

## International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693  
 ISSN Online: 2617-4707  
 IJABR 2024; 8(2): 640-648  
[www.biochemjournal.com](http://www.biochemjournal.com)  
 Received: 06-12-2023  
 Accepted: 10-01-2024

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## Genetic diversity analysis and character association of rice hybrids

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DOI: <https://doi.org/10.33545/26174693.2024.v8.i2h.645>

### Abstract

The current investigation was performed at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur, during *Kharif* 2022. 104 rice genotypes were planted in Randomized Complete Block design with three replications. The present study was initiated to obtain the promising rice hybrids in respect of various yield and grain quality traits in rice hybrids. High GCV and PCV was observed for number of tillers/plants, number of effective tillers/plants, panicle weight per plant, plant weight, biological yield/plant, sterile spikelet/panicle, fertile spikelets/panicle, total no. of spikelet, spikelet density %, harvest index, panicle index, and grain yield/plant. Grain yield per plant shared positive significant correlation with biological yield/plant and panicle weight/plant. The genotypes of cluster III and cluster VI showed higher inter cluster distance, hence the parental lines fell in these clusters may be utilized for broaden the genetic base of rice. On the basis of PCA ranking for yield attributing five genotypes viz., R 671 × NPT 29, Kranti × JNPT 1058, Kranti × WGL -14, Shyamla × IR 64 and 29A × P3123 crosses were found superior both for yield and attributing traits.

**Keywords:** Genetic variability, rice, hybrids, correlation

### Introduction

Rice, a prominent staple food worldwide, is classified within the genus *Oryza*. This genus encompasses two cultivated types, *Oryza sativa* and *Oryza glaberrima* alongside 22 wild species. As per the most up-to-date taxonomic data, within these wild variants, 14 are diploid, featuring a chromosome count of  $2n = 2x = 24$ , whereas the remaining 8 are tetraploid, having a chromosome count of  $2n = 4x = 48$ . Both cultivated types, *Oryza sativa* and *Oryza glaberrima*, exhibit diploidy with an identical chromosome count of  $2n = 2x = 24$ . Particularly, *Oryza sativa* functions as a primary dietary staple for approximately 3.5 billion individuals, holding an esteemed status as the most vital food crop cultivated on a global scale. Rice plays a crucial role in global nutrition, providing a significant source of dietary carbohydrates for billions of people. Additionally, it offers valuable energy, protein, vitamins, essential fatty acids, minerals, zinc and iron, as highlighted by Zinc and iron are particularly important for their role in supporting overall health and preventing deficiencies. Beyond its nutritional value, rice holds symbolic significance as a unifying element in various cultures across the globe. It is commonly referred to as the "grain of life" due to its indispensability in daily food. Notably, rice showcases exceptional genetic diversity, with over one hundred thousand distinct landraces and improved cultivars, reflecting its position as one of the few crop species exhibiting such remarkable genetic variation (Samal *et al.* 2014) [6]. The worldwide rice production in 2022–2023 was 511.6 MT on a territory of 164.19 million hectares with such a productivity of 4560 kg/hectare (FAO, 2023). So far, the first advance estimations covering primarily kharif crops for the current agricultural year 2022-23 have been produced, with kharif rice output estimated at 104.99 million tonnes. (Ministry of agriculture and farmers, 2023). Achieving high yield, quality and resistance are the primary breeding goals to facilitate cost-effective and efficient cultivation. There is a growing demand for hybrid rice seeds and it is projected that the area dedicated to hybrid rice cultivation will increase from the current 3.5 million hectares to approximately 8–10 million hectares in the next 5–10 years.

The majority of seed production for hybrid rice is expected to take place in Andhra Pradesh and Telangana. In India till 2022, a total of 133 rice hybrids exists, with 40 developed by the public sector and 93 by the private sector. These hybrids have varying durations, ranging from 110 to 150 days, and cover approximately 3.5 million hectares, which accounts for 8% of the total rice acreage in the country. Ensuring the genetic purity of parental lines and their hybrids is crucial for the successful adoption of hybrid rice technology throughout the nation. The selection of suitable parents with advantageous alleles, which, when crossed, may yield heterotic hybrids, might also speed success. Rice hybrids created with parental lines that are regionally adaptive and have tolerance to biotic and abiotic challenges are likely to perform well, particularly under favourable environmental conditions. The main aim of hybrid development is high yield and resistance. Conducting a critical analysis of genetic variability parameters is an essential requirement for plant breeders involved in crop improvement programmes, especially when dealing with traits of economic importance. These parameters include genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), heritability and genetic advance. Such analysis provides valuable insights into the extent of genetic variation within a population. Studies on path coefficients offer useful information on the direct and indirect effects of various yield component traits on grain yield. This information aids in identifying effective selection criteria for improving yields more effectively. The degree of genetic divergence and the relative contributions of different components to overall divergence can be assessed through  $D^2$  analysis. Principal Component Analysis (PCA) is another technique that provides valuable information about the gene pool, enabling the selection of precise genetic resources for breeding programmes. These analytical approaches assist breeders in making informed decisions regarding the selection and utilisation of genetic resources for crop improvement. Conducting a thorough analysis of genetic variability parameters is crucial for plant breeders involved in crop improvement programs, especially when dealing with economically significant traits. These parameters, including genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), heritability and genetic advance, offers valuable insights into the extent of genetic variation within a population.

### Materials and Methods

The experimental material includes 104 rice genotypes were planted in a randomised complete block design with three replications in kharif season 2022 at seed breeding farm, JNKVV, Jabalpur. Geographically JNKVV, Jabalpur is located at 23.900 north latitude and 79.580 east longitudes at a 411.87 meters elevation of above mean sea level.

Each genotype was planted in three rows of five metres length with 15-20 cm spacing and one seedling per hill. All the standard package and practices were adopted to grow a good crop. The quantitative traits like days to flowering (day), flag leaf length (cm), flag leaf width (cm), stem thickness per plant (cm), culm length (cm), panicle length (cm), culm thickness, plant height (cm), number of tillers per plant, number of productive tillers per plant, average panicle weight per plant (g), number of spikelet per panicle, fertile spikelet per panicle, sterile spikelet per panicle, biological yield per plant (g), stem weight (g), spikelet

density (%), spikelet fertility (%), panicle index (%), harvest index (%), grain yield per plant (g) and 1000 grain weight (g) were recorded manually. All the statistical analyses were carried out using INDOSTAT software.

### Results and Discussion

The analysis of variance declared that mean sum of square had high significance for all yield attributing traits. Maximum variability was observed for total spikelets per panicle and lowest for flag leaf width (Table 1.). The values of phenotypic coefficient of variation for all the traits under study were found to be more than genotypic coefficient of variation and very small difference was present in between genotypic and phenotypic coefficients of variation revealing very little influence of environment for their expression (Table 2). This finding was in partial consonance with the findings of Bharath *et al.* (2018) [7], Pragma *et al.* (2018) [8], Kujur *et al.* (2017) [9] and Rahangdale *et al.* (2019a) [2]. High GCV and PCV were recorded for the traits *viz.*, Stem thickness (25.87%) followed by number of tillers/plant (26.05% & 26.64), number of effective tillers/plant (26.28% & 26.73%), panicle weight per plant, plant weight, biological yield plant, sterile spikelet/panicle, fertile spikelets/panicle, total no. of spikelet, spikelet density %, harvest index, panicle index, grain yield/plant, While moderate value of GCV and PCV were recorded for flag leaf length, grain breadth, decorticated grain breadth, length to breadth ratio for decorticated grain, grain length, flag leaf width, stem length, fertility percentage, head rice recovery %, thousand grain weight, However, low magnitude of GCV and PCV were observed for days to flowering, panicle length, decorticated grain length, plant height, hulling %, milling %. Heritability and genetic advance are potent method for predicting the gene action and effect. These are significant parameters for assessing the transmit ability and genetic gain of the economic trait in selection programme. Heritability and genetic advance are important selection parameters. High heritability accompanied with high genetic advance showed by traits *viz.* Days to flowering, flag leaf length, flag leaf width, stem length, Plant height, stem thickness, number of tillers, number of effective tillers, stem weight per plant, panicle weight, biological yield, sterile spikelets, fertile spikelets, total number of spikelets, fertility percentage, spikelet density, grain length, grain breadth, decorticated grain length, decorticated grain breadth, head rice recovery, thousand grain weight, harvest index, panicle index, length breath ratio for decorticated grain, and grain yield per plant. High heritability accompanied with moderate genetic advance showed by Hulling percentage, Milling percentage, Panicle length. This indicates the preponderance of additive gene action and therefore could be taken as aim important traits for the direct selection programme. The findings were supported for trait spikelet fertility by Nath *et al.* (2021) [10]; total spikelets per panicle by Nath *et al.* (2021) [10], Nagaraju *et al.* (2013) [11], Tomar *et al.* (2000) [12] and Sabu *et al.* (2009) [13]. The interrelationship between the traits could be extracted through the correlation analysis and those traits which are directly correlated with seed yield per plant can be taken for direct selection (Table 3). The current investigation revealed the significant and positive correlation of traits with yield are biological yield, panicle weight, number of tiller/plants, stem weight/plant, total number of spikelets, flag leaf length, spikelet density, harvest index, panicle length, stem

thickness, stem length, panicle index, grain weight, decorticated grain width, head rice recovery, milling %, fertility %. Therefore, enhancement of magnitudes of these traits would directly influence the grain yield in positive aspects. Trait negatively correlate with grain yield per plant were length: breath ratio for decorticated grain, days to flowering, decorticated grain length. Hence, reduction in magnitude of these traits would enhance grain yield. The findings were supported for trait spikelet fertility by Nath *et al.* (2021) <sup>[10]</sup>; total spikelets per panicle by Nath *et al.* (2021) <sup>[10]</sup>, Nagaraju *et al.* (2013) <sup>[11]</sup> and Tomar *et al.* (2000) <sup>[12]</sup>. The path analysis separates the effect on grain yield into direct and indirect effect (Fig.1). The direct effect influences the yield directly, while indirect effect enhance yield though some other traits. The high positive direct effect was reported by traits such as plant height, fertile spikelet, sterile spikelet, harvest index, spikelet density, panicle weight, stem weight, number of tillers per plant, decorticated grain width, hulling%, length: breath for decorticated grain, flag leaf length, and grain length. It indicates true relationship between them and direct selection for these traits will be rewarding for yield improvement (Table 4&5). But selection should be restrained for traits with negative direct effects *viz.*, total number of spikelets/panicles, stem length, panicle length, biological yield/plant, panicle index, number of effective tillers, fertility %, milling %, head rice recovery %, decorticated grain length, and grain width all showed negative direct effects. The genetic divergence revealed that stem length, fertile spikelets, panicle weigh, thousand grain weight, sterile spikelets, grain yield per plant, panicle index, harvest index, and stem weight per plant. Days to flowering, total number of spikelets, grain length, decorticated grain length, head rice recovery%, decorticated grain width, and flag leaf length all contributed less than 1% to genetic divergence. The selection of these traits proves to be beneficial for

selection breeding programme. The selection would find to be ineffective for traits which doesn't contributes in genetic divergence, which are Flag leaf length, stem length, panicle length, plant height, number of tillers, number of productive tillers per plant, panicle weight, biological yield, spikelet density, grain weight, hulling%, milling%, and length: breath ratio for decorticated grain. The findings were in propinquity with Pratap *et al.* (2018) <sup>[14]</sup> for plant height Rahangdale and Singh (2019b) <sup>[3]</sup> for spikelet density, panicle weight/plant, decorticated grain length/breadth ratio, number of tiller per plant, decorticated grain width and flag leaf length; Pratap *et al.* (2018) <sup>[14]</sup> and Chandra *et al.* (2017) <sup>[15]</sup> for fertile spikelet/panicle; Kumari *et al.* (2020) <sup>[16]</sup> for harvest index. According to the Mahalanobis D<sup>2</sup> analysis, the highest intra clusters distance was recorded in cluster VII (Table 6). Highest inter cluster distance was found in cluster III (32B) & VI(R 671 × NPT 29, 31A X MTU 1081 × NPT 111) followed by Cluster IV(Shyamla) & VII(25A X NPT 26-1, 25A X NPT 14-7), Cluster V(NPT 10-24 × R 712, NPT 10-65 × JNPT 58, 3A X NPT 13-01, 3A X Swarnyapriya, 29B, 97B)& VI(R 671 × NPT 29, 31A X MTU 1081 × NPT 111), Cluster VI(R 671 × NPT 29, 31A X MTU 1081 × NPT 111) & VII(25A X NPT 26-1, 25A X NPT 14-7), Cluster II(Kranti × JNPT 1058, Kranti × WGL - 14, Kranti × NPT 26-1, Shyamla x IR 64, 32A X MTU 1081 × NPT 13-01, NPT 23, NPT 26-1, JNPT-58, NPT 14-7) & V (NPT 10-24 × R 712, NPT 10-65 × JNPT 58, 3A X NPT 13-01, 3A X Swarnyapriya, 29B, 97B) Table 7&8. This displayed that cross between these clusters are expected with sufficient heterosis and thus could be chosen as a parent for the hybridization in rice improvement programme. Similar findings were obtained by Bhushan *et al.* (2019) <sup>[17]</sup>, Kushwaha *et al.* (2020) <sup>[18]</sup> and Archana *et al.* (2018) <sup>[19]</sup> for 1000 seed weight. Tiwari *et al.* (2019) <sup>[20]</sup> Archana *et al.* (2018) <sup>[19]</sup> for fertile spikelets.

**Table 1:** ANOVA for yield and quality attributing traits in fertility restorer lines

S. No	Source of variance	D.F.	Mean sum of square										
			DTF	FLL	FLW	SL	PL	PH	ST	NOT	NOETPP	SWPP	PW
1.	Replication	2	4.46	3.67	0.0094	3.05	1.65	8.23	0.00038	0.077	0.36	0.38	0.15
2.	Genotype	103	208.96**	101.15*	0.20	187.31***	14.30 ***	241.35*	8.04**	18.75***	17.54**	438.93***	654.69**
3.	Error	206	1.34	0.90	0.0037	2.22	1.17	3.032	0.0004	0.28	0.20	0.42	0.29

S. No	Source of Variance	D.F.	Mean sum of square							
			BY	SS	FS	TNOS	HI%	PI%	GYPP	H%
1.	Replication	2	1.013	3.52	14.15	26.0032	0.55	1.200	0.088	0.793
2.	Genotypes	103	1757.21**	5555.69**	16100.58***	18278.74***	328.10***	2217.94**	241.74***	49.25*
3.	Error	206	0.48	3.92	6.93	7.029	0.75	1.03	0.22	50

S. No	Source of variance	D.F.	Mean sum of square									
			M%	L/B	F%	SD%	GL	GW	DGL	DGW	HRR%	1000GW
1.	Replication	2	9.097	0.0094	0.45	0.25	0.019	0.034	0.00053	0.006	16.69	0.047
2.	Genotypes	103	49.50**	1.014*	549.09**	27.43**	2.55**	0.34*	0.92*	0.23*	216.01*	52.51*
3.	error	206	2.094	0.010	0.65	0.25	0.022	0.015	0.012	0.0025	3.30	0.043

\*\* , \*\*\*significant difference at p

**Table 2:** Parameters of genetic variability for yield, yield attributing and quality traits in rice genotypes

S. No.	Traits	Mean	Range		Coefficient of variation		H <sup>2</sup> (Bs) %	Genetic Advance as % of Mean
			Min.	Max.	GCV (%)	PCV (%)		
1	DTF	101.93	80.33	126.00	8.16	8.23	98.10	21.33
2	FLL	34.12	23.26	49.26	16.93	17.16	97.30	44.12
3	FLW	1.39	0.75	1.98	18.61	19.11	94.80	47.84
4	SL	74.53	53.93	97.33	10.53	10.72	96.50	27.33
5	PL	24.96	19.06	31.41	8.37	9.43	78.80	19.62
6	PH	99.50	75.40	123.53	8.95	9.12	96.30	23.20
7	ST	6.32	2.31	10.10	25.87	25.87	95.90	68.29
8	NOT	9.52	5.96	18.66	26.05	26.64	95.60	67.24
9	NOETPP	9.14	5.76	18.66	26.28	26.73	96.70	68.21
10	SWPP	28.52	13.30	77.06	42.38	42.44	99.70	111.73
11	PW	32.56	11.13	93.37	45.34	45.37	99.90	119.64
12	BY	61.09	26.80	160.97	39.60	39.62	99.90	104.52
13	SS	43.88	10.33	273.66	98.02	98.13	99.80	258.51
14	FS	214.56	64.00	354.66	34.13	34.15	99.90	90.06
15	TNOS	258.44	100.33	446.33	30.19	30.21	99.90	79.67
16	F%	83.07	22.62	96.78	16.27	16.30	99.60	42.88
17	SD%	10.35	4.14	22.48	29.06	29.47	97.20	75.66
18	GL	8.97	6.50	12.12	10.24	10.37	97.40	26.67
19	GW	2.64	1.94	3.35	12.58	13.41	88.00	31.16
20	DGL	6.38	4.85	7.90	8.65	8.82	96.20	22.39
21	DGW	2.10	1.46	2.77	13.15	13.37	96.80	34.16
22	HRR%	62.95	41.65	78.41	13.37	13.68	95.50	34.51
23	1000GW	21.32	10.46	31.13	19.61	19.63	99.80	51.71
24	HI%	40.26	13.19	83.93	25.94	26.03	99.30	68.25
25	PI%	78.84	24.38	209.45	34.47	34.50	99.90	90.95
26	H%	78.35	51.81	87.93	5.09	5.32	91.30	12.84
27	M%	75.13	50.24	81.36	5.29	5.63	88.30	13.12
28	LBR	3.10	2.02	5.06	18.62	18.91	97.00	48.44
29	GYPP	23.65	14.15	60.70	37.93	37.99	99.70	100.01

**Table 3:** Estimation of phenotypic correlation for various yield and quality attributing traits.

Traits	DTF	FLL	FLW	SL	PL	PH	ST	NOT	NOETPP	SWPP	PW	BY	SS	FS	TNOS
DTF	1	-0.0485	0.2947 ***	0.2184	0.0165	0.1969 ***	0.2238 ***	-0.1439 *	-0.152**	0.1063	-0.1376 *	-0.0308	0.0664	0.0033	0.0397
FLL		1	0.3621 ***	0.3064 ***	0.2881 ***	0.3450 ***	0.3333 ***	0.0074	0.0417	0.4019 ***	0.2535 ***	0.3557 ***	0.2342 ***	0.4433 ***	0.5452 ***
FLW			1	0.3969 ***	0.0237	0.3559 ***	0.3900 ***	-0.2533 ***	-0.2345***	0.2543 ***	0.1057	0.1917 ***	0.0427	0.3803 ***	0.3804 ***
SL				1	0.3403 ***	0.9695 ***	0.3406 ***	-0.2040 ***	-0.1777**	0.2130 ***	0.1712 **	0.2110 ***	0.0686	0.2359 ***	0.2593 ***
PL					1	0.5599 ***	0.3166 ***	0.2779 ***	0.3115***	0.3406 ***	0.3928 ***	0.4101 ***	0.2258 ***	0.2182 ***	0.3293 ***
PH						1	0.3812 ***	-0.1075	-0.0754	0.2760 ***	0.2527 ***	0.2923 ***	0.1202 *	0.2654 ***	0.3154 ***
ST							1	-0.0314	-0.0071	0.3918 ***	0.2254 ***	0.3336 ***	0.0717	0.2723 ***	0.2951 ***
NOT								1	0.9761***	0.4971 ***	0.5850 ***	0.6058 ***	-0.0246	0.0105	-0.0037
NOETPP									1	0.5154 ***	0.6026 ***	0.6257 ***	-0.0314	0.0562	0.0354
SWPP										1	0.6177 ***	0.8772 ***	-0.0286	0.3051 ***	0.2706 ***
PW											1	0.9194 ***	-0.1757 **	0.4297 ***	0.3064 ***
BY												1	-0.1216 *	0.4149 ***	0.3223 ***
SS													1	-0.1788 **	0.3837 ***
FS														1	0.8400 ***
TNOS															1
GYPP	-0.0634	0.4303	0.1323	0.2295	0.3802	0.3010	0.2565	0.5020	0.5227	0.5028	0.6149	0.6269	0.0252	0.5170	0.4991

**Table 4:** Estimation of phenotypic correlation for various yield and quality attributing traits. (Continue)

Traits	F%	SD%	GL (mm)	GB (mm)	DGL (mm)	DGW (mm)	HRR	1000 GW	HI%	PI%	H%	M%	LBR
DTF	-0.0491	0.0401	0.2185 ***	-0.0045	-0.2910 ***	0.0382	0.2527 ***	0.0425	-0.0647	0.1425 *	-0.1166 *	0.0168	-0.1603 **
FLL	-0.0168	0.4903 ***	-0.065	0.2962 ***	-0.0468	0.1650 **	0.0699	0.1338 *	0.0916	0.2019 ***	0.1895 ***	-0.1481 **	-0.1656 **
FLW	0.1461 **	0.3905 ***	-0.2325 ***	0.3606 ***	0.3983 ***	0.3254 ***	0.2946 ***	-0.0047	-0.1476 **	0.0218	0.0706	0.0142	-0.4446 ***
SL	0.0861	0.1534 **	0.1729 **	0.3962 ***	-0.1420 *	0.3312 ***	0.3887 ***	0.3657 ***	0.0157	0.0265	0.1172 *	0.1177*	-0.3031 ***
PL	-0.0762	-0.0128	0.3596 ***	0.0283	0.1953 ***	-0.005	0.1334 *	0.1895 ***	0.02	-0.0446	0.0692	0.1721**	0.0893
PH	0.0553	0.1331 *	0.2464 ***	0.3580 ***	-0.0746	0.2914 ***	0.3777 ***	0.3707 ***	0.0089	0.0119	0.1209 *	0.1477 **	-0.2445 ***
ST	0.0605	0.2178	0.1845 **	0.0771	-0.003	0.1461 **	0.1118 *	0.2308 ***	0.1104	0.0835	-0.2101 ***	0.086	-0.1340 *
NOT	-0.0592	-0.0907	0.0024	-0.0986	-0.0049	-0.0282	0.0563	-0.036	-0.1602 **	-0.2309 ***	0.002	0.1865 ***	0.0167
NOETPP	-0.0336	-0.0582	0.0182	-0.0828	0.0071	-0.0071	0.0627	-0.016	-0.1614 **	-0.2314 ***	-0.0075	0.1706 **	0.009
SWPP	0.1235 *	0.1884 ***	0.1168 *	0.1671 **	-0.0133	0.2414 ***	0.2908 ***	0.2962 ***	-0.3736 ***	-0.1194 *	-0.0131	0.0504	-0.1893 ***
PW	0.2643 ***	0.1835 **	0.0381	0.1763 **	0.0254	0.1578 **	0.2938 ***	0.1044	-0.3357 ***	-0.5097 ***	0.2104 ***	0.3329 ***	-0.1196 *
BY	0.2231 ***	0.2062 ***	0.0817	0.1912 ***	0.0088	0.2171 **	0.3248 ***	0.2119 ***	-0.3918 ***	-0.3709 ***	0.1218 *	0.2285 ***	-0.1677 **
SS	-0.8934 ***	0.3088 ***	0.1263 *	0.3071 ***	-0.1184 *	-0.0332	-0.0209	-0.1273 *	0.2323 ***	0.3660 ***	-0.3638 ***	-0.2606 ***	-0.0615
FS	0.5093 ***	0.8126 ***	-0.1515 **	0.1702 **	-0.1545 **	0.0926	0.1276 *	-0.0657	0.0683	-0.0123	0.0866	0.063	-0.1810 **
TNOS	-0.0147	0.9330 ***	-0.0726	0.3291 ***	-0.2103 ***	0.0686	0.1083	-0.1319 *	0.1922 ***	-0.1194 *	-0.0845	-0.2038 ***	
F%	1	0.0233	-0.1531 **	-0.1969 ***	0.0882	0.0503	0.0422	0.1066	-0.1214 *	-0.2450 ***	0.3516 ***	0.1951 ***	0.0142
SD%		1	-0.1996 ***	0.3206 ***	-0.2832 ***	0.0589	0.0524	-0.1929 ***	0.1819 **	0.2189 ***	-0.2029 ***	-0.1955 ***	-0.2306 ***
GL (mm)			1	-0.1521 **	0.4197 ***	-0.2149 ***	-0.0253	0.2604 ***	-0.0421	0.0218	-0.1259 *	0.0158	0.3769 ***
GW (mm)				1	-0.2502 ***	0.4779 ***	0.4947 ***	0.2284 ***	0.0749	0.0814	0.0097	0.0313	-0.4736
DGL (mm)					1	-0.2842 ***	-0.3246 ***	0.2710 ***	-0.0359	-0.0573	-0.0539	-0.1339 *	0.6906 ***
DGW (mm)						1	0.4321 ***	0.2893 ***	-0.0448	-0.0202	0.1046	0.0187	-0.8625 ***
HRR %							1	0.2245 ***	-0.1446 *	-0.1837 **	0.2961 ***	0.3623 ***	-0.4588 ***
1000GW								1	-0.1270 *	-0.0225	0.0232	0.0384	-0.0567
HI %									1	0.8103 ***	-0.1566 ***	-0.1136 *	0.028
PI %										1	-0.3793 ***	-0.3749 ***	0.0005
H %											1	0.7414 ***	-0.0854
M %												1	-0.0509
LBR													1
GYPP (gm.)	0.1521	0.3835	0.0327	0.2039	-0.0622	0.1913	0.1754	0.0383	0.3826	0.2159	0.0369	0.1664	-0.1729



**Table 5:** Estimation of Genotypic Path coefficient showing direct and indirect effect of various components on seed yield

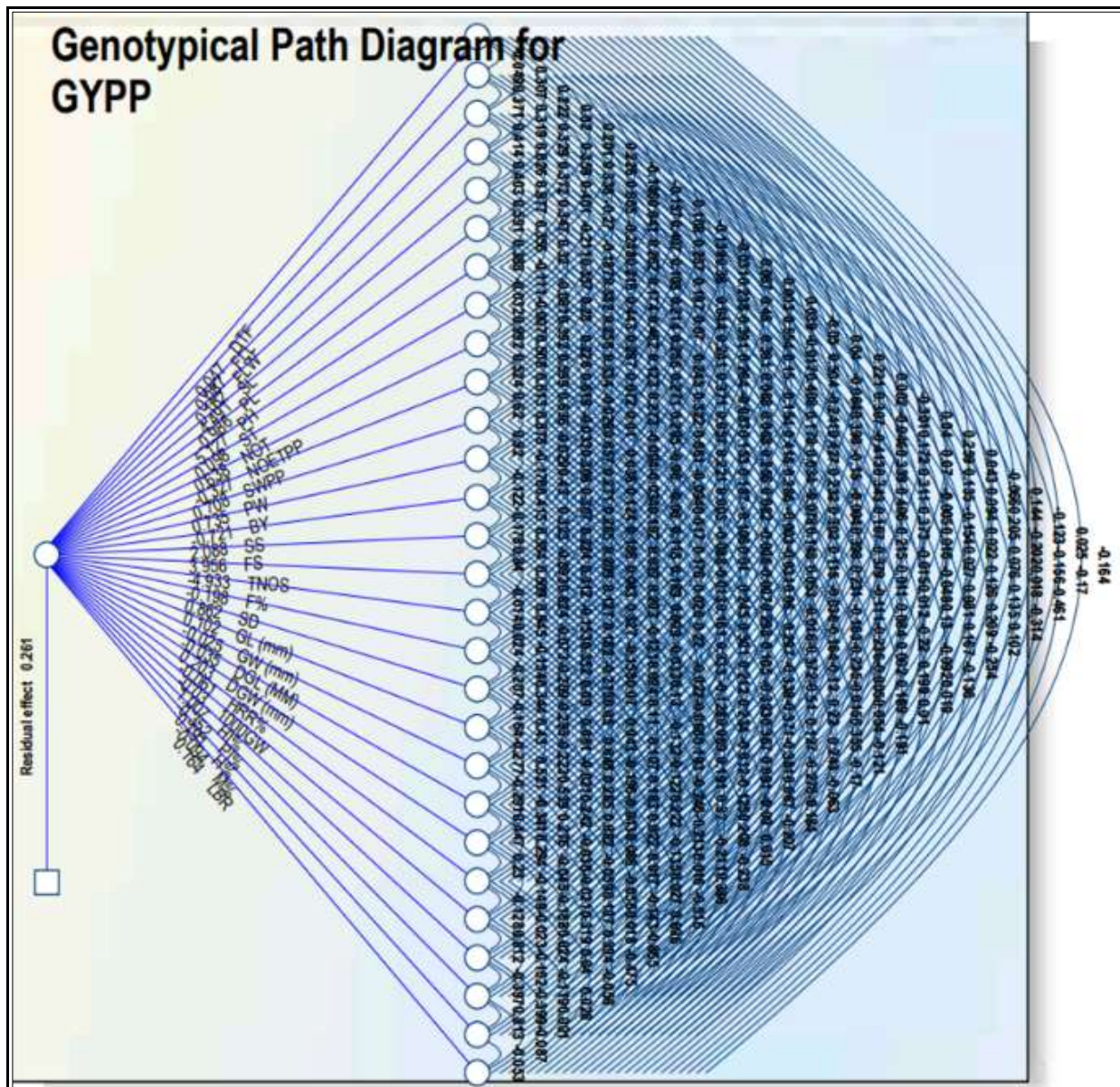
	DTF	FLL	FLW	SL	PL	PH	ST	NOT	NOETPP	SWPP	PW	BY	SS	FS	TNOS
DTF	0.0472	-0.0023	0.0145	0.0105	0.0009	0.0095	0.0107	-0.0069	-0.0074	0.0051	-0.0066	-0.0015	0.0032	0.0001	0.0019
FLL	-0.0042	0.087	0.0323	0.0277	0.0286	0.0312	0.0294	0.0004	0.0035	0.0354	0.0224	0.0313	0.0207	0.0392	0.0482
FLW	0.0496	0.0601	0.1618	0.067	0.0042	0.0601	0.0649	-0.0436	-0.0402	0.0424	0.0175	0.0319	0.0071	0.0632	0.0633
SL	-0.9967	-1.4317	-1.8608	-4.491	-1.8086	-4.3854	-1.5571	0.9489	0.8394	-0.9718	-0.7826	-0.9631	-0.3128	-1.0806	-1.1865
PL	-0.0195	-0.324	-0.0257	-0.397	-0.9858	-0.5821	-0.3514	-0.3157	-0.3515	-0.3769	-0.4371	-0.4551	-0.2527	-0.2416	-0.3661
PH	1.0285	1.8385	1.9059	5.0067	3.0277	5.1272	1.9911	-0.5709	-0.4162	1.4377	1.3211	1.5246	0.6293	1.3878	1.6493
ST	0.0222	0.0332	0.0394	0.0341	0.035	0.0381	0.0982	-0.0032	-0.0007	0.0385	0.0222	0.0328	0.007	0.0268	0.029
NOT	-0.0934	0.0032	-0.1719	-0.1348	0.2042	-0.071	-0.0205	0.6378	0.6327	0.3239	0.3818	0.3949	-0.0166	0.0067	-0.0029
NOETPP	0.0512	-0.0133	0.0812	0.0611	-0.1166	0.0265	0.0024	-0.3243	-0.3269	-0.1713	-0.2005	-0.208	0.0108	-0.0187	-0.0116
SWPP	0.0762	0.288	0.1854	0.1532	0.2706	0.1985	0.2778	0.3594	0.3709	0.7078	0.4385	0.6213	-0.0204	0.2164	0.1918
PW	-0.1022	0.1888	0.0796	0.128	0.3258	0.1893	0.1658	0.4399	0.4506	0.4553	0.7348	0.676	-0.1294	0.3161	0.2254
BY	0.0225	-0.2597	-0.1421	-0.1547	-0.3329	-0.2145	-0.2407	-0.4465	-0.4588	-0.6331	-0.6635	-0.7212	0.0879	-0.2996	-0.2327
SS	0.1403	0.4964	0.092	0.1454	0.5352	0.2563	0.1498	-0.0542	-0.0688	-0.0603	-0.3677	-0.2545	2.088	-0.3726	0.8013
FS	0.0102	1.7812	1.5461	0.9519	0.9698	1.0709	1.0783	0.0415	0.2263	1.2096	1.7021	1.6432	-0.706	3.9563	3.3239
TNOS	-0.1947	-2.7307	-1.929	-1.3033	-1.8318	-1.5868	-1.4568	0.0221	-0.1752	-1.3369	-1.513	-1.5914	-1.8929	-4.1443	-4.9329
F%	0.0098	0.0034	-0.0296	-0.0175	0.0172	-0.0112	-0.012	0.0119	0.0066	-0.0245	-0.0524	-0.0442	0.1765	-0.1006	0.0028
SD%	0.0346	0.4345	0.3517	0.1327	0.0583	0.1318	0.1906	-0.081	-0.0514	0.1655	0.1604	0.1805	0.2694	0.7105	0.8153
GL(mm)	0.0226	-0.0065	-0.0246	0.0182	0.0427	0.0262	0.0191	0.0003	0.0017	0.0121	0.004	0.0085	0.013	-0.0156	-0.0075
GW(mm)	-0.0001	-0.0078	-0.0101	-0.0108	-0.0009	-0.0098	-0.0021	0.0027	0.0022	-0.0045	-0.0048	-0.0052	-0.0083	-0.0046	-0.0089
DGL(mm)	0.0104	0.0016	0.0143	0.0052	-0.0081	0.0027	0.0001	0.0002	-0.0003	0.0004	-0.0009	-0.0003	0.0042	0.0055	0.0074
DGW(MM)	0.0081	0.0349	0.0689	0.0698	-0.0009	0.0615	0.0301	-0.0064	-0.0014	0.0497	0.0327	0.0448	-0.0067	0.0192	0.0143
HRR%	-0.0158	-0.0043	-0.0189	-0.0247	-0.0101	-0.0242	-0.007	-0.0032	-0.0037	-0.0181	-0.0183	-0.0202	0.0013	-0.0079	-0.0067
1000GW	-0.0013	-0.0041	0.0001	-0.0114	-0.0065	-0.0115	-0.007	0.0011	0.0005	-0.009	-0.0032	-0.0065	0.0039	0.002	0.004
HI%	-0.0663	0.0946	-0.1547	0.0164	-0.0154	0.0111	-0.1116	-0.1637	-0.1647	-0.3749	-0.3406	-0.3952	0.2353	0.0692	0.1946
PI%	-0.0507	-0.0721	-0.0077	-0.0094	0.0169	-0.0043	-0.0294	0.0831	0.0828	0.0422	0.1794	0.1306	-0.129	0.0043	-0.0671
H%	-0.0235	-0.0388	0.0145	0.0242	0.0156	0.0249	-0.042	0.0004	-0.001	-0.0029	0.0421	0.0243	-0.073	0.0175	-0.0238
M%	-0.0023	0.0146	-0.0016	-0.0127	-0.0195	-0.0157	0.0086	-0.0186	-0.0177	-0.005	-0.0332	-0.0228	0.026	-0.0063	0.0084
LBR	-0.0269	-0.0279	-0.0757	-0.0515	0.0168	-0.0416	-0.0223	0.0031	0.0016	-0.0314	-0.0199	-0.0278	-0.0103	-0.0302	-0.0341
GYPP	-0.064	0.4367	0.1351	0.2336	0.4327	0.3077	0.2569	0.5147	0.533	0.5049	0.6149	0.6276	0.0254	0.5181	0.5002
PARTIAL R <sup>2</sup>	-0.003	0.038	0.0219	-1.0489	-0.4265	1.5774	0.0252	0.3283	-0.1742	0.3574	0.4518	-0.4526	0.053	2.0497	-2.4675

**Table 5:** Estimation of Genotypic Path coefficient showing direct and indirect effect of various components on seed yield (Continue...)

	F%	SD	GL (mm)	GW (mm)	DGL (MM)	DGW (mm)	HRR%	1000GW	HI%	PI%	H%	M%	LBR
DTF	-0.0023	0.0019	0.0104	0.0001	-0.0142	0.0019	0.0122	0.0021	-0.0031	0.0068	-0.0058	0.0012	-0.0077
FLL	-0.0015	0.0438	-0.0056	0.0267	-0.004	0.0149	0.0061	0.0117	0.0082	0.0178	-0.0176	-0.0136	-0.0148
FLW	0.0243	0.066	-0.0389	0.0644	-0.0668	0.0548	0.0503	-0.0007	-0.0249	0.0036	0.0122	0.0028	-0.0747
SL	-0.3967	-0.6909	-0.8016	-1.9156	0.6718	-1.5415	-1.825	-1.6764	-0.0731	-0.1195	-0.567	-0.6075	1.4103
PL	0.0859	-0.0667	-0.4121	-0.034	-0.2291	0.0043	-0.1647	-0.2116	0.0151	0.0474	-0.0801	-0.2058	-0.1007
PH	0.2908	0.7837	1.3141	1.9793	-0.3976	1.5507	2.0419	1.9425	0.0566	0.0629	0.6666	0.8583	-1.3001
ST	0.006	0.0217	0.0184	0.0081	-0.0003	0.0146	0.0113	0.0227	-0.0109	0.0082	-0.0216	-0.009	-0.0133
NOT	-0.0383	-0.0599	0.002	-0.0679	-0.0035	-0.02	0.0337	-0.023	-0.1037	-0.1507	0.0014	0.1266	0.0119
NOETPP	0.011	0.0195	-0.0055	0.0288	-0.0032	0.0023	-0.0198	0.0052	0.0535	0.0769	0.0018	-0.0618	-0.0033
SWPP	0.0879	0.1358	0.0836	0.1245	-0.009	0.1732	0.2109	0.2104	-0.2636	-0.0848	-0.0105	0.038	-0.1354
PW	0.1948	0.1366	0.0287	0.1386	0.0189	0.1181	0.2211	0.077	-0.2486	-0.3747	0.1616	0.2608	-0.0891
BY	-0.1614	-0.151	-0.0598	-0.1464	-0.0067	-0.1589	-0.2398	-0.1532	0.2831	0.2676	-0.0914	-0.1756	0.1224
SS	-1.8654	0.6523	0.2659	0.6831	-0.252	-0.0691	-0.045	-0.2663	0.4879	0.7659	-0.7961	-0.5798	-0.1313
FS	2.0153	3.2595	-0.6046	0.7219	-0.6239	0.3733	0.514	-0.2603	0.2719	-0.0489	0.3608	0.2655	-0.7283
TNOS	0.071	-4.6635	0.3612	-1.7343	1.0582	-0.3468	-0.5429	0.6514	-0.9535	-0.9401	0.6144	0.4443	1.0233
F%	-0.1975	-0.0048	0.0305	0.0413	-0.0178	-0.01	-0.0085	-0.0211	0.0242	0.0485	-0.0731	-0.041	-0.003
SD	0.0209	0.8624	-0.1783	0.297	-0.2546	0.0526	0.0418	-0.1693	0.1578	0.1911	-0.1834	-0.182	-0.2051
GL (mm)	-0.0158	-0.0211	0.1022	-0.0168	0.0439	-0.0228	-0.0021	0.027	-0.0044	0.0022	-0.0138	0.0016	0.0395
GW (mm)	0.0053	-0.0088	0.0042	-0.0254	0.007	-0.0132	-0.0137	-0.0062	-0.0021	-0.0022	-0.0004	-0.0007	0.0131
DGL (MM)	-0.0031	0.0102	-0.0149	0.0096	-0.0347	0.0101	0.0118	-0.0096	0.0013	0.0021	0.0019	0.005	-0.0241
DGW (mm)	0.0103	0.0124	-0.0452	0.1059	-0.0591	0.2032	0.0908	0.0598	-0.0091	-0.0044	0.0218	0.0036	-0.1759
HRR%	-0.0026	-0.0029	0.0013	-0.0327	0.0207	-0.0271	-0.0607	-0.0139	0.009	0.0114	-0.0194	-0.0239	0.0288
1000GW	-0.0032	0.006	-0.008	-0.0074	-0.0084	-0.009	-0.007	-0.0304	0.0039	0.0007	-0.0007	-0.0012	0.0018
HI%	-0.1232	0.1843	-0.0432	0.0828	-0.0387	-0.0452	-0.1499	-0.1285	1.0069	0.8181	-0.1636	-0.1202	0.028
PI%	0.0864	-0.078	-0.0076	-0.0302	0.0209	0.0075	0.0663	0.008	-0.2858	-0.3518	0.1396	0.1403	-0.0003
H%	0.0708	-0.0407	-0.0259	0.0032	-0.0107	0.0205	0.0611	0.0045	-0.0311	-0.076	0.1914	0.1555	-0.0167
M%	-0.0194	0.0197	-0.0015	-0.0026	0.0134	-0.0017	-0.0368	-0.0038	0.0112	0.0373	-0.076	-0.0935	0.0049
LBR	0.0025	-0.039	0.0634	-0.0848	0.1142	-0.142	-0.0779	-0.0095	0.0046	0.0001	-0.0144	-0.0086	0.1642
GYPP	0.1526	0.3884	0.0332	0.2173	-0.065	0.1947	0.1797	0.0386	0.3812	0.2156	0.0387	0.1792	-0.1759
Partial R <sup>2</sup>	-0.0301	0.335	0.0034	-0.0055	0.0023	0.0396	-0.0109	-0.0012	0.3839	-0.0759	0.0074	-0.0168	-0.0289

**Table 6:** Distribution of rice hybrid in different clusters

Cluster No.	No. of genotype	Genotypes
1	83	IR 64, Kranti × WGL 32100, IR 64 × Pusa tarangini, NPT 10-24 × WGL 32100, 97 x NPT 29,56Ax NPT 13-01, 3A X MTU 1081 × NPT 13-01,3A X MTU 1081 × PS-4, 3A X JNPT 514-22, 3A X AVT 1 IME 3535, 3A X AVT-1 IME-3536, 3A X IVT- 1 IME-3664, 3A X Pusa tarangini, 97A x NPT 65, 3A X MTU 1010 × 25B × NPT 101, 3A X JNPT 23-1, R-671 × WGL 32183, NPT 10-24 × WGL 32183, Kranti ×WGL 32183, 31A X JNPT 1059-10, 25A X JNPT 1059-925A X Sonam, 32A X MTU 1081 × NPT 111, 32A X JNPT 1059-10, 32A X AVT-1 IME-3531, Sonam, Pusa Tarangini , Swarnyapriya, R 712, R 671, NPT-29, NPT 13-01, NPT-25, NPT 65, NPT 10-24, NPT 10-65, JNPT 1058, JNPT 23-01, JNPT 514-22, JNPT 1059-9, JNPT 1059-10, MTU 11320, P 3123, MC -13, RTCNP -28, WGL 32100, MTU 1081 X NPT 111, MTU 1010 ×25B × NPT 101, AVT- 1 IME- 3531, AVT -1 IME- 3535, AVT -1 IME- 3536, IVT IME-3624, JR 206, 3B, 99B, 22B, 25B, 31B, 56B, WGL 32183, WGL 14, MTU 1010×PS-5, MTU 1081 X PS-4, MTU 1081 X NPT 13-01, 56A X NPT 23, 56A XJNPT 1058, 56A X WGL- 14, 56A X RTCNP-28, 97A X JR 206, 97A X P 3123, 99A X NPT- 25, 99A X JNPT- 1058, 99A X MTU 1010×PS-5, 99A X MTU 11320, 99A X MC-13, Kranti, IR 64, 22A X Pusa tarangini, 22A X Swarnyapriya, 29A X R 712, 29 A X P 3123, 31A X MTU 1081 × PS-4, JRH 19
2	9	Kranti × JNPT 1058, Kranti × WGL -14, Kranti × NPT 26-1, Shyamla x IR 64, 32A X MTU 1081 × NPT 13-01, NPT 23, NPT 26-1, JNPT-58, NPT 14-7
3	1	32B
4	1	Shyamla
5	6	NPT 10-24 × R 712, NPT 10-65 × JNPT 58, 3A X NPT 13-01, 3A X Swarnyapriya, 29B, 97B
6	2	R 671 × NPT 29, 31A X MTU 1081 × NPT 111
7	2	25A X NPT 26-1, 25A X NPT 14-7



**Fig 1:** Genotypical Path Diagram for Grain yield per plant

**Table 7:** Intra and Inter cluster D<sup>2</sup>-value

Intra Clusters Distance	D <sup>2</sup> value	Inter Clusters Distance	D <sup>2</sup> value
VII	9597.17	III & VI	61668.56
V	7516.79	IV & VII	61668.56
II	7019.05	V & VI	61562.77
VI	5563.38	VI & VII	44685.27
I	4970.09	II & V	39006.85

**Table 8:** Cluster means value of different character

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
DTF	101.47	106.63	98	108.67	101.28	99.83	103.17
FLL	33.31	39.98	35.03	30.62	32.49	38.56	43.43
FLW	1.38	1.61	0.99	1.03	1.29	1.53	1.5
SL	73.48	82.33	70.1	62.27	76.5	77.88	82.63
PL	24.78	26.06	23.75	23.33	24.06	27.47	29.51
PH	98.26	108.39	93.85	85.6	100.56	105.35	112.13
ST	6.21	9.11	3.71	3.74	3.44	9.18	7.31
NOT	9.58	8.97	9.67	9	9.37	12.91	7
NOETPP	9.22	8.75	9	8	8.74	12.48	6.67
SWPP	26.27	42.56	20.93	14.65	30.48	70.16	22.29
PW	32.15	33.74	21.03	18.4	27.24	90.21	16
BY	58.41	76.29	41.97	33.05	57.72	160.36	38.29
SS	36.36	51.44	56.33	55.67	67.11	28	256.17
FS	214.13	270.04	124.67	122	174.83	264	143.83
TNOS	250.49	321.48	181	177.67	241.94	292	400
F%	84.96	84.54	68.88	68.67	73.16	91.07	34.58
SD	10.11	12.73	7.62	7.62	9.96	10.64	13.53
GL (mm)	8.88	9.35	10	10	8.58	10.08	10.17
GW (mm)	2.61	2.72	2.39	2.49	2.79	2.91	3.16
DGL (mm)	6.35	6.48	6.71	7	6.41	6.98	6.42
DGW (mm)	2.1	2.2	2	1.57	2.1	2.31	2.02
HRR%	62.56	65.35	58.75	72.07	61.75	72.93	59.46
1000GW	20.73	24.98	23.5	24.08	21.53	27.11	20.79
HI%	39.97	39.62	33.72	52.84	42.79	19.4	65.59
PI%	75.06	98.09	67.27	94.92	89.96	34.1	158.59
H%	78.81	74.93	80.43	73	79.86	80.05	70.26
M%	75.48	72.85	77.52	74.59	74.61	79.53	67.66
LBR	3.09	3	3.36	4.48	3.18	3.06	3.18
GYPP	23.14	28.9	14.15	17.46	22.27	31.07	25.76

On the basis of PCA findings, among all genotypes contributing their presence in more than one PC with high PC score twenty five crosses viz., R 671 × NPT 29, Kranti × JNPT 1058, Kranti × WGL -14, 29A × P3123, Shyamla × IR 64 while, Kranti × WGL 32100 and IR 64 × Pusa tarangini, Kranti × NPT 26-1, NPT 10-24 × WGL 32183, NPT 10-24 × R 712, 3A × NPT 13-01, 97A × NPT 65, 3A × NPT 13-01, 31A × MTU1081 × NPT 111, 31A × MTU 1081 × PS-4, 32A × AVT-1 IME 3531, 56A × JNPT 1058, 3A × AVT-1 IME-3536, 56A × WGL-14 and 97A × JR206, 25A × JNPT 1059-9, 32A × MTU 1081 × NPT 111, 99A × JNPT 1058, 99A × MC-13, 3A × IVT-1 IME-3624. Confine with desirable yield as well as quality associated PCs, and had high score for yield as well as quality traits. These lines

might be utilized in hybridization programme for the transfer of good yield as well as good quality traits in the recipient rice lines for the development of promising rice cultivars. On the basis of their nutrient concentrations (Zn & Fe) some genotypes found to be best for cooking quality 25A × NPT 26-1, 25A × NPT 14-7, 29A × R 712, 31A × MTU 1081 × PS-4, IR 64 × Pusa tarangini, Shyamla × IR 64, Kranti × JNPT 1058, 3A × MTU 1081 × NPT 13-01, 3A × NPT 13-01, R-671 × WGL 32183 and NPT 10-24 × WGL 32100. The findings with Eigen value more than 1 were found in first four components by Kumari *et al.* (2019) [21]; first five components by Rahangdale *et al.* (2021) [1], Singh *et al.* (2020) [5], Gour *et al.* (2017) [22]; first six components by Tiruneh *et al.* (2019) [4].

**Table 9:** Summary of principal component analysis

PC	Eigen values	Variability %	Cumulative %
PC1	6.478	22.340	22.340
PC2	4.296	14.815	37.155
PC3	3.338	11.512	48.667
PC4	2.816	9.710	58.377
PC5	2.278	7.855	66.231



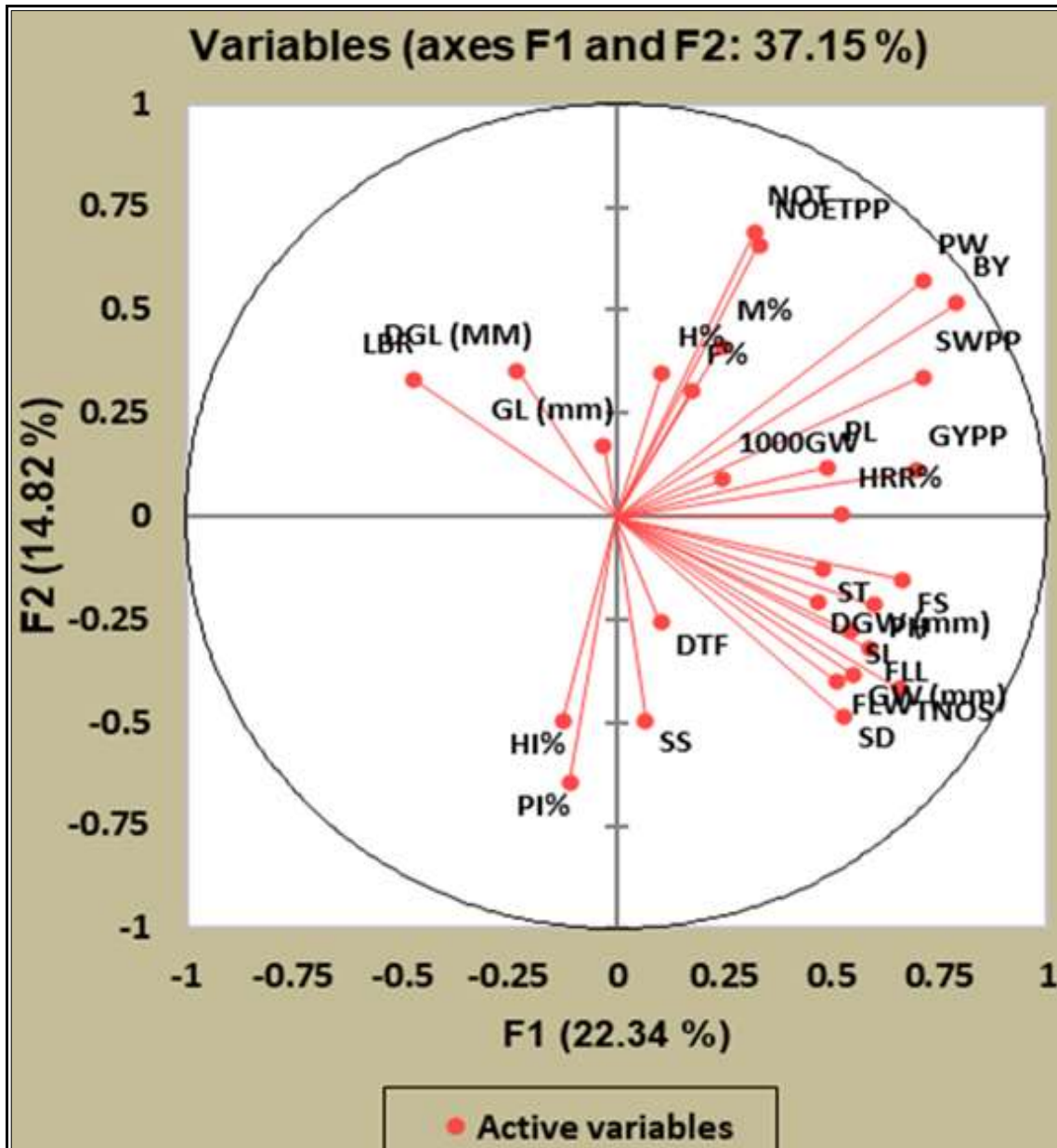


Fig 2: PC Biplot

**Acknowledgment**

I express my sincere gratitude to Department of Plant Breeding and Genetics, JNKVV, Jabalpur for facilitate me to carried all the experimentation.

**References**

1. Rahangdale S, Singh Y, Upadhyay PK, Koutu GK. Principal component analysis of JNPT lines of rice for the important traits responsible for yield and quality. *Indian Journal of Genetics and Plant Breeding*. 2021;81(01):127-131.
2. Rahangdale S, Singh Y, Koutu GK, Tiwari S. Genetic Variability, Correlation and Path Coefficient Studied for Yield and Quality Traits in JNPT Lines of Rice (*Oryza sativa* L.). *Int. J. Curr. Microbiol. App. Sci*. 2019a;8(10):1025-1037.
3. Rahangdale S, Singh Y. Genetic diversity analysis in JNPT lines of rice (*Oryza sativa* L.). *IJCS*. 2019b;7(6):2267-2271.
4. Tiruneh A, Gebrselassie W, Tesfaye A. Genetic diversity study on upland rice (*Oryza sativa* L.) genotypes based on morphological traits in southwestern Ethiopia. *Asian Journal of Crop Science*. 2019;11:17-24.
5. Singh SK, Habde SV, Khaire A, Mounika K, Majhi PK, Singh DK. Principal component analysis in f2 mapping population for high grain zinc content in rice (*Oryza sativa* L.). *Plant Archives*. 2020;20(2):6935-6941.
6. Samal P, Pote TD, Krishnan SG, Singh AK, Salgotra RK, Rathour R. Integrating marker-assisted selection and doubled haploidy for rapid introgression of semi-dwarfing and blast resistance genes into a Basmati rice variety ‘Ranbir Basmati’. *Euphytica*. 2014;215:1-13.
7. Bharath HA, Chandan MC, Vinay S, Ramachandra TV. Modelling urban dynamics in rapidly urbanising Indian cities. *The Egyptian Journal of Remote Sensing and Space Science*. 2018;21(3):201-210.
8. Pragma K, Krishna KVR, Rao LVS, Suneetha K. Studies on morphological characterization in soft rice (*Oryza sativa* L.) genotypes. *International Journal of Current Microbiology and Applied Sciences*. 2018;7(5):1348-1374.
9. Kujur N, Bhandarker S, Shrivastava Y, Tirkey A. Assessment of Variability of Aromatic Rice Using



- Agro-Morphological Characterization. Int. Journal Curr. Microbiol. App. Sci. 2017;6(11):1835-1846.
10. Nath S, Kole PC. Genetic variability and yield analysis in rice. Electronic Journal of Plant Breeding. 2021;12(1):253-258.
  11. Nagaraju D, Sao A, Sarawgi AK, Singh P. Genetic divergence studies in some indigenous scented rice (*Oryza sativa* L.) accessions of Central India. Asian J Pl Sci. 2013;5(2):197–200.
  12. Tomar JB, Dabas BS, Gautam PL. Genetic variability, correlation coefficient and path analysis for quantitative characters under rainfed ecosystem in the native land races of rice. J Plant Genet Resour. 2000;13(3):229–246.
  13. Sabu KK, Abdullah MZ, Lim LS, Wickneswari R. Analysis of heritability and genetic variability of agronomically important traits in *Oryza sativa* x *O. rufipogon* cross. Agron Res. 2009;7(1):97-102.
  14. Pratap A, Bisen P, Loitongbam B, Singh PK. Assessment of Genetic Variability for Yield and Yield Components in Rice (*Oryza sativa* L.) Germplasms. Int J Bio-resource Stress Manage. 2018;9(1):87-92.
  15. Chandra BS, Devi KR, Lingaiah N, Hari Y, Venkanna V. Analysis of variability, correlation and path coefficient studies for yield and quality traits in rice (*Oryza sativa* L.). Agric Sci Digest. 2017;37(1):1-9.
  16. Kumari N, Parmar M. Correlation and path coefficient analysis for grain yield and yield components in rice (*Oryza sativa* L.) under aerobic condition. Int J Chem Stud. 2020;(8):927-930.
  17. Bhushan B, Kumar B, Sudan SK, Singh P, Razdan AK. Nature and magnitude of genetic diversity among locally adapted rice (*Oryza sativa* L.) genotypes. J Pharmacogn Phytochem. 2019;8(3):2526-2530.
  18. Kushwaha N, Kant R, Kumar R, Nilanjaya, Chhaya R, Sinha N, *et al.* Study of genetic divergence in lowland rice genotypes of Bihar. Int J Curr Microbiol Appl Sci. 2020;9(2):88-94.
  19. Archana RS, Rani MS, Vardhan KMV, Fareeda G. Genetic diversity studies among rice (*Oryza sativa* L.) genotypes for grain yield, yield components and nutritional traits in rice. Int J Chem Stud. 2018;6(6):134-137.
  20. Tiwari DN, Tripathi SR, Tripathi MP, Khatri N, Bastola BR. Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. Adv Agric; c2019. p. 1-9.
  21. Kumari B, Mallick MA, Solanki MK, Solanki AC, Hora A, Guo W. Plant growth promoting rhizobacteria (PGPR): modern prospects for sustainable agriculture. Plant Health Under Biotic Stress: Microbial Interactions. 2019;2:109-27.
  22. Gour G. Quantum resource theories in the single-shot regime. Physical Review A. 2017 Jun 8;95(6):062314.