

Genetic Divergence and Variability Studies for Yield and Quality Traits in Elite Rice (*Oryza sativa* L.) Genotypes

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Authors' contributions

This work was carried out in collaboration among all authors. Author KRD designed the study, performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Authors BSC, YH and KRP managed the analyses of the study. Authors NL and PJMR managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

Genetic divergence and variability was assessed among 33 elite germplasm lines which were evaluated in RBD at Regional Agricultural Research Station, Warangal with an objective to classify and understand the nature and magnitude of genetic diversity and variability with regard to grain yield, yield components and quality traits using Mahalanobis D^2 statistics. Genotypes were grouped into eight clusters and cluster I was the largest comprised of 23 genotypes followed by cluster II which consists of 4 genotypes and rest of the clusters from cluster III to cluster VIII contain one genotype each. The maximum cluster distance was found between cluster II and cluster IV (2178.98) followed by cluster III and cluster VIII (2160.16). The minimum inter cluster distance was observed between cluster I and cluster III (540.96). The intra cluster distance was maximum for cluster II (354.1) indicating existence of variability within the cluster. A perusal of results on cluster means revealed that cluster VIII recorded highest cluster mean for yield/plant, panicle length, test

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weight, plant height, volume expansion ratio, kernel length after cooking, length/breadth ratio, kernel length and kernel width, The most important trait causing maximum divergence was plant height (31.8) which ranked 168 times first followed by alkali spreading value, days to 50% flowering and test weight were responsible for differentiating the genotypes studied. Phenotypic coefficient of variation (PCV) was slightly higher than genotypic coefficient of variation (GCV) for all the traits. Moderate GCV and PCV estimates were observed for filled seeds/panicle, test weight, alkali spreading value, volume expansion ratio, yield/plant, water uptake and head rice recovery. High heritability coupled with moderate genetic advance as percent of mean was observed for test weight (98.5:46.62), filled seeds/panicle (92.6:46.26), alkali spreading value (90.9:43.15), yield/plant (78;35.30), head rice recovery (78.9:27.46) and volume expansion ratio (69.1:37.3). In this study the genotypes WGL 1143, WGL 1150, WGL 1149, Tellahamsa in cluster II and WGL 1062 in cluster IV and WGL 915 in cluster VIII were widely divergent and crosses may be effected among the genotypes of the clusters to get more heterosis and subsequently better recombinants in segregating generations.

Keywords: Rice; yield; quality; diversity; variability.

1. INTRODUCTION

Rice (*Oryza sativa* L.) belongs to family poaceae (Graminae) and one of the most important food grain crops in the world forms the diet of more than 3.0 billion people Krishnan et al. [1]. Globally it is grown extensively with wide range of ecosystems under varying temperatures and water regimes in more than 114 countries and is referred as global grain. Rice is life was the theme of International year of rice 2004 denoting its overwhelming importance as an item of food and commerce. Among the rice growing countries in the world India has the largest area under rice cultivation and ranks second in production next to China. However to meet the food demands of the growing population and to achieve food security in the country, the production levels need to be increased by 2 million tonnes every year, which is possible through heterosis breeding and other innovative breeding approaches Padmavathi [2]. In order to meet the food requirement of growing population, development of high yielding varieties is essential Chun et al. [3]. Enhancing crop yield is one of the most priorities in crop breeding programmes and quality traits yet another important consideration. Development of new high yielding and quality rice varieties superior to the existing varieties mostly depends upon the amount of genetic diversity and variability present in the population. The parents involved in the development of varieties should be divergent. The germplasm provides immense scope for wide variability Zafer et al. [4]. Genetic diversity is one of the potent techniques of measuring genetic divergence in various breeding materials. The nature and magnitude of genetic divergence

would help the plant breeder in choosing right choice of parents for crossing programmes in order to obtain higher amount of heterotic expression in F_1 and broad spectrum of variability in subsequent segregating generations Vivekanandan and Subramanian [5]. Genetic variability for agronomic and quality traits are the key components of breeding programmes for broadening the gene pool of rice. Genetic parameters like GCV and PCV are useful in detecting the amount of variability present in the germplasm. Heritability coupled with high genetic advance would be more useful tool in predicting the resultant effect in selection of the best genotypes for quality, yield and its attributing traits and it helps in the determining the influence of environment on the expression of genotypic and reliability of characters. Recognizing the importance of genetic diversity and variability in plant breeding experiments, present research work was undertaken with an objective to classify and understand the nature and magnitude of genetic diversity and variability with regard to grain yield, yield components and quality traits in rice.

2. MATERIALS AND METHODS

The study was conducted during *Kharif*, 2017 at Regional Agricultural Research Station, Warangal, Telangana state, India. The experimental material comprised of 33 rice genotypes and it was laid out in RBD with two replications. Each plot consists of 3 rows of 4 m length. Thirty days old seedlings were transplanted with a spacing of 20 cm between rows and 15 cm between the plants at the rate of 20 plants per row grown with the application of

fertilizers N, P, K at the rate of 120:60:40 kg/ha respectively and the recommended package of practices were followed for raising a healthy crop. A composite of 10 plants from the middle row was used to record observations on the plants for yield components like plant height (cm), effective tillers, panicle length(cm), filled seeds/panicle, yield/plant (g) and test weight (g) except days to 50% flowering which was computed on plot basis. Data was recorded on physical and chemical quality characters viz., hulling percent (%), milling percent (%), head rice recovery (%), kernel length (mm), kernel width (mm), length/breadth ratio, kernel length after cooking (mm), kernel width after cooking (mm), kernel elongation ratio, water uptake (ml) and alkali spreading value. Observations on hulling and milling were taken with the help of Satake company make laboratory huller and polisher. Data on head rice recovery was recorded. Kernel length and kernel width of 20 whole milled rice were measured by means of dial caliper and length and breadth ratio was computed as per Murthy and Govindaswamy [6]. Kernel elongation was determined by soaking 5g of whole milled rice in 12 ml distilled water for 10 minutes and later cooked for 15 minutes in water bath. Observation on the length and breadth of cooked kernels and elongation ratio were recorded with the help of graph sheet to quantify cooking traits, while water uptake, volume expansion ratio and alkali spreading value by following the standard procedures.

The treatment means for all the characters were subjected to analysis of variance techniques on the basis of model proposed by Panse and Sukhatme [7]. The genotypic and phenotypic variances were calculated as per formulae proposed by Burton [8]. Heritability in broad sense (h^2_b) was calculated by the formulae given by Lush [9]. From the heritability estimates the genetic advance (GA) was calculated by the formula given by Johnson et al. [10]. Genetic divergence analysis was done following the D^2 statistics proposed by Mahalanobis [11] and described by Rao [12].

3. RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences for all the characters (Table 1) indicating the existence of considerable amount of variability among the genotypes selected for study. The perusal of results revealed that all the 33 genotypes were clustered

into 8 clusters based on minimum D^2 values and confirmation of tentative grouping by Tocher's method (C.R.Rao1952) (Table 2) and (Fig. 1). Among the clusters, cluster I was the largest comprised of 23 genotypes followed by cluster II which consists of four genotypes and rest of the clusters from cluster III to cluster VIII contain one genotype each as genotypes were divergent from each other as also from rest of the varieties, hence each of them form separate cluster. Cluster II containing WGL 1143, WGL 1150, WGL 1119 and WGL 1149 were Tellahamsa derived near isogenic lines including Tellahamsa were grouped into one cluster. Therefore the 33 genotypes falling as many as eight clusters is an indication of prevalence of good extent of diversity in the material. Maximum genotypes were included in cluster I (23) followed by cluster II (4) with 69.6 and 12.1 proportion from the studied genotypes. Clustering did not follow any particular pattern with respect to origin were also reported earlier in rice by Nibedita et al. [13] and Rukmini devi et al. [14].

The discrimination of germplasm lines into so many clusters suggested presence of high degree of genetic diversity in the material studied. Earlier workers have also reported substantial genetic divergence in the rice material. Presence of substantial genetic diversity among the germplasm lines screened in the present study indicated that this material may serve as good source for selecting the diverse parents for hybridization programmes aimed at isolating desirable segregants for grain yield and other important characters, moreover selection and choice of parents mainly depends upon contribution of characters. These results are in accordance with Chandramohan et al. [15], Devi et al. [16]. Cheema et al. [17] advocated that the number of clusters formed, number of genotypes in clusters and super position of the genotypes within the clusters indicated the possibility of genetic improvement for yield and yield components. The choice of the suitable diverse parents based on genetic divergence analysis would be more fruitful than the choice made on the basis of geographical distances Murthy and Arunachalam [18] stated that genetic drift and selection in environment could cause greater diversity than geographic distance. Genetic diversity plays an important role because hybrids between genotypes of diverse origin generally display a greater heterosis and throw more recombinants than those between closely related parents.

Table 1. Analysis of variance (Mean squares) for grain yield and quality traits in rice (*Oryza sativa* L.)

S. no.	Characters	Replication(d.f=1)	Treatments (d.f=32)	Error (d.f=32)
1	Days to 50% flowering	0.74242	162.4**	1.461174
2	Plant height(cm)	3.782424	262.38**	1.193362
3	Effective tillers	0.007424	0.911913**	0.242424
4	Panicle length (cm)	0.001650	11.262752**	0.104019
5	Filled seeds /Panicle)	740.015100	6998.656250**	270.358902
6	Yield/ha(kg)	186349.2	2739023.93**	338626.66
7	Test weight(g)	0.000123	32.387055**	0.252154
8	Hulling percent(%)	3.500606	27.232585**	4.336544
9	Milling percent (%)	12.220610	17.867614**	7.689981
10	Head rice recovery (%)	170.242400**	152.561174**	17.948049
11	Kernel length(mm)	0.228097**	0.582204**	0.018925
12	Kernel width (mm)	0.000873	0.020917**	0.002720
13	Length/breadth ratio	0.013388	0.072389**	0.029285
14	Kernel length after cooking(mm)	0.213068*	0.951250**	0.034474
15	Kernel breadth after cooking (mm)	0.009456	0.031138**	0.003978
16	Kernel elongation ratio	0.033188**	0.008313**	0.001407
17	Volume expansion ratio	0.018668	0.354664**	0.064731
18	Water uptake (ml)	284.378800	6804.7500947**	2319.972538
19	Alkali spreading value	0.875152*	2.466771**	0.117339

*Significant at 5% level, ** Significant at 1 % level

Table 2. Clustering composition with distribution of 33 genotypes in rice by Tocher's method

Cluster no	No of genotypes	Entry no	Genotypes
I	23	1,7,2,3,6,21,17,31,19,14,4,10,18,8,13,23,11,12,30,26,25,24,29	WGL-810,WGL-347,WGL-811,WGL-401,WGL-32100,WGL-505,RNR-15048,WGL-1067,WGL-825,WGL-914,WGL-962,WGL-1152,BPT-5204,WGL-676,WGL-1021,WGL-739,WGL-697,WGL-965,WGL-1121,WGL-1131,WGL-1151,WGL-1127
II	4	22,27,28,33	WGL-1143,WGL-1150,WGL-1149,TELLAHAMSA
III	1	30	WGL-1119
IV	1	16	WGL-1062
V	1	5	SIDDHI
VI	1	15	WGL-1003
VII	1	32	RP-1
VIII	1	9	WGL-915

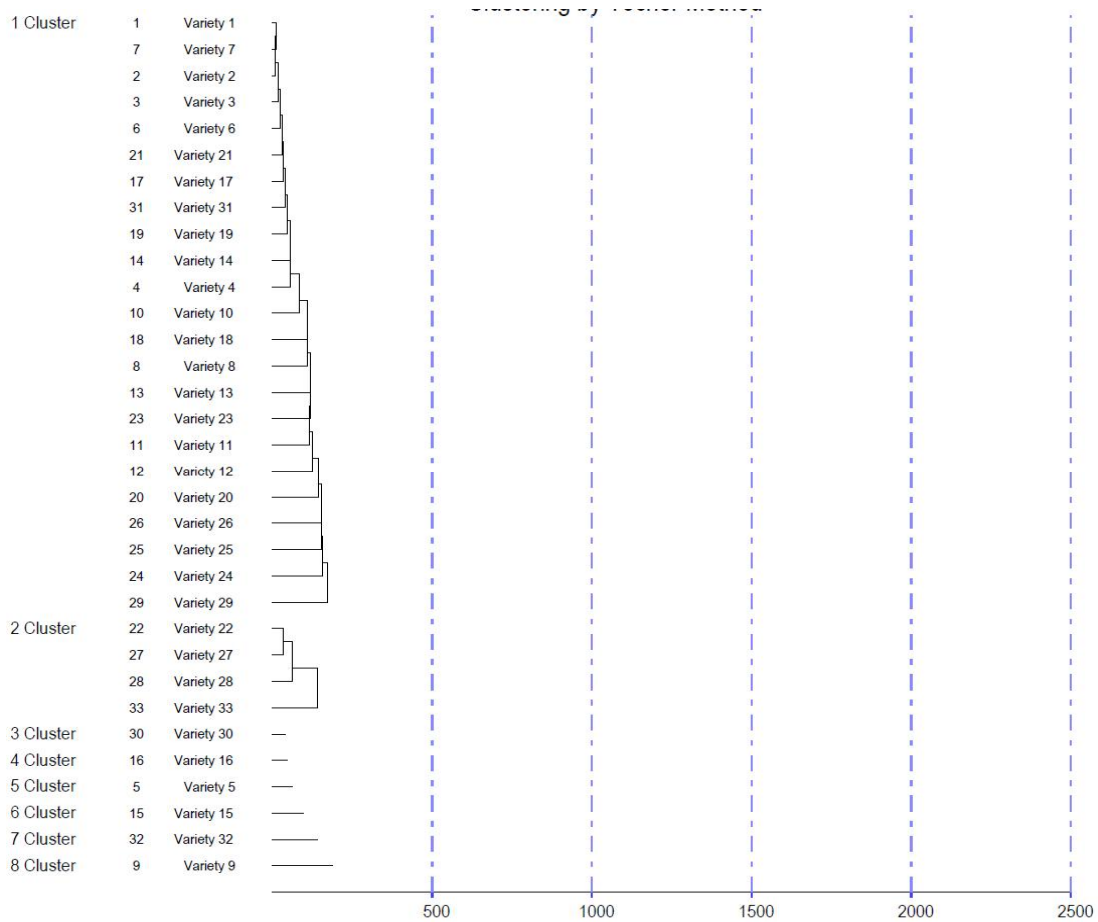


Fig. 1. Clustering pattern of 33 Promising Germplasm lines in Rice according to Tocher's method

The genotypes grouped within a cluster exhibit narrow range of genetic variability, whereas different clusters indicate wider variability. The average inter cluster and intra cluster distances are presented in Table 3 and Fig. 2. The maximum inter cluster distance was found between cluster II and cluster IV (2178.98) followed by cluster III and cluster VIII (2160.16), cluster IV and cluster VIII (2107.82), cluster VII and cluster VIII (2117.03), cluster V and cluster VIII (2095.57) and cluster II and cluster VI (1976.51). The minimum inter cluster distance was observed between cluster I and cluster III (540.96) and cluster I and cluster V (587.71) indicated that the genotypes included in them were closely related. Greater the distance between two clusters wider the genetic diversity among the genotypes of these clusters and such highly divergent high performing genotypes would be of great use in recombination breeding programme in order to get high heterotic

recombinants. Avoidance of selection of parents from genetically homogeneous clusters should be preferred to maintain relatively broad genetic base. It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters. But a plant breeder the objective is not only high heterosis but also performance of the genotypes for important yield and quality traits evaluated. Keeping in view it is indicated that hybridization between the genotypes of cluster II (WGL-1143, WGL-1150, WGL-1149 and Tellahamsa) with WGL 1062 of cluster IV, the genotype of cluster III (WGL 1119), cluster IV (WGL 1062), cluster V (Siddhi), cluster VII (RP-1) with WGL 915 of cluster VIII and genotypes (WGL 1143, WGL 1150, WGL 1149, Tellahamsa) of cluster II with cluster VI (WGL 1003) are expected to produce highly heterotic hybrids. The genotypes of these clusters may be used as parents in the crossing

programme to generate breeding material with high genetic diversity. According to Rahaman et al. [19] crossing between highly divergent genotypes would produce a broad spectrum of variability enabling further selection and improvement. Thus selection of parents from these clusters for a crossing programme will produce desirable transgressive segregants. The intra cluster distance indicating poor diversity.

Gradual increase in D^2 value over the range without any sudden jumps in the values among the genotypes may be result of their evolution with the same ancestral parents or due to evolution under near indicated ecological parameters or they might have been subjected to similar natural selection. Similar results were also reported by Rukmini Devi et al., 2020.

Table 3. Intra-Inter cluster distances among eight clusters in 33 genotypes of rice (*Oryza sativa* L.)

	I cluster	II cluster	III cluster	IV cluster	V cluster	VI cluster	VII cluster	VIII cluster
I cluster	326.55	1142.97	540.96	329.75	587.79	789.30	662.15	1275.51
II cluster		354.10	1007.79	2178.98	1049.44	1976.51	914.60	1378.15
III cluster			0.00	1245.67	187.73	1965.94	590.48	2160.16
IV cluster				0.00	1045.46	711.77	786.53	2107.82
V cluster					0.00	1909.35	653.39	2095.57
VI cluster						0.00	1542.74	848.97
VII cluster							0.00	2117.03
VIII cluster								0.00

Bold values: Intra cluster distances

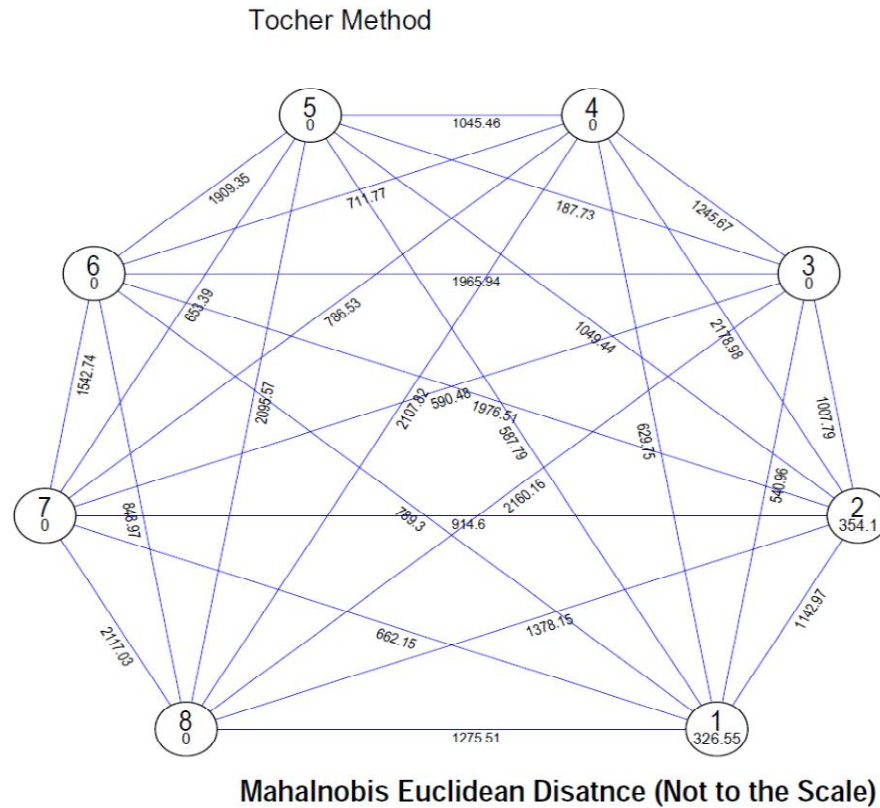


Fig. 2. Intra and inter cluster distances of 33 rice (*Oryza sativa* L.) genotypes in eight clusters by Tocher’s method

Table 4. Estimation of Mean values of eight clusters by Tocher's method for 33 genotypes of rice for yield and yield components (*Oryza sativa* L.)

	Days to 50% flowering	Plant height(cm)	Effective tillers	Panicle length(cm)	Filled seeds/panicle	Yield/pl (g)	Test weight(g)	Hulling percent (%)	Milling percent (%)	Head rice recovery (%)
I cluster	99.89	110.8	10.4	25.23	266	17.9	16.98	83.57	71.92	55.05
II cluster	91.63	92.75	11	22.36	132	10.8	21.23	76.20	68.41	50.76
III cluster	88.5	94	11.5	22	276	16.8	13.70	86.15	74	57.6
IV cluster	127.5	117.1	10	26.3	311	13.9	12.95	83.3	73.7	50.85
V cluster	99	91.6	11.5	25.5	254	18.08	13.05	85.5	71.4	59.6
VI cluster	112.5	132	9	28.95	264	19.5	21.75	81.40	69.35	58.85
VII cluster	113.5	98.9	10	19.8	186	15.6	13	76.15	75.75	49.55
VIII cluster	100.5	127.1	10	30.45	268	20.2	30	81.8	68.9	56.25

Table 4(a). Estimation of Mean values of eight clusters by Tocher's method for 33 genotypes of rice for quality traits (*Oryza sativa* L.)

	Kernel length (mm)	Kernel width (mm)	Length/ Breadth ratio	Kernel length after cooking (mm)	Kernel breadth after cooking (mm)	Kernel elongation ratio	Volume expansion ratio	Water uptake (ml)	Alkali spreading value
I cluster	4.96	1.54	3.25	6.30	2.04	1.27	1.72	248.24	4.58
II cluster	5.67	1.63	3.42	7.24	2.00	1.3	2.16	296.0	7.00
III cluster	4.66	1.44	3.25	5.75	2.00	1.24	1.20	131.5	4.00
IV cluster	4.53	1.49	3.11	5.78	2.00	1.28	1.88	219.0	5.5
V cluster	4.54	1.53	3.00	5.88	2.00	1.30	1.20	319.0	4.00
VI cluster	5.39	1.68	3.15	6.65	2.00	1.24	1.75	279.0	6.50
VII cluster	5.69	1.47	3.55	6.75	1.95	1.19	1.00	179.0	5.50
VIII cluster	6.58	1.68	3.85	7.48	2.55	1.14	2.43	271.5	4.00

Table 5. Contribution of different characters towards genetic divergence in 33 genotypes of rice (*Oryza sativa* L.)

S. no.	Source	Times ranked 1st	Contribution (%)
1	Days to 50% flowering	66	12.5
2	Plant height(cm)	168	31.8
3	Effective tillers	-	-
4	Panicle length (cm)	49	9.28
5	Filled seeds /Panicle)	2	0.38
6	Yield/ha (kg)	1	0.19
7	Test weight(g)	74	14.01
9	Hulling percent (%)	2	0.38
8	Milling percent (%)	-	-
10	Head rice recovery (%)	2	0.38
11	Kernel length(mm)	6	1.14
12	Kernel width (mm)	2	0.38
13	Length/breadth ratio	-	-
14	Kernel length after cooking(mm)	36	6.81
15	Kernel breadth after cooking(mm)	1	0.18
16	Kernel elongation ratio	-	-
17	Volume expansion ratio	-	-
18	Water uptake (ml)	13	2.46
19	Alkali spreading value	106	20.07

Table 6. Components of genetic parameters for yield and quality traits in rice (*Oryza sativa* L.)

Character	Mean	Range	PV	GV	PCV	GCV	Heritability in broad sense (%)	Genetic advance as percent of mean
Days to 50% flowering	100	88-128	81.9	80.5	9.36	8.955	98.2	18.28
Plant height(cm)	108.5	82-132	131.8	130.6	10.58	10.54	99.1	21.61
Effective tillers	10.47	9-12	0.57	0.33	7.25	5.52	58	8.66
Panicle length (cm)	24.93	20-30	5.683	5.58	9.56	9.47	98.2	19.33
Filled seeds /Panicle)	248.5	117-362	3634.5	3364.14	24.26	23.34	92.6	46.25
Yield/ha (kg)	5645.4	2896-7414	1538825	200199	21.97	19.40	78	35.3
Test weight(g)	17.57	12-30	16.32	16	22.98	22.80	98.5	46.6
Hulling percent(%)	82.46	73-87	15.78	11.44	4.81	4.10	72.5	7.19
Milling percent (%)	71.54	63-77	12.77	5.0	4.99	3.15	39.8	4
Head rice recovery (%)	54.6	34-66	85.1	67.15	16.89	15	78.9	27.4
Kernel length(mm)	5	5-7	0.3	0.282	10.76	10.4	93.7	20.7
Kernel width (mm)	1.55	1-2	0.01	0.009	6.99	6.13	77	11
Length/breadth ratio	3.28	3-4	0.05	0.022	6.87	4.47	42.4	6
Kernel length after cooking(mm)	6.42	5-8	0.49	0.45	10.92	10.53	93	20.93
Kernel breadth after cooking (mm)	2	2-3	0.01	0.14	6.48	5.70	77.3	10.33
Kernel elongation ratio	1.26	1.1-1.3	0.005	0.003	5.51	4.64	71.1	8
Volume expansion ratio	1.74	1-3	0.21	0.14	26.21	21.8	69.1	37.3
Water uptake (ml)	251.28	132-347	4562.36	2242.38	26.88	18.84	49.1	27.2
Alkali spreading value	4.93	4-7	1.29	1.17	23	21.97	90.9	43.15

Different characters revealed by cluster means are presented in Table 4. It is always desirable to look for genotypes having more than one desirable trait but belonging to different clusters based on cluster mean values. The results indicate that the selection of genotypes with higher cluster mean values for particular trait could be used in the hybridization programme for improvement of the character. The contrasting genotypes for days to 50% flowering were present in cluster III, cluster II and cluster IV for plant height, cluster V and cluster VIII for panicle length, cluster III and cluster VIII for test weight, cluster VII, V and cluster VIII and for yield cluster IV and cluster VIII. To get early maturing varieties the genotypes WGL 1143, WGL 1150, WGL 1149 and Tellahamsa present in cluster II and WGL 1119 of cluster III can be involved and for developing late maturing varieties the genotype WGL 1062 in cluster IV may be involved in crossing. For developing fine grain varieties genotypes from cluster III, cluster IV, cluster V and cluster VII may be involved. Obtaining bold grain types also possible by using genotypes from cluster II, VI and VIII. The genotype WGL 915 in cluster VIII recorded high mean for yield/plant, panicle length, test weight, kernel length, kernel length after cooking, kernel width after cooking and volume expansion ratio.

A critical appraisal of the observations indicated that none of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. Therefore hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits requires hybridization between the selected genotypes from divergent clusters. Similar results also reported by Ramakrishna Prasad et al.[20]. A wide range of variation for several characters among single as well as multi genotypic clusters was observed (Table 5). However the most important trait showing maximum genetic divergence was the plant height (31.8) which ranked 168 times first and was responsible for differentiating the genotypes studied. In general semi dwarf plant height with strong culm and non lodging plant type is very much essential in rice to increase biological yield thereby economic yield. The trait alkali spreading value (20.07) followed by test weight (14.01) days to 50% flowering (12.50) and panicle length were also important traits contributing to total genetic divergence. Hence it is advisable to select divergent parents based on these three characters and attempt crossing between them so as to achieve a broad spectrum of favourable

genetic variability for yield improvement in rice. Similarly Latif et. al. [21] for plant height, Banumathy et al. [22] for plant height and days to 50% flowering, Bose and Pradhan [23], Chandramohan et al [15], Rukmini Devi et al. (2020) also reported higher genetic diversity due to days to 50% flowering and test weight in rice. On other hand effective tillers, milling percent, length/breadth ratio and volume expansion ratio have no role towards genetic divergence in the present studies. Yield per plant (0.19), kernel breadth after cooking (0.18), filled seeds/panicle (0.38), head rice recovery (0.38) were least responsible for contributing towards the total divergence. These results indicated presence of more diversity for plant height, alkali spreading value, test weight and panicle length in the present experimental material and due importance could be given for these traits for crop improvement.

The extent of variability for any character is very important for the improvement of crop through breeding. The estimates of mean, range, genotypic variation, phenotypic variation, genotypic coefficient of variation, phenotypic coefficient of variation, heritability in broad sense and genetic advance as percent of mean for 19 characters have been presented in Table 6. The highest genotypic variation was found for filled seeds/panicle (3364.15) and lowest magnitude of genotypic variation was observed for kernel elongation ratio (0.003). Moderate PCV and GCV estimates were observed for filled seeds/panicle (23.34), test weight (22.81), alkali spreading value (21.9), volume expansion ratio(21.8), yield/plant (19.41), water uptake (18.8), head rice recovery (15.0), whereas lowest values were observed for milling percent (3.153), hulling percent (4.103), length/breadth ratio (4.475), kernel elongation ratio (4.648), effective tillers (5.524), kernel breadth after cooking, kernel width, days to 50% flowering, plant height, kernel length after cooking and panicle length and kernel length. Selection for these traits would offer better scope for genotypes under study and there is a need for creation of variability either by hybridization or mutation followed by selection. These results are in consonance with the findings of Venkata subbaiah et al. [24], Singh et al. [25]. Rukmini Devi et al. [26] reported lower PCV and GCV estimates for kernel width, days to 50% flowering, kernel breadth after cooking, panicle length, kernel elongation ratio, milling percent, hulling percent. Dhurai et al. [27] for days to 50% flowering, kernel length, kernel width and length/breadth ratio and Ravindra

Babu et al. [28] for kernel width, Genotypic coefficient of variation measures the variability of any trait. Allard [29] reported the extent of the environmental influence on any trait is indicated by the magnitude of difference between the genotypic and phenotypic coefficients of variation. Large differences reflects high environmental influence, while small differences reveal high genetic influence. In this study phenotypic coefficient of variation was slightly higher than genotypic coefficient of variation for days to 50% flowering, plant height, panicle length, test weight, kernel length after cooking, kernel elongation ratio, alkali spreading value, effective tillers indicate significant genetic variability for these traits which may facilitate selection. These results are in conformity with findings of Rukmini Devi et al. [30] for days to 50% flowering, plant height, test weight and kernel length after cooking. High to moderate differences between genotypic and phenotypic coefficient of variation were observed for filled grains/panicle, yield/plant, volume expansion ratio, kernel length, kernel width, length/breadth ratio, hulling percent, milling percent, head rice recovery and water uptake indicated the high influence of environment on these traits. These results were in conformity with the findings of Venkata Subbaiah et al. [24] for effective tillers, filled grain/panicle, yield/plant, test weight, kernel length and kernel width. The amount of genetic variation recorded alone was not be of much use to the breeder unless supplement with the information on heritability estimates, which gives a measure of heritable portion of the total variation. It has been suggested by Burton and Devane [31]. Genotypic coefficient of variation along with heritability estimates could provide a better picture of the amount of advance to be expected by phenotypic selection. Since genetic advance is dependent on phenotypic variability and heritability in addition to selection intensity. The heritability estimates in conjunction with genetic advance will be more effective and reliable in predicting the response to selection (Johnson et al 1955) The heritability estimates obtained for the studied traits ranged between 39.8 (milling percent) to 99.1 (plant height). High broad sense heritability estimates observed for plant height (99.1), test weight (98.5), days to 50% flowering (98.2), panicle length (98.2), kernel length (93.7), filled seeds/panicle (92.6), alkali spreading value (90.9), head rice recovery (78.9), yield/plant (78.0), kernel breadth after cooking (77.3), kernel width (77.0), hulling percent (72.5) and kernel elongation ratio (71.1). It suggests high component of heritable portion

of variation, it is the portion which is exploited by the breeder. High heritability values indicate that the characters under study are less influenced by environment in their expression. Broad sense heritability useful in selection of elite types from homozygous lines whereas narrow sense heritability useful in selection of elite lines from segregating material and requires crossing in definite fashion. The plant breeder therefore adopt simple selection method on the basis of phenotype of the characters which ultimately improve the genetic background of the traits. Irdis and Mohammed [32] reported high heritability for days to 50% flowering, plant height, panicle length, filled seeds/panicle, yield/plant, test weight, hulling percent, head rice recovery, kernel length, kernel width, kernel length after cooking and kernel breadth after cooking. Heritability will help the plant breeder in selection of elite genotypes from diverse genetic population. It is a good index of transmission of characters from parents to off springs.

Low broad sense heritability observed for milling percent (39.8), length/breadth ratio (42.4) and water uptake (49.1) indicating influence of environment on these traits. The low heritability recorded for the traits indicate that direct selection for these traits will be in effective. Sahu et al. [33] reported low heritability for length/breadth ratio and high heritability for alkali spreading value and kernel length after cooking. High heritability do not always indicate high genetic gain. Heritability with genetic advance considered together should be used in predicting the ultimate effect for selecting superior genotypes.

The estimates of genetic advance as percent of mean provide more reliable information regarding the effectiveness of selection in improving the traits. Genetic advance denotes the improvement in the genotypic value of the new population over the original population Johnson et al (1955) categorized the genetic advance as percent of mean as high (>20%) moderate (10-20%) and low (<10%). The traits test weight (46.6%), alkali spreading value (43.1), volume expansion ratio (37.3), yield/plant (35.3), head rice recovery (27.5), water uptake (27.2), plant height (21.6), kernel length after cooking (20.9) and kernel length (20.77) recorded high estimates of GA as percent of mean, while panicle length (19.3), days to 50% flowering (18.2), kernel width (11.08) and kernel breadth after cooking (10.334) showed moderate estimates of GA as percent of mean. Thus suggested that these traits are

primarily under genetic control and selection for these can be achieved through their phenotypic performance in order to obtain maximum genetic gain for yield and quality traits in rice by simple selection procedure. According to Panse [34] if a character is governed by non additive gene action it may give heritability but low genetic advance where as if it is governed by additive gene action, high heritability (>60%) along with high genetic advance (>20%) helps good scope for improvement. The traits test weight (98.5:46.6), filled seeds/panicle (92.6; 46.3), alkali spreading value (90.9:43.2), yield/plant (78:35.3), head rice recovery (78.9;27.5) and volume expansion ratio (69.1;37.33) exhibited high heritability with high genetic advance. Similar findings were also reported by Rukmini Devi et al. [35] and for yield/plant, head rice recovery, volume expansion ratio and Idris and Mohammed (2013) for filled seeds/panicle.

High heritability with low genetic advance was observed for panicle length, hulling percent, kernel length, kernel width, kernel breadth after cooking, kernel elongation ratio, days to 50% flowering and plant height indicate non additive type of gene action and genotypic environmental interaction plays a significant role in the expression of the traits.

4. CONCLUSION

The present study revealed that the selection of parents should be on the basis of their inter cluster distance and superior mean performance for yield, yield components and quality traits and contribution of different characters towards total genetic divergence. The genotypes WGL 915, WGL 1062, WGL 1143, WGL 1150, WGL 1149 and Tellahamsa were widely divergent and crossing may be effected for obtaining a wide spectrum of variation among the segregants. The characters plant height, days to 50% flowering, test weight, panicle length and alkali spreading value were found to be important contributing characters for genetic divergence and due weight age should be given while formulating breeding schedule WGL 915 in cluster VIII recorded high mean for yield/plant and other yield contributing traits and quality traits hence the genotype can be used as ultimate parent for inclusion in the crossing programme. The characters filled seeds/panicle, test weight, yield/plant, head rice recovery showed moderate GCV, high heritability and moderate genetic advance would particularly encourage the breeders to achieve higher grain yield, hence these traits could be selected in

existing germplasm for genetic improvement of yield of rice.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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