Assessment of Genetic Diversity, Correlation and Principal Component Analysis of Restorer Lines of Hybrid Rice

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ABSTRACT

Rice is the premier food crop for more than half of the world population. So achieving high-yield potential is always a dominant objective in rice breeding. This experiment was taken to study the genetic parameters like variability, heritability, genetic advance, correlation, clustering and PCA analysis of thirty promising restorer lines of rice using Randomized Complete Block Design with three replications. Both GCV and PCV, heritability and genetic advance was high for most of the quantitative parameters. Correlation and path coefficient reflected significant variation in most of the yield components. Principal Component Analysis showed that out of 21 quantitative characters only seven principal components (PCs) exhibited more than 1.00 eigen value and showed about 80.91% cumulative variability. PC1 had the highest variability (21%) followed by PC2 (16.7%). Cluster analysis grouped thirty rice cultivars in four clusters. Maximum genetic diversity was found between Cluster I and Cluster IV whereas minimum in between Cluster III and Cluster IV. Cluster III consisted of 7 cultivars showed maximum mean grain yield. The cultivars from these clusters with desirable characters may be used for parental line improvement program (R×R). According to the results obtained from the studies, it was concluded that traits like number of effective tillers, number of grains per panicle and 1000-grain weight were useful for direct selection criteria for higher grain yield. Cultivars like LP 106R, ACI 1R, Hera 10R could be used as a source of pollen parent for developing new hybrid combinations in hybrid rice breeding programs.

Keywords: *Rice, yield components, floral traits, genetic variability, heritability*

1. INTRODUCTION

Rice is the most significant staple food crop in which more over half of the world's population relies on [1]. The primary goal of plant breeders is to increase the output of basic foods in order to accommodate the rapidly growing population. By 2030, it is anticipated that rice production will need to increase by 60% from 1995 levels. [2]. Therefore, increasing rice production is crucial for ensuring food security and reducing poverty.

Food grain production is no doubt increasing year by year through the adoption of modern crop production techniques, but due to higher growth rate of population, there is a sustained demand for increase in food production. Several attempts are being made to enhance food production through both conventional and non-conventional breeding methods with available approaches. Exploitation of hybrid vigour is considered as one of the practically feasible tools to break the yield plateau in rice. Successful and long-lasting hybrid program depends on development of component lines using CMS source. The discovery of CMS in rice suggested that breeding could develop a commercially viable F_1 hybrid [3]. Components lines development is considered as the backbone of any sustainable hybrid rice program. In comparison to the best traditional rice varieties, the most prospective hybrids produced yields that were 20–30% [4] and 15–20% higher. According to Siddiq [5], selective enhancement of primary yield components can result in a significant yield increase (20–30%). If the hybrids' parental lines

are regionally adapted and sufficient information about their agronomic and floral characteristics is acquired, it may result in self-sufficient F_1 seed production. Therefore, it is crucial to understand the agronomic and floral characteristics of R lines.

In breeding programs, direct selection based upon crop yields is paradoxical due to its complicated polygenically inherited nature. Rice yield is a complicated quantitative trait that is controlled by pleiotropic genes as well as greatly regulated by the environment and influenced by a variety of other traits. Additionally, making a decision only based on yield may not always be accurate. The selection procedure will be more successful if there is proof of character connection and the direct and indirect impacts each character adds. When establishing a systematic breeding program in a circumstance like this, having a clear understanding of the genotypes and range of linked responses to selection for yield and yield qualities would be quite beneficial. It is possible to create hybrids with better yield potential than the parents and conventional check varieties by carefully choosing restorer lines based on their genetic diversity [6]. A population with high levels of variability offers the chance for selection to create a variation with desired characteristics. Assessment of genetic diversity among and within groups or clusters is crucial for the right parent selection and a more effective search for heterosis.

In order to clarify information on variability, heritability, character associations and the path towards yield and to distinguish superior restorer lines in regard to various floral and yield-contributing traits, the current investigation was carried out in this context.

2. MATERIALS AND METHODS

At the experimental site of Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur, which is situated at the center of the Madhupur Tract (90^o26 E longitude and 24^o29 N latitude) and is 8.2 meters above sea level, thirty restorer lines were grown in Randomized Complete Block Design with three replications during *Aman,* 20018-19.

The experimental fields are divided into three blocks. Every line's seedlings were nurtured in a bed before being transplanted into the experimental plots at the age of 30 days. Two seedlings per hill were transplanted, with a row-to-row distance of 20 cm and a plant-to-plant distance of 15 cm. By spraying urea-TSP-MoP-gypsum-ZnSO4 at 150:100:70:60:10 kg/ha respectively, to maintain proper soil fertility. During the last stage of land preparation, Total TSP, MoP, Gypsum, and ZnSO4 were used. At 15, 30, and 45 days after transplantation (DAT), total urea was applied in three separate applications.

Each plot's five sample plants, excluding the border plants, were chosen at random for the purpose of collecting traits. Before anthesis, the length and breadth of the anther, stigma, and filament were measured under a microscope using an ocular micrometer (level 1). On the basis of the Randomized Complete Block Design model developed by Cochran and Cox [7], quantitative characters were statistically analyzed. Tests to determine the significance of treatment critical difference were conducted using [8]. According to Burton, phenotypic and genotypic coefficients of variation (PCV and GCV) were assessed [9]. According to the procedures outlined by Allard [10], heritability in the broad sense and genetic progress were assessed and arranged according to Johnson et al [11]. The Miller et al. algorithm was used to calculate correlation coefficients for all quantitative character combinations at the phenotypic, genotypic, and environmental levels [12]. Wright [13] path coefficient analysis was used to examine the direct and indirect effects of different characteristics on yield. Cluster analysis and principle component analysis is done by R studio 4.2.1.

3. RESULT

3.1. ANALYSIS OF VARIANCE
Tables 1a and 1b provide the analysis of variance for the twenty-one traits. All of the investigated characters had notable differences, according to the ANOVA.

3.2. GENETIC VARIABILITY
The estimates of mean, range, phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV), heritability (h^2) and genetic advance as per cent of mean (GAM) are presented in Tables 2 and 3 respectively and described character wise here under. All of the traits examined in this study had higher phenotypic co-efficients of variance than genotypic co-efficients of variation.

High (>20%) phenotypic co-efficient of variation was observed for number of tiller/hill, number of panicle/plant, thousand grain weight, stigma length, stigma breadth, pollen fertility, filament length and grain yield/hill. However, moderate (10-20%) genotypic and phenotypic coefficients of variation were recorded in the

present study for 50% flowering, No. of grain per panicle, Filled grain, Flag leaf breath, Anther length, Anther breath. In comparison, the genotypic and phenotypic coefficents of variation were estimated to be low (10%) in for days to maturity, plant height, panicle length, Grain length, Grain breath, Spikelet fertility. For almost all of the variables examined, heritability estimates in the broadest meaning (h^2b) were comparatively higher (>60%). High heritability and high genetic advance as percent mean was observed for 50% days to flowering, number of tillers/hill, number of panicle/plant, number of grain/panicle, thousand grain weight, filled grain/panicle, flag leaf length, flag leaf breath, anther length, anther breath, stigma length, stigma breadth, filament length and grain yield/hill. On the other hand, moderate genetic advance and high heritability in terms of mean percent were seen for Days to maturity, plant height, panicle length, pollen fertility, spikelet fertility (Table 3).

High GCV and PCV, together with high heritability and high genetic advance in percent of mean were found in the current investigation for number of tillers/hill, number of panicles/plant, number of grains/panicle, thousand grain weight, flag leaf length, stigma length, stigma breath, filament length, grain yield per plant (Table 3).

Table- 1a. Analysis of variance for restorer lines

Source of variation	d.f	50% F	DMT	PH (cm)	PL (cm)	NT/H	NP/P	NG/P	GW(mm)	GL(mm)	Filled	Yield/hill
Replication	2	0.0	0.000	0.385	5.254	5.544	2.100	52.478	0.006	0.023	36.011	0.329
Genotype	4	123.72**	100.952**	177.069**	8.03**	40.554**	27.807**	1613.93**	0.206**	0.944**	1405.95**	255.45**
Error	58	0.0	0.000	2.624	0.22	0.315	0.617	21.719	0.003	0.003	22.517	0.450

50% F = Days to 50% flowering, DMT = Days to maturity, PH = Plant height, PL = Panicle length, NT/H = Number of tiller per hill NP/P = Number of panicle per tiller, NG/P = Number of grain per panicle, GL= Grain length, GW = Grain width

Table- 1b. Analysis of variance for restorer lines

Source of variation	d.f	FLL (cm)	FLW (cm)	TW (gm)	AL (μm)	AB (μm)	SL (μm)	SB (μm)	FL (μm)	PF (%)	SF (%)
Replication	2	7.945	0.057	6.452	33.403	4.836	4.544	2.303	108.386	0.001	37.200
Genotype	4	147.855**	0.203**	77.31**	6991.934**	274.389**	5202.412**	588.975**	10470.173**	220.083**	96.164 **
Error	58	0.292	0.002	0.370	34.673	4.842	12.016	3.780	10.719	0.001	6.844

FLL = Flag leaf length, FLW = flag leaf width , TW = Thousand weight , AL= Anther length ,AB= Anther breadth, SL= Stigma length, SB= Stigma breadth, FL= Filament length, PF= Pollen fertility , SF= Spikelet fertility

** = Significant 1% level, d.f = Degrees of freedom

Table- 2. Mean performance of 30 restorer lines for 30 characters in rice (*Oryza sativa* L.)

Restorer	50% F	DMT	PH	PL	NT/H	NP/P	NG/P	TGW	Filled grain	GL	GW	Yield	FLL	FLW	AL (µm)	AB (µm)	SL (µm)	SB (µm)	FL (µm)	PF (%)	SF (%)
BUdhan 2R	70	91	122.3	24.13	9	8	155	16.17	124.3	10.1	3.3	15.7	31.3	1.2	433.3	75.7	213.0	45.3	213.3	90	80
Shokti R	58	88	117.3	21.22	7	7	123	18.2	115.7	10.0	2.7	13.8	34.6	1.5	383.7	65.3	189.7	52.3	171.7	95	94
Hera 5R	61	91	103.4	23.05	9	8	134	19.63	126.7	10.5	3.1	8.3	28.3	1.5	424.3	75.3	214.3	41.3	222.7	92	95
Moyna R	61	93	110.3	23.6	7	7	125	26.73	112.7	9.6	3.5	21.6	33.7	1.9	389.0	75.3	173.3	55.0	175.0	70	90
BU 7R	49	81	107.7	23.98	10	9	85	25.27	72	11.1	3.3	14.9	14.7	1.6	445.0	66.3	110.7	37.6	234.0	73	85
BHD 2R	60	81	110.5	22.11	11	10	156	27.83	130.3	10.6	3.0	34.2	33.0	1.1	350.0	60.0	110.7	24.7	162.0	98	83
Gold R	60	95	112.4	23.79	8	8	116	32.97	109	10.0	3.2	25.1	17.7	1.5	481.0	75.7	212.7	46.7	163.7	95	94
China2R	61	91	109.1	26.05	10	9	124	24.67	120	10.1	3.1	26.5	27.7	1.1	389.0	68.0	140.0	66.3	184.7	95	97
Doyel R	61	91	104.6	25.11	13	11	135	18.83	113.3	10.6	3.2	23.8	27.6	1.6	351.3	72.0	79.3	25.3	213.3	95	84
BU 1R	62	92	112.3	23.6	9	8	77	28.17	68.67	9.8	3.1	14.7	27.7	1.6	387.0	72.3	172.3	49.7	272.7	90	89
BHD 3R	60	90	116.3	21.03	11	10	84	28.17	76	10.0	2.8	22.1	37.8	1.6	413.3	67.0	145.0	55.0	194.3	90	90
LP 106R	64	90	110.4	24.19	17	14	126	27.7	117.7	10.2	3.1	47.7	30.7	1.5	399.0	42.7	84.0	30.0	215.7	94	94
KatariboghR	85	113	128.3	23.25	23	19	130	13.77	113.3	10.1	3.0	28.6	31.8	1.6	365.8	75.7	121.3	66.7	215.3	60	88
MItali R	64	90	119.8	23.64	7	6	144	28.53	121	10.6	2.6	17.2	35.7	1.0	403.3	58.3	101.3	38.7	276.0	95	84
LP 108R	67	96	108.4	22.79	9	8	114	32.47	104.7	10.0	2.9	22.7	22.7	1.6	413.3	69.0	170.7	66.7	192.0	90	92
China 1R	61	95	118.1	20.94	11	10	64	32.1	54	9.8	3.1	16.2	34.7	1.4	356.3	60.7	166.0	60.0	245.0	98	84
BU 329R	64	91	115.6	23.14	15	13	148	22.27	122.7	10.1	3.1	33.5	28.7	1.8	391.3	71.7	174.0	55.7	361.3	92	83
Restorer	**50% F**	**DMT**	**PH**	**PL**	**NT/H**	**NP/P**	**NG/P**	**TGW**	**Filled grain**	**GL**	**GW**	**Yield**	**FLL**	**FLW**	**AL (µm)**	**AB (µm)**	**SL (µm)**	**SB (µm)**	**FL (µm)**	**PF (%)**	**SF (%)**
BHD 1R	65	91	117.7	23.07	10	9	131	17.8	113	9.4	3.2	20.8	34.0	1.6	357.7	99.7	97.3	35.3	307.3	93	86

LP 70R	59	83	111.6	24.05	8	7	138	25.43	132	9.4	3.0	25.1	35.0	1.6	378.7	58.0	140.0	64.3	196.7	90	96
ACI 1R	58	90	113.9	25.97	8	8	148	25	145	9.1	2.7	29.7	28.7	1.3	538.3	62.7	180.3	30.3	164.0	96	99
BU 521R	69	91	114.7	24.94	10	9	130	22.87	110	8.9	2.6	22.3	36.7	1.7	391.7	71.3	175.0	64.7	170.3	90	85
MuktagachR	66	89	139	28.19	8	7	132	20.72	106.7	11.1	2.0	14.8	42.7	1.2	491.8	75.2	107.7	16.5	182.7	95	80
HB 9R	57	78	114.4	25	14	12	152	18	145	9.2	2.7	31.8	30.8	1.1	413.0	66.7	176.0	41.0	213.7	90	96
Hera 10R	59	89	109.6	24.94	10	9	162	25.1	151	9.9	2.8	33.9	42.7	1.9	364.0	61.7	53.3	30.0	163.0	95	93
SL 8R	73	90	101.2	22.15	9	8	126	28.1	118.3	9.8	3.0	68.0	20.7	1.8	374.7	71.7	156.7	43.7	187.7	85	94
HB 8R	67	96	111.3	23.72	13	12	131	29.8	115.7	10.0	3.1	40.7	44.3	1.7	347.0	65.7	163.3	53.3	214.3	90	89
BU 3R	66	98	127.7	25.28	14	12	127	18.03	101.7	9.8	3.0	21.4	28.9	1.8	413.3	67.0	144.3	55.3	223.3	95	80
BU 2R	65	90	112.6	24.15	17	16	137	25.03	108.7	9.1	3.0	41.7	25.2	1.4	417.0	66.7	175.0	61.7	353.7	95	79
IR 509R	65	92	112.4	24.78	15	14	136	22.04	114.7	9.1	2.6	34.9	23.7	1.1	321.3	80.0	164.3	54.7	373.5	90	84
BU 507R	53	91	115.4	20.94	14	13	118	21.44	103.7	9.6	2.9	23.5	23.3	1.1	316.0	60.0	110.7	43.3	216.3	100	88

50% F = Days to 50% flowering, DMT = Days to maturity, PH = Plant height, PL = Panicle length, NT/H = Number of tiller per hill, NP/P = Number of panicle per tiller, NG/P = Number of grain per panicle, GL= Grain length, GW = Grain width, FLL = Flag leaf length, FLW = flag leaf width, TW = Thousand grain weight, AL= Anther length, AB= Anther breadth, SL= Stigma length, SB= Stigma breadth, FL=Filament length, PF= Pollen fertility ,SF= Spikelet fertility.

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Table- 3. Mean, range, genetic variability, heritability (broad sense) and genetic advance as percent of mean for yield and its component traits for 30 restorer lines of rice

| Sl.No | Character | Mean | Range | Coefficient of variation | | Heritability (%) | GAM (%) |
				PCV(%)	GCV(%)		
1	50% flowering	63.122	49.0-85.0	10.2453	10.229	99.69	21.039
2	Days to maturity	91.533	78.0-98.0	6.3312	6.3083	99.28	12.948
3	Plant height (cm)	114.26	101.21-128	6.8224	6.673	95.68	13.447
4	Panicle length (cm)	23.761	20.94-28.18	7.0723	6.798	92.19	13.431
5	Number of tiller/hill	11.388	7.00-23.3	32.5324	32.157	97.71	65.481
6	No. of panicle/plant	10.133	6.0- 15.6	30.704	29.709	93.62	59.217
7	No. of grain/panicle	126.94	64.33- 162.3	18.5155	18.147	96.07	36.642
8	1000 grain wt.(g)	24.094	13.76-32.96	21.17	21.018	98.58	42.989
9	Filled grain	112.24	54.00-145.0	19.52	19.13	95.34	38.48
10	Grain length (mm)	9.911	9.06-11.13	5.679	5.648	98.90	11.571
11	Grain breath (mm)	2.92	2.03-3.26	9.106	8.896	95.43	17.902
12	Flag leaf length (cm)	30.501	14.66-44.33	23.062	22.994	99.41	47.227
13	Flag leaf breath (cm)	1.456	1.03-1.86	18.055	17.753	96.68	35.958
14	Anther length(μm)	396.66	316.0-538.3	12.231	12.141	98.53	24.825
15	Anther breath(μm)	68.572	58.00-99.66	14.190	13.823	94.89	27.738
16	Stigma length(μm)	147.422	53.33-214.3	28.	28.215	99.31	57.922
17	Stigma breath (μm)	47.039	24.66-66.66	29.978	29.692	98.10	60.581
18	Filament length (μm)	222.63	162.0-373.5	29.39	29.69	98.79	54.54
19	Pollen fertility (%)	90.46	60.0-100.0	29.56	26.52	99.69	19.31
20	Spikelet fertility (%)	88.43	79.33-98.66	6.84	6.17	81.31	11.46
21	Yield/hill (g)	25.09	8.25-47.71	36.83	36.73	99.37	75.47

3.3. CORRELATION COEFFICIENT

Correlation coefficients between yield and other characters and inter relations among them were estimated and presented in fig 1. Grain yield was observed to be positively and significantly associated with number of effective tiller per hill (0.60**), number of panicle per plant (0.63**), number of grains per panicle (0.40*) and filled grain (0.39*). Positive non-significant association found for panicle length (0.18), thousand grain weight (0.15), spikelet fertility (0.07), stigma breadth (0.03), filament length (0.19) and pollen fertility (0.05). On the contrary negative association was noticed for plant height (-0.27), anther length (-0.2), anther breadth (-0.36) (Fig 1).
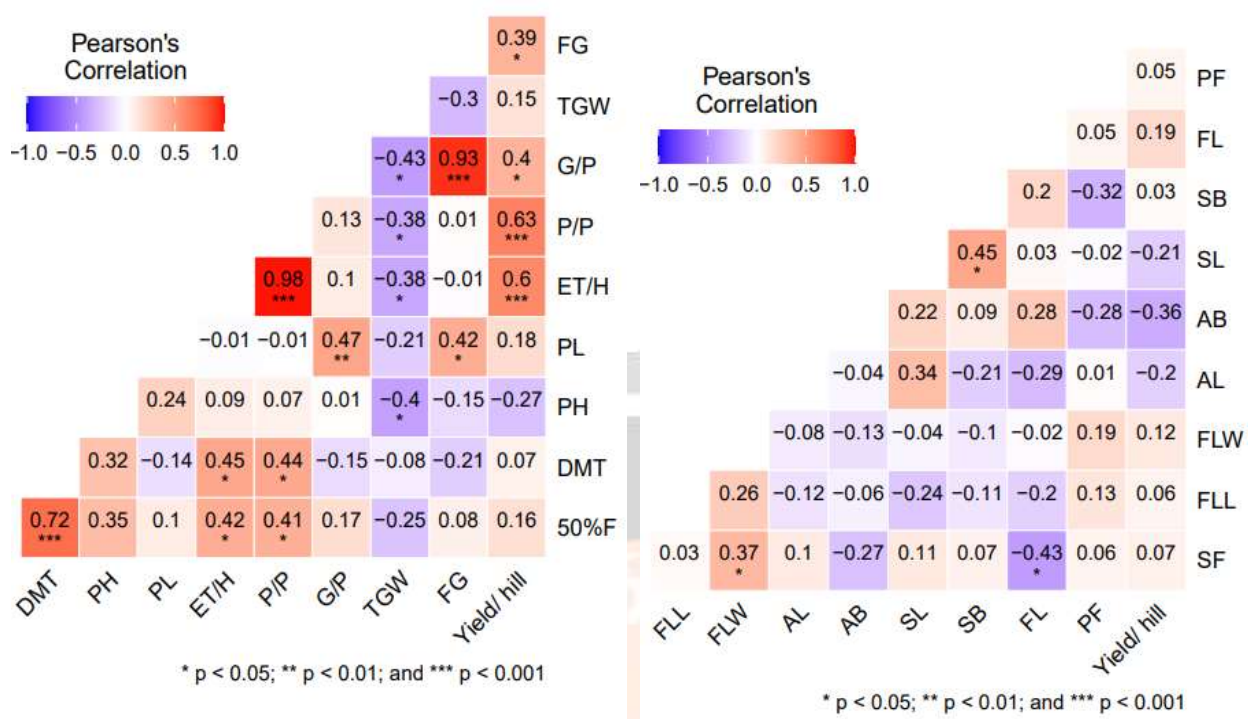
Fig- 1 Correlation analysis between traits

3.4. PATH ANALYSIS

Through path analysis at the phenotypic and genotypic levels, the direct and indirect effects of yield were determined. The results are shown in the Tables 4a, 4b. Path coefficient analysis revealed that plant height, panicle length, number of tiller per hill, number of grain per panicle, thousand grain weight, spikelet fertility, grain width, anther length, stigma length and filament length exhibited positive direct effects possessed the highest positive direct effect on grain yield. The negative direct relationship between plant height and days to 50% flowering and yield suggested that short-lived rice hybrids may be created without compromising grain output. Except for plant height, panicle number, and filled grain, most of the examined parameters revealed a positive indirect relationship between panicle length and grain yield.

The residual impact for the first 10 characters in Table 4a was 0.351, which means that they were responsible for 65% of the variation in grain yield. The remaining ten characters in Table 4b had a value of 0.103, which meant that they were responsible for 90% of the variation in grain yield. This result suggests that few traits other than those present in the current experiment may also influence yield.

3.5. SCREE PLOT

Scree plot explained the percentage of variance associated with each principal component obtained by drawing a graph between eigenvalues and principal component numbers. Principal component analysis (PCA) using 21 traits produced ten principal components which cumulatively accounted for 100 % of the total phenotypic variance.

Table- 4a. Direct and indirect effects (phenotypic) of floral and agronomical characters on yield of restorer lines of rice

Character	Days to 50% flowering	Days to maturity	Plant height	Panicle length	Number of tiller /hill	Number of panicle /plant	Number of grain /panicle	Grain weight	Filled grain	Spikelet fertility
Days to 50% flowering	**-.1323**	-.2180	.0310	.0021	1.3043	-.8149	1.274	-.1778	-.5859	-.5354
Days to maturity	-.0938	**-.3074**	.0301	-.0035	1.4853	-.9564	-.6305	-.0609	1.097	-.4966
Plant height	-.0430	-.0967	**.0955**	.0064	.5008	-.2977	.2192	-.2963	.7980	-1.091
Panicle length	-.0120	.0472	.0268	**.0229**	-.0313	.0755	2.5617	-.1796	-2.249	-.1240
Number of tiller per hill	-.0550	-.1455	.0152	-.0002	**3.1318**	-2.140	.5885	-.2499	.0196	-.5866
Number of panicle/tiller	-.0505	-.1377	.0133	-.0008	3.1463	**-2.135**	.6280	-.2463	.0058	-.6062
Number of grain/panicle	-.0271	.0312	.0034	.0094	.2970	-.2156	**6.2176**	-.2998	-5.655	.0336
Grain weight	.0323	.0258	-.0389	-.0056	-1.078	.7231	-2.563	**.7273**	1.872	.4825
Filled grain	-.0129	-.0560	-.0127	.0085	-.0102	.0020	5.8358	-.2260	**-6.025**	.7805
SF	.0325	.0699	-.0478	-.0013	-.8436	.5931	.0957	.1608	-2.154	**2.1823**
Yield	**.1477**	**.0637**	**-.2051**	**.1375**	**.5835**	**.6167**	**.3944**	**.1766**	**.3961**	**.0868**

Residue effect = 0.351

Table- 4b. Direct and indirect effects (phenotypic) of floral and agronomical characters on yield of restorer lines of rice

Character	Grain length	Grain width	Flag leaf length	Flag leaf width	Anther length	Anther breadth	Stigma length	Stigma breadth	Filament length	Pollen fertility
Grain length	**-.5251**	0.0151	.0000	.0029	.0009	.0569	.0659	.1016	-.0511	.0081
Grain width	-.0393	**.2014**	-.0528	-.0031	-.0014	-.0265	-.0184	-.048	.0492	.0152
Flag leaf length	-.002	-.0928	**.1145**	-.0075	-.0008	.0462	.0486	.0255	-.0560	-.0179
Flag leaf width	.0575	.0241	.0325	**-.0263**	-.0006	.0657	.0142	.0217	-.0093	-.0231
Anther length	-.0794	-.0448	-.0154	.0025	**.0062**	.0056	-.0658	.0537	-.0729	-.0015
Anther breadth	.0637	.0114	-.0113	.0037	-.0001	**-.4685**	-.0473	-.016	.0758	.0327
Stigma length	.1745	.0187	-.0281	.0019	.0021	-.1118	**-.1982**	-.1081	.0120	.0052
Stigma breadth	.2369	.0429	-.0130	.0025	-.0015	-.0334	-.0951	**.2252**	.0500	.0401
Filament length	.1008	.0372	-.0241	.0009	-.0017	-.1336	-.0089	-.0423	**.2660**	-.0071
Pollen fertility	.0314	-.0225	.0151	-.0045	.0001	.1132	.0076	.0667	.0139	**-.1355**
yield	**-.3248**	**.0763**	**.0596**	**.1564**	**.2118**	**-.3558**	**.2319**	**.0043**	**.1873**	**.0855**

Residue effect = 0.1030

The first PC explained 21 % of the total variance and the PC2 explained an additional 16.7 % of the total variance which was the highest variance of the total variance (Fig 2). For this reason, we selected the PC1 and PC2 for this explanation. The Eigenvectors decreased significantly from PC1 (21 %) to PC3 (13.1 %). This shows that more principle components did not adequately capture variation after PC3. Thus, only the initial three PCs were considered. Rotated component matrix results revealed that PC1 had the highest level of variability (21%) and was therefore the most significant component and highly filled with characters like number of effective tiller per hill (0.864) and number of panicle per plat (0..875) contributed in positive direction whereas days to maturity (-0.661), days to 50% flowering (-0.680), plant height (-0.309) and panicle length (-0.032) contributing in a negative way. It was made abundantly evident that, with the exception of panicle length, yield features are the main cause of PC1's variance. PC2 contributed to 16.67% of the total variation which was loaded with characters like grain per panicle (0.890), number of effective tillers per plant (0.198), panicle length (0.565), filled grain (0.885) and spikelet fertility (0.119) contributed in positive direction while characters like days to maturity (0.194) contributed in negative direction (Table 5).
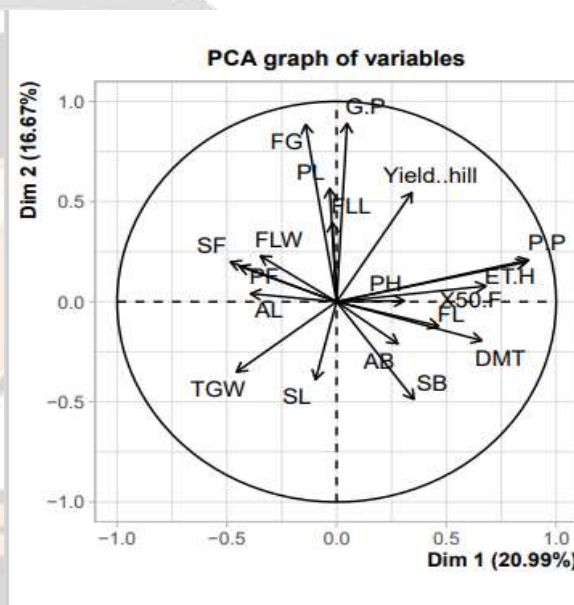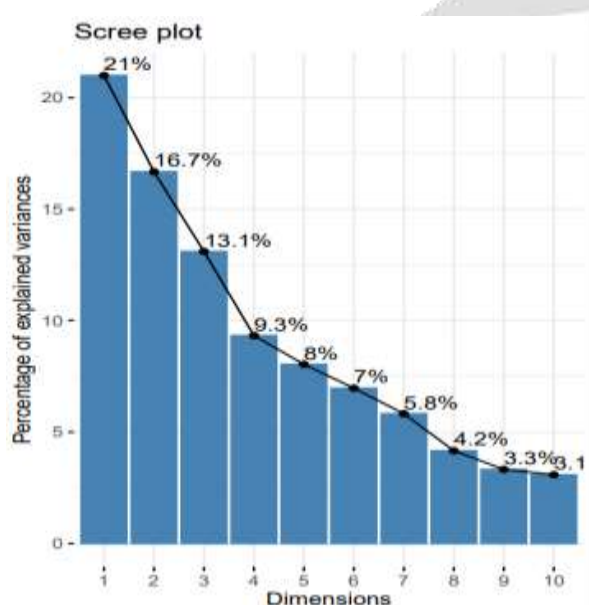

Fig- 2 Scree plot showing variation of rice genotypes   **Fig- 3** Distribution of strength of correlation among various traits

3.6. PRINCIPAL COMPONENT ANALYSIS (PCA)

The degree of association between them in this PCA-Biplot is explained by how near the trait vectors are to one another. Strong neutral correlation results when the angle between the trait vectors is less than 90^0, If it is higher than 90^0, there is a negative correlation and it is said to be linear or have a perfect connection when it is 0^0. In here yield had strong correlation with panicle length, grain per panicle, flag leaf length, effective tiller per hill and filled grain. The higher the coefficients, regardless of the sign, the more effective they will be in discriminating between traits. To demonstrate a distinct pattern of arranging genotypes in the factor plane, a scatter plot between PC1 and PC2 was created. PC1 showed 21 % variability with the Eigen value of 3.99 (Table 5). After PC3 started to straighten out, an elbow line was discovered, and it is evident that PC1 had the greatest variation of all the PCs. Scatter plot fig 4 was drawn between PC1 and PC2 that depicted Every genotype was dispersed widely among many areas. The genotypes were occupying the convex region of the hull displaying the outliers were Hira 10R, ACI 1R, Shokti R, BU 1R, China 10R and Kataribhog R (Fig 4).

Fig- 4 Distribution of rice genotypes across the various components

Table- 5. Eigen value and percent of total variation and component matrix for the principal component axes

Principal Components	1	2	3	4	5	6	7
Eigen values	3.99	3.17	2.49	1.77	1.52	1.32	1.11
% of Variance	21	16.67	13.1	9.32	8.04	6.97	5.82
Cumulative %	21	37.67	50.77	60.08	68.12	75.09	80.90
Component Matrix							
Days to 50% flowering	-0.680	-0.078	0.251				
Days to maturity	-0.661	-0.194	0.102				
Plant height	-0.309	-0.004	-0.741				
Number of effective tiller per hill	0.864	0.198	-0.308				
Panicle length	-0.032	0.565	0.437				
Number of panicle per plant	0.875	0.209	-0.311				
Grain per panicle	0.048	0.890	0.147				
Thousand grain weight	0.456	0.351	0.447				
Filled grain	0.142	0.885	0.017				
Spikelet fertility	-0.484	0.119	-0.294				

3.6. CLUSTER ANALYSIS:

Cluster analysis cluster 30 rice cultivars in four clusters. The largest cluster, Cluster II, had 14 genotypes. Cluster IV was next with 8 genotypes (Table 6). According to dendogram Cluster I was monogenotypic clusters include Kataribhog R. Cluster II included maximum genotypes those are Shokti R, Hera 5R, Moyna R, BU 7R, Gold R, China2R, BU 1R, BHD 3R, MItali R, LP 108R, China 1R, LP 70R, SL 8R, BU 507 R. Cluster III includes BHD 2R, Doyel R, LP 106R, ACI 1R, HB 9R, Hera 10R, HB 8R. Cluster IV includes BUdhan 2R, BHD1R, BU 521R Muktagacha R ,BU 3R, BU 2R IR 509R, BU 329R. Dendogram showed that maximum genetic distance is present between Cluster Cluster I and Cluster VI indicated that they had diverse genetic material (Fig 5). Although they

belong to the same species but the parents involved in theory cross were different and may had different origin. Within cluster II Gold R and BU 507R had most diversity which was probably due to the involvement of different parents in their crosses or may be due to some sort of mutation while BU 507R was most similar to the BU 7R. Cluster III and Cluster IV have the least amount of genetic diversity. Cultivars with higher grain production and associated favorable traits are included in Cluster III.
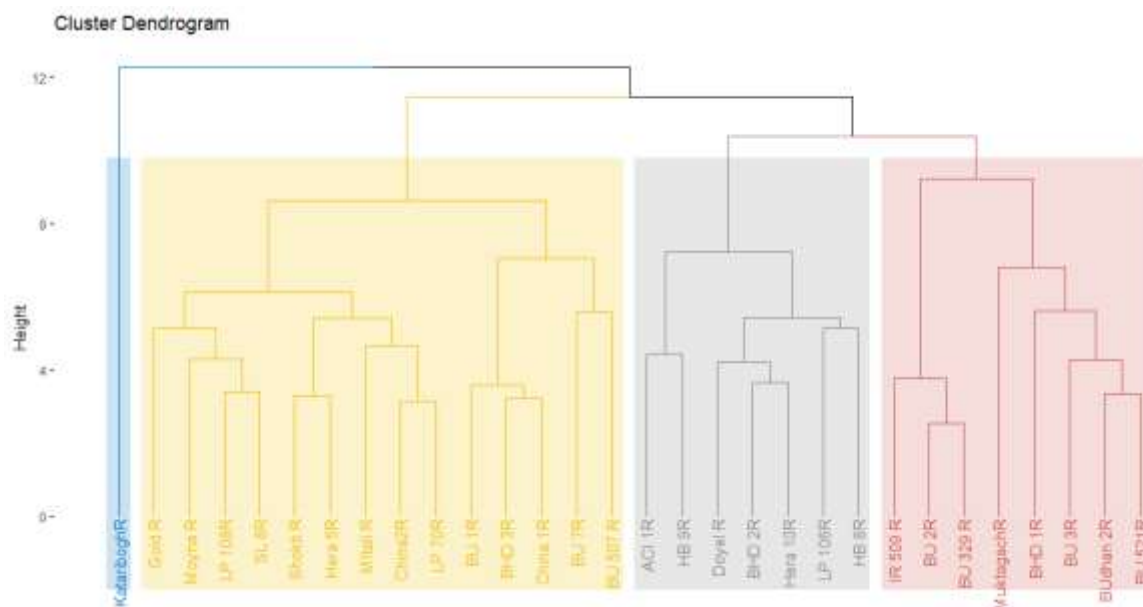
Fig- 5 Cluster analysis of the 209 rice landraces by Hierarchical cluster analysis of the FactoMineR (Factor analysis and data mining with R) package.

Table- 6. Relative contributions of the 30 rice genotypes into 4 cluster

Cluster	Number	Genotypes
I	1	Kataribhog R
II	14	Shokti R, Hera 5R, Moyna R, BU 7R, Gold R, China2R, BU 1R, BHD 3R, MItali R, LP 108R, China 1R, LP 70R, SL 8R, BU 507 R
III	7	BHD 2R, Doyel R, LP 106R, ACI 1R, HB 9R, Hera 10R, HB 8R
IV	8	BUdhan 2R, BHD1R, BU 521R Muktagacha R ,BU 3R, BU 2R IR 509R, BU 329R

4. DISCUSSION:
4.1. GENETIC VARIABILITY
All of the phenotypes examined in the current analysis showed higher phenotypic than genotypic co-efficients of variance, showing the influence of environment. Mamta Singh et al. reported similar conclusions [14].

High phenotypic co-efficients of variation (>20%) were noted for number of tillers/hill, number of panicles/plant, thousand grain weight, flag leaf length, stigma length, stigma breadth, filament length, pollen fertility and grain yield/hill. Therefore, improving grain yield through selection of these genotypes based on phenotype may be successful. Hossain et al. had reported similar outcomes [15]. But in this investigation, modest (10–20%) genotypic and phenotypic coefficients of variance found for 50% flowering, number of grain/panicle, Filled grain, flag leaf breath, anther length, anther breath. These results concur with those of Bornane et al [16] for 1000 grain weight. In contrast, the present study found that estimations of the genotypic and phenotypic coefficients of variance were lower (10%) for days to maturity, plant height, panicle length, Grain length, Grain breath, Spikelet fertility. For plant height, similar results were previously reported by Satish et al. [17].

Nearly all of the examined traits had heritability estimates in the broad sense (h^2b) that were considerably higher (>60%). Similar results in hybrid rice were reported by Iftekharuddula et al. in [18]. Evaluations of high heritability have been found to be useful in choosing superior genotypes based on phenotypic performance.

High heritability and high genetic advance as a percentage mean were observed for 50% days to flowering, number of tillers/hill, number of panicles/plant, number of grains/panicle, thousand grain weight, filled grains/panicle, flag leaf length, flag leaf breath, anther length, anther breath, stigma length, stigma breadth, filament length and grain yield/hill indicating that the high heritability is caused by the cumulative effects of gene action and Selection for these characters might be worthwhile. Adilakshmi and Girijarani noted similar results [19] for 1000-seed weight and Madhavilatha et al. [20] for yield per plant. On the other hand strong heritability and moderate genetic advance in percent of mean were observed for days to maturity plant height, panicle length, pollen fertility, spikelet fertility indicating both non-additive and additive gene effects contribute to the control of the characteristics. The outcomes match those of the reports of Seyoum et al. [21]. To provide a better understanding of the effectiveness of selection, additional information on genetic variation has been informed along with heritability and genetic advance assessments.

High GCV and PCV, together with high heritability and high genetic advance in percent of mean, were found in the current study for number of tiller/hill, number of panicles/plant, number of grains/panicle, thousand grain weight, flag leaf length, stigma length, stigma breath, filament length, grain yield/plant showing that additive gene activity predominates and as a result, there is opportunity for selection-based improvement of the attribute. Mohana Krishna et al. earlier reported similar findings [22].

4.2. CORRELATION COEFFICIENT

Effective selection strategies for complex (polygenic) traits depend on the information of the association/relationship between these traits [23]. Grain yield was observed to be positively and significantly associated with number of effective tiller per hill, number of panicle per plant, number of grains per panicle and filled grain indicating with an increase in these features, increase in grain production. Therefore, while making selections to improve yield, priority should be given to these features. The results concur with those of Manikaminnie et al. [24] about the number of reproductive tillers per hill. Positive non-significant relationship found for panicle length, thousand grain weight, spikelet fertility, stigma breadth, filament length and pollen fertility. The findings are in agreement with the reports of Akter et al. [25]. On the contrary negative association was noticed for plant height (-0.27), anther length (-0.2), anther breadth (-0.36).

4.3. PATH ANALYSIS

Path co-efficient analysis revealed that panicle length, number of tiller per hill, number of grain per panicle, thousand grain weight, spikelet fertility, grain width, anther length, stigma length and filament length showed favorable immediate results had the greatest favorable direct impact on grain yield and Consequently, it would be possible to pick individuals directly based on these attributes. Hasan et al. [26] found similar positive direct effect of thousand grain weight on grain yield. The negative direct relationship between plant height and days to 50% flowering and yield suggested that short-lived rice hybrids may be created without compromising grain output. Except for plant height, panicle number, and filled grain, most of the examined parameters revealed a positive indirect relationship between panicle length and grain yield. The path coefficient and correlation showed that panicle length, number of grains/panicle, thousand grain weight, filled grains/panicle, stigma breadth, filament length, pollen fertility and spikelet fertility were the most essential features of the examined restorers lines and Exploiting the yield potential of rice hybrids might benefit from selection based on these traits.

4.5. SCREE PLOT

Results revealed that the PC1 which accounted for positive direction with characters such as number of effective tiller per hill and number of panicle per plant whereas days to maturity, days to 50% flowering, plant height and panicle length contributing in a bad way. That indicated that the variation in PC1 is mainly contributed by yield characters except panicle length. PC2 contributed to grain per panicle, number of effective tillers per plant, panicle length, filled grain and spikelet fertility while characters like days to maturity contributed in negative direction. Therefore, the important features have a propensity to stick together and come together in several principle components, which help to explain the variability. This could be taken into account when using these traits in a later breeding program.

4.5. PRINCIPAL COMPONENT ANALYSIS (PCA)

The PCA's findings provided an explanation for the genetic diversity of the rice collection. The identified characteristics within the axes showed a significant influence on the phenotypic of germplasm lines. For the

characterization of various rice germplasm lines, researchers like Yugandhar et al. [27] and Ilieva et al. [28] have used PCA. In the selection process of a breeding program, PCA helps us relate the traits that have a significant impact on the phenotypic of various genotypes of rice. The genotypes occupied the convex portion of the hull that displayed the outliers like Hira 10R, ACI 1R, Shokti R, BU 1R, China 10R and Katarivhog R. Similarly Fenty et al. [29] reported that less components should be dealing with it by removing components having an eigenvalue of 1. Sharma et al. [30] reported that PCA highlights the significance of the main source of variation at each differentiation axis. Khare et al. [31] also stated that PCA condenses a big set of variables into smaller sets of components that summarize the correlations.

4.7. CLUSTER ANALYSIS

There was no correlation between the eco-geographical distribution of genotypes and genetic divergence, as evidenced by the clustering pattern that showed the genotypes from various locations clustered together. The open exchange of germplasm among breeders from various places may be the reason why genotypes of various origin are grouped together in one cluster. Similar findings were reported by Rashid et al. [32] and Sabesan [33]. This shows that selection has been directed toward the same objective in the various genotype origin sites, yet there is enough genetic variation to clearly distinguish them into 13 clusters. It was concluded that Cultivars like BHD 2R, Doyel R, LP 106R, ACI 1R, HB 9R, Hera 10R, HB 8R might be used for rice hybridization and improve programs for developing new rice varieties.

5. CONCLUSION

Results of the present study on variability, heritability, genetic advance, correlation, path analysis, PCA and Cluster analysis revealed a potential for improving restorer lines' grain yield through selection and using of suitable parent for developing new hybrid combinations. The highest mean performance for yield was found in LP 106 R followed by BU 2R, ACI 1R, Hera 10R. For the creation of early-maturing rice hybrids BU7R, BHD 2R, LP 70R and dwarfness SL 8R, Doyel R can be used. The majority of the examined characters displayed notable genetic variation. Studies on path coefficients and character association demonstrated the value of the number of tillers, number of panicle, number of grain, stigma breadth and filament length as selection criteria for effective yield improvement as they contain highest positive direct effect on yield. The genotypes potentially be categorized into several groups, according to cluster analysis and principal component analysis. Breeders can identify potential genotypes that could be employed as parents in upcoming breeding programs by using such groupings.

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