Original Research Article

GENETIC DIVERSITY ANALYSIS FOR YIELD AND MORPHO-PHYSIOLOGICAL TRAITS IN ELITE RICE (*ORYZA SATIVA* L.) GENOTYPES UNDER SEMI DRY SYSTEM THROUGH D^2 STATISTICS

ABSTRACT:

Genetic divergence is a useful tool for choosing the parents to employ in a hybridization programme. The current study was conducted at Agricultural College, Aswaraopet, Telangana, to evaluate genetic diversity among 30 rice genotypes during *Kharif* 2021 using D^2 analysis under semi-dry system. Based on the analysis, thirty genotypes were divided into ten clusters based on D^2 values. Cluster II was found largest with twelve genotypes followed by cluster I had with ten genotypes and clusters III, IV, V, VI, VII, VIII, IX, and X had one genotype each, indicating that there was a sizable amount of variation among the genotypes. Cluster II (284.13) had the highest intra-cluster D^2 value, followed by cluster I. (242.63) while highest inter-cluster distance was found between Cluster VIII and IV (1503.42) followed by cluster VI and IV (1316.83), cluster VI and III (1316.15), cluster IX and IV (1303.55), cluster VIII and X (1261.09), cluster VIII and IX (1132.95), V and III (1113.91), and cluster VII and V (1101.7) suggesting that crosses involving lines from these clusters would produce wider and more desirable recombinations. The average inter-cluster distance for Cluster VIII and VI was the lowest (231.01), followed by Cluster IX and X (394.3) and Cluster III and IV (397.72). The genotypes of these clusters have the most gene complexes, as shown by the shortest inter-cluster distance. The findings revealed that, root biomass contributed the most to genetic divergence (24.59 percent), ranking first followed by total biomass (21.60%), root length (17.70%) and grain yield/plant (14.02%), culm strength (8.04%), plant height (5.74%), 1000 grain weight (4.36 %). The traits *viz.*, root biomass, total biomass, root length, grain yield/plant and culm strength contributed 85.95% of the total deviation and need to be exploited to develop varieties suitable for semi-dry system in rice. The genotypes BPT 5204, WGL 697, RNR 21278, RNR 28361, WGL 915, PR 126 and JGL 28545 were to be better for further hybridization programmes to develop varieties for semi-dry system.

Key words: Genetic diversity, D^2 statistics, rice, elite genotypes, semi-dry system

1. INTRODUCTION

Rice (*Oryza sativa* L.,) is one of the most important staple food crop for than half of the world's population and is the primary staple food crop in Asia. It is mostly grown in Asia, Latin America and Africa which represents semitropical climate with alternating wet and dry seasons (Rao et al. 2016). Globally it is grown in an area of 158 million acres with the production of 700 million tonnes. With an area, production and productivity of 43.6 mha, 118.88 mt, and 2722 Kg ha-1 respectively, India is one of the largest producers of rice. In Telangana, rice is grown in an area of 2.01 million ha producing 7.42 million tonnes with the productivity of 3644 Kg ha-1 (www.indiastat.com, 2019-20).

Currently no varieties are available that are amenable for alternate tillage and establishment techniques, especially in unpuddled or zero tillage soil conditions with direct seeding in Asia (Fukai, 2002; Watanabe *et al*., 1997) due to more focus of breeding efforts on developing varieties suitable for TPR. Semi dry (direct dry seeded) rice requires specially bred cultivars having good mechanical strength in the coleoptiles to facilitate early emergence of the seedlings, early seedling vigour for weed competitiveness (Jannik *et al*., 2000; Zhao *et al*., 2006), efficient root system for anchorage and to tap soil moisture from lower layers in peak evaporative demands (Clark *et al*., 2000; Pantuvan *et al*., 2002) along with yield stability, ability to germinate under anaerobic conditions, tolerance to early submergence (Ismail *et al*., 2009), early heading and short intermediate height (Fukai, 2002), high specific leaf area during vegetative growth and low specific leaf area with high chlorophyll content during reproductive phase (Jones *et al*., 1997b; Jones *et al*., 1997a). In the present context of shifting of rice cultivation from traditional transplanting system to alternate rice establishment techniques like drum seeding and direct seeding keeping in view of conserving natural resources, energy and increasing cost of cultivation, there is an urgent need to develop varieties suitable for alternate rice establishment techniques by evaluating existing germplasm / elite genotypes. Genetic diversity is the pre-requisite for any crop improvement programme as it helps in the development of superior recombinants (Manonmani and Fazlullah Khan 2003), through selection of parents having wider variability for different characters (Nayak *et al*. 2004). In order to identify suitable diverse genotypes possessing traits of interest under semi-dry system, the present work was taken up to estimate the extent of genetic divergence among 30 elite rice genotypes through D^2 statistics (Mahalanobis, 1936) and grouping of genotypes by using Tocher's method as suggested by Rao (1952).

2. MATERIAL AND METHODS

The material for present study comprised of thirty elite rice genotypes consisting of short, medium and long duration rice varieties. All the 30 genotypes were sown at Agricultural College, Aswaraopet, Telangana state during *Kharif*, 2021 to identify diverse genotypes that possessed desirable traits for semi-dry system. All the 30 genotypes were sown through dibbling method in a randomized block design replicated thrice, with a spacing of 20 cm between rows and 10 cm between plants. To ensure uniform plant population per replication, all appropriate precautions were taken and the crop was raised by following all the package of practices. Observations recorded were recorded on field emergence at 7 and 14 DAS, plant stand per m^2, days to 50% flowering number of productive tillers per plant, plant height (cm), culm strength, panicle length (cm), spikelet fertility (%), 1000 – grain weight (g), grain yield per plant (g), specific leaf area (cm^2), root length (cm), root biomass (g), total biomass (g) and harvest index by randomly choosing five plants from each entry in each replication and their means were used for the statistical analysis.

3. RESULTS AND DISCUSSION:

The perusal of the results of present study revealed that thirty genotypes were grouped into ten groups (Table 1 and Fig. 1) based on D^2 values. Cluster II was found largest with twelve genotypes, followed by clusters I with ten genotypes, and clusters III, IV V, VI, VII, VIII, IX and X with a single genotype each, suggesting a significant degree of variation across the genotypes. The intra and inter cluster distance are presented in (Table 2). D^2 values within clusters ranged from zero (cluster III, IV, V, VI, VII, VIII, IX, X) to 284.13(cluster II). Cluster II had the greatest intra cluster distance (284.13) followed by cluster I (242.63) indicating that there was still substantial genetic divergence among the genotypes. This could be used to enhance yield through recombination breeding under semi-dry system. Similar results were also reported earlier by Ovung *et al*. (2012).

The highest divergence was found between cluster VIII and IV (1503.42) followed by cluster VI and IV (1316.83), cluster VI and III (1316.15), cluster IX and IV (1303.55), cluster VIII and X (1261.09), cluster VIII and IX (1132.95), V and III (1113.91) and VII and V (1101.7) implying that selection of genotypes and crosses among them would result in wider and more desirable recombinations between traits under consideration. Cluster VIII and VI had the lowest average (231.01) followed by Cluster IX and X (394.3) and Cluster III and IV (397.72). The genotypes of these clusters have the most gene complexes as indicated by the minimum inter cluster distance. The results were found to be on par with the results of earlier workers viz., Mishra *et al*. (2003) and Chaturvedi and Maurya (2005).

The greater the distance between two clusters, the more is the genetic diversity between genotypes. The genotypes in the most divergent clusters may be able to take advantage of the maximum heterosis. It is indicated that hybridization between the genotypes BPT-5204 (cluster III), RNR 21278 (cluster IX), WGL 697, PR 121 and JGL 28545 (cluster II), RNR 15048 and WGL 915 (cluster I), RNR 28361 (cluster VIII), JGL 1798 (cluster IV) and PR 126 (cluster X) may be exploited for development of varieties suitable for semi-dry system with higher yield as they were found to posses desirable traits (Table 3). It was found that no cluster had at least one genotype with all of the required features, shutting out the possibility of selecting one genotype for immediate use and hence, hybridization between selected genotypes from divergent clusters is essential to selectively incorporate all of the targeted traits.

A perusal of results of cluster means in (Table 4) revealed that cluster VI has the highest mean value for 1000-grain weight, panicle length, plant height while cluster III has the highest mean value for number of productive tillers per panicle, grain yield per plant and plant height, cluster II has the highest mean value for 50% flowering and root length.

The contribution of each trait to total divergence is presented in (Table 5). Among the traits studied, contribution of root biomass was highest towards genetic divergence (24.59%) by taking 107 times ranking first, followed by total biomass (21.60%) by taking 94 times, root length (17.70%) by taking 77 times, grain yield/plant (14.02%) by 61 times, followed by culm strength (8.04%) by 35 times, plant height (5.74%) by 25 times, 1000-grain weight (4.36%) by 19 times to genetic divergence in decreasing order. Root biomass, total biomass, root length, grain yield/plant, culm strength together contributed 85.95% towards total divergence. As a result, these characteristics should be prioritized during hybridization and population selection in order to develop varieties amenable for semi-dry system. These results are in conformity with the findings of Vennila *et al.* (2011)

4. CONCLUSION:

A significant range of variation was evident among thirty elite rice genotypes upon evaluation. The thirty rice genotypes were grouped into ten clusters which was in consonance with the clustering pattern obtained by Mahalanobis D^2 statistics. The parents for hybridization program should be selected on the basis of magnitude of genetic distance, contribution of different characters towards the total divergence and magnitude of cluster means for different characters to manifest heterosis. Hybridization between the genotypes *viz*., BPT 5204, RNR 21278, WGL 697, PR 121, JGL 28545, RNR 15048, WGL 915, RNR 28361, JGL 1798 and PR 126 may be attempted in future breeding programmes to develop varieties suitable for semi-dry system. In view of this, genotypes from clusters III, IX, II, I, VIII, IV and X were found to be expected to manifest high heterosis in desirable direction for most of the morpho-physiological traits under study, accumulation of favorable genes in subsequent segregating generations.

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Table 1. Clustering pattern among 30 rice Genotypes

Cluster Number	Number of genotypes in the cluster	Names of the Genotypes
I	10	PR-128, WGL-32100, WGL-14, PR-127, PR129, PNR-29325, RNR-15048,WGL-915, JGL-11470, PR-114
II	12	PR-121, JGL-24423, WGL-44, WGL-962, WGL-3962, WGL-697, JGL-28545, Sugandha samba, RNR-11718, MTU-1061, Krishna, WGL-739
III	1	BPT-5204
IV	1	JGL-1798
V	1	JGL-18047
VI	1	Tellahamsa
VII	1	RNR-28361
VIII	1	PR-124
IX	1	RNR-21278
X	1	PR-126

Table 2. Intra (diagonal) and inter-cluster average of D^2 values of 30 rice genotypes

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
Cluster I	242.63	537.83	461.66	404.09	684.0	866.51	505.15	1043.19	712.33	516.44
Cluster II		284.13	1057.89	888.57	464.67	417.16	527.99	537.91	532.52	624.65
Cluster III			0.00	397.72	1113.91	1316.15	1050.17	1762.61	902.21	409.51
Cluster IV				0.00	788.81	1316.83	1031.6	1503.42	1303.55	561.97
Cluster V					0.00	425.36	1101.7	458.46	877.22	577.28
Cluster VI						0.00	960.99	231.01	583.26	845.67
Cluster VII							0.00	1068.78	502.41	675.3
Cluster VIII								0.00	1132.95	1261.09
Cluster IX									0.00	394.3
Cluster X										0.00

Table 3: Cluster-wise genotypes with possessing desirable morpho-physiological characters

S.No.	Cluster Number	Genotype	Morpho-physiological characters
1	III	BPT 5204	Plant height, field emergence at 7 days after sowing, total biomass, root biomass and number of productive tillers per plant
2	IX	RNR 21278	1000-grain weight, culm strength, specific leaf area, root length
3	II	WGL 697	Field emergence at 7 days after sowing, spikelet fertility, root length and plant height
		PR 121	Panicle length, plant stand/m^2, specific leaf area
		JGL 28545	Grain yield per plant
4	I	WGL 915	Culm strength
		RNR 15048	Specific leaf area
5	VIII	RNR 28361	Culm strength, root length
6	X	PR 126	Grain yield per plant, 1000-grain weight and number of productive tillers per plant
7	IV	JGL 1798	Panicle length and total biomass

Table 4 Cluster mean of different characters in 30 rice genotypes

Cluster Number	Days to 50% flowering	Plant height (cm)	Number of productive tillers per Plant	Panicle Length (cm)	Harvest Index	Grain yield per plant (g)	1000 grain weight	Field emergence at 7 days	Field emergence at 14 days
I	59.37(VI)	83.31(IX)	14.37(V)	20.63(VI)	0.41(V)	21.51(VIII)	19.09(IX)	87.50(V)	87.93(V)
II	63.58(II)	87.82(VII)	14.42(IV)	21.38(V)	0.43(IV)	24.40(VI)	20.47(VII)	86.56(VI)	86.78(VI)
III	54.33(VIII)	113.87(1)	15.67(I)	20.17(VIII)	0.46(III)	29.53(II)	20.69(VI)	92.33(II)	92.67(II)
IV	59.67(V)	90.77(V)	14.33(VI)	25.10(I)	0.34(VII)	28.37(IV)	18.43(X)	73.00(X)	73.67(X)
V	62.67(IV)	73.03(X)	14.33(VI)	20.33(VII)	0.81(I)	25.33(V)	23.00(IV)	75.00(IX)	76.00(IX)
VI	51.33(IX)	99.33(III)	12.33(IX)	23.17(II)	0.39(VI)	23.42(VII)	25.44(I)	88.00(IV)	88.33(IV)
VII	63.00(III)	86.80(VIII)	13.33(VII)	21.77(IV)	0.39(VI)	18.29(IX)	20.19(VIII)	90.00(III)	90.33(III)
VIII	50.67(X)	99.67(II)	12.67(VIII)	22.60(III)	0.50(II)	15.35(X)	22.29(V)	92.67(I)	93.33(I)
IX	58.33(VII)	89.07(VI)	14.67(III)	18.93(X)	0.50(II)	29.30(III)	24.75(II)	84.00(VIII)	85.00(VIII)
X	66.00(I)	98.73(IV)	15.33(II)	20.00(IX)	0.39(VI)	32.83(I)	24.62(III)	86.00(VII)	86.33(VII)

Cluster Number	Plant stand/m^2	Culm strength	Spikelet Fertility	Specific Leaf area	Root length	Total biomass	Root Biomass
I	79.07(VII)	27.82(V)	85.73(V)	0.89(VII)	16.35(IV)	85.93(IV)	24.47(III)
II	83.06(V)	28.59(IV)	84.86(VII)	1.14(V)	16.43(III)	63.71(VIII)	16.51(VIII)
III	73.00(X)	27.26(VI)	91.33(I)	0.32(X)	15.20(V)	101.5(I)	27.99(I)
IV	83.67(IV)	24.37(VII)	85.67(VI)	1.66(III)	13.23(VIII)	95.72(II)	26.75(II)
V	73.67(IX)	18.07(X)	78.33(VIII)	0.83(VIII)	10.50(X)	75.44(VII)	17.78(VII)
VI	74.00(VIII)	22.59(IX)	87.67(IV)	0.55(IX)	15.10(VI)	55.53(IX)	16.37(IX)
VII	82.67(VI)	50.70(I)	77.67(IX)	1.24(IV)	19.43(II)	85.88(V)	20.12(V)
VIII	84.67(III)	24.30(VIII)	77.33(X)	1.10(VI)	12.17(IX)	53.29(X)	13.88(X)
IX	88.67(II)	35.33(II)	90.00(II)	1.95(I)	20.10(I)	76.73(VI)	19.59(VI)
X	89.67(I)	35.03(III)	89.00(III)	1.78(II)	14.27(VII)	94.33(III)	23.31(IV)

Chart 1: Cluster number and variability parameter

Table 5: Percentage of contribution of each character towards total divergence

SL.NO	**Character**	**No. of times ranked first**	**Contribution (%)**
1.	Days to 50% flowering	2	0.45
2.	Plant height	25	5.74
3.	No.of productive tillers	1	0.02
4.	Panicle length	12	2.75
5.	Harvest Index	1	0.06
6.	Grain yield / plant	61	14.02
7.	1000 - grain weight	19	4.36`
8.	Field emergence at 7 DAS	1	0.17
9.	Field emergence at 14 DAS	2	0.45
10.	Plant stand / m2	1	0.02
11.	Culm strength	35	8.04
12.	Spikelet fertility	1	0.01
13.	Specific leaf area	1	0.02
14.	Root length	77	17.70
15.	Total biomass	94	21.60
16.	Root biomass	107	24.59

Fig. 1: Cluster analysis of 30 genotypes by Tocher method