

#### **RESEARCH ARTICLE**

# Unveiling Genetic Variation in Rice Hybrids Through Hierarchical Clustering and Principal Component Analysis

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#### Abstract

The present investigation was carried out with 67 rice hybrids along with eight checks (four varietal and four hybrid checks) to ascertain the extent of genetic diversity for yield and yield associated traits through multivariate techniques like hierarchical clustering and principal component analysis (PCA). By using Wards method of clustering, 67 rice hybrids along with eight checks were aggregated into eight clusters based on different traits in which cluster VI comprised of 15 hybrids is the largest one followed by cluster III and IV with 12 hybrids. The hybrids in cluster I and II had highest values for test weight and effective bearing tillers /m<sup>2</sup> respectively. Similarly, the hybrids in cluster III recorded maximum values for plant height and Grain yield. In PCA, the total variation was bisected into 10 major principal components (PCs) in which PC1, PC2, PC3 and PC4 with eigen values more than one describing 24.76%, 23.26%, 14.54 and 13.22%, respectively attributing for overall variation of 75.80%. From the present study, the hybrids *viz.*, NRH 24, NRH 46, NRH 40, NRH 38, NRH 53, NRH 2; Hybrid checks HC2 (US 314), HC4 (HRI 174) and varietal check VC1 (BPT 5204) were identified to be genetically potential for commercial exploitation to enhance yield and its attributing traits in rice.

Keywords: Rice, Genetic diversity, Cluster analysis, Principal component analysis

#### Introduction

Rice (*Oryza sativa* L.), a global food grain and an important staple food crop for half of the global population. Globally, India holds second place in rice production next to China. The major rice producing states in India include West Bengal, UP, Andhra Pradesh, Punjab, Telangana and Tamil Nadu. Besides, West Bengal and Uttar Pradesh produce 30% of total quantity of rice produced in the country. In India, the rice crop reported a production of 203.6 million tonnes from 47.8 million ha with average productivity of 4259 Kg/ha (https://ipad.fas.usda.gov/countrysummary/Default.aspx?id=IN&crop=Rice). In Andhra Pradesh, the crop is cultivated in total area of 2.13 million ha with production of 12.63

million tonnes and productivity of 5932 million tonnes (Agricultural statistics at a glance, 2022-23, Directorate of Economics and Statistics, Government of Andhra Pradesh, 2022-23). In the present national scenario, the population growth rate is reached to 1.58% and the requirement of rice was estimated to be around 140.7 million tonnes by 2025 (http:// worldfood.apionet.or.jp). In order to make India selfsufficient in rice, enhancement of rice productivity to larger extent is a prime requisite (Hossain, 1996; Mishra, 2002). Despite this, task is quite challenging for breeders as the options available are very limited. Hence, breeders need to identify genetically diverse and potential hybrids for their inclusion in crop

improvement programme by divergence studies for yield and its attributing traits.

Although yield is a complex and challenging trait which depends mainly on environment and other different variables. For an efficient selection, breeder can reduce the number of characteristics and this can be made possible by using a method known as PCA. PCA is one of the multivariate techniques utilized in data analysis that converts data into a series of new orthogonal variables called principal components by linearly combining the variables that account for majority of variance in the original variables (Abdi and Williams, 2010) and it comprehends non-parametric strategy from a complicated set of data (Tiwari et al., 2022). The main advantage of using PCA over cluster analysis is that each genotype can be assigned to one group only (Mohammadi, 2002). The cluster analysis is a pertinent method for concluding relationship among hybrids and amount of genetic distance from each other (Mellingers, 1972). Divergence analysis using PCA and hierarchical cluster analysis has been shown to be effective in determining potential hybrids useful for hybridization (Chaudhary et al., 2015). The prime objective of this investigation was to unveil genetic diversity and identify the best divergent hybrids for their inclusion in commercial rice improvement programme.

## **Materials and Methods**

The experimental material consisted of 67 rice hybrids along with eight checks (four varietal and four hybrid checks) which were evaluated at Regional Agricultural Research Station (RARS), Nandyal, Andhra Pradesh, India during *kharif*, 2023. All the hybrids were evaluated in Augmented Block Design with plot size of 10 m<sup>2</sup> per hybrid with a spacing of 20 cm x 15 cm. All the agronomic practices recommended by Acharya N.G. Ranga Agricultural University were followed to raise a healthy crop. Data was collected from five competitive and randomly selected plants for recording yield and yield attributes *viz.*, Days to 50% flowering (DFF), Days to maturity (DM), Plant height (cm) (PH), Effective bearing tillers/m<sup>2</sup> (EBT/ m<sup>2</sup>), Panicle length (cm) (PL), Filled Grains per panicle (FGP), Unfilled grains per panicle (UFGP), Total grains per panicle (TGP), Spikelet fertility % (SF %), Test weight (g) (TW) and grain yield (Kg/m<sup>2</sup>)(GY) whereas DFF and DM data was recorded on plot basis. PCA (Hotelling, 1936) and cluster analysis were used to identify the most contributing traits for variation and diversity among hybrids, respectively (Peeters and Martinelli, 1989). The data generated by evaluation of hybrids s forwarded to statistical analysis to estimate genetic diversity through PCA and hierarchical clustering using JMP 17.0 statistical software (SAS Institute Inc., Cary, NC, USA).

## **Results and Discussions**

The performance of 67 rice hybrids together with eight checks evaluated for eleven yield and yield attributes is presented in Table 1. The hybrid NRH 3 was found to be early flowering (81 days), while VC2(MTU 1262) was identified as late flowering (114 days). DM ranged from 109 days (NRH2) to 144 days (NRH 51). NRH 36 was found as taller (123 cm) whereas VC1 (BPT 5204) noticed as shorter (87.70 cm) with an average of 106.98 cm. The hybrid NRH 43 was found to bear a greater number of effective tillers (726 /  $m^2$ ), while least number of effective tillers  $(238 / m^2)$  was displayed by hybrid, NRH 8. The mean value of PL was found to be 25.19 cm with range of 21.22 cm (HC2) to 27.86 cm (NRH 55). The TGP ranges from 160 (HC 2) to 599 (NRH 40) with mean value of 337. The mean SF % was recorded as 84.55% in which NRH 34 topped the list with 93.64% and NRH 17 occupied the bottom position with 60.06%. The TW ranged from 11.27 g (NRH 40) to 23.27 g (NRH 11) with average TW value of 15.98 g. The mean GY was recorded as 1.27Kg/m<sup>2</sup> with ranges from 0.612 Kg/m<sup>2</sup> (NRH 26) to 2.152 Kg/m<sup>2</sup> (NRH 5) among the studied hybrids. Vasudeva Reddy et al., (2023) reported same kind of experimental results while evaluating hybrids for yield and its component traits in rice.

S. No.	Entry	Cross Combination	DFF	DM	PH (cm)	$EBT/m^{2}$	PL(cm)	FGP	UFGP	TG/P	SF %	TW (G)	GY (kg/sq.m)	
-	NRH 1	IR 58025A/RTCNP 67	92	120	103.8	389	24.90	193	50	243	79.57	20.24	1.246	
7	NRH 2	IR 68888 A/AE 1325	82	109	95.3	310	24.90	296	22	318	92.96	15.20	0.870	
ю	NRH 3	IR 79156 A / AE 1305	81	110	97.2	277	25.90	301	21	322	93.60	16.52	1.002	
4	NRH 4	APMS 6A / M 652	82	110	92.3	277	24.34	298	33	331	90.02	14.23	1.152	
5	NRH 5	APMS 6A / RTCNP 103	67	125	109.4	442	26.06	239	19	258	92.56	16.23	2.152	
9	NRH 6	APMS 6A / RTCNP 152	88	115	106.5	422	23.94	240	25	265	90.55	17.29	1.304	
7	NRH 7	APMS 6A / RTCNP 67	85	113	96.9	479	25.40	336	42	377	88.98	14.47	1.542	
~	NRH 8	APMS 6A / SN 698	87	125	95.5	238	24.90	307	26	333	92.30	16.21	1.354	
6	NRH 9	APMS 9A / BM 559	96	125	96.8	403	25.70	270	26	296	91.14	13.80	1.020	
10	NRH 10	APMS 9A / RTCNP 151	66	128	114.6	432	27.80	294	50	344	85.53	19.36	1.631	
=	NRH 11	APMS 9A / RTCNP 167	97	125	105.1	640	25.08	296	43	339	87.32	23.27	1.782	
12	NRH 12	APMS 9A / RTCNP 168	66	126	111.2	353	25.68	245	99	310	78.80	20.95	1.186	
13	NRH 13	APMS 9A / RTCNP 67	101	130	103.7	653	25.94	204	45	249	81.90	16.23	0.963	
14	NRH 14	PMS 3A / RTCNP 66	102	129	109.0	317	24.70	271	82	353	76.68	15.83	1.846	
15	NRH 15	CMS 23A / BPT 2782	95	124	113.4	370	26.50	315	37	352	89.49	18.20	1.470	
16		APMS 11A	87	116	103.4	436	25.76	277	26	303	91.55	18.30	1.752	
17	NRH 17	APMS 11A/RTCNP 152	60	116	109.9	376	26.52	206	137	343	60.06	19.35	0.881	
18	NRH 18	APMS 11A/RTCNP 167	101	133	103.5	386	26.22	214	37	251	85.26	15.50	1.709	
19	NRH 19	APMS 11A/RTCNP 170	95	125	110.6	389	26.64	197	63	260	75.67	18.77	1.201	
20	NRH 20	APMS 11A/RTCNP 176	98	128	105.9	574	25.40	201	32	233	86.27	16.77	1.494	
21	NRH 21	APMS 11A/RTCNP 66	95	123	115.3	686	25.04	216	52	268	80.60	19.45	1.134	
22	NRH 22	APMS 11A/RTCNP 67	97	125	106.5	614	25.48	257	41	298	86.25	18.93	1.422	
23	NRH 23	APMS 11A/RTCNP 99	66	128	99.1	548	26.14	248	52	300	82.67	17.74	1.368	
24	NRH 24	APMS 14A / RTCNP 167	111	137	104.7	409	24.18	189	76	265	71.42	17.32	0.695	
25	NRH 25	APMS 15A / BM 563	90	117	106.1	389	26.50	370	26	396	93.39	15.54	0.987	
26	NRH 26	APMS 15A / CM 458	92	117	98.5	330	25.30	336	53	388	86.45	15.55	0.612	
27	NRH 27	APMS 15A / NICRA P3	83	112	106.3	350	26.46	340	39	380	89.63	17.74	1.674	
28	NRH 28	15A/	86	116	106.3	429	25.00	335	42	377	88.76	16.30	1.602	
29	NRH 29	APMS 15A / RTCNP 169	107	136	108.7	393	24.32	218	83	301	72.38	15.86	1.220	
30	NRH 30	APMS 15A / RTCNP 67	102	130	114.9	541	26.70	301	41	342	88.00	14.21	1.467	
31	NRH 31	APMS 15A / SN 698	88	118	102.6	396	26.00	324	27	350	92.40	14.26	0.828	
32	NRH 32	APMS 16A / RTCNP 150	94	124	88.9	488	24.10	197	52	249	79.12	13.24	1.035	
33	NRH 33	APMS 16A / RTCNP 170	105	135	114.1	409	24.96	250	85	336	74.57	16.22	1.040	
34	NRH 34	16A /	95	124	119.1	703	25.70	324	22	346	93.64	13.93	1.233	
35	NRH 35	APMS 16A / RTCNP 66	66	128	106.1	568	24.56	224	43	267	83.92	14.52	1.233	
36	NRH 36	APMS 16A / RTCNP 67	100	128	123.0	535	25.66	260	28	288	90.29	15.64	1.693	
37	NRH 37	APMS 16A / SN 698	96	125	100.5	422	26.40	339	LL LL	415	81.51	11.51	0.906	
38	NRH 38	APMS 17A / CM 449	90	118	92.4	350	22.40	422	105	528	80.06	13.30	0.690	
39	NRH 39	APMS 17A / CM 454	97	127	101.7	376	24.20	352	57	409	86.05	15.40	1.521	
40	NRH 40	APMS 17A / NICRA P3	96	125	106.4	403	00 90	485	114	509	80.03	11 77	1 1 2 2	
			2	1		225	1001			~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	00.00	11.41	1.144	



S. No.	Entry	Cross Combination	DFF	DM	PH (cm)	EBT/m <sup>2</sup>	PL(cm)	FGP	UFGP	TG/P	SF %	TW (G)	GY (kg/sq.m)	Heterosis %
42	NRH 42	APMS 17A / RTCNP 66	102	130	114.6	673	24.40	198	42	240	82.50	14.75	1.242	-13.51
43	NRH 43	APMS 17A / RTCNP 67	97	125	101.5	726	24.80	277	48	325	85.21	14.28	1.341	-6.62
44	NRH 44	APMS 18A / CM 460	97	127	108	409	25.10	496	72	568	87.26	13.84	1.038	-27.72
45	NRH 45	APMS 18A / RTCNP 145	98	127	106	528	26.46	356	51	407	87.47	14.18	1.146	-20.19
46	NRH 46	APMS 18A / RTCNP 166	106	133	111.9	449	27.10	286	132	418	68.49	15.69	1.366	-4.89
47	NRH 47	APMS 18A / RTCNP 172	97	125	108.9	380	24.90	212	87	298	70.96	17.96	1.673	16.52
48	NRH 48	APMS 18A / RTCNP 176	66	130	114.7	373	25.04	301	103	404	74.48	14.83	1.293	-9.99
49	NRH 49	APMS 18A / RTCNP 66	93	120	118.3	475	25.50	273	36	309	88.33	16.61	0.99	-31.06
50	NRH 50	APMS 18A / RTCNP 84	104	128	107.2	350	24.68	320	74	394	81.17	16.30	0.958	-33.30
51	NRH 51	APMS 18A / RTCNP 97	105	134	115.8	413	25.74	318	86	404	78.77	16.42	1.304	-9.17
52	NRH 52	APMS 18A / RTCNP 99	104	132	105.9	370	26.00	394	67	462	85.40	14.41	1.643	14.38
53	NRH 53	APMS 19A / BM 563	91	119	108.7	403	25.42	469	61	531	88.47	15.11	0.840	-41.50
54	NRH 54	APMS 19A / BM 571	98	127	105.1	422	24.78	394	35	430	91.76	12.19	1.512	5.29
55	NRH 55	APMS 19A / RTCNP 103	97	126	113.4	383	27.86	392	99	458	85.64	14.90	1.278	-11.00
56	NRH 56	APMS 19A / RTCNP 133	66	129	112.5	462	25.34	478	78	556	85.98	16.64	1.506	4.87
57	NRH 57	APMS 19A / RTCNP 167	93	120	109.7	502	24.56	194	32	226	85.84	11.89	1.381	-3.83
58	NRH 58	APMS 19A / RTCNP 171	94	124	111.1	363	22.10	205	89	294	69.75	14.76	1.019	-29.03
59	NRH 59	APMS 19A / RTCNP 172	94	127	110.1	383	25.28	263	76	338	77.66	17.20	1.418	-1.24
60	NRH 60	APMS 19A / RTCNP 173	100	130	109.7	399	25.08	296	59	355	83.33	17.56	1.361	-5.20
61	NRH 61	APMS 19A / RTCNP 174	98	127	111.1	396	22.58	286	23	309	92.49	17.67	1.471	2.45
62	NRH 62	APMS 19A / RTCNP 175	66	129	113.3	389	24.46	198	41	239	82.69	18.33	1.116	-22.28
63	NRH 63	APMS 19A / RTCNP 176	98	130	115.3	373	25.68	310	76	386	80.37	13.63	1.480	3.05
64	NRH 64	APMS 19A / RTCNP 66	95	124	119.9	455	25.70	247	33	280	88.21	15.03	1.412	-1.67
65	NRH 65	APMS 19A / RTCNP 67	90	118	121.4	561	24.30	236	25	261	90.41	15.68	1.386	-3.48
99	NRH 66	APMS 19A / RTCNP 97	98	128	106.1	406	26.44	299	71	370	80.78	14.89	1.339	-6.73
67	<b>NRH 67</b>	APMS 19A / RTCNP 99	106	132	110.8	380	24.50	325	71	396	82.04	11.60	1.417	-1.30
68	VC1	BPT 5204	111	140	87.7	502	23.04	175	22	197	88.73	14.30	1.160	
69	VC2	MTU 1262	114	144	106.9	386	24.76	363	42	405	89.62	12.57	0.990	
70	VC3	NDLR 7	100	129	97.4	360	23.72	250	22	272	91.77	13.19	1.315	
71	VC4	NDLR 8	96	126	103.9	432	23.96	175	30	205	85.19	15.59	1.366	
72	HC1	US 312	96	125	107.2	393	26.48	296	37	333	88.88	18.16	0.831	
73	HC2	US 314	85	115	106.6	452	23.92	143	18	160	89.03	20.43	1.250	
74	HC3	27 P 63	96	126	108.9	403	21.22	267	38	305	87.54	14.98	1.356	
75	HC4	HRI 174	101	130	106.6	386	24.28	165	30	195	84.72	20.49	1.436	
Mean			96	125	106.9	435	25.19	285	52	337	84.55	15.98	1.27	
Maximum	um		114	144	123	726	27.86	496	137	599	93.64	23.27	2.15	
Minimum	um		81	109	87.7	238	21.22	143	18	160	60.06	11.27	0.61	
SD			6.74	6.82	7.22	100.35	1.20	77.44	26.81	87.90	6.78	2.36	0.29	
SE			0.778	0.788	0.834	11.588	0.139	8.942	3.096	10.150	0.783	0.274	0.034	
DFF-day TGP-tota	s to 50% flo I grains per	DFF-days to 50% flowering, DM-days to maturity, PH-plant height, EBT/m <sup>2</sup> - Effective b TGP-total grains per panicle, SF %- spikelet fertility %, TW-test weight, GY- grain yield	H-plant ] %, TW-1	neight, E est weig	(BT/m <sup>2</sup> - Effe tht, GY- grain	ctive bearir n yield	ıg tillers/m²,	PL-pani	cle length,	FGP-fill	ed grains	per panicle	t, EBT/m²- Effective bearing tillers/m², PL-panicle length, FGP-filled grains per panicle, UFGP-unfilled grains per panicle, eight, GY- grain yield	ains per panicle,

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Hierarchical cluster analysis was conducted with 67 rice hybrids along with eight checks using Wards method which provides the best result to get the finest possible classification. The cluster analysis revealed the aggregation of hybrids into eight clusters (**Table 2 and Figure 1**). The cluster means computed for eleven major yield attributing characters revealed the existence of ample amount of variation among the clusters (**Table 3**). The highest and lowest cluster means were recorded for the traits EBT/m<sup>2</sup> (631.4) and GY (1.00), respectively. Maximum cluster mean of overall traits was noticed in cluster VII (174.60) followed by cluster VIII (154.20). In contrast, the least cluster mean was displayed by cluster I

(121.70). This clearly infers the existence of ample amount of genetic divergence in the hybrids of these clusters. Further, among the eight divergent clusters, the highest numbers of hybrids were grouped in cluster VI with 15 hybrids followed by 12 hybrids in cluster III and IV. The hybrids in cluster IV showed highest mean values for DFF, DM, PH, EBT/m<sup>2</sup> and SF %. The hybrids of cluster III and cluster VIII showed maximum value for GY. Ravikumar *et al.*, (2015), Tejaswani *et al.*, (2016), Tejaswini *et al.*, (2018), Muthuramu and Sakthivel (2018), Dhakal *et al.*, (2020), Kusuma Kumari *et al.*, (2021) and Amudha and Ariharasutharsan (2021) also documented same kind of clustering of accessions into distinct clusters.

Table 2: Grouping of different hybrids into different clusters

Cluster	No. of hybrids	Hybrids
Ι	5	NRH 1, NRH 12, NRH 19, NRH 62,HC4
II	9	NRH 11, NRH 13, NRH 35, NRH 42, NRH 43, NRH 20, NRH 22, NRH 23, NRH 21
III	12	NRH 5, NRH 18, NRH 10, NRH 15, NRH 30, NRH 45, NRH 55, NRH 34, NRH 36, NRH 64, NRH 49, NRH 65
IV	12	NRH 2, NRH 3, NRH 4, NRH 25, NRH 31, NRH 26, NRH 41, HC1, NRH 7, NRH 28, NRH 16, NRH 27
V	11	NRH 6, HC2, NRH 61, HC3, NRH 8, NRH 9, VC3, NRH 32, NRH 57, VC4, VC 1
VI	15	NRH 14, NRH 47, NRH 48, NRH 63, NRH 51, NRH 50, NRH 59, NRH 60, NRH 66, NRH 46, NRH 24, NRH 29, NRH 33, NRH 58, NRH 17
VII	6	NRH 37, NRH 40, NRH 44, NRH 53, NRH 56, NRH 38
VIII	5	NRH 39, NRH 54, NRH 52, NRH 67,VC2

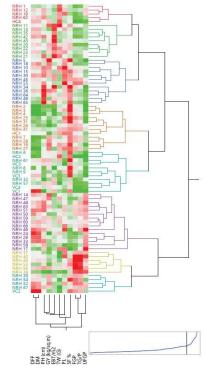


Figure 1: Dendrogram showing clustering by Wards method

DFF-days to 50% flowering, DM-days to maturity, PH-plant height, EBT/m<sup>2</sup>- Effective bearing tillers/ m<sup>2</sup>, PL-panicle length, FGP-filled grains per panicle,

UFGP-unfilled grains per panicle, TGP-total grains per panicle, SF %- spikelet fertility %, TW-test weight, GY- grain yield



Cluster No.	DFF	DM	PH	EBT/m <sup>2</sup>	PL	FGP	UFGP	TGP	SF %	TW	GY	Mean
Cluster I	96.9	125.7	109.1	381.5	25.2	199.5	50.0	249.4	80.3	19.8	1.2	121.7
Cluster II	98.3	126.9	106.4	631.4	25.2	235.6	44.2	279.9	84.1	17.3	1.3	150.1
Cluster III	96.8	125.5	114.7	484.3	26.2	287.6	37.1	324.7	88.7	15.8	1.5	145.7
Cluster IV	87.1	115.5	101.2	373.5	25.7	322.4	34.6	357.1	90.4	16.2	1.2	138.6
Cluster V	94.8	124.5	101.2	417.9	23.8	227.5	28.6	256.1	88.5	15.3	1.3	125.4
Cluster VI	100.5	129.3	110.5	386.1	25.1	263.0	87.7	350.7	74.7	16.3	1.3	140.5
Cluster VII	94.8	123.8	104.8	408.1	25.3	448.2	84.6	532.8	84.0	13.6	1.0	174.6
Cluster VIII	103.7	132.2	106.1	386.8	24.8	365.7	54.6	420.3	87.0	13.2	1.4	154.2
Mean values	96.6	125.4	106.7	433.7	25.2	293.7	52.7	346.4	84.7	15.9	1.3	

Table 3: Cluster means of various characters of rice hybrids under study

Bold figures indicate maximum and minimum values in each character. DFF-days to 50% flowering, DMdays to maturity, PH-plant height, EBT/m<sup>2</sup>- Effective bearing tillers/m<sup>2</sup>, PL-panicle length, FGP-filled grains per panicle, UFGP-unfilled grains per panicle, TGP-total grains per panicle, SF %- spikelet fertility %, TW-test weight, GY- grain yield

The constellation plot based on Wards method (Figure 2) depicts relationship among the 67 hybrids together with eight checks. The hybrids are grouped as end points and every cluster join as a new point with lines drawn will act as membership in constellation plot. The plot divided the total hybrids into 8 clusters with membership of 5,9,12,12,11,15,6 and 5. The Clustering pattern divulged that majority of hybrids congregated in cluster VI (15), followed by Cluster III (12) and Cluster IV (12). The hybrids with longer line representing greater genetic distance between the clusters. Further, the identified hybrids with maximum genetic distance are considered as superior and exploited commercially in yield improvement programme in rice.

The PCA an authentic tool utilized for successful selection of divergent genotypes in crop improvement programme. The results of PCA revealed the significance of first four PCs in discriminating 67 rice hybrids along with eight checks. The first four PCs, PC1, PC2 PC3 and PC4 exhibited eigen value

greater than one explaining 75.80% of total variation. The eigen values and total cumulative per centage of variances explained by PCs is furnished in **Table 4**. PC1 with eigen value of 2.724 contribute 24.76% of the total variability, PC2, PC3 and PC4 with eigen value of 2.559, 1.604 and 1.455 attributed 23.62%, 14.54% and 13.22% of the total variability, respectively. The first PC displayed high positive weight to UFGP (0.850), DFF (0.645), TGP (0.624) and DM (0.622). The second PC displayed highest positive loading to DFF (0.569), DM (0.563) and EBT (0.438). Likewise, the third and fourth PCs gave positive loading to GY (0.588) and TW (0.661), respectively (**Table 5**).

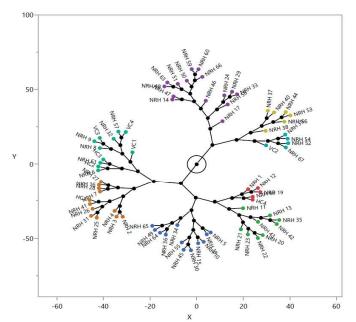


Figure 2: Constellation plot of 67 hybrids along with eight checks into Eight clusters based on Euclidean distance

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Components	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
Eigen values	2.724	2.559	1.604	1.455	0.862	0.682	0.56	0.506	0.033	0.012
Proportion variance %	24.76	23.262	14.547	13.229	7.83	6.21	5.14	4.60	0.30	0.11
Cumulative variance %	24.76	48.03	62.577	75.806	83.65	89.86	94.99	99.59	99.89	100.00

Principal	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
Components	ICI	102	105	104	103	100	107	100	109	1010
DFF	0.645	0.569	0.150	-0.402	0.075	0.184	0.106	0.076	0.129	-0.007
DM	0.622	0.563	0.164	-0.420	0.154	0.193	0.095	0.060	-0.126	0.008
PH (cm)	0.283	0.344	0.509	0.379	-0.095	-0.398	0.403	-0.257	-0.002	0.0007
EBT/m2	-0.115	0.438	0.435	-0.120	-0.654	-0.161	-0.273	0.247	-0.007	0.0007
PL	0.219	-0.201	0.500	0.480	-0.182	0.571	-0.119	-0.234	-0.000	-0.0001
FGP	0.414	-0.807	0.336	-0.087	0.029	-0.064	0.076	0.209	-0.006	-0.0320
UFGP	0.850	-0.034	-0.321	0.338	-0.023	-0.130	-0.184	0.035	0.010	0.0741
TGP	0.624	-0.722	0.198	0.026	0.018	-0.096	0.011	0.195	-0.002	-0.0056
SF %	-0.629	-0.389	0.500	-0.383	0.055	0.079	0.190	0.050	0.014	0.0740
TW (G)	-0.292	0.384	-0.021	0.661	0.128	0.168	0.235	0.477	-0.001	0.0029
GY (Kg/sq.m)	-0.145	0.277	0.588	0.149	0.581	-0.186	-0.400	0.010	0.007	-0.0034

Table 5: Factor loading of different characters with respect to different principal factor in rice hybrids

DFF-days to 50% flowering, DM-days to maturity, PH-plant height, EBT/m<sup>2</sup>- Effective bearing tillers/m<sup>2</sup>, PL-panicle length, FGP-filled grains per panicle, UFGP-unfilled grains per panicle, TGP-total grains per panicle, SF %- spikelet fertility %, TW-test weight, GY- grain yield

The greater portion of the variance (24.76%) was noticed in PC1and was strongly convinced DFF, DM, PH, PL, FGP, UFGP, TGP. Similarly, PC2 was influenced by DFF, DM, PH, EBT/m<sup>2</sup>, TW and GY. Likewise, PC3 and PC4 are primarily influenced by UFGP, TW and DFF, DM, EBT/m<sup>2</sup>, FGP, SF, respectively. Similar kind of results are in agreement with findings of Nachimuthu *et al.*, (2014), Allam *et al.*, (2017), Riaz *et al.*, (2018), Umadevi *et al.*, (2019), Sudeepthi *et al.*, (2020), Singh *et al.*, (2020), Pushpa *et al.*, (2021), Christina *et al.*, (2022), Lakshmi *et al.*, (2022), Mushtaq and Kumar (2023), Nayak *et al.*, (2023), in rice.

The interaction between the characters and the genotypes that perform better for the traits are depicted in the biplot diagram. The length of the vector for each trait represents its offering to total divergence, longer the vector length, more is the contribution of concerned traits. The biplot depicted the relationship of 67 rice hybrids along with eight checks for 11 traits (Figure 3). The trait TG/P displayed greater vector length implying its contribution to the total divergence followed by DFF, SF %and FGP. These results are in congruence with the research findings of Lakshmi *et al.*, (2022), Tiwari *et al.*, (2022) and Gayathridevi *et al.*, (2023).

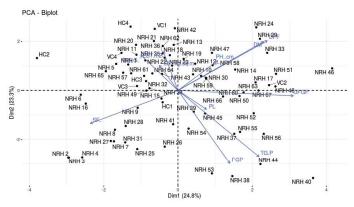


Figure 3: Biplot comprising of 67 rice hybrids along with eight hybrids studied for eleven yield and yield attributing traits

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DFF-days to 50% flowering, DM-days to maturity, PH-plant height, EBT/m<sup>2</sup>- Effective bearing tillers/ m<sup>2</sup>, PL-panicle length, FGP-filled grains per panicle, UFGP-unfilled grains per panicle, TGP-total grains per panicle, SF %- spikelet fertility %, TW-test weight, GY- grain yield

The angle formed by the vectors of the traits indicates the association between the traits. A right angle (90°) between the vectors denotes no correlation, while an obtuse angle (>90°) denotes a negative correlation and an acute angle (<90°) between vectors suggests a positive correlation. All the traits studied displayed positive correlation with grain yield per plant except UFGP which noticed no correlation. From the biplots, the 11 yield and yield attributing traits were divulged into four groups. GY, TW and EBT were grouped in same cluster. DFF, DM and PH were grouped in same cluster. The traits UFGP, PL, TGP and FGP were grouped in another cluster. Whereas, SF % alone grouped as one cluster. The selection of hybrids with desirable highest score (0.588) for grain yield in PC3 will be desirable for developing high grain yielders in rice. The study showed that NRH 24, NRH 46, NRH 40, NRH 38, NRH 53, NRH 2; Hybrid checks HC2 (US 314), HC4 (HRI 174) and varietal check VC1 (BPT 5204) were located at extreme ends of distinct quadrants of the plot. Hence, theses hybrids and checks were recognized as highly divergent and found to be potential for exploitation in hybridization programme to enhance heterotic potential in rice crop. These results are in congruence with findings of Rahimi et al., (2013), Pandit et al., (2016), Sharafi et al., (2018), Divya et al., (2022), in rice.

## Conclusion

PCA concluded that the first four PCs with eigen values more than one describing 24.76%, 23.26%, 14.54 and 13.22%, respectively attributed 75.80% of total variation. The cluster analysis exhibited

high genetic diversity, indicating a great chance for crop improvement by employing hybrids from other clusters. NRH 24, NRH 46, NRH 40, NRH 38, NRH 53, NRH 2 were identified as promising hybrids and can be used in developing diverse and heterotic inbred lines. Besides, the hybrids *viz.*, NRH 5 (49.89%), NRH 14 (28.54%), NRH 11(24.09%), NRH 16 (22.01%), NRH 18 (19.02%), NRH 36 (17.90%), NRH 27 (16.57%), NRH 47 (16.52%) were recognized as best heterotic hybrids for yield over best hybrid check HC4 (HRI 174) that governed by dominant genes and hence these hybrids can be advanced to evaluate under multi-location trails and further forwarded for commercial exploitation.

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