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Research Note

Assessment of genetic variability and diversity analysis in medium duration rice accessions

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Abstract

A total of 64 medium duration rice accessions were evaluated for their genetic variability and genetic divergence during *Rabi* season 2020 at Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal. Analysis of variance revealed significant differences for all the traits considered for the study. The traits spikelets per panicle and filled grains per panicle recorded high GCV as well as PCV thereby indicating that these traits would be improved effectively through selection. Other yield component traits viz., plant height, productive tillers per plant, spikelets per panicle, filled grains per panicle, fertility per cent, grain weight and single plant yield revealed high heritability coupled with high genetic advance, indicating that simple selection could be effective for improving these characters. The D^2 values and hierarchical clustering analysis grouped the 64 germplasm into seven clusters. In both the clustering methods, the genotype Gold 44 was grouped under separate clusters indicating that, this is a diverse genotype among all the genotypes taken for study. Further, genotype AD 16124 was grouped under the same cluster in both the clustering methods with the highest cluster mean for grain yield per plant. Hence, this genotype could be efficiently utilized for the yield improvement programme in rice.

Keywords: Variance, Heritability, Genetic advance, Diversity, Cluster and Rice.

Rice is the major staple food of South and South East Asia, wherein 90 per cent of the world's rice is produced and consumed. The global area under rice cultivation during the year 2020 was 166 M.ha with production of about 750 MT. In India, the total area under rice cultivation was 43.77 M.ha with a production of about 169.14 MT and productivity of 3.86 tonnes per hectare (Pathak *et al.*, 2020). Quantum jump in rice productivity has been achieved with the development of high yielding varieties for commercial cultivation. However, rice being major food crop in Southern, Eastern and North Eastern states of India, improving its productivity has become a crucial importance in these states (Subbaiah *et al.*, 2011). During late samba and thaaladi seasons, medium duration rice varieties like CO(R) 43, Improved White Ponni (IWP),

BPT 5204, ASD(R) 19, ADT(R) 39 and ADT(R) 46 are grown by the farmers in Karaikal region in Pondicherry state. The information on the nature and magnitude of genetic variation of yield contributing traits is essential for genetic improvement of the crop.

The estimates of mean, variability, heritability and genetic advance will be useful for an efficient selection process in crop improvement. Assessment of PCV and GCV is essential criteria to select better performing lines among the divergent groups (Kahani and Hittalmani, 2016). Heritability and Genetic Advance are useful in predicting the genetic gain under selection than heritability alone. Genetic diversity analysis is used for estimating and establishing of genetic relationship in germplasm

collection and identifying diverse genotypes having wider variability for various characters. The information on genetic diversity has been successfully used for efficient germplasm utilization and genotype selection. Mahalanobis's D^2 statistics (1936) is a powerful tool to quantify the degree of genetic divergence between the genotypes and to relate clustering pattern with the geographic origin. Genetic diversity analysis is helpful in estimating and establishing of genetic relationship of genotypes in germplasm collection, identifying the diverse genotypes having wider variability for various characters and for efficient selection of parents for hybridization programme. Considering these views in mind, the present experiment was formulated to study the genetic variability and its magnitude, genetic divergence and clustering pattern of medium duration rice germplasm to select the suitable parental lines for further rice breeding programmes.

The testing material for the present study comprised of 64 medium duration rice accessions obtained from the Indian Institute of Rice Research (IIRR), Hyderabad and was laid in a Randomized Block design (RBD) with three replications in Eastern farm of PJN College of Agriculture and Research Institute, Karaikal during *Rabi*, 2020. Biometrical observations were recorded on five randomly selected plants in each replication, for nine yield and yield contributing traits *viz.*, flowering duration, plant height, productive tillers per plant, panicle length, spikelets per panicle, filled grains per panicle, fertility per cent, grain weight and single plant yield. The biometrical values were recorded on single plant basis for all the characters, except flowering duration, which was recorded on individual plot basis. The mean values in each replication for all the nine characters were subjected to analysis of variance to test the significance for each character in accordance with the methodology of Panse and Sukhatme (1967). The variances due to genotypic as well as phenotypic values, as well as the coefficient of variations due to genotype and phenotype were estimated by the formulae given by Burton and de Vane (1953). Genetic diversity among

the 64 accessions were subjected to Mahalanobis D^2 statistics as suggested by Rao (1952). Statistical analysis for variability was performed using the TNAU STAT software (Manivannan, 2014) and for hierarchical clustering with UPGMA (Unweighted Pair-Group Method using Arithmetic Average) by using arithmetic means for construction of dissimilarity measures. The construction of phylogenetic tree was derived by the greater similarity of the genotypes (Matta *et al.*, 2015). The dissimilarity matrix was calculated with adjusted mean values for nine quantitative characters using STAR statistical program (version 2.0.1)

The genetic variability available in any crop species is the basic resource for selecting the better performing lines among the divergent group of germplasm lines and later quantifying the extent of variability created for the traits of interest (Kahani and Hittalmani, 2016). In this study, the analysis of variance revealed the presence of significant differences among the genotypes for all the nine traits, indicating the presence of heterogeneity. The phenotypic coefficient of variation (PCV) was found to be higher than the genotypic coefficient of variation (GCV) for all the nine traits (**Table 1**) indicating that the influence of environment on these traits were at a lower level. These are in accordance with the reports of Rashid *et al.* (2017) and Gyawali *et al.* (2018). Higher phenotypic as well as genotypic coefficient of variations were recorded for spikelets per panicle, filled grains per panicle, single plant yield and productive tillers per plant; moderate values were recorded for fertility per cent and plant height and the least values were recorded for flowering duration and panicle length. Further, the differences in PCV and GCV ranged from 0.08 to 4.22 and this is probably due to lesser influence of environmental on all the nine traits studied. Therefore, selection based on phenotype can be effective in those traits having high and moderate variability for yield improvement. The reports of Kishore *et al.* (2015), Rashid *et al.* (2017) and Devi *et al.* (2020) support the above findings. The highest difference between PCV and GCV were observed in productive tillers

Table 1. Genetic variability parameters for grain yield and its component traits in Rice

Traits	Variance		PCV (%)	GCV (%)	h ²	GA	GA as per cent of mean
	Phenotypic	Genotypic					
Flowering duration	67.16	62.68	8.65	8.36	93.33	15.76	16.63
Plant height (cm)	173.48	169.62	10.71	10.59	97.77	26.53	21.56
Productive tillers per plant	7.14	6.57	17.90	17.17	92.02	5.07	33.93
Panicle length (cm)	4.20	3.94	8.85	8.57	93.81	3.96	17.11
Spikelets per panicle	1391.10	1360.95	24.51	24.24	97.83	75.17	49.40
Filled grains per panicle	945.70	905.38	24.19	23.67	95.74	60.65	47.71
Fertility per cent	76.27	73.77	10.45	10.28	96.72	17.40	20.82
Grain weight (g)	7.40	7.00	13.58	13.21	94.59	5.30	26.46
Single plant yield (g)	26.96	26.56	19.58	19.43	98.52	10.54	39.73

per plant whereas, the least difference was exhibited by flowering duration. This reveals that some degree of environmental influence does exist on the phenotypic expression of these characters and selection based on these traits would be effective for rice yield improvement programmes.

Heritability indicates the extent of inheritance of characters from parents to their off springs and can helpful to predict the genetic gain, which is .nothing but the reliability of the phenotypic value to achieve higher breeding value during selection process. In the present study, all the nine traits recorded high heritability ranging from 92.02 to 98.52 per cent (**Table 1**). Among them highest heritability per cent was recorded by single plant yield (98.52 per cent) followed by spikelets per panicle (97.83 per cent), plant height (97.77 per cent), fertility per cent (96.72 per cent) and filled grains per panicle (95.74 per cent). The higher heritability per cent of these traits suggests that environmental factors did not greatly affect their phenotypic expression. Therefore, we can adopt simple selection methods by using these highly heritable traits for yield improvement. Similar results with high heritability estimates were reported by Hasan *et al.* (2019) and Roy and Shil (2020) supports our findings.

The heritability is the combined effect of additive as well as non-additive genes. However, its practical utility cannot be fully achieved unless it is corroborated with genetic advance. Genetic advance gives the understanding on the type of gene action, especially for quantitative traits. Highest genetic advance was recorded for spikelets per panicle (75.17 per cent) followed by filled grains per panicle (60.65 per cent); moderate value was recorded by plant height (26.53 per cent) and the least value was

recorded for panicle length (3.96 per cent) and productive tillers per plant (5.07 per cent). Genetic advance as per cent of mean is a more reliable parameter than genetic advance. The highest genetic advance as per cent of mean was recorded by spikelets per panicle (49.40 per cent), followed by filled grains per panicle (47.71 per cent) and single plant yield (39.73 per cent); moderate values by productive tillers per plant (33.93 per cent), grain weight 26.46 per cent), plant height (21.56 per cent) and fertility per cent (20.82 per cent); whereas the lowest was recorded by flowering duration (16.63 per cent) and panicle length (17.11 per cent). High genetic advance indicated the predominance of the additive gene action. Hence, selection based on the above traits with high genetic advance would be very effective and the selected genotypes can be used as a parental line for the varietal development program. The findings of Khare *et al.* (2014) are in accordance to our results.

High heritability coupled with high genetic advance is an indication of preponderance of additive gene action and such trait is effective for phenotypic selection. (Johnson *et al.*, 1955). High heritability coupled with high genetic advance as per cent of mean was recorded in five component traits *viz.*, spikelets per panicle, filled grains per panicle, single plant yield, productive tillers per panicle and grain weight (**Table 1**). These were in accordance with the findings of Khare *et al.* (2014), Rashid *et al.* (2017), Girma *et al.* (2018) and Osman *et al.* (2020). In general, traits with high heritability coupled with high genetic advance as per cent of mean demonstrates the preponderance of additive gene action in them and it is likely to respond effectively to phenotypic selection. (Johnson *et al.*, 1955).

Table 2. Clustering pattern of 64 medium duration rice genotypes in D² analysis

Clusters	Number of genotypes	Rice accessions
I	23	CB 16118, RP 6329-251-10-3-2, CR 2916-10-2-1-1, CR 2906-253-56-3, KAU PTB 0614-10-14-17, OR 2500-1-1, WGL-1380, CR 3564-1-1-3-2-1-1, RP 6481-RAF20-GSR IR-1 DQ136-Y3-Y2, CR 4121-36-24-1, RP 6195-MC/RIL-SM2, MTU 1348 (MTU 2689-45-1-1), RP 5564 PTB 1-4-1, BPT 3050, ORJ 1352 (TP 30601), HURS-19-3, KJT-2010-3, BRR 0136 (IR 125026-73-1-1), MTU 1347 (MTU 2414-5-1-1-1-1), R 1641-914-1-400-1-20, RP 6112-MS-M-47-2-6-9-4-5-33, RP Bio 5479-248 JF 12 RIL, NWGR-8001
II	20	HKR 15-35, CR 4202-300-1-2-1, CR 4004-14228-2-1-3-2-1-4, KJT 9-2-12-2-8, CR 2851-S-1-6-2B-4-2, RGL 7020, TRC 2020-9, CRAC 3998-124-1, Jaya, Pusa 5278-3-7-1-93-1-1-2, PAU 8442-2K14-3583-422-1 (RYT 3784), OR 2573-11, TTBDR 207-3-2, CB 16101, MSN 109, OROI-8- IR 88228-33-3-5-2, BRM-Brahma, TKM 13, RCPR 67-RP 5484, WGL-1377
III	14	Pusa 5000-1-1-1, RP 6460-C397, CR 4315 -3-1-1-2-1, MTU 1275 (MTU 2385-123-1-2-3), CR 4113-1-2-1-1-1, NDR 359, R 741-1-55-2-1-R-1-5, CR 3564-1-1-4-2-2-1, RTN 0901-1-1-3-1, UPR 4283-7-1-1-1, AD 17764, RP 5405-13-1-3-1-1-1, JGL 33138, PAU 7180-7-26-0-0-0 (RYT 3866)
IV	4	G12 RNR 28399, RP 6476-29-12-5-3, R 1624-82-1-60-1, NVSR-598
V	1	Gold-44
VI	1	AD 16124
VII	1	RP 6328-218-B-29-1

Table 3. Average intra (diagonal) and inter (off-diagonal) cluster D² and D values among seven clusters in medium duration rice

Cluster	I	II	III	IV	V	VI	VII
I	1634.79 (40.43)	6305.95 (79.41)	7814.64 (88.40)	3647.30 (60.39)	8008.39 (89.48)	3731.60 (61.08)	18500.11 (136.02)
II		2411.32 (49.11)	21551.23 (146.80)	7199.94 (84.85)	3292.10 (57.38)	4378.29 (66.17)	31707.65 (178.06)
III			2817.83 (53.08)	10305.56 (101.52)	22519.35 (150.06)	15126.15 (122.99)	11969.05 (109.40)
IV				3661.24 (60.51)	7642.67 (87.42)	5761.63 (75.91)	13453.65 (115.98)
V					0.00	7769.62 (88.15)	29165.07 (107.78)
VI						0.00	26202.73 (161.87)
VII							0.00

Diagonal values – Intra cluster distance; Off-diagonal – Inter-cluster distance

The mean biometrical values recorded on nine quantitative characters for 64 rice accessions were subjected to D² analysis using TNAUSTAT software and clustering of genotype was performed by Tocher's method. The 64 rice accessions were grouped into seven clusters (Table 2). Among the seven clusters, cluster I constituted the maximum of 23 accessions, followed by cluster II (20 accessions). The cluster III had 14 accessions, while the cluster IV had four accessions. The clusters V, VI and VII are monotypic which indicates that these clusters contain the most diverse genotypes.

The D values within and between the seven clusters are presented in Table 3. The highest intra cluster D value was observed in cluster IV (60.51), followed by cluster III (53.08), cluster II (49.11) and cluster I (40.43). The least intra cluster distance was recorded for clusters V, VI and VII indicating the presence of single accession per cluster. The cluster IV exhibited the highest intra-cluster distance and hence its accessions are more diverse than any other clusters. The least inter cluster distance was observed between cluster II and V (57.38) followed by cluster I and IV (60.39), revealing that the genotypes belonging to these clusters were relatively closer to each other and hence crossing among the genotypes belonging to these clusters would not produce desirable recombinants whereas the maximum inter cluster distance was observed between II and VII with of 178.06 followed by cluster VI and VII of 161.87. To realize much variability and high heterotic effects for grain yield and its concerned traits parents should be selected from these two clusters because of wider inter-cluster distance (Mishra *et al.*, 2003). Based on Euclidean distance the accessions were grouped into seven clusters (Table 4 and Fig. 1). Among them, cluster IV is the largest with 25 accessions followed by cluster II with ten accessions and cluster I and V with

nine accessions each and cluster III with eight accessions. However, Cluster VII has only one accession, while cluster VI with two accessions. In addition to divergence, the performance of genotypes and characters that contribute most to divergence should also be taken into account as they seem beneficial for crop improvement. Among all the nine traits, spikelets per panicle exhibited the maximum contribution (30.21%) towards diversity followed by filled grains per panicle (26.38%), spikelet fertility per cent (16.52%), plant height (13.14%), 1000 grain weight (9.92%), grain yield per plant (9.03%), flowering duration (4.61%), productive tillers per plant (0.31%) and panicle length (3.31%) (Table 5). Similar results were reported by Singh *et al.* (2021) and Lakshmi *et al.* (2022).

In both the clustering methods, AD 16124 was grouped under the same cluster with the maximum cluster mean of 45.95 g for single plant yield. It indicates that this genotypes could be efficiently utilized for the yield improvement programme of rice. The Gold 44 is grouped under separate cluster in both the clustering methods which indicates that, this is a diverse genotype among all the genotypes studied (Dey *et al.*, 2020).

The prime objective of this study was to access the genetic variability among the quantitative traits to select the promising medium duration rice genotypes. High magnitude of genetic variability was expressed for spikelets per panicle and filled grains per panicle. Hence, the selection based on these characters would be effective for the betterment for rice breeding programme. Seven out of nine characters *viz.*, plant height, productive tillers per plant, spikelets per panicle, filled grains per panicle, spikelet fertility per cent, grain weight and single plant yield recorded high heritability as well as high genetic advance, indicating the governance of these traits by flexible additive

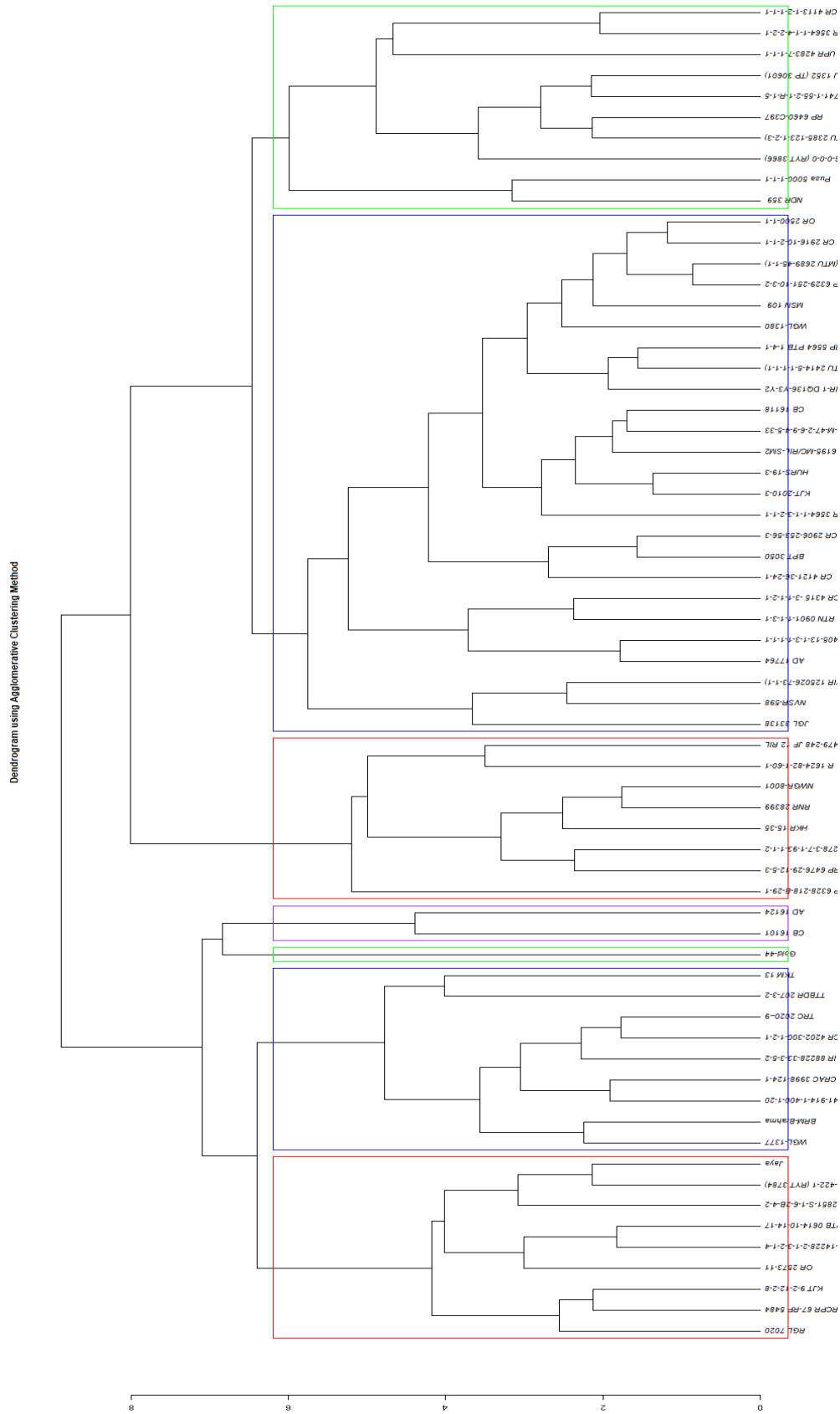


Fig. 1. Dendrogram using Hierarchical (Agglomerative) clustering method for seven clusters in medium duration rice

Table 4. Distribution of genotypes into different clusters in hierarchal cluster analysis for medium duration rice accessions

Cluster	Number of genotypes	Rice accessions
I	9	RCPR 67-RP 5484, PAU 8442-2K14-3583-422-1 (RYT 3784), KJT 9-2-12-2-8, OR 2573-11, CR 2851-S-1-6-2B-4-2, RGL 7020, CR 4004-14228-2-1-3-2-1-4, KAU PTB 0614-10-14-17, Jaya
II	10	CR 3564-1-1-4-2-2-1, MTU 1275 (MTU 2385-123-1-2-3), R 741-1-55-2-1-R-1-5, PAU 7180-7-26-0-0-0 (RYT 3866), NDR 359, G33 ORJ 1352 (TP 30601), CR 4113-1-2-1-1-1, Pusa 5000-1-1-1, UPR 4283-7-1-1-1, RP 6460-C397
III	8	R 1624-82-1-60-1, RNR 28399, HKR 15-35, RP 6476-29-12-5-3, Pusa 5278-3-7-1-93-1-1-2, NWGR-8001, RP 6328-218-B-29-1, RP Bio 5479-248 JF 12 RIL
IV	25	CR 3564-1-1-3-2-1-1, AD 17764, NVSR-598, BPT 3050, RP 6195-MC/RIL-SM2, JGL 33138, MTU 1347 (MTU 2414-5-1-1-1-1), KJT-2010-3, RP 6112-MS-M-47-2-6-9-4-5-33, CR 4121-36-24-1, MSN 109, WGL-1380, RP 6481-RAF20-GSR IR-1 DQ136-Y3-Y2, CB 16118, RTN 0901-1-1-3-1, CR 2916-10-2-1-1, RP 6329-251-10-3-2, MTU 1348 (MTU 2689-45-1-1), RP 5405-13-1-3-1-1-1-1, BRR 0136 (IR 125026-73-1-1), CR 4315 -3-1-1-2-1, G50 HURS-19-3, RP 5564 PTB 1-4-1, CR 2906-253-56-3, OR 2500-1-1
V	9	WGL-1377, OROI-8- IR 88228-33-3-5-2, TTBDR 207-3-2, BRM-Brahma, R 1641-914-1-400-1-20, CRAC 3998-124-1, CR 4202-300-1-2-1, TRC 2020-9, TKM 13
VI	2	CB 16101, AD 16124
VII	1	Gold-44

Table 5. Cluster mean values and relative contribution percentage of nine traits to diversity

Clusters	I	II	III	IV	V	VI	VII	Contribution %
FDR	95.72	95.75	94.86	88.5	<u>73.5</u>	109.5	80.5	4.61
PHT	131.51	117.42	124.21	122.7	<u>95.9</u>	131.1	102.3	13.14
PTL	14.48	15.7	14.24	<u>13.68</u>	21.9	19.5	14	0.31
PNL	23.32	22.62	23.69	23.63	<u>19.4</u>	23.8	23	0.31
SPP	153.7	<u>107.63</u>	207.56	165.53	108.6	121.3	253.4	26.38
FGP	132.04	<u>88.44</u>	176.67	120.66	99.3	104.7	178.8	30.21
FPT	86.14	82.05	85.14	73	91.45	86.35	<u>70.55</u>	16.52
GWT	19.54	20.36	21.1	18.74	19.35	<u>17.3</u>	18.1	9.92
GYP	26.62	24.74	29.35	23.3	<u>19</u>	45.95	21	9.03

FDR: Flowering duration, PHT: Plant height (cm), PTL: Productive tillers per plant, PNL: Panicle length (cm), SPP: Spikelets per panicle, FGP: Filled grains per panicle, FPT: Fertility per cent, GWT: Grain weight (g), GYP: Grain yield per plant (g).

Bold faced indicates the maximum cluster mean values; Underlined indicates the minimum cluster mean value

gene effects and as such simple phenotypic selection would be highly effective and rewarding for improving these traits. In both clustering methods, the genotype AD 16124 can be efficiently utilized for the yield improvement programme of rice.

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