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Assessment of Yield and Quality Traits in Rice (*Oryza sativa* L.) Restorer Lines through Genetic Diversity and Principal Component Analysis

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ABSTRACT

The experiment was conducted during *kharif* (July to November, 2020) at Seed Breeding Farm, Rice Improvement Project, Department of Plant Breeding & Genetics, College of Agriculture, JNKVV, Jabalpur, Madhya Pradesh, India to study genetic diversity and principal component analysis (PCA) in 80 fertility restorer lines of rice. Using the Tocher method, the genotypes were divided into 13 clusters, with Cluster I being the largest, comprising 64 genotypes. Cluster V included five genotypes, while the other clusters each contained only one genotype. The D^2 statistics revealed that Cluster V, which comprised the genotypes Laxmi-144, CANP-318, ANP-526, JNPT-782, and JNPT-767, exhibited the highest intra-cluster distance. Maximum inter-cluster distance was found between Clusters IX and XIII, followed by Clusters IV and XIII. Cluster mean values suggest that genotypes R-710 and 1E-TP-2 contribute major yield and quality traits, while genotype AD02207 contribute to improve yield-attributing traits. PCA identified eight principal components with Eigenvalue exceeding 1.00, captured 77.4% of total variability. These PCs contributed the traits having high value in terms of yield and quality. The rotated component matrix revealed that the PC1 accounted for the highest variability. Genotypes JNPT-782, AD02207, NP-9165 and ANP-526 reported elevated scores in these PCs hence will lead to superior cross combinations in terms of both yield and quality. Biplot analysis was also performed for trait-based genotype selection.

KEYWORDS: Rice, PCA, fertility restorer lines, eigenvalues

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Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

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1. INTRODUCTION

Rice is a primary food source that feeds the majority of the global population (Parida et al., 2022; Chaudhary et al., 2023). Rice is predominantly consumed in Asia, which accounts for 90% of its global consumption (Futakuchi et al., 2021, Anonymous, 2024) and it will likely continue to be a staple in Asian diets for the foreseeable future (Mohidem et al., 2022). Rice is a strategic global commodity essential for food security, economic growth, employment and social stability (Bin Rahman et al., 2023; Bray, 2023). Cultivated rice (*Oryza sativa* L.) is a self-pollinated, annual, diploid monocot belonging to the family *Poaceae* (*Graminae*) and having genome size of 430 Mb with chromosome number 2n=2x=24. Starchy endosperm is the highest composition in rice caryopsis (Shakri et al., 2021). In 2022–23, global rice production was 514 mt, and India contributed 135.75 million tons (Anonymous, 2023). To achieve national rice self-sufficiency, rice production must increase by approximately 1.1% annually over the next four decades (Nayak et al., 2022).

However, low-yielding cultivars alone cannot meet increasing demand; hence, hybrid production and cultivation need to be promoted to fill the yield gap by uplifting the production potential (Rout et al., 2020). Hybrid rice leads to an average yield advantage of 20% over inbred rice varieties (Liao et al., 2021; Abebrese et al., 2018). The three line system or cytoplasmic genetic male sterility system is an effective method of hybrid seed production in rice (ElShamey et al., 2022; Ashraf et al., 2024) based on three different lines namely A (CMS line), B (maintainer line), and R (restorer line) (Toriyama et al., 2019; Azad et al., 2022).

The primary objective in identifying and breeding new parental lines of rice is to determine genotypes with high yield and fertility restoration ability (Awad-Allah et al., 2022). Fertility restorer lines are essential for enhancing productivity by exploiting genetic variability (Prakash et al., 2024), and selecting suitable restorer lines is a major challenge in hybrid breeding to achieve the desired heterotic combinations. However, this limitation can be resolved by grouping these lines into different clusters or heterotic groups based on their divergence level, using different diversity analysis methods such as Mahalanobis D^2 statistics (Bhattarai et al., 2019). Moreover, crossing diverse parents from different clusters results in the most promising hybrids through the complementary interaction of diverse parental genes (Ovung et al., 2012). Therefore, hybrids with tremendous yield potential may be created by carefully selecting restorer lines based on their genetic diversity. The Mahalanobis D^2 statistics is a widely used tool for measuring genetic diversity within a population and identifying superior, diverse parets (Bhargavi et al., 2023) and it is useful for assessing genetic divergence at the genotypic level (Shanmugam et al., 2023). It also indicates the total genetic divergence among genotypes by providing estimates of the distances between clusters and within clusters.

Principal Component Analysis (PCA) proved to be a valuable multivariate statistical tool for revealing patterns in datasets and minimizing redundancy (Beena et al., 2021; Maji and Shaibu, 2012). It identifies the key components based on their contribution to the overall variability in a dataset. PC1 explains the most variation, followed by PC2, which explains the second most, and so on (Gupta and Khandelwal, 2022; Thakur et al., 2023). Principal components are generally derived from either the correlation matrix or the covariance matrix (Christina et al., 2021).

In light of the considerations above, current study has been planned to determine genetic diversity and principal component analysis (PCA) using 80 fertility restorer rice lines.

2. MATERIALS AND METHODS

The study was conducted during *kharif* (July–November, 2020) at Seed Breeding Farm, Rice Improvement Project, Department of Plant Breeding & Genetics, College of Agriculture, JNKVV, Jabalpur, Madhya Pradesh, India. The experiment included 80 rice genotypes (Table 1) in a Randomized Complete Block Design replicated thrice. Jabalpur is situated at 411.78 meter above the mean sea level at 23.900 N latitude and 79.580 E longitude. Each genotype was planted with one seedling hill^{-1} in three rows of five meters following spacing of 15×20 cm. Five plants were chosen at random from each replication. Observations were recorded on 29 yield and quality traits, i.e., Days to panicle initiation (DTPI), Days to maturity (DM), Number of tillers plant^{-1} (NOT), Number of effective tillers plant^{-1} (NOET), Plant height (PH), Stem length (SL), Stem thickness (ST), Flag leaf length (FLL), Flag leaf width (FLW), Panicle length (PL), Panicle weight (PW), Total spikelets panicle^{-1} (TSPP), Fertile spikelets panicle^{-1} (FSPP), Sterile spikelets panicle^{-1} (SSPP), Spikelet fertility % (SF%), Spikelet density (SD%), Thousand seed weight (1000 SW), Grain length (GL), Grain breadth (GB), Decorticated grain length (DGL), Decorticated grain breadth (DGB), Decorticated grain Length Breadth^{-1} ratio (DGL/B), Hulling % (H%), Milling % (M%), Head rice recovery (HRR), Biological yield (BY), Panicle index (PI), Harvest index (HI), Grain yield plant^{-1} (GYPP). The mean values of randomly selected plants from all the replications were used to compile the experimental data. Statistical analysis was carried out using the software IndoStat for cluster analysis and RStudio for PCA. The data were analysed in conformity

Table 1: List of 80 rice restorer lines used in the study programme

Sl. No.	Genotype	Sl. No.	Genotype	Sl. No.	Genotype
1.	Mahamaya	28.	Laxmi-144	55.	JNPT-81
2.	R-548	29.	IR09N26	56.	JNPT-782
3.	R-650	30.	IR-79854-38-2-4	57.	NPT14-12
4.	R-704	31.	IR-79854-48-2-1	58.	JNPT767
5.	Abhya	32.	AD02207	59.	JR-81
6.	R-321	33.	PAU-3832-79-4-3-1	60.	NPT-3803
7.	R-296	34.	RP5219-9-6-7-3-2-1-1	61.	NPT-3804
8.	R-712	35.	MTU1153	62.	NPT-3805
9.	R-710	36.	UPR2628-9-1-1	63.	NPT-3806
10.	R-304	37.	MTU11320-41-2-1	64.	NPT-3810
11.	JR-503	38.	P-3123	65.	NPT-3817
12.	Sugandha-3	39.	MC-13	66.	NPT-3820
13.	NPT-10	40.	TRC2013-2	67.	NPT-3821
14.	NPT-13-01	41.	VNR-212	68.	E-TP-1001
15.	NPT-15	42.	CR3424-2-2-5	69.	E-TP-1008
16.	NPT-29	43.	HRI-183	70.	E-TP-1014
17.	NPT-35-01	44.	NP-9165	71.	E-TP-1018
18.	NPT-37	45.	CR3703-11-1	72.	E-TP-1019
19.	NPT-65	46.	RP5911-52-13-3-2-2-1	73.	E-TP-1021
20.	NPT-70	47.	CR2829-PLN-32	74.	E-TP-1023
21.	NPT(S) 81	48.	CANP-318	75.	E-TP-1054
22.	JNPT809	49.	ANP-526	76.	E-TP-1062
23.	NP-72	50.	ANP-553	77.	E-TP-1064
24.	NP-1024	51.	Johar	78.	IME-1101
25.	NP-8421	52.	PR35766-B-24-3-18	79.	E-TP-1124
26.	PSP-456	53.	IR838614-678-8	80.	1E-TP-2
27.	Gemini	54.	HRT-181		

with the multivariate analysis of genetic divergence using D^2 statistics by Mahalanobis (1928). The average inter- and intra-cluster D^2 mean values were estimated according to the procedure given by Singh and Chaudhary (1977), and the genotype grouping was done following Tocher method. The PCA analysis was conducted following the procedures outlined by Massay (1965) and Jolliffe (1986).

3. RESULTS AND DISCUSSION

3.1. Genetic diversity analysis

Analysis of variance revealed significant variation among the genotypes for all studied traits. (Table 2). Almost all the variables except days to maturity, number of tillers, number of effective tillers, plant height, stem thickness, panicle length, decorticated grain L/B ratio, and grain yield plant^{-1} contributed to genetic divergence. The characters that contributed the most to the genetic divergence listed in Table 3. Palaniyappan et al. (2020), also reported similar findings for traits such as the number of spikelets panicle, fertile spikelets panicle^{-1} and grain length. Many researchers, such as Vennela et al. (2017) and Rahangdale et al. (2022) have utilized Mahalanobis D^2 statistic for multivariate analysis and highlighted its effectiveness in examining genetic divergence in rice genotypes.

The 80 rice genotypes were divided into 13 clusters using the tocher method (Figure 1). Cluster I was the largest among all the clusters, consisting of 64 genotypes. Cluster V contained five genotypes. The remaining clusters, including Clusters

Table 2: ANOVA for yield and quality attributing traits in fertility restorer lines

Source of variation	d.f.	Mean sum of squares									
		DTPI	DTM	NOT	NOET	PH (cm)	SL (cm)	ST (mm)	FLL (cm)	FLW (cm)	PL (cm)
Replication	2	1.21	26.22	0.02	0.34	5104.55	4.37	1.09	6.30	0.00	0.14
Genotype	79	111.03**	128.14**	6.56**	5.74**	5375.57**	334.38**	2.74**	170.32**	0.23**	12.97**
Error	159	0.36	21.25	0.42	0.38	4863.62	3.39	0.16	2.14	0.01	1.09
Source of variation	d.f.	Mean sum of squares									
		PW	TSPP	FSPP	SSPP	SF (%)	SD	1000 SW (g)	GL (mm)	GB (mm)	DGL (mm)
Replication	2	0.16	19.06	32.60	5.41	0.73	0.04	0.16	0.04	0.00	0.01
Genotype	79**	78.32**	14104.72**	10382.48**	519.71**	47.29**	24.05**	57.46**	3.78**	0.45**	3.97**
Error	159	0.41	105.94	78.92	5.68	0.79	0.27	0.37	0.09	0.02	0.04
Source of variation	d.f.	Mean sum of squares									
		DGB (mm)	DG L/B	H (%)	M (%)	HRR (%)	BYPP (g)	PI (%)	HI (%)	GYPP (g)	
Replication	2	0.003	0.002	3.110	6.920	3.881	0.091	36.962	0.001	2.397	
Genotype	79	0.270**	0.972**	43.960**	74.408**	77.748**	251.316**	194.072**	0.018**	69.728**	
Error	159	0.011	0.031	1.358	1.322	1.277	2.691	14.550	0.001	1.419	

*Significant at (*p*=0.05) level; ** Significant at (*p*=0.01) level; DTPI: Days to panicle initiation; DTM: days to maturity; NOT: Number of tillers plant^{-1}; NOET: Number of effective tillers plant: 1; PH: Plant height; SL: stem length; ST: Stem thickness; FLL: Flag leaf length; FLW: Flag leaf width; PL: Panicle length; PW: Panicle weight; TSPP: Total spikelet panicle^{-1}; FSPP: fertile spikelets panicle^{-1}; SSPP: Sterile spikelet panicle^{-1}; SF%: Spikelet fertility%; SD: Spikelet density; 1000 SW: Thousand seed weight; GL: Grain length; GB: Grain Breadth; DGL: Decorticated grain length; DGB: Decorticated grain breadth; DG L/B ratio: Decorticated length/breadth; H%: Hulling %; M%: Milling %; HRR: Head rice recovery; BYPP: Biological yield plant^{-1}; PI: Panicle index; HI: Harvest index; GYPP: Grain yield plant^{-1}

Table 3: Contribution of different characters towards genetic divergence

S1. No.	Character	Times ranked 1st	PCTTD
1.	Sterile spikelets panicle^{-1}	817	25.85%
2.	Total spikelets panicle^{-1}	553	17.50%
3.	Days to panicle initiation	468	14.81%
4.	Panicle weight(g)	256	8.10%
5.	Milling %	252	7.97%
6.	1000 seed weight (g)	216	6.84%
7.	Biological yield plant^{-1} (g)	116	3.67%
8.	Fertile spikelets panicle^{-1}	104	3.29%
9.	Stem length (cm)	86	2.72%
10.	Decorticated grain length (mm)	74	2.34%
11.	Head rice recovery (%)	74	2.34%
12.	Spikelet fertility (%)	56	1.77%
13.	Flag leaf length (cm)	33	1.04%

PCTTD: Percentage (%) contribution of traits towards divergence

II, III, IV, VI, VII, VIII, IX, X, XI, XII and XIII, consisted of a single genotype (Table 4). These results followed the findings of Ashok et al. (2016) and Palaniyappan et al. (2020) for the largest cluster and clusters containing a single genotype. Several mono-genotypic clusters (having a single genotype) may have developed due to geographic restrictions on gene mobility or severe natural and human selection for diverse and adaptive gene complexes.

Cluster V, which included the genotypes Laxmi-144, CANP-318, ANP-526, JNPT-782, and JNPT767, had the greatest intra-cluster distance, indicating the presence of a more significant amount of genetic variation (Figure 2, Table 5). Ashok et al. (2016) also concluded that the cluster with the highest intra-cluster distance exhibits significant heterogeneity.

Clusters IX and XIII had the highest inter-cluster distance, followed by clusters IV and XIII (Figure 2, Table 5). Palaniyappan et al. (2020) and Thomas and Lal (2012) recommended selecting genotypes from diverse clusters with greater inter-cluster distances to maximize heterosis. In this way, hybridization among genotypes like 1E-TP-2 (cluster

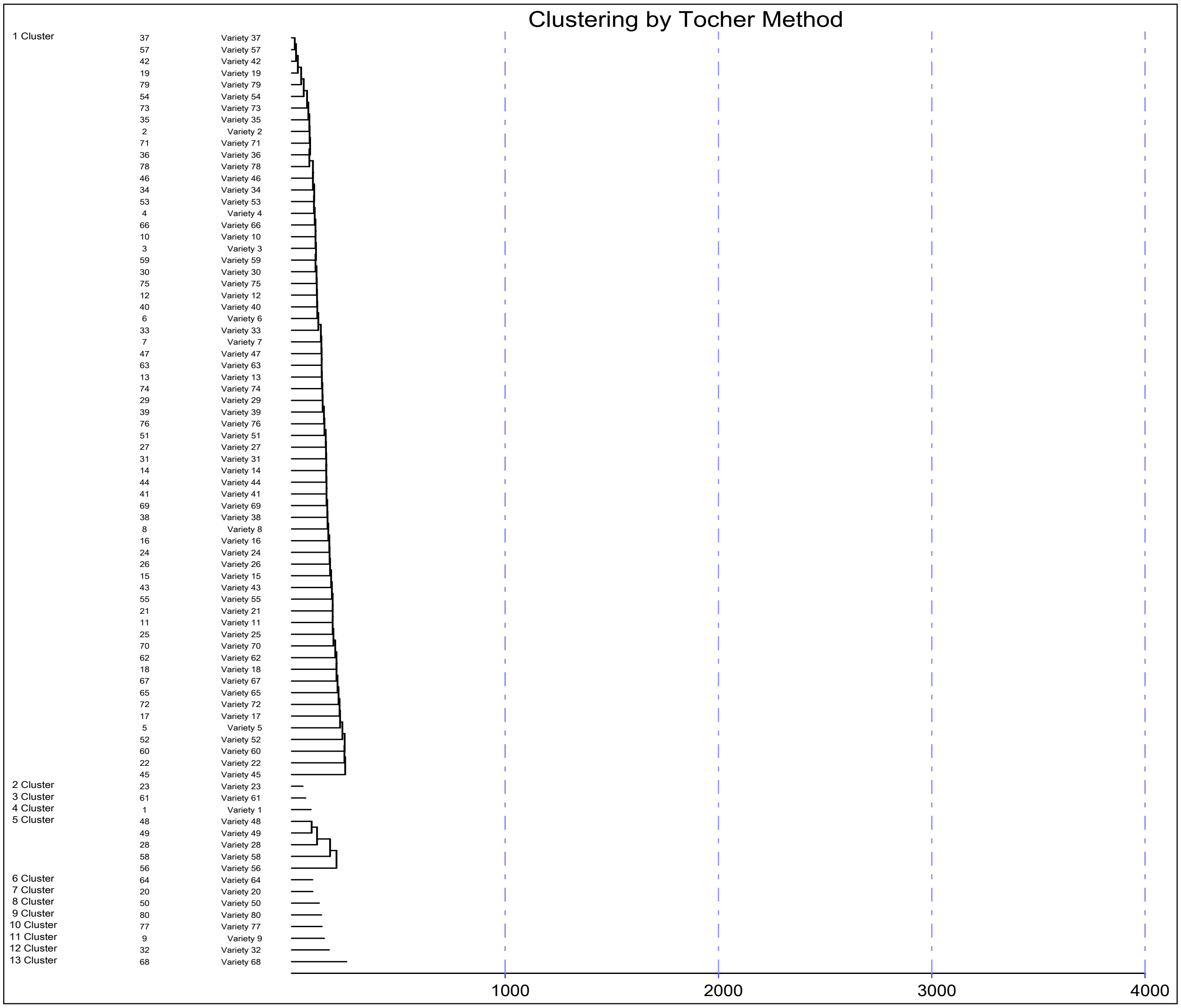

Figure 1: Clustering of genotypes by tocher method

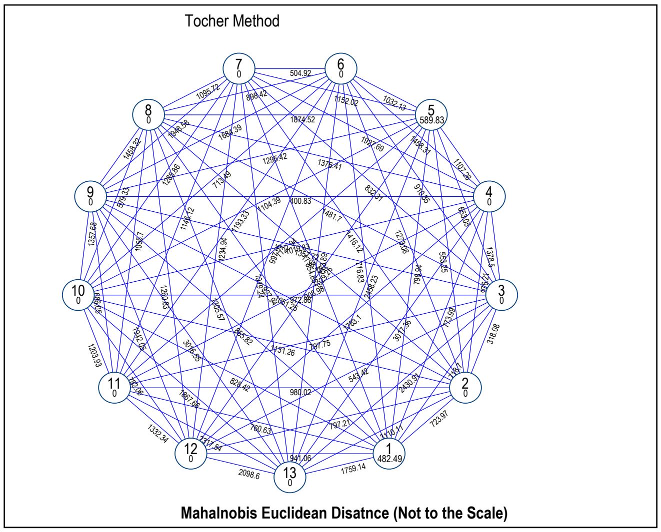

Figure 2: Illustration of Mahalanobis Euclidean Distance

XIII) with E-TP-1001 (cluster IX) and Mahamaya (cluster IV) with 1E-TP-2 (cluster XIII) would produce desirable hybrids or segregants with the accumulation of desirable genes. Cluster VI and XIII had the smallest inter-cluster distance, followed by clusters XII and I. The genotypes in these clusters should be avoided in hybridization programmes to maintain a broad genetic base. Alternatively, they can be mated to isolate superior parental lines with better allelic blends.

The cluster mean values for all the characters (Table 6) used in the study suggested a wide range of variability. Cluster IX and cluster XI recorded the highest cluster mean values for grain length, decorticated grain length, and decorticated grain breadth. Additionally, cluster IX recorded the highest mean values for panicle length and grain yield plant^{-1}, while cluster XI recorded the highest mean values for 1000 seed weight and hulling %. This indicates that genotype 1E-TP-

2 (cluster IX) and R-710 (cluster XI) can be employed to enhance yield and quality-related attributes.

Cluster XII recorded the highest mean value for days to panicle initiation, days to maturity, number of tillers, number of effective tillers, and panicle index, showing that genotype AD02207 can be used to develop potential early maturing cultivars. The highest mean values for total spikelets panicle^{-1}, fertile spikelets panicle^{-1}, decorticated grain LB

Table 4: Distribution of fertility restorer lines in different clusters

Cluster No.	No. of genotype	Genotypes
1	64	R-548, R-650, R-704, Abhya, R-321, R-296, R-712, R-304, R-304, JR-503, Sugandha-3, NPT-10, NPT-13-01, NPT-15, NPT-29, NPT-35-01, NPT-37, NPT(S) 81, JNPT809, NP-1024, NP-8421, PSP-456, IR09N26, IR-79854-48-2-1, RP5219-9-6-7-3-2-1-1, MTU1153, UPR2628-9-1-1, MTU11320-41-2-1, P-3123, TRC2013-2, VNR-212, HRI-183, NP-9165, CR3703-11-1, RP5911-52-13-3-2-2-1, CR3424-2-2-5, NPT-65, E-TP-1054, PAU-3832-79-4-3-1, NPT-3806, MC-13, CR2829-PLN-32, Johar, PR35766-B-24-3-18, IR838614-678-8, HRT-181, JNPT-81, NPT14-12, JR-81, NPT-3803, NPT-3804, NPT-3805, NPT-3817, NPT-3820, NPT-3821, E-TP-1008, E-TP-1014, E-TP-1018, E-TP-1019, E-TP-1021, E-TP-1023, E-TP-1062, IME-1101, E-TP-1124,
2	1	NP-72
3	1	NPT-3804
4	1	Mahamaya
5	5	Laxmi-144, CANP-318, ANP-526, JNPT-782, JNPT767
6	1	NPT-3810
7	1	NPT-70
8	1	ANP-553
9	1	1E-TP-2
10	1	E-TP-1064
11	1	R-710
12	1	AD02207
13	1	E-TP-1001

Table 5: Average Inter and Intra cluster D^2 value for fertility restorer lines

	I	II	III	IV	V	VI	VII
I	482.49	723.97	718.7	773.99	798.94	716.83	854.85
II		0	318.08	976.21	553.25	1273.08	1416.12
III			0	1378.5	653.05	910.35	832.31
IV				0	1107.26	1458.31	1927.69
V					589.83	1032.13	1152.02
VI						0	504.92
VII							0
VIII							
IX							
X							
XI							
XII							
XIII							

Table 5: Continue...

	VIII	IX	X	XI	XII	XIII
I	927.94	855.82	828.42	760.63	941.06	1759.14
II	1798.45	1051.25	1131.26	980.02	797.21	3110.11
III	1481.7	1357.72	972.88	797.75	543.42	2430.91
IV	1376.41	400.83	1019.83	908.98	1783.1	3017.36
V	1874.52	1295.42	1104.39	1122.94	1029.26	2458.23
VI	898.42	1684.39	713.49	1193.33	997.65	683.89
VII	1095.72	1948.58	1285.86	1146.12	1234.94	1019.24
VIII	0	1458.32	579.33	1055.7	1260.83	1305.57
IX		0	1357.68	686.05	1942.05	3016.55
X			0	1203.93	782.06	1867.66
XI				0	1332.34	2317.54
XII					0	2098.6
XIII						0

ratio, milling % and head rice recovery were observed in Cluster VII, demonstrating how NPT-70 can affect both yield and quality traits. Nayak et al. (2004), Rahangdale et al. (2022) and Tiwari et al. (2022) also reported that the characters' contributions to divergence heavily influence the choice of parents.

3.2. Principal component analysis (PCA)

PCA was performed using yield and quality components for rice genotypes. Additionally, a scree plot graph between Eigenvalues and principal components was created to

Table 6: Cluster mean values for yield and yield attributing traits of fertility restorer lines

	Clusters												
Traits	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
DTPI	94.62	107.33	109.33	88.67	101.47	91.33	97.33	83.33	90.33	92.00	92.67	110.00	81.33
DTM	123.93	139.67	137.67	119.00	129.73	118.33	126.67	111.33	121.00	121.33	122.33	140.00	112.00
NOT	8.98	8.07	8.27	8.27	9.52	8.83	6.27	8.90	10.00	10.60	8.67	13.83	10.97
NOET	7.48	6.67	6.67	7.33	7.59	7.87	4.67	7.47	8.67	9.27	7.33	11.73	9.47
PH (cm)	121.10	122.07	114.77	111.23	136.23	98.33	110.47	104.80	118.80	116.53	105.20	107.10	98.83
SL (cm)	88.89	96.20	89.63	87.57	110.34	77.73	86.80	79.13	85.63	93.50	79.30	84.03	70.57
ST (cm)	4.57	6.83	7.17	4.17	5.37	4.33	4.83	4.17	4.00	4.17	5.67	4.33	4.17
FLL (cm)	38.18	41.97	27.57	34.40	50.01	28.40	47.33	27.47	46.10	31.37	34.10	32.40	39.57
FLW (cm)	1.28	1.63	1.53	1.10	1.55	1.37	1.43	0.83	1.47	1.17	1.53	1.10	1.27
PL (cm)	26.57	25.87	25.13	23.67	25.89	20.60	23.67	25.67	33.17	23.03	25.90	23.07	28.43
PW	27.48	29.87	25.69	34.00	27.51	23.95	23.67	19.34	32.09	23.20	17.50	13.90	15.22
TSPP	204.67	203.00	248.33	177.33	262.53	305.67	332.67	140.67	138.33	237.00	73.00	51.67	235.67

Where; DTPI: Days to panicle initiation; DTM: days to maturity; NOT: Number of tillers plant^{-1}; NOET: Number of effective tillers plant^{-1}; PH: Plant height; SL: stem length; ST: Stem thickness; FLL: Flag leaf length; FLW: Flag leaf width; PL: Panicle length; PW: Panicle weight; TSPP: Total spikelet panicle^{-1}

Table 6: Continue...

	Clusters												
Traits	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
FSPP	171.91	166.67	207.33	160.67	220.20	254.67	282.33	117.33	124.00	197.67	58.00	42.00	196.33
SSPP	32.77	36.33	41.00	16.67	42.33	51.00	50.33	23.33	14.33	39.33	15.00	9.67	39.33
SF%	83.87	82.08	83.49	90.57	83.46	83.32	84.88	83.40	89.63	83.41	79.56	81.30	83.31
SD	7.75	7.86	9.88	7.50	10.12	14.86	14.05	5.48	4.17	10.29	2.84	2.25	8.35
1000 SW (g)	22.42	13.87	19.80	31.63	18.79	17.00	23.37	21.97	31.60	18.83	33.57	13.60	15.63
GL (mm)	8.86	9.00	9.00	9.00	8.20	7.33	8.00	10.67	12.00	9.00	12.00	8.33	7.33
GB (mm)	2.70	2.33	3.00	3.00	2.77	2.50	2.17	2.83	2.00	2.50	2.00	3.00	3.00
DGL (mm)	7.73	8.17	8.00	8.00	7.10	6.00	7.00	9.67	11.00	8.00	11.00	6.33	6.00
DGB (mm)	1.98	2.00	2.50	2.17	1.90	2.00	1.67	2.33	3.00	2.00	3.00	2.00	2.00
DG L/B	3.95	4.08	3.20	3.73	3.78	3.00	4.28	4.17	3.67	4.00	3.67	3.17	3.00
H %	78.24	78.00	78.67	72.67	76.93	76.17	78.33	73.13	75.50	77.17	78.83	73.83	58.00
M %	72.84	73.17	73.17	66.33	73.23	70.33	74.83	56.00	74.00	56.17	74.33	59.33	56.00
HRR %	63.45	66.17	63.67	61.03	64.10	62.33	68.67	51.50	57.33	48.17	65.83	52.33	44.83
BYPP(g)	51.08	62.40	61.45	53.02	63.12	41.03	48.03	41.08	56.66	42.60	61.03	49.77	29.50
PI %	81.56	63.35	78.76	79.99	83.69	79.59	78.68	79.10	87.77	81.16	66.81	111.96	80.09
HI %	0.44	0.30	0.33	0.51	0.37	0.47	0.39	0.37	0.50	0.44	0.19	0.31	0.41
GYPP (g)	22.46	18.94	20.23	27.20	23.24	19.07	18.63	15.30	28.17	18.83	11.70	15.48	12.20

Where; FSPP: fertile spikelets panicle^{-1}; SSPP: Sterile spikelet panicle^{-1}; SF%: Spikelet fertility %; SD: Spikelet density; 1000 SW: Thousand seed weight; GL: Grain length; GB: Grain Breadth; DGL: Decorticated grain length; DGB: Decorticated grain breadth; DG L/B ratio: Decorticated length/breadth; H%: Hulling %; M %: Milling %; HRR: Head rice recovery ; BYPP: Biological yield plant^{-1}; PI: Panicle index; HI: Harvest index; GYPP: Grain yield plant^{-1}

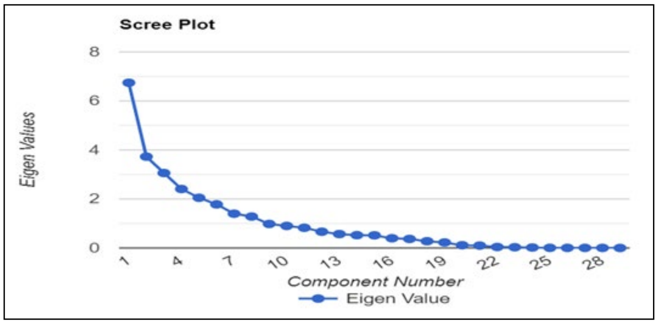

Figure 3: Scree plot of rice fertility restorer lines

describe the percentage of total variation explained by each PC (Figure 3). Of the twenty-nine traits, eight principal components (PCs) with Eigenvalues >1 captured 77.4% total variability. PC1 accounted for 23.3%, followed by PC2 (12.9%), PC3 (10.6%), PC4 (8.3%), PC5 (7.1%), PC6 (6.1%), PC7 (4.8%), and PC8 (4.4%) of the variation among genotypes. The analogous results were obtained by Tiwari et al. (2022).

As presented in Table 7, the rotated component matrix revealed that the PC1 accounted for the highest variability. These results were in agreement with Sheela et al. (2020) and Tiruneh et al. (2019) for PC1. PC scores suggested that yield-related traits, such as stem length, fertile spikelets panicle^{-1}, sterile spikelets panicle^{-1}, spikelet fertility %, panicle weight plant^{-1}, total spikelets panicle^{-1}, biological yield plant^{-1}, harvest index, grain yield plant^{-1}, and quality traits like grain breadth, decorticated grain length, and milling %, dominated in PC1. PC2 was dominated by phenological traits like days to panicle initiation and days to maturity (Figure 4). PC3 (1000 seed weight, decorticated grain length, grain length), PC4 (panicle length, grain

Table 7: Interpretation of rotated component matrix for the traits having highest value (>1) in each PCs

PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Stem length (cm)	Days to panicle initiation (days)	100 seed weight (g)	Panicle length(cm)	Stem thickness (mm)	Hulling %	Flag leaf length (cm)	No. of tillers plant^{-1}
Fertile spikelets panicle^{-1}	Days to maturity (days)	Grain length (mm)	Grain Breadth (mm)	Decorticated Grain L/B ratio	Head rice recovery %	Flag leaf width (cm)	
Sterile spikelets panicle^{-1}		Decorticated GL (mm)	Decorticated grain breadth(mm)				
Spikelet fertility(%)			Panicle Index %				
Panicle weight plant^{-1} (g)							
No. of spiklets panicle^{-1}							
Grain breadth (mm)							
Decorticated GL (mm)							
Biological yield Panicle^{-1} (g)							
Hervest index%							
Grain yield plant^{-1} (g)							
Milling %							

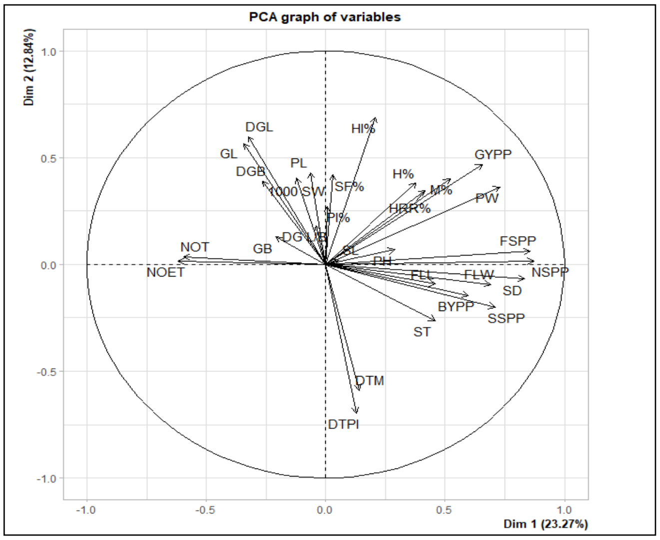

Figure 4: Clustering of variables for different principal components

breadth, decorticated grain breadth, panicle index), and PC5 (stem thickness, decorticated grain length breadth^{-1} ratio) also contributed to yield and quality attributes. PC6 contributed to quality attributes, such as head rice recovery and hulling %. PC7 was characterized by flag leaf length and width, while PC8 had the highest values for the number of tillers plant^{-1}.

Additionally, the biplot depicted in figure 5 between first two major principal components revealed the scattering and extent of variability among the genotypes and studied traits. Almost all genotypes and traits included in the present study exhibited high degree of variation. The genotype E-TP-1064 expected to be promising for improving the harvest index (Figure 5) when used as one of the parents in a heterosis breeding program. Similar results were reported for genotype ANP-526 for head rice recovery %, NPT-3821

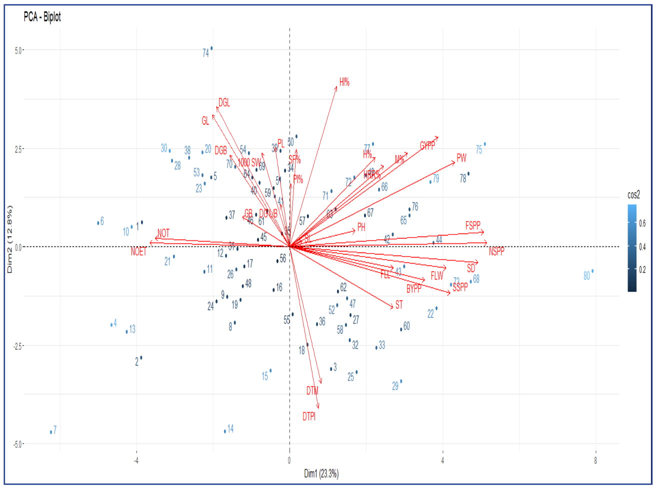

Figure 5: Biplot diagram for studied 80 genotypes and associated traits

for plant height, E-TP-1054, IME-1101 and E-TP-1124 for panicle weight, NPT14-12 for stem length ANP-553 for SF%, NPT-37, R-650 and NP-8421 for earliness traits, NPT-3803 for stem thickness, RP5911-52-13-3-2-2-1, NPT-3804 for grain breadth and decorticated grain L/B ratio, MC-13 for panicle length, E-TP-100, NPT-3810, E-TP-1014 and for 1000 SW and Mahamaya and R-304 for number of tillers and number of effective tillers.

The PC scores serve as the basis for proposing precise selection indices, with the intensity of these indices determined by the variability explained in each principal component. According to Singh and Chaudhary (1977), a high PC score for a genotype in a specific component indicates elevated values for the associated variables. The selection criteria involved choosing genotypes with top PC scores exhibiting positive values greater than 1.5 in each of the 8 principal components for all the rice genotypes studied.

The PC scores (Table 8) indicated that genotypes JNPT-782, AD02207, NP-9165, and ANP-526 fell in yield and quality-associated PCs with elevated scores indicated a substantial value in terms of both yield and quality. Among genotypes which is found to be common in yield as well quality associated PCs, maximum positive value recorded for JNPT-782 (3.027). Rahangdale et al. (2022) also suggested that genotypes that fall in principal components with high PC scores have high values for yield and quality traits. Therefore, designing intensive selection procedures based on PC analysis can rapidly improve yield and quality attributes.

Table 8: PC scores of genotypes having positive values >1 in each PC

PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
JNPT-782 (3.027)	AD02207 (2.409)	R-710 (3.684)	ANP-526 (2.407)	R-650 (2.886)	NP-9165 (2.323)	MC-13 (2.148)	NPT-35-01 (2.726)
NP-9165 (1.949)	ANP-526 (2.407)	NPT-13-01 (1.913)	AD02207 (2.053)	JR-503 (2.65)			
	VNR-212 (2.038)	NPT-3806 (2.082)	E-TP-1014 (2.003)				
NPT-15 (1.811)	Laxmi-144 (1.766)	NP-72 (1.726)	RP5219-9-6-7-3-2-1-1 (1.85)	NPT-3821 (2.234)	HRI-183 (2.001)	Gemini (2.027)	HRT-181 (1.601)
NP-8421 (1.788)	NP-72 (1.636)		CR3703-11-1 (1.816)	E-TP-1023 (1.885)	Abhya (1.689)	IR-79854-38-2-4 (2.026)	
JNPT-81 (1.613)	NP-1024 (1.621)		NPT-3803 (1.776)	CR2829-PLN-32 (1.863)	NPT-3810 (1.529)	JR-81 (1.765)	
	NPT-13-01 (1.606)		JNPT-782 (1.611)	Laxmi-144 (1.712)	IR09N26 (1.52)		
			IME-1101 (1.587)				
			R-548 (1.52)				

4. CONCLUSION

Due to their high inter-cluster distance, genotype 1E-TP-2 with E-TP-1001 and Mahamaya with 1E-TP-2 could lead to superior hybrid combinations. Cluster mean values suggested that genotypes 1E-TP-2, R-710, and AD02207 contributed to major yield and quality traits, while NPT-70 contributed to major yield-related traits. On the basis of PCA, genotypes JNPT-782, AD02207, NP-9165, and ANP-526 were found to be superior in both yield and quality-related principal components. Biplot analysis highlighted the trait-based genotype selection.

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