__Original Research Article__

Unraveling the Genetic Architecture of Rice (*Oryza sativa* L.) Using Variability, Correlation, Path analysis and Diversity Analysis: Insights for Crop Improvement Strategies

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ABSTRACT

The present study aimed to assess the genetic architecture of ricethrough various biometrical techniques that was achieved through a field experiment conducted during the *Kharif* 2022 season utilizing 23 distinct genotypes of rice. The trial was performed at the field experimentation center, Department of genetics and plant breeding, School of agriculture, Lovely Professional University. The research concluded that the highest genotypic and phenotypic coefficients of variation were for the number of productive tillers per plant, grain L/B ratio and grain yield per plant. Additionally, high heritability was observed for all traits except for kernel breadth. The investigation also explains high genetic advance as a percent of the mean was observed for all traits except spikelet fertility and kernel breadth. Grain yield per plant had a significant positive genotypic correlation with the number of productive tillers per plant, filled grains per panicle, and total number of grains. Path analysis revealed that kernel L/B ratio, kernel length, filled grains per panicle, total number of grains, and number of productive tillers per plant had the maximum positive direct effects. The study suggests that selection based on these traits could be more effective in improving rice yield.The germplasms falling in different clusters with high mean for grain yield and other component characters can be utilized for hybridization programme to obtain elite segregants.

Comment [I1]: were

Keywords: Variability, Correlation, Path analysis, Diversity, Rice

1. INTRODUCTION

Rice is one of the chief cereals consumed across the world. Rice proteins are known for having amino corrosive substances and are uniquely wealthy in lysine content [1]. India ranks first in the area of rice production and also first in rice exports. The interest in food is consistently extending with the increment of populace, making a yearly increment of 3% for each year popular rice [2]. The production of rice in India, for example, was estimated to be around 118.87 MT in the year 2020-2021, according to the Ministry of Agriculture and Farmers' Welfare. Variation among the varieties for the economical yield and associated traits is the foundation of any selection program in breeding.

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The heritable variability within the population or intermating resource can be concluded by genetic diversity. This helps to succeed in the subject of plant breeding by projecting genetic variation, and keen information about the concerned traits in the given resource. The information about the gene exchange to offspring's can be evaluated using heritability. Heritability provides information about the capability of a trait that can be transmitted to possible generations. Heritability estimates thus helps to predict the expression of traits in further generations. A combination of genetic advance and heritability is helpful for proper selection is said by [3]. High heritability coupled with high genetic advance results helps breeder to select preferable estimations in breeding programme. Correlation studies can provide information on the improvement of multiple characteristics simultaneously.

Comment [I3]: selection as said

Therefore, knowledge of the relationship between yield and its contributing characters is essential in rice breeding programs. Path coefficient analysis is a partial regression coefficient and well-established technique practiced in breeding to conclude the relation between grain yield and its contributing characters. The path coefficient analysis predicts the direct and indirect effects of source variables to the expressing variable. The nature of effect like direct or indirect effect of yield and its characteristics can be explained through path coefficient analysis [4]. Thereafter this method can be used in selection techniques which helps to read about specific traits resulting in correlation between grain yield and other traits.

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2. MATERIAL AND METHODS

The study was conducted at the Field Experimentation Centre, Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University in Punjab.

The experimental material for this study consisted of 23 genotypes sourced from various places, such as Punjab Agricultural University (PAU) and Agricultural Research Station (ARS) in Nellore,Andhra Pradesh. The genotypes were used for a field experiment conducted during the *Kharif* 2022 season. The experimental design used was a randomized block design with three replications, and the spacing between rows and plants was 30cm and 15cm, respectively. The cultural practices followed during the experiment were based on recommended guidelines to ensure proper growth and development of the plants.

2.1 Recorded observations

Five randomly selected plants from each entry and replication were evaluated for traits like Days to 50% flowering(DF), Plant height(PH) (cm), Panicle length(PL) (cm), Number of tillers per plant(NTL), Number of productive tillers per plant(NPL), Number of Spikelet's per panicle (NSP), spikeletfertility(SF), Flagleaflength(FL) (cm), Number of filled grains per panicle(NFG), Days to maturity(DM), Single plant yield(SYP) (gm), 1000 grain weight (TW) (gm), Biological yield(BY) (gm), and Harvest index(HI).

2.2 Statistical analysis

The techniques suggested by Singh and Chaudhary [5] are used to evaluate the genotypic coefficient of variation (GCV) and the phenotypic coefficient of variation (PCV). Heritability in broad sense is concluded using the formula established by [6]. Genetic advance is estimated using the method proposed by [3]. The path analysis is calculated by the method of Dewey and Lu [7].The concept of D^2 statistics was originally developed by P.C. Mahalanobis [8].

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3. RESULTS AND DISCUSSION

The analysis of variance conducted in this study indicated that the genotypes used in the experiment showed significant differences for each trait studied, as shown in Table 1. This indicates the presence of genetic variation among the genotypes used in the study [27]. The mean performance of the genotypes also showed a wide range, indicating the existence of significant variation among the genotypes. Similar results highlighting the presence of variation in different quantitative traits of rice have been reported in other studies [9-11].

Table1: Analysis of variance for grain yield and yield components in rice

Source of variation	d.f	DF	PH	PL	NTL	NPL	NSP	SF
Replication	**2**	13.43	62.26	9.33	12.28	6.44	78.98	6.04
Treatment	**23**	40.57	588.82	21.75	6.66	8.16	2317.76	42.33

Error	**44**	3.27	8.19	1.48	2.99	1.89	20.50	2.55
C.V.		**2.17**	**2.35**	**4.14**	**13.95**	**12.07**	**1.85**	**1.84**

Source of variation	**d.f**	**FL**	**DM**	**BY**	**SPY**	**TW**	**NFG**	**HI**
Replication	**2**	11.75	54.91	87.62	24.78	9.49	6.64	0.03
Treatment	**23**	19.52	236.23	168.78	17.77	9.34	1565.38	0.006
Error	**44**	2.92	13.16	26.73	7.18	2.48	9.60	0.001
C.V.		**5.71**	**2.88**	**5.92**	**8.08**	**6.80**	**1.46**	**9.70**

3.1 GCV and PCV of variation

The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) disguise the environmental effect over several traits. Estimates of minute difference between the PCV and GCV defines the environmental effect on the appearance of traits. Low estimates of PCV and GCV recorded for Days to 50% Flowering, Panicle Length, Spikelet fertility, Flag Leaf Length, Days to Maturity, Biological Yield, Grain Yield per Plant and 1000 Seed Weight, similar findings recorded for Days to 50% Flowering, Panicle Length, Spikelet fertility by [9], days to maturity by [12] which say direct selection for these traits is not recommended. Moderate PCV and GCV recorded for plant height, number of productive tillers, number of spikelets per panicle, and number of filled grains per panicle. Similar findings recorded for plant height, harvest index, this is the indication of appreciable amount of genetic variability and negligible influence of environment over the expression of the trait and suggests the scope of improvement of these genotypes for the traits, relevant discovery by [13-15]. Number of total tillers per plant was recorded as low PCV and Medium GCV. Here no recorded high PCV and GCV.

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3.2 Heritability and Genetic advance

As mentioned in (Table 2), the estimated heritability varied between (55.17-99.39) percent between days to 50% flowering to harvest index. High heritability recorded characteristics for days to 50% flowering, plant height, panicle length, number of spikelet's per panicle, number of filled grains per panicle, spikelet fertility, flag leaf length, days to maturity, biological length,1000 grain weight, harvest index and, harvest index shows the presence of additive gene action. Similar results recorded for days to 50 % flowering by [16], Plant height by [17], Moderate heritability recorded characteristics for number of total tillers per plant, single plant yield, Similar results recorded for number of total tillers per plant by [18]. Low heritability was not recorded, likewise results in [19]. Low or moderate estimates of heritability coupled with genetic advance indicated the presence of non-additive gene action, this criterion observed in traits like, single plant yield and no. of tillers per plant.

The genetic advancement percentage mean observed range from (1.69-56.75) days to 50% flowering to harvest index the presence of high GA percentage is observed in plant height, number spikelet's per panicle, number of filled grains per panicle, likewise results observed for plant height, spikelet's per panicle by [18]. Moderate GA percentage are observed in days to maturity, biological yield, and similar results for days to maturity by [20]. Low GA percentage observed in days to 50% flowering, panicle length, number of total tillers per plant, number of productive tillers, spikelet fertility, flag leaf length, single plant yield,1000 grain weight, harvest index similar results recorded for days to 50 % flowering by [16] and spikelet fertility for [21].

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Table 2: Coefficient of variation, heritability, and genetic advance of rice genotypes.

Characters	General mean	Range		Variance		Coefficient of variation		Heritability (%)	Genetic advance (5%)	G.A. as percentage of mean
		Min.	Max.	Genotypic	Phenotypic	Genotypic	Phenotypic			
DF	83.26	74.33	91.33	12.43	13.52	4.23	4.41	91.9	6.96	8.36
PH	121.52	91.47	136.13	193.5	196.20	11.44	11.52	98.6	28.45	23.41
PL	29.36	24.87	33.47	6.755	7.24	8.85	9.16	93.1	5.16	17.60
NTP	12.39	10.33	15.70	1.225	2.22	8.93	12.02	55.17	1.69	13.66
NPL	11.39	9.33	15.03	2.0894	2.71	12.68	14.47	76.82	2.60	22.90
NSF	245.07	170.13	286.93	765.75	772.58	11.29	11.34	99.1	56.75	23.15
SF	86.69	81.20	94.86	13.261	14.11	4.20	4.33	93.9	7.27	8.38
FL	29.95	25.83	33.67	5.532	6.50	7.85	8.51	85.03	4.46	14.91
DM	125.78	118.67	142.67	74.3584	78.74	6.85	7.05	94.43	17.26	13.72
BY	87.28	77.20	105.67	47.3509	56.20	7.88	8.59	84.16	13.04	14.90
SPY	33.18	28.73	36.40	3.5304	5.923	5.66	7.33	59.6	2.98	9.04
TW	23.17	20.20	29.40	2.2849	3.11	6.52	7.61	73.41	2.66	11.51
NFP	211.88	142.53	245.53	518.5	521.79	10.74	10.78	99.39	46.76	22.07
HI	0.38	0.28	0.47	0.01	0.02	11.10	12.44	79.72	0.07	20.43

3.3 Correlation coefficient analysis

The genotypic and phenotypic correlation values are showing minute differences, which destinates the effect of environment is low on these traits. The grain yield per plant is showing positively correlated with panicle length, no. of tillers per plant, no. of productive tillers per plant, no. of spikelet's per panicle, spikelet fertility, days to maturity, no. of filled grains per panicle and harvest index which designates that these traits are positively arbitrary at both phenotypic and genotypic levels. Similar results recorded for panicle length, number of productive tillers per plant, total tillers, days to maturity, total tillers per plant, and number of filled grains per panicle by [22]. Hence the selection of these traits for high yield is recommended. Negatively correlated traits for both phenotypic and genotypic correlations, like days 50% Flowering, plant height, flag leaf length, biological yield, and thousand seed weight, similar results recorded for plant height by [23], flag leaf length by [14] are not suggested for trait selection to improve the grain yield.

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3.4 Path Coefficient analysis

The outcome of path coefficient analysis says that the seven traits *viz*, panicle length, number of productive tillers per panicle, flag leaf length, biological yield, number of filled grains per panicle, and harvest index have a direct positive effect and accordingly these traits are useful for selection to improve the grain yield. Similar results for flag leaf length and panicle length by [24]. It is always known characters showing high positive effects for grain yield also resemble high direct effects. Negative direct effect on grain yield are days to 50 percent flowering, plant height, number of total tillers per panicle, number of spikelets per panicle, spikelet fertility, days to maturity, and test weight. Similar results for days to maturity by [15] plant height by [25-16].

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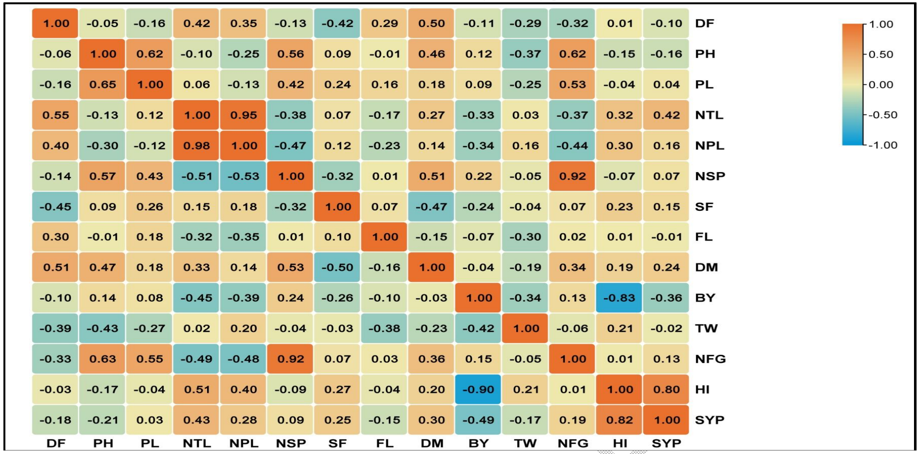
Fig.1 Phenotypic (r_p) (above diagonal) and Genotypic (r_g) (below diagonal) correlation coefficients among 14 characters in 23 genotypes



DF	PH	PL	NTL	NPL	NSP	SF	FL	DM	BY	TW	NFG	HI	SYP	
1.00	-0.05	-0.16	0.42	0.35	-0.13	-0.42	0.29	0.50	-0.11	-0.29	-0.32	0.01	-0.10	DF
-0.06	1.00	0.62	-0.10	-0.25	0.56	0.09	-0.01	0.46	0.12	-0.37	0.62	-0.15	-0.16	PH
-0.16	0.65	1.00	0.06	-0.13	0.42	0.24	0.16	0.18	0.09	-0.25	0.53	-0.04	0.04	PL
0.55	-0.13	0.12	1.00	0.95	-0.38	0.07	-0.17	0.27	-0.33	0.03	-0.37	0.32	0.42	NTL
0.40	-0.30	-0.12	0.98	1.00	-0.47	0.12	-0.23	0.14	-0.34	0.16	-0.44	0.30	0.16	NPL
-0.14	0.57	0.43	-0.51	-0.53	1.00	-0.32	0.01	0.51	0.22	-0.05	0.92	-0.07	0.07	NSP
-0.45	0.09	0.26	0.15	0.18	-0.32	1.00	0.07	-0.47	-0.24	-0.04	0.07	0.23	0.15	SF
0.30	-0.01	0.18	-0.32	-0.35	0.01	0.10	1.00	-0.15	-0.07	-0.30	0.02	0.01	-0.01	FL
0.51	0.47	0.18	0.33	0.14	0.53	-0.50	-0.16	1.00	-0.04	-0.19	0.34	0.19	0.24	DM
-0.10	0.14	0.08	-0.45	-0.39	0.24	-0.26	-0.10	-0.03	1.00	-0.34	0.13	-0.83	-0.36	BY
-0.39	-0.43	-0.27	0.02	0.20	-0.04	-0.03	-0.38	-0.23	-0.42	1.00	-0.06	0.21	-0.02	TW
-0.33	0.63	0.55	-0.49	-0.48	0.92	0.07	0.03	0.36	0.15	-0.05	1.00	0.01	0.13	NFG
-0.03	-0.17	-0.04	0.51	0.40	-0.09	0.27	-0.04	0.20	-0.90	0.21	0.01	1.00	0.80	HI
-0.18	-0.21	0.03	0.43	0.28	0.09	0.25	-0.15	0.30	-0.49	-0.17	0.19	0.82	1.00	SYP

TABLE 3: Genotypic path coefficient for grain yield and its component traits in rice

Traits	DF	PH	PL	NTL	NPL	NSP	SF	FL	DM	BY	TW	NFG	HI	SYP
DF	**-0.2134**	0.0135	0.0344	-0.1163	-0.0862	0.029	0.0952	-0.0647	-0.109	0.0219	0.0841	0.0706	0.0055	**-0.178**
PH	0.0033	**-0.0515**	-0.0336	0.0068	0.0153	-0.0292	-0.0048	0.0007	-0.0241	-0.0071	0.0221	-0.0323	0.0087	**-0.2093**
PL	-0.0248	0.1003	**0.1536**	0.0186	-0.0184	0.0666	0.0403	0.0276	0.0282	0.0117	-0.0411	0.0846	-0.0064	**0.0251**
NTL	-0.1494	0.0362	-0.0333	**-0.2741**	-0.2828	0.1398	-0.0405	0.0864	-0.0917	0.1244	-0.0053	0.1333	-0.1388	**0.4318**
NPL	0.186	-0.1364	-0.055	0.4748	**0.4603**	-0.2451	0.0836	-0.1589	0.0632	-0.178	0.0943	-0.2232	0.1823	**0.2782**
NSP	0.634	-2.6435	-2.021	2.3774	2.4815	**-4.661**	1.5028	-0.0444	-2.4492	-1.123	0.1759	-4.3014	0.4019	**0.0904**
SF	0.9127	-0.1896	-0.5363	-0.302	-0.3714	0.6597	**-2.046**	-0.2117	1.0279	0.5288	0.0634	-0.1376	-0.5582	**0.2514**
FL	0.0457	-0.0019	0.0271	-0.0475	-0.0521	0.0014	0.0156	**0.1508**	-0.0245	-0.0145	-0.0568	0.0044	-0.0067	**-0.1545**
DM	-0.0534	-0.0488	-0.0192	-0.035	-0.0144	-0.0549	0.0525	0.017	**-0.1046**	0.0034	0.0236	-0.0372	-0.0209	**0.2989**
BY	-0.1084	0.1454	0.0803	-0.4792	-0.4083	0.2544	-0.2729	-0.1014	-0.0348	**1.0559**	-0.4383	0.1633	-0.9479	**-0.4935**
TW	0.1035	0.1125	0.0703	-0.0051	-0.0538	0.0099	0.0081	0.0989	0.0594	0.109	**-0.2626**	0.0136	-0.0553	**-0.1687**
NFG	-1.4649	2.7753	2.4369	-2.1514	-2.146	4.084	0.2976	0.1299	1.5765	0.6843	-0.2295	**4.4254**	0.053	**0.1863**
HI	-0.0489	-0.3207	-0.0792	0.9648	0.7545	-0.1643	0.5199	-0.0847	0.3816	-1.7104	0.4014	0.0228	**1.9053**	**0.8223**

RESIDUAL EFFECT = 0.1178

3.5 Diversity analysis

A range of variation was observed among twenty-three rice germplasms that were evaluated. These germplasms were then grouped into different clusters based on their similarity, as determined by the Mahalanobis D^2 statistical method. To select parents for a hybridization program that can lead to maximum heterosis, it is recommended to consider the magnitude of genetic distance, the contribution of different characters to total divergence, and the magnitude of cluster means for different characters' performance. The germplasms in clusters I & III, II & I, III & I, IV & III, and V & I exhibit significant variability, and it is expected that subsequent generations will accumulate favorable genes, leading to high heterosis.

Fig. 2 Graphical depiction of a dendrogram that shows the clustering of 23 rice genotypes based on 14 observable traits.

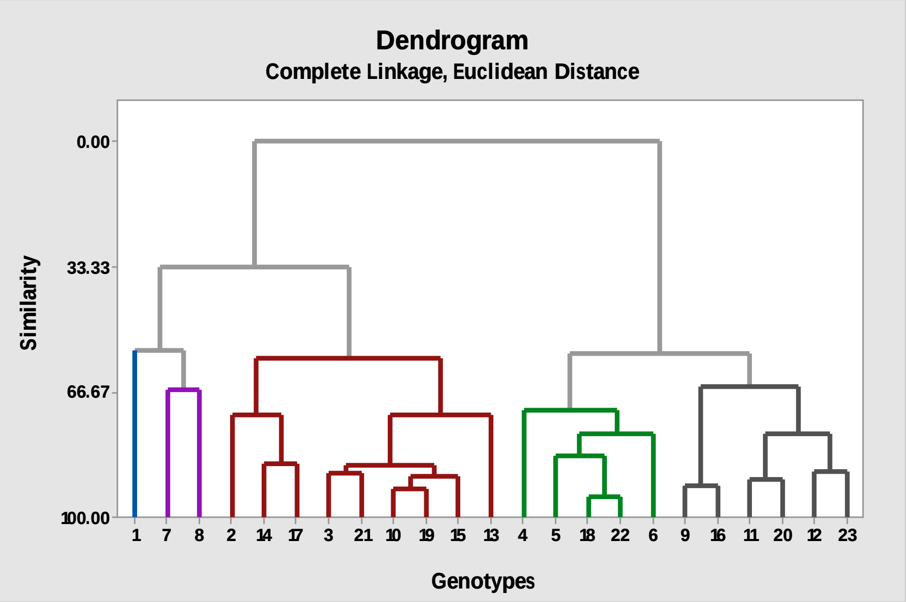


Table 4 Average inter and intra-cluster distance values in rice

	cluster1	cluster 2	cluster 3	cluster 4	cluster5
cluster 1	**0**	64.074	101.963	46.8275	99.7712
cluster 2	64.075	**21.91**	45.863	35.3407	38.1032
cluster 3	101.963	45.8629	**14.34**	79.1143	23.5643
cluster 4	46.828	35.3407	79.114	**20.71**	71.0568
cluster 5	99.771	38.1032	23.564	71.0568	**16.81**

4. CONCLUSION

It is concluded that the high heritability coupled with high genetic advance possesses the additive gene action which prioritizes selection of traits for breeding program and our experiment also concludes that the same for traits like plant height, no. of productive tillers per plant, 1000 seed weight and harvest index shows high heritability and high genetic advance. The genotypic and phenotypic correlations result the positive and direct effect of harvest index, number of tillers per plant on grain yield, which indicates the true association between the traits and environmental effect is not evident. Hence concluded the selection among the trats is preferred to increase the yield of rice per plant.

Comment [l20]: traits

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