

ELUCIDATION OF RICE ADVANCED BREEDING LINES (F₆ GENERATION) FOR GENETIC DIVERSITY THROUGH PRINCIPAL COMPONENT AND HIERARCHICAL CLUSTERING ANALYSIS

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ABSTRACT

The current study aimed to evaluate 200 advanced breeding lines along with three checks during *kharif*, 2024 to delineate the extent of genetic diversity for yield and its component traits using multivariate techniques using Principal Component Analysis (PCA), Hierarchical clustering and correlation. In PCA, the principal components having eigen values greater than one *viz.*, PC1, PC2, PC3, PC4 and PC5 detailing 20.3%, 16.7%, 14%, 12.8% and 12.7% respectively with a cumulative effect of 76.7% of the total variation. Based upon Wards method of hierarchical clustering, 200 rice advanced breeding lines along with three checks were divulged into 14 clusters based on different traits studied, in which cluster I topped with 30 advanced breeding lines followed by cluster XIII and VI with 29 and 25 advanced breeding lines, respectively. The advanced breeding lines confined to cluster X registered higher cluster mean values for grain yield. Besides, cluster XIV showed highest values for panicle length, ear bearing tillers/m² and grains per panicle. The trait grain yield registered positive association with days to 50 % flowering, days to maturity, ear bearing tillers/m², grains per panicle and test weight through correlation analysis. From the present study, the advanced breeding lines *viz.*, NDRA 78, NDRA 225, NDRA 226, NDRA 227 and NDRA 50 were identified as genetically potential advanced breeding lines for commercial exploitation for enhancing yield and component traits in rice.

Keywords: Correlation, Genetic diversity, Hierarchical cluster analysis, Principal component analysis, Rice.

INTRODUCTION

Rice (*Oryza sativa* L.) is foremost food crop feeding over half of the world's population (Ricepedia, 2025). Globally, India ranks second in rice production next to China. Despite, India produces 22% of the world's rice supply, population growth in the country is predicted to threaten food security by 2050 and increase demand for rice (Fathima *et al.*, 2021). In India,

during 2024-25 rice crop reported a production of 226.5 million tonnes from 51 million ha with average productivity of 4441 Kg/ha. In Andhra Pradesh, the crop is cultivated in total area of 1.92 million ha with production of 11.26 million tonnes and productivity of 5861 million tonnes (Season and Crop Report, 2023-24, Directorate of Economics and Statistics, Govt. of Andhra Pradesh). Even though the green revolution

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significantly increased rice production and productivity, a yield plateau prevented future advancement mainly due to various biotic and abiotic stresses. Hence, guaranteeing food security in future is a big challenging task, particularly, for rice breeders in India as rice is pivotal for food and nutritional security in the country. Despite this, options for breeders are very limited. Hence, breeders need to identify genetically diverse and potential advanced breeding lines for their inclusion in crop improvement programme by divergence studies for yield and its attributing traits.

Among various multivariate analysis tools viz., Principal Component Analysis (PCA) and cluster analysis have been reported to be effective for evaluating the phenotypic diversity in addition to identifying genetically distant clusters of genotypes and selecting important traits contributing to the total variation in the genotypes (Sudeepthi *et al.*, 2020a). PCA has an edge over the other as it eliminates multicollinearity among the independent variables and shows the relevance of the largest contributor to the total variance at each differentiation axis and it comprehends non-parametric strategy from a complicated set of data. Hierarchical cluster analysis of quantitative traits is used to measure the genetic divergence and to classify the genetic stock into distinct groups (Pavan Kumar *et al.*, 2019). Genetic divergence analysis using PCA and hierarchical cluster analysis is productive in determining potential advanced breeding lines useful for hybridization. The prime objective of this examination was to delineate/elucidate genetic diversity and identify the superior advanced breeding lines for their inclusion in the commercial rice improvement programme.

MATERIAL AND METHODS

The prevailing examination was laid out with 200 advanced breeding lines of rice in F_6

generation together with three checks (NDLR 7 (tolerant to BPH and Blast with potential yield of 6.5-7 (t/ha), NDLR 8 (tolerant to BPH, leaf folder and moderately tolerant to Blast with potential yield of 6 – 7.5 (t/ha) and BPT 5204 (tolerant to BLB and Blast with potential yield of 6 (t/ha) during *kharif*, 2024 at Regional Agricultural Research Station (RARS), Nandyal, Andhra Pradesh, India during *kharif*, 2024. All the advanced breeding lines were evaluated in an Augmented Block Design with plot size of 10 m² per line with a spacing of 20 x 15 cm. All the standard cultural and agronomic practices recommended by Acharya N.G. Ranga Agricultural University were adopted to achieve good crop growth. Data was gathered from five competitive and randomly selected plants for recording yield and yield attributes viz., Plant height (PH), Ear bearing tillers/m² (EBT/m²), Panicle length (PL), Grains per panicle (GP), Test weight (TW) and Grain yield (Kg/ha)(GY) however data on days to 50% flowering (DFF) and days to maturity (DM) data was measured on plot basis. To assess genetic diversity among advanced breeding lines, PCA and cluster analysis were used to identify the most contributing traits for variation and diversity among advanced breeding lines, respectively. The obtained data through evaluation of advanced breeding lines is subjected to statistical analysis to delineate genetic diversity through hierarchical clustering and PCA using JMP 18.0 statistical software (SAS Institute Inc., Cary, NC, USA).

RESULTS AND DISCUSSION

The descriptive statistics of eight studied traits in 200 advanced breeding lines along with three checks is documented in Table 1. The advanced breeding lines, NDRA 3, NDRA 7, NDRA 20, NDRA 25, NDRA 30, NDRA 47, NDRA 62 and NDRA 94 (97 days) was observed to be early flowering, while NDRA 225 was late flowering (111 days). The line NDRA 94 (129)

Table 1. Descriptive statistics of eight yield and yield component characters in rice advanced breeding lines

S.No	Characters	Mean	Minimum	Maximum	SD	SE
1	DFF	105.06	97	112	1.91	0.13
2	DM	135.31	125	142	2.65	0.19
3	PH (cm)	89.53	70.42	109.34	6.78	0.48
4	PL	22.90	20.5	25.28	0.89	0.06
5	EBT/m ²	521.80	336.6	778.8	91.09	6.39
6	GP	280.99	160.8	530.6	60.80	4.27
7	TW (G)	12.86	9.07	15.3	1.29	0.09
8	GY(Kg/ Ha)	6473.02	4650	8760	888.67	62.37

noticed early maturity while NDRA 58 and NDRA 80 (142) matured late than other advanced breeding lines. The PH ranged from 70.42 cm (NDRA 86) to 109.34 cm (NDRA164) with an average plant height of 89.53 cm. The mean value of PL was found to be 22.90 cm with range from 20.5 cm (NDRA 101) to 25.28 cm (NDRA 135). The hybrid NDRA 98 was found to bear a greater number of ear bearing tillers (778 / m²), while least number of ear bearing tillers (336 / m²) was displayed by hybrid, NDRA 150. The trait GP varied from 160 (NDRA 191) to 530 (NDRA 81) with mean value of 280. The advanced breeding lines NDRA 50 (9.07) and NDRA 001 (15.3) recorded minimum and maximum TW among all the advanced breeding lines. The mean GY (Kg/ha) was recorded as 6473 Kg with range from 4650 Kg (NDRA79) to 8760 Kg (NDRA 45) among the studied advanced breeding lines. The presence of significant variability among the advanced breeding lines for yield and yield component traits is the key for success in crop improvement programme. Vasudeva Reddy *et al.*, 2023 and Vijay Kumar *et al.*, 2024 reported the similar experimental results while evaluating advanced breeding lines for yield and its component traits in rice.

The PCA is an authentic tool utilized for successful selection of divergent genotypes in

crop improvement programme. The results of PCA revealed the significance of first five PCs in discriminating 200 advanced breeding lines along with three checks. The first five PCs viz. PC1, PC2, PC3, PC4 and PC5 exhibited eigen value greater than one explaining 76.7% of total variation. The eigen values and total cumulative percentage of variances explained by PCs is furnished in Table 2. PC1 with eigen value of 1.63 contributes 20.3% of the total variability, PC2, PC3, PC4 and PC5 with eigen value of 1.33, 1.12, 1.02 and 1.02 attributed 16.7%, 14.0%, 12.8%, and 12.7% of the total variability, respectively. The first PC displayed high positive weight to DFF (0.686), and DM (0.634). The second PC displayed highest positive loading to TW (0.734) and GY (0.364). The third PC displayed highest positive loading to EBT/m² (0.643). Likewise, the fourth and fifth PCs gave positive loading to PL (0.753) and PH (0.709), respectively (Table 3).

The greater portion of the variance (20.3%) was noticed in PC1 and was strongly convinced by DFF, DM, EBT/m² and GY. PC2 was influenced by DM, PL, TW and GY. Similarly, PC3 was influenced by EBT/m², GY, GP and TW. Likewise, PC4 and PC5 are primarily influenced by PL, PH and PH, GY respectively. Similar kind of results are in agreement with findings of Sudeepthi *et al.*

Table 2. Total variances explained by different principal components in rice advanced breeding lines

Components	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Eigen values	1.63	1.33	1.12	1.02	1.02	0.85	0.68	0.32
Proportion variance %	20.3	16.7	14.0	12.8	12.7	10.6	8.58	4.01
Cumulative variance %	20.3	37.1	51.1	63.9	76.7	87.4	95.9	100

Table 3. Factor loading of different characters with respect to different principal factors in rice advanced breeding lines

Principal Components	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
DFF	0.686	-0.155	-0.110	0.101	-0.745	-0.064	-0.194	0.659
DM	0.634	0.194	-0.114	0.279	-0.132	0.048	0.305	-0.596
PH (cm)	-0.044	-0.202	-0.156	0.456	0.709	0.459	0.079	0.051
PL	-0.247	0.354	-0.005	0.753	-0.113	-0.591	-0.003	0.077
EBT/m ²	0.117	-0.399	0.643	-0.87	0.160	-0.215	0.573	20.070
GP	-0.098	-0.253	0.370	0.343	-0.570	0.569	-0.146	0.000
TW (G)	-0.083	0.734	0.134	0.078	-0.050	0.239	0.441	0.418
GY (Kg/ Ha)	0.181	0.364	0.617	0.059	0.326	-0.615	-0.563	-0.144

Bold figures indicate maximum and minimum values in each character.

2020a, Venkata Ratnam *et al.*, 2022, Edukondalu *et al.*, 2024 and Paramanik *et al.*, 2025 in rice.

The biplot depicted the relationship of 200 advanced breeding lines along with three checks for eight traits (Fig. 1). From the biplots, the eight yield and yield attributing traits were divulged into four groups. GY and DM were grouped in same cluster. DFF and EBT/m² were grouped in same cluster. The traits PL and TW were grouped in another cluster. Whereas, PH and GP together grouped as one cluster. The selection of advanced breeding lines with highest score (0.617) in PC3 will be desirable for developing high grain yielders in rice. The study showed that NDRA 78, NDRA 225 (NDLR 7 check), NDRA 226 (NDLR 8 check), NDRA 227 (BPT 5204 check) and NDRA 50 were located at extreme ends of distinct quadrants of the plot. Hence, these advanced breeding

lines and checks were recognized as highly divergent and found to be potential for exploitation in hybridization programme to enhance heterotic potential in rice crop.

Hierarchical cluster analysis was conducted with 200 advanced breeding lines along with three checks using Wards method which provides the best result to get the finest possible classification. The cluster analysis revealed the aggregation of advanced breeding lines into fourteen clusters (Table 4 and Fig.2). The cluster means computed for eight major yield attributing characters revealed the existence of ample amount of variation among the clusters (Table 5). The highest and lowest cluster means were recorded for the traits GY (7902.86) and TW (11.44), respectively. Maximum cluster mean of overall traits was noticed in cluster X (7902.86) followed by cluster XIV (673.20). In contrast, the least

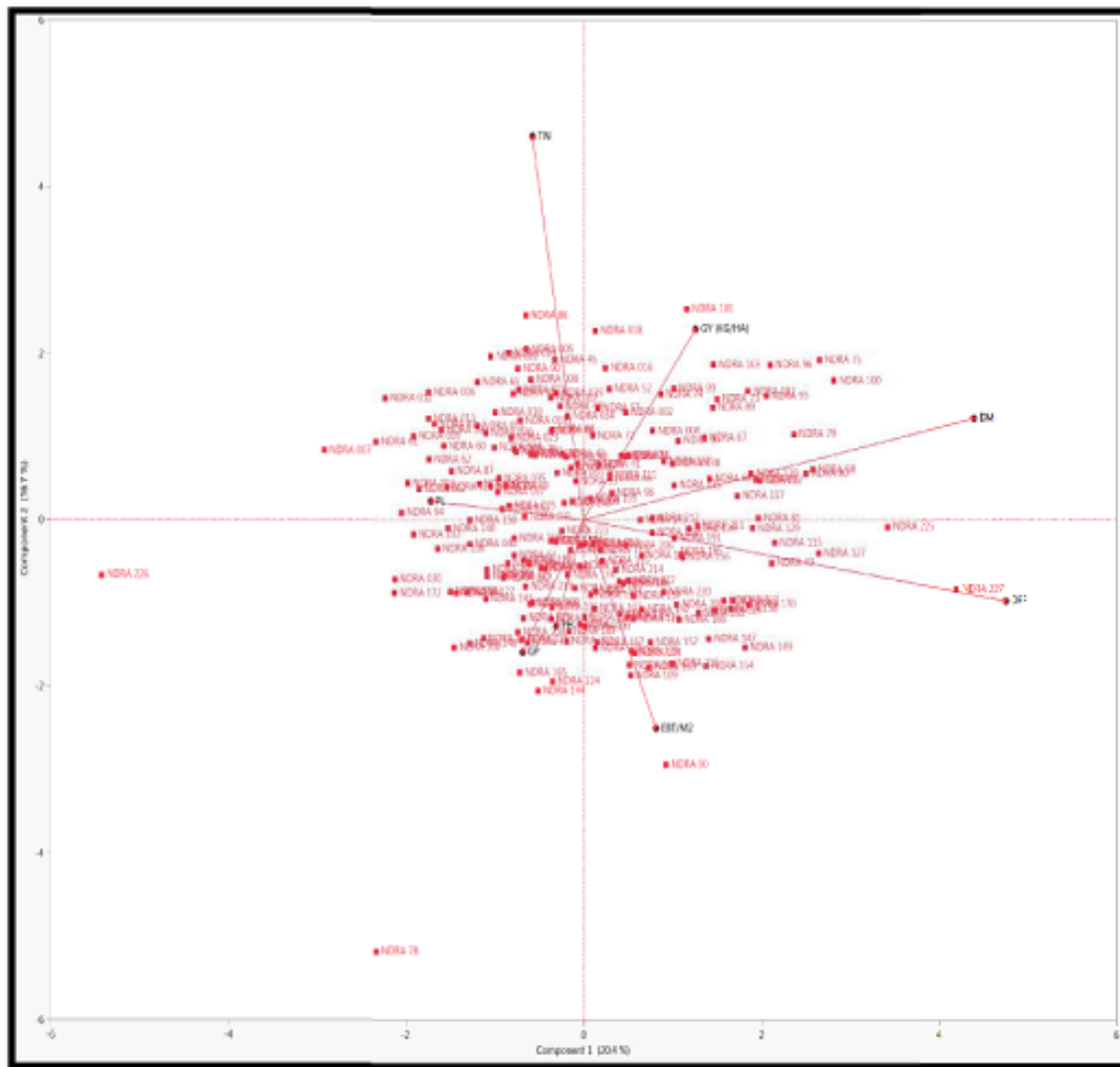


Fig 1. Biplot comprising of 200 rice advanced breeding lines along with three checks for eight yield and yield attributing traits

cluster mean was displayed by cluster XIV(11.44). This clearly infers the existence of ample amount of genetic divergence in the advanced breeding lines of these clusters. Further, among the fourteen divergent clusters, the highest numbers of advanced breeding lines were grouped in cluster I with 30 advanced breeding lines followed by 29 advanced breeding lines in cluster XIII and 25 advanced breeding lines in cluster VI. The advanced breeding lines in cluster XI showed highest mean values for DFF and DM. Similarly, the advanced breeding lines of cluster XIV showed maximum values for PL, EBT/m² and GP. The

advanced breeding lines in cluster X displayed maximum cluster value for GY. Ravi Kumar *et al.*, 2015, Kusuma Kumari *et al.*, 2021, Mondal *et al.*, 2024 and Howlander *et al.*, 2025 also documented same kind of clustering of accessions into distinct clusters.

The constellation plot based on Wards method (Fig. 3) depicts relationship among the 200 advanced breeding lines along with three checks. The advanced breeding lines 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 advanced breeding lines into

Table 4. Grouping of different advanced breeding lines into different clusters

Cluster	No. of advanced breeding lines	Advanced breeding lines
I	30	NDRA 001, NDRA 002, NDRA 74, NDRA 016, NDRA 41, NDRA 97, NDRA 017, NDRA 019, NDRA 77, NDRA 53, NDRA 93, NDRA 003, NDRA 69, NDRA 71, NDRA 87, NDRA 020, NDRA 025, NDRA 031, NDRA 64, NDRA 036, NDRA 037, NDRA 181, NDRA 42, NDRA 49, NDRA 040, NDRA 201, NDRA 023, NDRA 035, NDRA 032, NDRA 61
II	15	NDRA 018, NDRA 88, NDRA 022, NDRA 90, NDRA 47, NDRA 62, NDRA 59, NDRA 65, NDRA 60, NDRA 76, NDRA 029, NDRA 45, NDRA 66, NDRA 111, NDRA 72
III	16	NDRA 005, NDRA 008, NDRA 011, NDRA 014, NDRA 91, NDRA 015, NDRA 024, NDRA 021, NDRA 033, NDRA 63, NDRA 006, NDRA 010, NDRA 012, NDRA 013, NDRA 007, NDRA 009
IV	7	NDRA 034, NDRA 48, NDRA 44, NDRA 039, NDRA 46, NDRA 51, NDRA 52
V	15	NDRA 030, NDRA 172, NDRA 110, NDRA 159, NDRA 150, NDRA 136, NDRA 146, NDRA 177, NDRA 219, NDRA 209, NDRA 164, NDRA 205, NDRA 204, NDRA 206, NDRA 223
VI	25	NDRA 108, NDRA 151, NDRA 157, NDRA 176, NDRA 128, NDRA 152, NDRA 113, NDRA 143, NDRA 185, NDRA 174, NDRA 183, NDRA 214, NDRA 199, NDRA 109, NDRA 112, NDRA 203, NDRA 213, NDRA 119, NDRA 142, NDRA 122, NDRA 169, NDRA 125, NDRA 163, NDRA 198, NDRA 167
VII	10	NDRA 94, NDRA 144, NDRA 165, NDRA 224, NDRA 148, NDRA 175, NDRA 197, NDRA 207, NDRA 221, NDRA 226
VIII	16	NDRA 114, NDRA 130, NDRA 140, NDRA 193, NDRA 116, NDRA 182, NDRA 141, NDRA 179, NDRA 194, NDRA 208, NDRA 168, NDRA 171, NDRA 196, NDRA 178, NDRA 180, NDRA 210
IX	15	NDRA 004, NDRA 95, NDRA 81, NDRA 79, NDRA 80, NDRA 038, NDRA 57, NDRA 70, NDRA 58, NDRA 103, NDRA 73, NDRA 96, NDRA 89, NDRA 99, NDRA 102
X	7	NDRA 67, NDRA 75, NDRA 85, NDRA 100, NDRA 68, NDRA 127, NDRA 101
XI	7	NDRA 43, NDRA 115, NDRA 139, NDRA 166, NDRA 135, NDRA 225, NDRA 227
XII	10	NDRA 86, NDRA 145, NDRA 195, NDRA 117, NDRA 129, NDRA 120, NDRA 138, NDRA 212, NDRA 211, NDRA 156
XIII	29	NDRA 50, NDRA 124, NDRA 202, NDRA 131, NDRA 92, NDRA 118, NDRA 173, NDRA 191, NDRA 107, NDRA 186, NDRA 220, NDRA 184, NDRA 192, NDRA 222, NDRA 187, NDRA 98, NDRA 137, NDRA 153, NDRA 155, NDRA 121, NDRA 147, NDRA 123, NDRA 200, NDRA 149, NDRA 126, NDRA 170, NDRA 158, NDRA 154, NDRA 215
XIV	1	NDRA 78

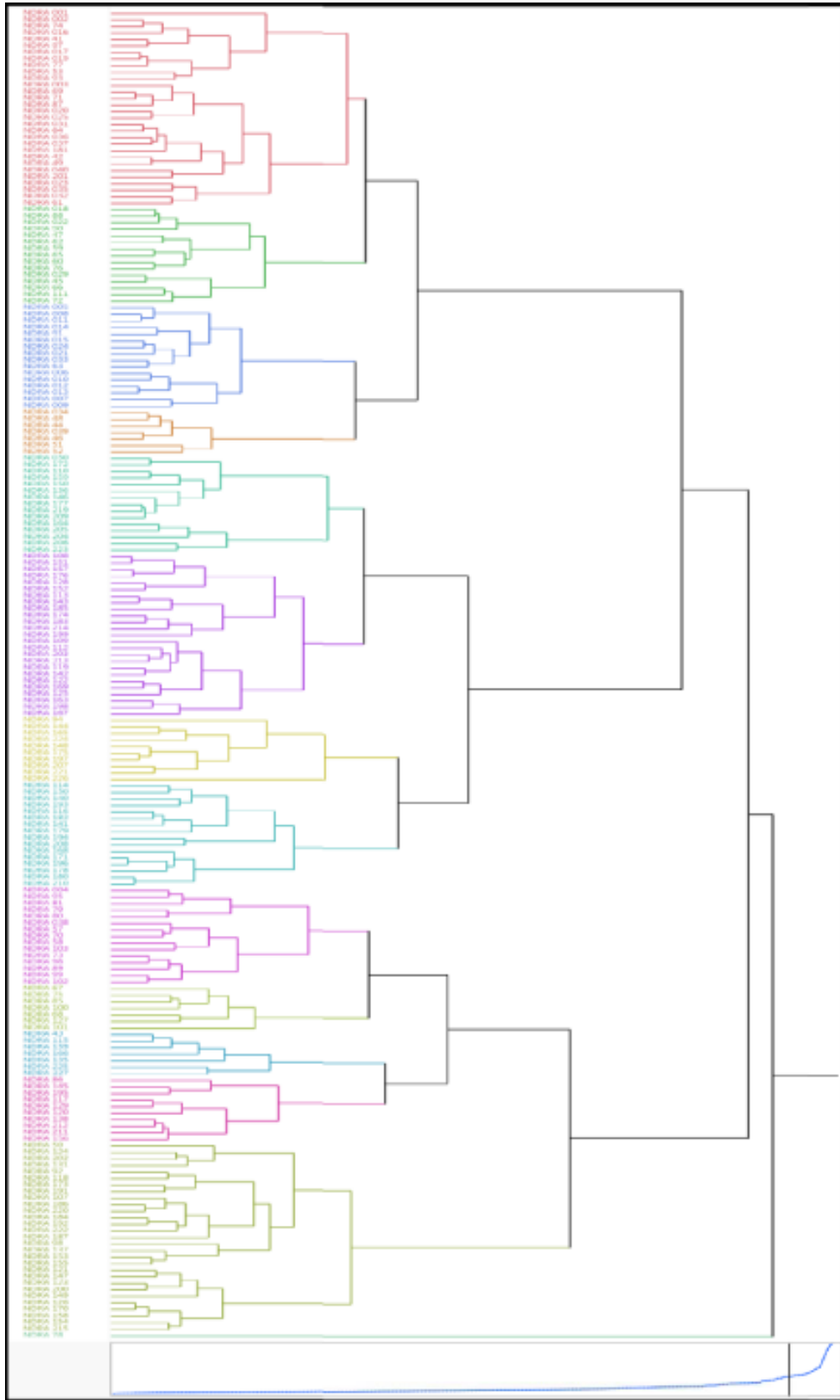


Fig 2. Dendrogram showing clustering by Wards method

Table 5. Cluster means of various characters of rice advanced breeding lines under study

Cluster No.	DFF	DM	PH	PL	EBT/m ²	GP	TW	GY(Kg/ha)	Mean
Cluster I	103.73	135.23	89.88	23.48	566.28	279.12	13.95	6616.00	978.46
Cluster II	103.67	134.20	90.10	23.25	481.80	292.35	13.73	7820.00	1119.89
Cluster III	103.50	134.06	86.47	23.14	438.90	298.80	14.56	5923.13	877.82
Cluster IV	103.29	137.57	94.80	21.96	485.57	265.63	14.13	6300.00	927.87
Cluster V	104.60	133.40	96.53	23.40	428.12	274.05	11.93	5912.00	873.00
Cluster VI	105.72	135.56	93.91	23.27	553.87	279.26	11.79	5914.80	889.77
Cluster VII	103.10	131.50	96.14	22.44	613.15	294.57	12.02	6131.60	925.56
Cluster VIII	104.44	132.88	85.18	22.04	469.43	259.94	11.84	6073.13	894.86
Cluster IX	107.33	138.87	90.34	22.59	439.56	308.05	14.19	6458.00	947.37
Cluster X	107.00	137.71	89.91	21.18	521.40	258.23	13.79	7902.86	1131.51
Cluster XI	108.38	139.04	93.22	23.53	565.85	275.81	12.06	7280.98	1062.36
Cluster XII	106.40	137.60	79.81	23.48	432.96	293.50	12.05	6447.00	941.60
Cluster XIII	106.28	135.52	84.04	22.48	626.54	267.28	11.87	6580.34	979.30
Cluster XIV	104.00	133.00	86.86	23.66	673.20	400.38	11.44	5880.00	1364.50
Mean values	105.10	135.44	89.80	22.85	521.19	546.46	12.81	6517.13	

Bold figures indicate maximum and minimum values in each character.

14 clusters with membership of 30, 15, 16, 7, 15, 25, 10, 16, 15, 7, 7, 10, 29 and 1. The Clustering pattern divulged that majority of advanced breeding lines congregated in cluster I (30), followed by Cluster XIII (29) and Cluster VI (25). The advanced breeding lines with longer vector line represent greater genetic distance between the clusters. Further, the identified advanced breeding lines with maximum genetic distance are considered as superior and exploited commercially in yield improvement programme in rice.

The correlation analysis of eight traits (Fig 4) revealed that PH was positively correlated with PL and PL was positively associated with PH, GP and TW. Similarly, GP was positively associated with DM, PL and TW. Likewise, TW was associated with DM, GP and GY. Furthermore, GY was positively associated with DFF, DM, EBT/m², GP and TW and

negatively associated with PH and PL. Similar kind of association results were also in congruence with Sudeepthi *et al.*, 2020b, Roy *et al.*, 2024 and Howlader *et al.*, 2025.

CONCLUSION

PCA concluded that the first five 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 revealed high genetic diversity, suggesting a significant opportunity for crop improvement by utilizing advanced breeding lines from other clusters and recognized advanced breeding lines *viz.*, NDRA 78, NDRA 225, NDRA 226, NDRA 227 and NDRA 50 as superior and divergent advanced breeding lines for commercial exploitation. Furthermore, the advanced breeding lines *viz.*, NDRA 45, NDRA 90, NDRA

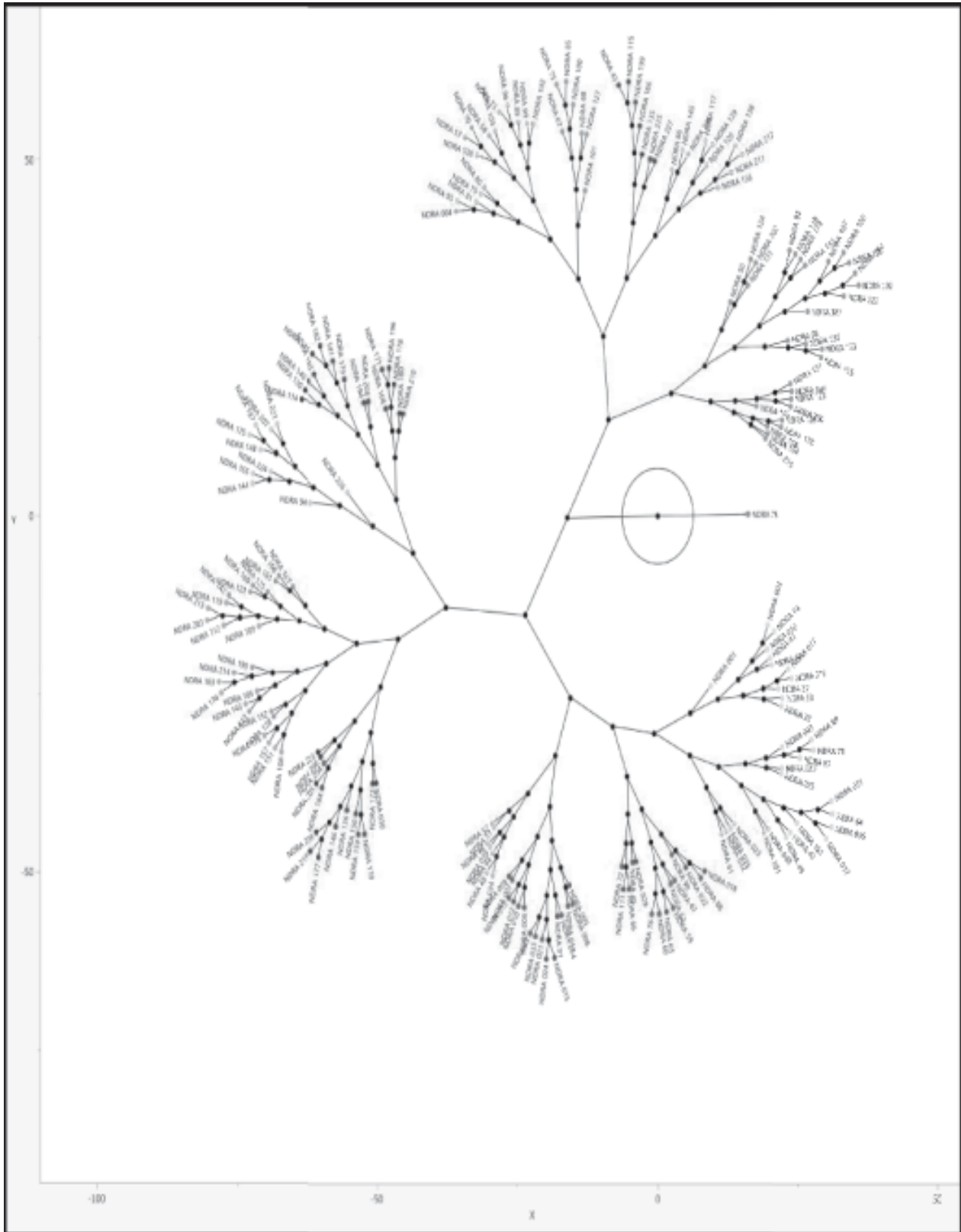


Fig 3. Constellation plot of 200 advanced breeding lines along with three checks into 14 clusters based on Euclidean distance

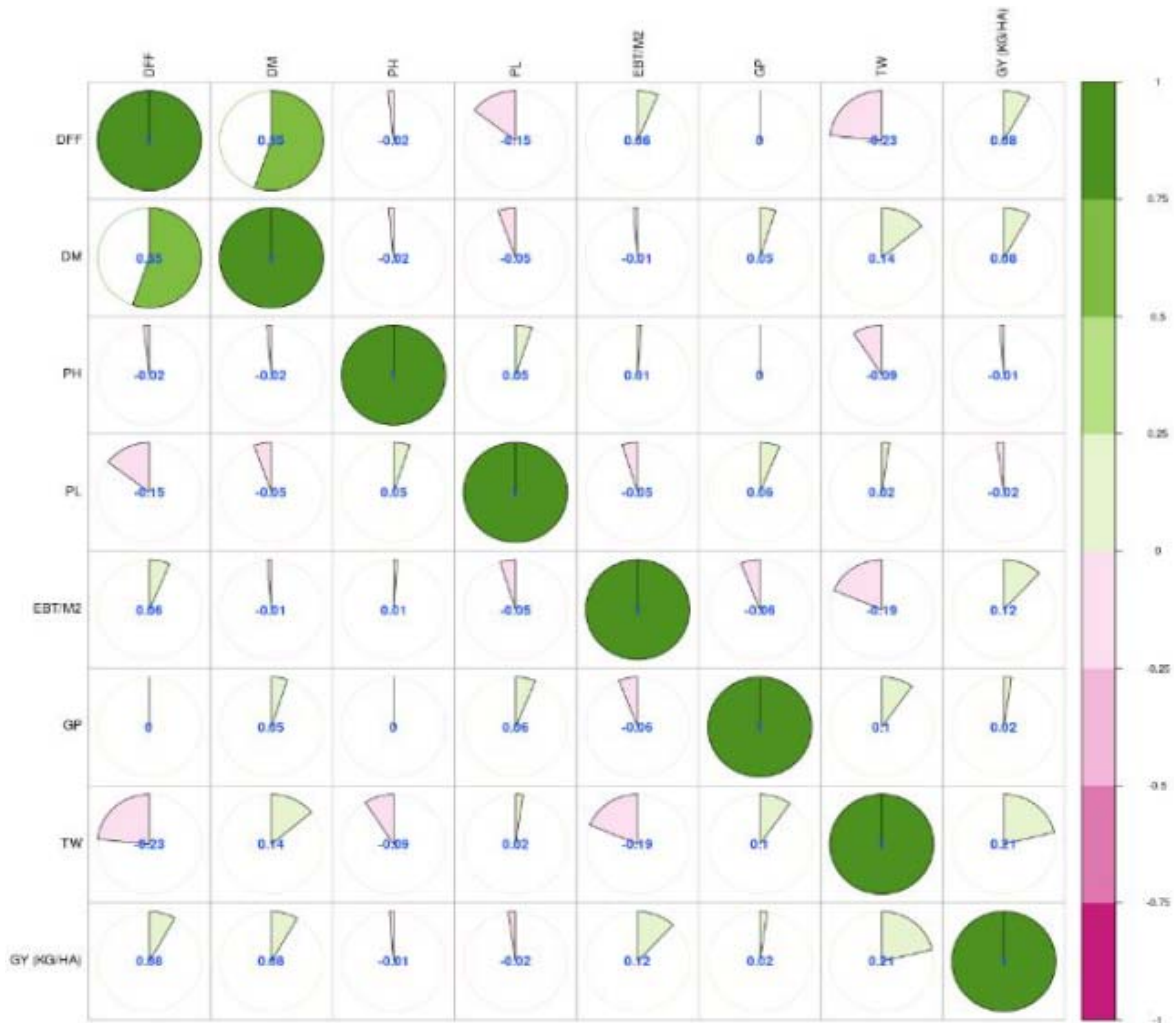


Fig 4. Correlation for yield and its components in rice advanced breeding lines

029 and NDRA 131 were identified as top grain yielders which can be exploited in crop improvement programme. Based on correlation analysis, GY was positively associated with DFF, DM, EBT/m², GP and TW and negatively associated with PH and PL.

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