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Genetic Diversity in Rice for Yield, Quality and Nutritional Traits (*Oryza sativa* L)

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ABSTRACT

Morphological divergence study among the forty eight genotypes based on twenty two yield, yield contributing, quality and nutritional characters through D^2 statistic indicated the presence of substantial diversity by forming large number of clusters with wide range of inter-cluster distances. The genotypes of rice under study were distributed into seven clusters based on Ward's minimum variance. Out of seven clusters, cluster I was the largest comprising of 12 genotypes, followed by cluster IV and V with nine, cluster III with seven, cluster II with five, cluster VI with four and cluster VII with two suggesting the existence of high degree of heterogeneity among the genotypes.

Key words: *Cluster Diversity, Genotypes and Rice.*

Rice occupies the enviable prime place among the food crops cultivated around the world. The slogan "Rice is life" is the most appropriate for India where this crop forms a livelihood for millions of rural households and describes its role in sustaining food and nutritional security. India is the second largest producer of rice next to China producing 111.008 m t with an average productivity of 2585 kg ha^{-1} from an area of 42.94 m ha. In Andhra Pradesh, rice is cultivated in 2.15 m ha with a production of 8.051 m t with an average productivity of 3741 kg ha^{1} (Indiastat, 2018). Study of diversity is the pre-requisite in any breeding programme**.** Genetic diversity is the most important tool in the hands of the plant breeder in choosing the right type of parents for hybridization programme. Various techniques such as morphological, biochemical characterization/ evaluation (allozyme) and DNA (or molecular) marker analysis were routinely used for the assessment of genetic diversity within and between plant populations. Estimation of degree of divergence between populations and contribution of different characters to total divergence can be done by D^2 statistics, which is more reliable method in selection of parents for hybridization programme. Genetic improvement of any crop mainly depends upon the amount of genetic variability present in the population. In order to generate variability, hybridization between genotypes of diverse origin is suggested to unlock new recombinations. Genetic divergence has been used as an indirect parameter of moderate effectiveness in selecting parents to produce high yielding progenies.

MATERIAL AND METHODS

The present investigation was conducted at Regional Agricultural Research Station (RARS), Maruteru, Andhra Pradesh, the experimental material were evaluated in Augmented Design comprised of 48 rice genotypes including with 3 checks during kharif 2014. Checks were replicated in nine blocks. The seedlings were transplanted on 28th day with spacing of 20 cm between rows and 15 cm between plants and observations were recorded for twenty two traits *viz.,* plant height at maturity (cm), days to 50 per cent flowering, panicle length (cm), number of productive tillers per hill, number of filled grains per panicle, number of total grains per panicle, spikelet fertility sterility (%), grain weight per panicle (g), grain yield per plant (g), kernel length (mm), kernel breadth (mm), L/B ratio, kernel length after cooking (mm), kernel elongation ratio, water uptake (ml), alkali spreading value, gel consistency (mm), amylose content (%) and iron and zinc (ppm) content in brown and polished rice grains (Shobha Rani *et al.,* 2014). Genetic diversity analysis was carried out following D^2 statistics proposed by Mahalanobis (1936) and clustering pattern was done using Ward's minimum variance method (Ward, 1963)

STATISTICAL ANALYSIS

The data collected were statistically analysed using WINDOSTAT - 9.2 version and the analysis of variance showed significant differences among the genotypes of rice under study. Genetic diversity analysis was carried out following D^2 statistics proposed by Mahalanobis.

Table 1. Contribution of different traits to genetic diversity in 48 rice genotypes

S.No	Characters	Contribution %
1	Days to 50 Per Cent Flowe	1.42
2	Panicle Length (cm)	0.01
3	Productive Tillers Per Hi	0.01
4	Filled Grains Per Panicle	17.82
5	Total Grains Per Panicle	30.14
6	Spikelet Fertility (%)	0.01
7	Grain Weight Per Panicle	0.01
8	Grain Yield Per Plant (g)	0.01
9	Plant Height At Maturity	9.04
10	Kernel Length (mm)	0.01
11	Kernel Breadth (mm)	0.01
12	L/B Ratio	0.01
13	Kernel Length After Cooking (mm)	0.01
14	Kernel Elongation Ratio	0.01
15	Water Uptake (ml)	40.96
16	Iron Content in brown rice (ppm)	0.01
17	Iron Content in polished rice (ppm)	0.01
18	Zinc Content in brown Rice (ppm)	0.01
19	Zinc Content in polished rice (ppm)	0.01
20	Alkali Spreading Value	0.01
21	Gel Consistency (mm)	0.62
22	Amylose Content (%)	0.01

Table 2. Clustering pattern among 48 genotypes of rice under study (Ward minimum variance)

No. clusters	No. of genotypes	Name of the genotypes
Cluster I	12	NLR 3042, NLR 34242, NLR 34449, BPT2615, BPT 3291, Improved Samba Mahsuri,Tellahamsa, MTU 1156, MTU 1010, MTU 7029, BPT 5204, Vamsadhara
Cluster II	5	KMP 105, IR 64, FL 478, GSR ZGY 1, GSR H.H.Z.5.SAL10
Cluster III	7	Anjali, Vandana, Savitri, Annada, Kaling III, Varalu, GSR T.M.E 80518
Cluster IV	9	Azucena, Warangal samba, Tapaswini, MTU 1121, Naveen, Pooja, Mahsuri, RNR 2354, NDLR 8
Cluster V	9	MTU 1075, Manoharsali, MTU 1061, Varsha, N22, Lunasuvarna, PLA 1100, Srikakulam sannalu, MTU 1166
Cluster VI	4	Burmadha, Isukaravalu, Gedanzibetan, FR13A
Cluster VII	2	Chittimutyalu, Godavari isukalu

Table 3. Average Inter and intra cluster distances of seven clusters (Euclidean²: Cluster Distances: Ward)

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	21.510	37.292	38.832	34.305	37.159	68.278	74.328
Cluster II		35.361	46.385	51.535	60.749	65.667	88.944
Cluster III			30.896	44.711	43.966	53.233	67.132
Cluster IV				28.929	39.050	49.843	52.935
Cluster V					28.574	60.488	73.190
Cluster VI						28.183	47.124
Cluster VII							13.865

Diagonal bold values indicate intra cluster distances

RESULTS AND DISCUSSION

The utility of D^2 statistics as a potential tool to quantify the extent of divergence in biological populations at genetic level is further enhanced by its applicability to estimate the relative contribution of the various plant characters to total genetic divergence. The characters water uptake contributed maximum (40.96%) towards genetic divergence followed by total grains per panicle (30.14%), number of filled grains per panicle (17.82%), plant height at maturity (9.04%), days to 50 % flowering (1.42%), gel consistency (0.62%) and all the remaining characters contributed 0.01%. (Table 1). These results are in confirmity with the findings of Thayumanavan *et al*. (2009), Padmaja *et al.* (2010) and Supriya *et al.* (2017) who reported major contribution to diversity through total number of grains per panicle; Priyanka *et al.* (2015*)* and Nirosha *et al*. (2016) through days to 50 % flowering.

All forty eight genotypes of rice under study were distributed into seven clusters based on D^2 values using Ward's minimum variance method (Ward, 1963). The distribution of genotypes into various clusters is presented in Table 2 and Figure 1. Out of seven clusters, cluster I was the largest comprising of 12 genotypes, followed by cluster IV and V with nine, cluster III with seven, cluster II with five, cluster VI with four and cluster VII with two suggesting the existence of high degree of heterogeneity among the genotypes.

Most of the landraces were grouped into cluster VI and VII. The varieties developed by CRRI, Cuttack (Anjali, Vandana, Savitri, Annada and Kaling III) were grouped into cluster III. NLR varieties (NLR-3042, NLR34449 and NLR34242) and BPT varieties (BPT 5204, BPT 3291 and BPT 2615 were grouped into cluster I along with maruteru varieties (MTU 7029, MTU 1010, MTU 1156) and MTU 1075, MTU 1166 and MTU 1061 were grouped into cluster V. Thus overall composition of the clustering pattern showed that genotypes from the same geographic origin were present in same clusters as they showed similarity. Similar finding has been reported by Singh *et al*., 2008, Allam *et al.,* 2014. Some of the genotypes of same geographic origin were distributed in different clusters. Similar findings have been reported by Sharma *et al*., 2011, Priyanka *et al*., 2015.

The average intra and inter cluster distance values (Table 3) showed that intra cluster distances ranged from 13.865 (cluster VII) to 35.361 (cluster II) (Table 3). Maximum intra cluster distance was observed in cluster II (35.361) followed by cluster III (30.896) and cluster IV (28.929) indicating that some genetic divergence still existed among the genotypes within each of these clusters. Selection within such clusters might be executed based on maximum mean value for the desirable characters. The inter cluster distance was higher than intra cluster distance, indicating the presence of wide genetic diversity among the genotypes under study. Maximum inter cluster distance was exhibited between clusters II and VII (88.944) followed by clusters I and VI (74.328), clusters V and VII (73.19) and clusters I and VII (68.278). The greater the distance between two clusters, the wider the genetic diversity among the genotypes of those clusters. Such highly divergent, high performing genotypes would be of great use in recombination breeding programme in order to get high heterotic recombinants. The lowest inter cluster divergence was noticed between clusters I and IV (34.305) followed by clusters I and V (37.159) and clusters I and II (37.292), indicating that the varieties included in them were closely related. Selection of parents from genetically homogeneous clusters should be avoided to maintain relatively broad genetic base. Keeping this in view, it could be concluded that landraces from clusters VII (Chittimutyalu and Godavari isukalu) and VI (Burmadha, Isukaravvalu, Gedanzibetan, FR13A) and varieties from clusters I, II and V may be used as parents in the hybridization programme to generate breeding material with high diversity.

The cluster means for each of 22 characters are presented in Table 4. From the data it can be inferred that considerable differences existed for all the traits studied among the clusters. Cluster I exhibited highest mean values for three traits *viz.* grain yield per plant (23.17g), L/B ratio (2.77) and elongation ratio (1.75) and lowest mean value for panicle length (21.54 cm). Cluster II was characterized by having highest mean value for kernel length after cooking (9.61mm). Varieties in cluster III expressed highest mean value for water uptake and lowest mean value for days to 50 % flowering (88.38 days). Cluster IV recorded maximum mean values for number of filled grains per panicle (233.374) and spikelet fertility (91.559 %) and minimum mean values for water uptake (199 ml). Cluster V exhibited highest mean value for number of productive tillers (9.044), number of total grains per panicle (266.861), grain weight per panicle (4.384g), days to 50 % percent flowering (114.926 days), alkali spreading value (5.35), gel consistency (65.69) and amylose content (25.24) and minimum mean value for iron content in brown rice (7.303 ppm). Cluster VI had highest mean values for plant height (179.48 cm) and panicle length (27.94 cm). Local landraces which were present in cluster VII recorded highest mean values for grain iron and zinc content in brown and polished rice and lowest mean values for grain weight per panicle, grain yield per plant, spikelet fertility, kernel length, kernel

Table 4. Cluster means for 22 characters among 48 genotypes of rice

	Days to 50 per cent flowering	Plant height at maturity (cm)	Panicle length (cm)	Number of productive tillers Per Hill	Number of filled grains per panicle	Number of total Grains per panicle	Spikelet fertility (%)	Grain weight per panicle (g)	Grain yield per plant (g)
Cluster I	98.611	109.868	21.543	8.981	194.715	217.228	89.490	3.532	23.170
Cluster II	90.733	98.203	22.541	8.820	104.741	123.761	85.270	2.855	20.670
Cluster III	88.381	113.361	24.357	8.843	169.843	200.929	84.892	3.638	21.898
Cluster IV	103.074	129.506	27.364	8.404	233.374	254.791	91.559	4.166	20.122
Cluster V	114.926	134.734	26.403	9.044	232.338	266.861	86.718	4.384	21.034
Cluster VI	107.250	179.488	27.944	8.000	135.321	162.296	84.438	3.708	17.566
Cluster VI	101.667	159.570	26.174	9.000	196.450	233.900	84.019	2.463	15.892

	Kernel Length (mm)	Kernel Breadth (mm)	L/B Ratio	Kernel Length After Cooking (KLAC)	Kernel Elongation Ratio (ER)	Water Uptake (ml)	Alkali Spreading Value	Gel Consistency (mm)	Amylose Content (%)
Cluster I	5.71	2.06	2.77	9.25	1.75	209.46	4.60	47.42	23.39
Cluster II	6.61	2.12	3.13	9.61	1.57	244.70	4.23	45.85	22.24
Cluster III	5.66	2.59	2.21	8.62	1.44	304.55	5.01	50.67	23.01
Cluster IV	5.53	2.05	2.72	8.46	1.55	199.00	3.60	51.26	21.83
Cluster V	5.55	2.18	2.55	8.40	1.56	259.65	5.35	65.69	25.24
Cluster VI	5.74	2.54	2.30	7.45	1.29	249.29	3.33	60.74	18.87
Cluster VI	4.08	1.99	2.06	5.60	1.45	236.83	3.44	41.22	21.86

	Iron Content in brown Rice ppm	Iron Content in polished rice (ppm)	Zinc Content in brown Rice (ppm)	Zinc Content in polished rice (ppm)
Cluster I	8.358	2.092	19.302	10.613
Cluster II	9.627	1.771	19.951	12.384
Cluster III	10.136	2.255	19.466	10.685
Cluster IV	10.42	2.413	20.554	12.956
Cluster V	7.303	1.773	20.102	10.719
Cluster VI	10.453	1.752	24.836	16.544
Cluster VII	12.138	3.827	25.419	18.928

breadth, L/B ratio, kernel length after cooking and gel consistency.

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.

The Cluster V had highest mean value for number of productive tillers, number of total grains per panicle, grain weight per panicle, days to 50 %, percent flowering, alkali spreading value gel consistency and amylose content and minimum mean value for iron content in brown rice. The Cluster I exhibited highest mean values for grain yield per plant, and lowest mean value for zinc content in brown rice. The cluster VII recorded highest mean values for grain iron and zinc content in brown and polished rice. The promising genotypes from these clusters with high mean values for different traits may be used as parents

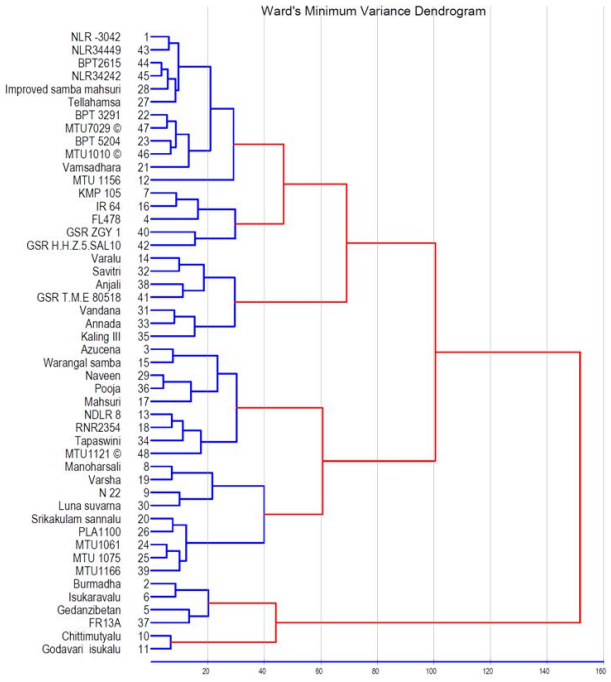

Fig 1. Ward's minimum variance dendrogram showing relationship among 48 rice genotypes

in future hybridization depending upon the objective of the breeding programme to derive superior transgressive segregants.

CONCLUSION

Based on the present objective, eight parents were selected from four clusters I, V, IV and VII based on genetic distance, cluster means and *per se* performance. Cluster I had 12 genotypes; among them BPT 5204, MTU 1156 and MTU 1010 which are having desirable quality were selected. Among the 9 genotypes of cluster V, MTU 1075 and N22 were selected. From cluster IV, MTU 1121 for its good quality and higher filled grains per panicle and Azucena with high iron and zinc content were selected. From the cluster VII, Chittimutyalu may be selected for possesing highest mean values for grain iron and zinc content in brown and polished rice. The promising varieties *viz.*, MTU 1075, MTU 1156, MTU 1010 and BPT 5204 may be crossed with Chittimutyalu, Azucena and N22 which showed high mean values for iron and zinc content.

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