	PH	LL	LW	DFF	NT	PL	NS/P	NFG/P	PB	SB	LPB	LSB	TW	GL	GW	DL	DL	SPY
Genotypes	52	1025.44 **	92.71 **	0.07 *	250.75 **	62.97 **	13.75 **	6941.55 **	6289.67 **	9.60 **	66.97 **	79.31 *	12.88 **	63.93 **	1.80 **	0.55 *	1.59 **	0.56 **	141.79 **
Replication	2	4.77	1.37	0.04	6.08	3.08	0.61	42.59	25.83	1.15	0.87	0.08	1.47	0.36	0.06	0.06	0.19	0.01	2.28
Error	104	2.68	2.48	0.02	35.40	3.36	2.21	9.86	3.03	0.47	1.69	1.69	0.13	2.83	0.13	0.05	0.09	0.03	0.46

* and ** - significant at 5% level and 1% level respectively
significant at 5% level.
PH-Plant height LL-Leaf length LW-Leaf width DFF-Days to 50% flowering NT-Number of tillers PL-Panicle length NS/P-Number of spikelets per panicle NFG/P-Number of filled grain per panicle PB-Primary branches SB-Secondary branches LPB- Length of Primary branches LSB- Length of Secondary branches TW-Test weight GL-Grain length GW-Grain width DL- Decorticated grain length DW- Decorticated grain width

secondary branches (31.17, 30.03) and similar findings was also reported by Fathima *et al.*(2021) and Lakshmi et al., 2022. The maximum environmental variance (EV) was noticed in days to 50 % flowering whereas the minimum was single plant yield, grain length and secondary branch length. This result was by the findings of Pratab *et al.* (2014). The broad sense heritability for all the character studied were high (>60 %) except for leaf width and it ranged from 53.81 % to 99.22 (**Table 3**). Heritability coupled with GAM could be more useful for selection (Johnson *et al.,* 1955). In the present study, GAM ranged from 15.75 - 110.25 for days to 50 %

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Table 3. Estimates of variability, heritability and genetic advance for yield and yield contributing traits

Characters	Phenotypic variance (PV)	Genotypic variance (GV)	PCV (%)	GCV (%)	Heritability	GAM (%)
PH	343.60	340.92	15.21	15.15	99.22	31.09
LL	32.56	30.08	18.74	18.02	92.38	35.67
LW	0.03	0.02	15.97	11.71	53.81	17.70
DFF	107.25	71.75	11.43	9.35	66.90	15.75
NT	23.23	19.87	31.27	28.92	85.52	55.09
PL	6.06	3.85	10.62	8.46	63.48	13.88
NS/P	2320.42	2310.56	48.21	48.10	99.58	98.88
NFG/P	2098.58	2095.55	53.60	53.56	99.86	110.25
PB	3.51	3.04	31.72	29.54	86.74	56.67
SB	23.45	21.76	31.17	30.03	92.80	59.59
LPB	27.56	25.88	29.91	28.98	93.87	57.85
LSB	4.38	4.25	28.20	27.78	96.99	56.35
TW	23.20	20.36	24.14	22.62	87.78	43.65
GL	0.69	0.55	10.23	9.15	80.07	16.88
GW	0.21	0.17	15.34	13.60	78.56	24.83
DL	0.59	0.50	12.71	11.72	84.95	22.24
DW	0.21	0.17	18.81	17.25	84.12	32.59
SPY	47.57	47.11	30.87	30.72	99.02	62.98

PH-Plant height LL-Leaf length LW-Leaf width DFF-Days to 50% flowering NT-Number of tillers PL-Panicle length NS/P-Number of spikelets per panicle NFG/P-Number of filled grain per panicle PB-Primary branches SB-Secondary branches LPB- Length of Primary branches LSB- Length of Secondary branches TW-Test weight GL-Grain length GW-Grain width DL- Decorticated grain length DW-Decorticated grain width SYP-Single plant yield

flowering and for a number of filled grains per panicle respectively. Most of the traits including single plant yield recorded high GAM (62.98%) with high heritability (99.02 %) indicating that these traits were less influenced by the environment and governed by additive gene action and can easily be selected based on phenotype. Days to 50 % flowering and leaf width recorded high heritability (66.90 %) and moderate GAM (17.7) indicating that these traits are governed by both additive and nonadditive gene action. These results clearly showed that there is a possibility of direct selection for these traits, similar result was also obtained by Girma *et al.(*2018).

The correlation coefficients between yield and yield components *viz*., plant height, Leaf length, leaf width, days to 50 % flowering, number of tillers/plant, panicle length, number of spikelets per plant, number of filled grains per plant, number of primary branches per plant, number of secondary branches per plant, length of primary branches, length of secondary branches, test weight, grain length, grain width, decorticated grain length, decorticated grain width and single plant yield were analysed and results are presented correlogram squares with values and significant indicates and a heat map were created and presented in **Fig. 1 & 2**. The non-significant values are marked as “X” and significant values are differentiated in colour intensity (**Fig.1**).Colour of each cell represents the strength and direction of the correlation, the darker colours indicate the strong association with the other character and the lighter colour indicates the weaker association among the characters.

The results disclosed that the single plant yield had a high significant positive correlation with the total number of spikelets per plant, the number of filled grains per plant and the number of primary branches per plant. The positive correlation of single plant yield with various traits was supported by- Shanthi *et al.*(2011), Basavaraja *et al.* (2011) and Jangala *et al.* (2022) for filled grains per panicle and a total number of spikelets per plant, Priya *et al*. (2017) and Jangala *et al*. (2022) for number of primary branches per plant. Direct selection of these traits with increased magnitude can help for yield improvement. The length of the primary branches was significantly negatively correlated with grain yield. This might be due to longer primary branches with fewer productive tillers and panicles, which could reduce the grain yield. By choosing short primary branches, it is possible to have more panicles leading to more grain yield. This result was confirmed with the KRISHI research data repository and knowledge management (Krishi.icar.gov.in). Days to 50 % flowering and plant height have a negative and non-significant association with single-plant yield. Shanthi *et al.* (2011) and Panwar and Ali *et al.* (2007)

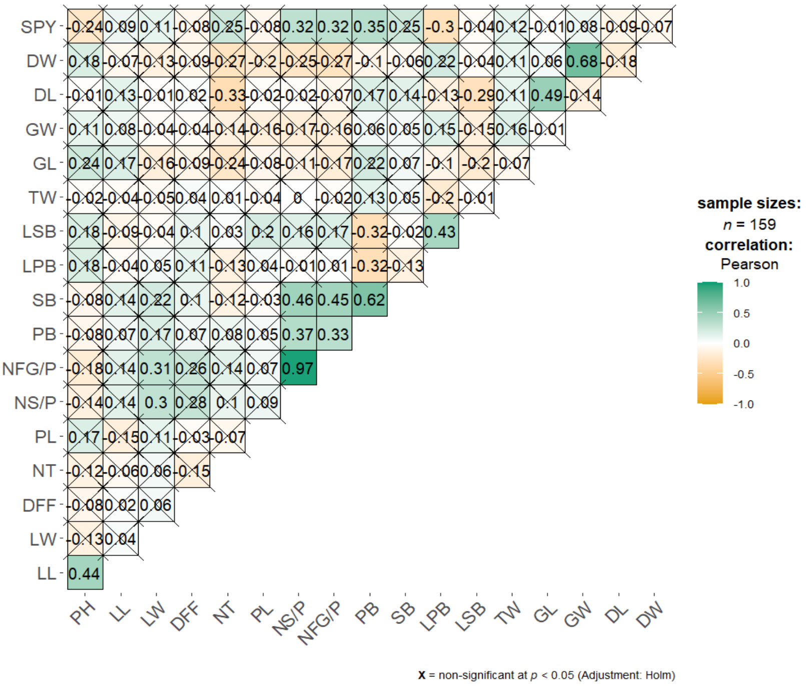

Fig. 1. Correlogram with significant among 18 characters for 53 genotypes

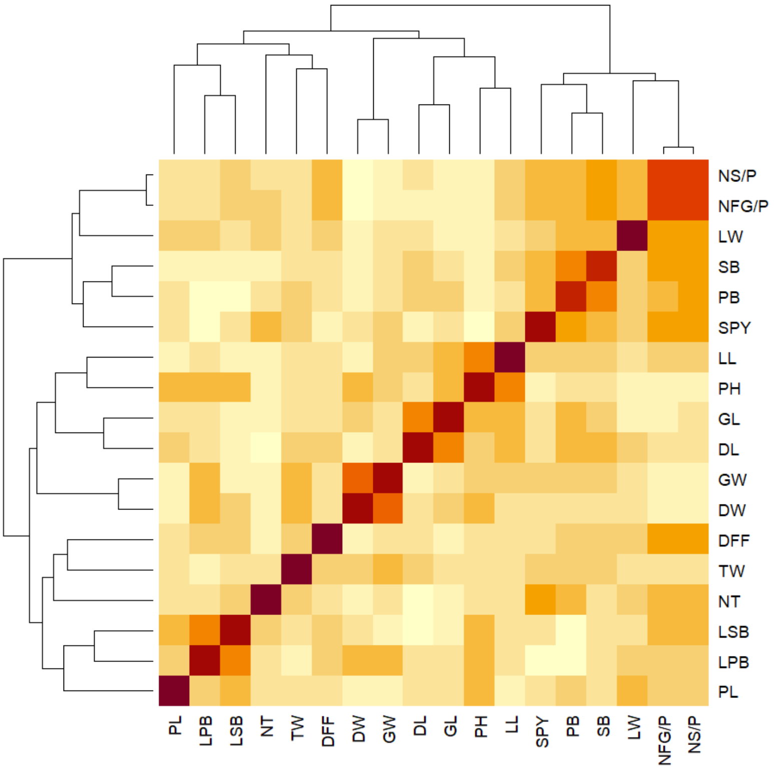

Fig. 2. Heatmap for correlation among 18 characters for 53 genotypes

obtained similar findings for these traits. Hence reduction in height and duration did not have much influence on yield.

Analysis of interrelation among the yield attributing traits revealed that the total number of spikelets per plant had the positive and highly significant correlation (0.97) with number of filled grains per panicle. Hence selecting the plants with a greater number of spikelets per panicle strongly improves the grain yield via higher filled grains per panicle. Similarly, primary branches per plant, secondary branches per plant and total number of spikelets per panicle and number of filled grains per panicle were significantly and positively correlated with each other. Plant height had significant and a positive correlation with leaf length. The above results revealed that selection in high degree of any one of the above characters simultaneously improves the grain yield and this finding was by the previous findings of Jangala *et al.*(2022), Singh *et al.* (2018) and Priya *et al.* (2017). Primary branches per plant had a negative and significant correlation with the length of primary and secondary branches and clearly shows that increasing number of the primary branches eventually reduces the length of primary and secondary branches.

Correlation studies allow a complete measure of the relationship between two traits. The real contribution of an attribute and its effect through different features should be arrived at by way of partitioning the correlation coefficients into direct and indirect effects by path coefficient analysis. This will be very useful in imparting due weightage to the important yield-attributing traits under selection process. Path coefficient analysis results (**Table 4**), indicated that the number of spikelets per panicle, primary branches per plant and length of secondary branches showed positive direct effect on yield. Consequently, indirect selection for these traits was likely to bring an overall improvement in grain yield per plant.

Negative directional selection is needed for some characters like plant height and days to 50 % flowering. In this study the plant height and days to 50 % flowering exhibited negative direct effect on yield. Hence direct selection for this character might be useful. A similar observations were also reported by Yadav *et al.* (2011), Shanthi *et al.* (2019) and Kumar *et al.* (2021). The residual effect in the present experiment was 0.0647, which means that the characters in the path analysis expressed the variability in grain yield by 94.36% and the remaining 5.64 % needs additional characterization for the future

Table 4. Estimates of direct and indirect effects between yield and yield component

	PH	LL	LW	DFF	NT	PL	NS/P	NFG/P	PB	SB	LPB	LSB	TW	GL	GW	DL	DW
PH	**-0.302**	0.080	-0.002	0.011	-0.017	-0.004	-0.038	0.010	-0.018	0.004	-0.045	0.038	-0.001	0.023	0.020	0.001	0.001
LL	-0.133	**0.182**	0.001	-0.003	-0.008	0.004	0.038	-0.008	0.016	-0.006	0.010	-0.019	-0.001	0.016	0.015	-0.012	0.000
LW	0.039	0.007	**0.019**	-0.008	0.008	-0.003	0.081	-0.017	0.038	-0.010	-0.013	-0.008	-0.002	-0.015	-0.007	0.001	0.000
DFF	0.024	0.004	0.001	**-0.138**	-0.021	0.001	0.076	-0.015	0.016	-0.004	-0.028	0.021	0.001	-0.009	-0.007	-0.002	0.000
NT	0.036	-0.011	0.001	0.021	**0.138**	0.002	0.027	-0.008	0.018	0.005	0.033	0.006	0.000	-0.023	-0.026	0.031	-0.001
PL	-0.051	-0.027	0.002	0.004	-0.010	**-0.026**	0.024	-0.004	0.011	0.001	-0.010	0.042	-0.001	-0.008	-0.029	0.002	-0.001
NS/P	0.042	0.025	0.006	-0.039	0.014	-0.002	**0.270**	-0.054	0.082	-0.020	0.003	0.034	0.000	-0.011	-0.031	0.002	-0.001
NFG/P	0.054	0.025	0.006	-0.036	0.019	-0.002	0.262	**-0.056**	0.073	-0.020	-0.003	0.036	-0.001	-0.016	-0.029	0.007	-0.001
PB	0.024	0.013	0.003	-0.010	0.011	-0.001	0.100	-0.018	**0.222**	-0.027	0.080	-0.067	0.005	0.021	0.011	-0.016	0.000
SB	0.024	0.025	0.004	-0.014	-0.017	0.001	0.124	-0.025	0.138	**-0.044**	0.033	-0.004	0.002	0.007	0.009	-0.013	0.000
LPB	-0.054	-0.007	0.001	-0.015	-0.018	-0.001	-0.003	-0.001	-0.071	0.006	**-0.250**	0.090	-0.007	-0.010	0.028	0.012	0.001
LSB	-0.054	-0.016	-0.001	-0.014	0.004	-0.005	0.043	-0.009	-0.071	0.001	-0.108	**0.210**	0.000	-0.019	-0.028	0.028	0.000
TW	0.006	-0.007	-0.001	-0.006	0.001	0.001	0.000	0.001	0.029	-0.002	0.050	-0.002	**0.037**	-0.007	0.029	-0.010	0.000
GL	-0.073	0.031	-0.003	0.012	-0.033	0.002	-0.030	0.009	0.049	-0.003	0.025	-0.042	-0.003	**0.096**	-0.002	-0.047	0.000
GW	-0.033	0.015	-0.001	0.006	-0.019	0.004	-0.046	0.009	0.013	-0.002	-0.038	-0.032	0.006	-0.001	**0.184**	0.013	0.002
DL	0.003	0.024	0.000	-0.003	-0.045	0.001	-0.005	0.004	0.038	-0.006	0.033	-0.061	0.004	0.047	-0.026	**-0.095**	-0.001
DW	-0.054	-0.013	-0.002	0.012	-0.037	0.005	-0.068	0.015	-0.022	0.003	-0.055	-0.008	0.004	0.006	0.125	0.017	**0.003**

Residual effect = 0.0647

PH-Plant height LL-Leaf length LW-Leaf width DFF-Days to 50% flowering NT-Number of tillers PL-Panicle length NS/P-Number of spikelets per panicle NFG/P-Number of filled grain per panicle PB-Primary branches SB-Secondary branches LPB- Length of Primary branches LSB- Length of Secondary branches TW-Test weight GL-Grain length GW-Grain width DL- Decorticated grain length DW-Decorticated grain width breeding program. A similar result was reported by Hailu *et al.* (2016). According to the partitioning of correlation values, many of the features were unable to establish a significant association with single plant yield, which may have been caused by extremely strong negative direct effects. Critical evaluation of consequences received from character association and its direction indicated that the grain yield per plant possessed a positive association with a total number of spikelets per plant, total number of fertile spikelets and number of tillers per plant with a positive direct effect (Panika *et al.,* 2022). Therefore, selecting for these features could bring improvement in yield and yield components.

Among the 18 principal components, only eight PC had Eigen values greater than 1.00 and accounted for approximately 80.18% of the total cumulative variability (**Table 5**). The scree plot displayed the percentage of variation explained by each PC's and indicated that PC1 had the highest amount of variability at approximately 17.89% with the greatest Eigen value. Furthermore, there was a continued decline in variability was observed in PC2, PC3, PC4, PC5, PC6 and PC8, with corresponding values of 13.66%, 11.77%, 9.75%, 8.48%, 6.64%, and 5.74%, respectively. The biplot diagram of the first two main components showed how the characteristics interacted with each genotype as well as with one another (**Fig. 3**). Each character's contribution to the total divergence is shown by the length of its vector; the longer the vector, the higher the contribution. Single plant yield, number of fertile spikelets, total number of spikelets per plant and number of tillers exhibited maximum vector length showed the maximum contribution to the total diversity. These results were in conformity with the findings of Lakshmi *et al.* (2022) and Tiwari *et al.*(2022).

In conclusion, the traits single plant yield, number of spikelets and fertile spikelets per plant, number of primary and secondary branches recorded high PCV and GCV, heritability coupled with GAM. Therefore, while selecting genotypes to increase yield, these attributes should be considered. Based on correlation and path analysis the grain yield was observed to have a positive and significant correlation with the total number of spikelets, number of filled grains and number of primary branches per plant and had a negative association with length of the primary branch. Path analysis results showed that the number of tillers also had a direct effect on grain yield. Hence during

Table 5. Eigen value, contribution of variability for the principal component of variance in the selected rice genotypes

Components	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Eigen value	3.2194	2.4586	2.1181	1.7543	1.5258	1.1958	1.1274	1.0332
Percentage of variance	17.89	13.66	11.77	9.75	8.48	6.64	6.26	5.74
Cumulative percentage of variance	17.89	31.54	43.31	53.06	61.53	68.18	74.44	80.18
PH	-0.06	0.26	-0.21	0.18	-0.48	0.34	0.06	-0.15
LL	0.09	0.28	-0.07	0.10	-0.26	0.26	0.59	0.01
LW	0.22	-0.13	-0.09	0.19	0.25	-0.22	0.18	-0.27
DFF	-0.02	-0.03	-0.16	0.16	0.46	0.35	0.16	0.48
NT	0.11	-0.35	0.27	0.05	-0.29	-0.06	0.26	-0.02
PL	0.04	-0.20	-0.28	0.00	-0.11	0.34	-0.48	-0.43
NS/P	0.41	0.10	-0.24	0.18	-0.19	-0.22	-0.20	0.20
NFG/P	0.39	0.04	-0.20	0.24	-0.17	-0.31	-0.14	0.24
PB	0.36	0.12	0.13	0.05	0.28	0.20	0.05	-0.37
SB	0.34	0.13	-0.05	0.23	0.33	0.04	0.07	-0.25
LPB	-0.25	0.01	-0.32	0.35	0.01	-0.20	-0.01	0.11
LSB	-0.15	-0.24	-0.34	0.29	0.07	0.31	-0.01	0.08
TW	0.09	0.08	0.39	0.13	-0.03	0.36	-0.39	0.29
GL	0.11	0.43	-0.14	-0.30	-0.09	0.02	-0.01	0.01
GW	-0.16	0.35	0.29	0.40	0.09	-0.02	-0.01	-0.06
DL	0.18	0.31	-0.17	-0.41	0.16	0.07	-0.10	0.19
DW	-0.26	0.36	0.21	0.30	0.03	-0.19	-0.23	-0.11
SPY	0.36	-0.19	0.32	0.14	-0.17	0.18	-0.03	0.18

PH-Plant height LL-Leaf length LW-Leaf width DFF-Days to 50% flowering NT-Number of tillers PL-Panicle length NS/P-Number of spikelets per panicle NFG/P-Number of filled grain per panicle PB-Primary branches SB-Secondary branches LPB- Length of Primary branches LSB- Length of Secondary branches TW-Test weight GL-Grain length GW-Grain width DL- Decorticated grain length DW-Decorticated grain width SYP-Single plant yield

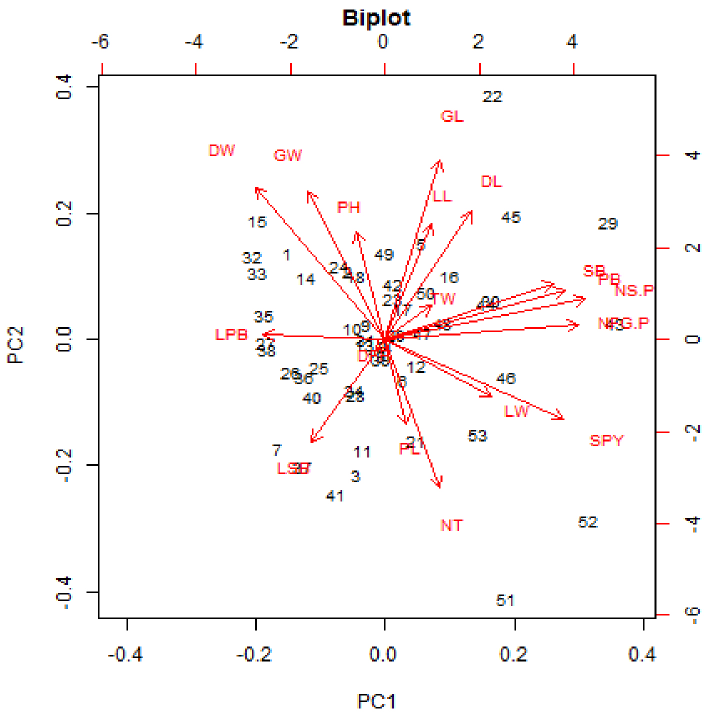

Fig. 3.Biplot diagram of PC1 and PC2

the selection process indirect selection of a total number of spikelets, number of filled grains and number of tillers per plant can improve the yield. In PCA analysis, single plant yield, number of fertile spikelets, total number of spikelets per plant and number of tillers had maximum vector length showed the maximum contribution to the total diversity and the varieties possessing high mean value for these traits could be used as a donor to improve the yield attributing traits in a future breeding program.

REFERENCES

Basavaraja, T., Gangaprasad, S., Dhusyantha Kumar, B. M. and Shilaja Hittlamani. 2011. Correlation and path analysis of yield and yield attributes in local rice cultivars (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, **2**(4):523-526.

Burton, GW. 1952. Quantitative inheritance in grasses. In: Proc 6th Int Grassland Congr 1: 356-363.

Dewey, D.R. and Lu, K. H. 1959. A correlation and path coefficient analysis of components crested wheat grass and seed production. *Agronomy Journal*, **52**:515-518. [Cross Ref]

Girma, B.T., Kitil, M.A., Banje, D.G, Biru, H.M. and Serbessa, T.B. 2018. Genetic variability, study of yield and yield related traits in rice (*Oryza sativa* L.) genotypes. *Adv Crop Sci Tech,* **6**: 381. doi:10.4172/2329-8863.100038

Hailu, A., Alamerew, S., Nigussie, M. and Assefa, E. 2016. Correlation and path coefficient analysis of yield and yield associated traits in barley (*Hordeum vulgare* L.) germplasm. *Advanced crop science technology*. **4**: 2. [Cross Ref]

Hasan, M.J., Kulsum, M.U., Majumder, R.R. and Sarker, U. 2020. Genotypic Variability for Grain Quality Attributes in Restorer Lines of Hybrid Rice. *Genetika* , **52**: 973–989. [Cross Ref]

Jangala, D. J., Amudha, K., Geetha, S. and Uma, D. 2022. Studies on genetic diversity, correlation and path analysis in rice germplasm. *Electronic Journal of Plant Breeding,* **13**(2): 655-662. [Cross Ref]

Johnson, H.W, Robinson, H.F. and Comstock, R. 1955. Estimates of Genetic and environmental variability in soybeans . *Agronomy Journal,* **47**: 314-318. [Cross Ref]

Khan, M.K., Pandey, A., Hamurcu, M., Hakki, E.E. and Gezgin, S. 2020. Role of molecular approaches in improving genetic variability of micronutrients and their utilization in breeding programs. In *Wheat and Barley Grain Biofortification*; Elsevier: Amsterdam, *The Netherlands* pp. 27–52. [Cross Ref]

Kumar, N.S., Reddy, V.R. and Chandramohan, Y. 2021. Correlation and path coefficient Studies of yield and quality traits in rice (*Oryza sativa* L.). *Research Journal of Agricultural Sciences,* **7** (3): 606-609.

Lakshmi, M., Shanmuganathan, M., Jeyaprakash, P. and Ramesh, T. 2022. Genetic variability and diversity analysis in selected rice (*Oryza sativa* L.) varieties. *Electronic Journal of Plant Breeding,* **13**(3): 955-966. [Cross Ref]

Lush, JL. 1940. Intra - sire correlation and regression of off spring on dams as a method of estimating heritability of characters. *Proc Am Soc Anim Prod,* **33**: 293-301.

Panika, N., Singh, Y., Singh, S. K., Rahangdale, S. and Shukla, R. S. 2022. Genetic variability, correlation and path coefficient study of indigenous rice (*Oryza sativa* L.). *Environment and Ecology*, **40** (4D): 2777-2786.

Panwar, L. L. and Ali, M. 2007. Correlation and path analysis of yield and yield components in transplanted rice. *Oryza*, **44** (2): 115-120.

Peng, Shaobing Khush, and Gurdev. 2003. Four decades of breeding for varietal improvement of irrigated lowland rice in the International Rice Research Institute. *Plant Production Science*: 157-164. [Cross Ref]

Priya, C. S., Suneetha, Y., Babu, D. R. and Rao, S. V. 2017. Inter-relationship and path analysis for yield and quality characters in rice (*Oryza sativa* L.). *Environment and Technology*, **6** (1): 381-390.

Shanthi, P., Ganesan K.N., Manivannan, N. and Natarajan, C. 2019. Correlation and path analysis in Blackgram (*Vigna mungo* L.). *Eelectronic Journal of Plant Breeding,* **10** (3): 1218 – 1222

Shanthi, P., Jebaraj, S. and Geetha, S. 2011. Correlation and path coefficient analysis of some sodic tolerant physiological traits and yield in rice (*Oryza sativa* L.). *Indian Journal of Agricultural Research*, **45**(3): 201-208. [Cross Ref]

Singh, R., Yadav, V., Mishra, D. N. and Yadav, A. 2018. Correlation and path analysis studies in rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry,* **7**(1S): 2084-2090.

Sivasubramanian, J. and Madhavamenon. 1973. Genotypic and phenotypic variability in rice. *Madras Agric J,* **12**: 15-16.

Snedecor, G. W. and Cochran, W. G.1956. Statistical methods applied to experiments in agriculture and biology. *5th ed. Ames, Iowa: Iowa State University.*

Tiwari, D.N., Tripathi, S.R, Tripathi, M.P, Khatri, N. and Bastola, B.R. 2019. Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. *Adv Agric,* **1** :1-9. [Cross Ref]

Tiwari, S., Singh, Y., Upadhyay P.K. and Koutu, G.K. 2022. Principal component analysis and genetic divergence studies for yield and quality-related attributes of rice restorer lines.*Indian J. Genet. Plant Breed,* **82**(1): 94-98. [Cross Ref]

Wright S. 1921.Correlation and causation. *Journal of Agricultural Research*, **20** (7):557-585.

Yadav, S.K., Pandey, P., Kumar, B. and Suresh, B.G. 2011. Genetic architecture, Inter-relationship and selection criteria for yield improvement in rice. *Pakistan Journal of Biological Sciences,* **14**(9): 540-545. [Cross Ref]