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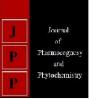Hyderabad, Telangana, India

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Genetic diversity studies for differential soil phosphorus content in rice (*Oryza sativa* L.)

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Abstract
Studies was carried out to assess the genetic divergence among 55 parental lines of rice using Mahalanobis D^2 under graded soil phosphorus condition *viz*., 20, 40 and 60 *kg P_2O_5 ha*[-1] at ICAR-Indian Institute of Rice Research, Hyderabad. 55 parental lines were grouped into eight clusters. Cluster I had highest number of genotypes (48) and remaining clusters showing one parental line in each cluster. Highest divergence occurred between cluster II and VII (14.49) and minimum inter cluster distance between the clusters V and II (4.63). The highest intra cluster distance was recorded for cluster no. I (4.47) and remaining clusters shows 0.00 showed minimum intra cluster distance

Keywords: Genetic divergence, mahalanobis D^2, Tocher's method, wilkins method, clusters distance, cluster mean value

Introduction

Rice is a self-pollinated cereal crop belonging to the family Gramineae (synonym-Poaceae) under the order Cyperales and class Monocotyledon having chromosome number 2n=24. Rice Globally, an area of 162.97 Mh, production- 495.03 Mt and productivity of 4530 kg ha-1 in 2017-18 (World Agricultural Production, USDA, 2019). India produced 112.91 Mt, Area- 43.80 Mha, average yield of 2578 kg/ha (Indiastat, 2017-18). The area under hybrid rice in India wet season (*Kharif* 2018) was around 3 m.ha. (6% of the total rice area of 44 m.ha i.e. 2.64 mha) Senguttuvel *et al.*, 2019. India is the 3rd largest producer and consumer of fertilizers. Overall production of fertilizers during FY18 has been 413 LMT.

Phosphorus (P) is one of the most important primary macronutrients which promotes plant growth and plays a vital role in improving crop productivity. Nearly 80% of applied inorganic P is wasted in processes such as fixation with iron/aluminium in acidic soils, calcium/magnesium in alkaline soils and slow diffusion leaving only 20% of it to be utilized by the plant. Thus P fertilizer use must be optimised (Yi *et al*., 2005, Plaxton and Tran, 2011, Vinod and Heuer, 2012, Herrera-Estrella and Lopez-Arredondo, 2016) [17, 9, 15, 6] particularly in India where P fertility of soils is extremely poor (Sanyal *et al*. 2015) [10]. Genetic diversity is one of the criteria of parent selection in the hybridization programme. The availability of transgressive segregant in any breeding program depends upon the diversity between the parents involves. The quantification of genetic diversity through biometrical procedures such as Mahalanobis's D^2- statistic which may be an efficient tool in the quantitative estimation of genetic diversity (Mahalanobis, 1936) [7]. The divergence analysis has a definite role to play in an efficient choice of divergent parents for hybridization to exploit maximum heterosis.

Methods and Material

The field experiment was carried out during the *kharif* 2016 in three different soil P *viz*., 20, 40 and 60 Kg P_2O_5 ha^{-1} at P- facility center in ICAR-IIRR Hyderabad. The materials used in this experiment consisted of 55 parental lines of rice which were maintained at ICAR- IIRR Hyderabad (Table-1). Data collected based on randomly selecting three plants in row excluding border plants. Days to 50% flowering, Plant height (cm), panicle length (cm), total tillers per plant, productive tillers per plant, spikelet fertility (%) and 1000 seed weight (g) and yield per plant (g) were measured from 3 randomly selected sample plant.

Statistical analysis: Homogeneity of error variance was tested using F-max test method of Hartley15, with the equation

$$F\text{ - max} = \frac{\text{Largest MSE}}{\text{Smallest MSE}}$$

Pooled ANOVA over 3 soil P condition was done using indostat version 9.2 software. Mahalanobis's D^2 statistics was used to examine the genetic distance between populations 17. The significance level of genetic distance between clusters was tested both at 1 and 5% level of probability using chi-square test. The D^2 values obtained for pairs of cluster were considered as the calculated values of chi-square ($\chi2$) and tested for P degree of freedom, where P is the number of characters considered (Singh and Chaudhary1985) [12].

Table 1: List of 55 parental lines of rice screened in differential soil P (20, 40 and 60 $Kg\ P_2O_5\ ha^{-1}$) plot of ICAR- IIRR, Hyderabad

Sl. No	Parental lines	Sources of origin	Sl. No	Parental lines	Sources of origin
1	AYT-21	IRRI, Philippines	29	KASALATH	aus Landrace
2	L-2182	IIRR, Hyderabad	30	KMR-3	College farm, Mandya
3	50-13	IIRR, Hyderabad	31	RPHR-1005	IIRR, Hyderabad
4	AR 7-65R	IIRR, Hyderabad	32	DR 714-1R	IIRR, Hyderabad
5	AR 7-75R	IIRR, Hyderabad	33	BK-36-167	IIRR, Hyderabad
6	AR 9-21R	IIRR, Hyderabad	34	BK-39-179	IIRR, Hyderabad
7	AR 19-42R	IIRR, Hyderabad	35	50-10	IIRR, Hyderabad
8	AR 19-18R	IIRR, Hyderabad	36	BK-35-155	IIRR, Hyderabad
9	PSV-15	IIRR, Hyderabad	37	SG-25-74	IIRR, Hyderabad
10	PSV-18	IIRR, Hyderabad	38	612-1	IIRR, Hyderabad
11	PSV-41	IIRR, Hyderabad	39	IBL-57	IIRR, Hyderabad
12	PSV-49	IIRR, Hyderabad	40	BK-49-42	IIRR, Hyderabad
13	NH-12-124R	IRRI, Philippines	41	BCW-56	IIRR, Hyderabad
14	NH-12-144R	IRRI, Philippines	42	RPHR-1096	IIRR, Hyderabad
15	ATR-304	IIRR, Hyderabad	43	SG-26-120	IIRR, Hyderabad
16	ATR-305	IIRR, Hyderabad	44	BK-49-80	IIRR, Hyderabad
17	ATR-224	IIRR, Hyderabad	45	RPHR-517	IIRR, Hyderabad
18	ATR-226	IIRR, Hyderabad	46	BK-52-104	IIRR, Hyderabad
19	ATR-253	IIRR, Hyderabad	47	619-2	IIRR, Hyderabad
20	ATR-256	IIRR, Hyderabad	48	RP-BIO4919-363-5	IIRR, Hyderabad
21	MTP-5	IIRR, Hyderabad	49	TCP963	IIRR, Hyderabad
22	MTP-7	IIRR, Hyderabad	50	TCP951	IIRR, Hyderabad
23	IR-68897B	IRRI, Philippines	51	TCP950	IIRR, Hyderabad
24	APMS-6B	RRS, Maruteru	52	TCP795	IIRR, Hyderabad
25	IR-79156B	IRRI, Philippines	53	TCP964	IIRR, Hyderabad
26	IR-58025B	IRRI, Philippines	54	PUSA-5B	IARI, New Delhi
27	CRMS-32B	NRRI, Cuttack	55	TCP-960	IIRR, Hyderabad
28	RASI	IIRR, Hyderabad			

Results and Discussions

In the present study combined analysis of variance revealed the performance of parental lines under different soil P condition was differ. D^2 values were calculated for 1485 possible pairs of combinations (n (n-1)/2) from means of 55 genotypes for 8 characters.

Significant differences among the genotypes for each individual character were first determined followed by the statistical significant differences between the genotypes based on the pooled effects of all the characters were carried out using the *Wilk's criterion*. The *Wilk's* criterion thus obtained was used in calculations of 'V' statistic. The significance of 'V' (statistic) was tested by % at 432 degrees of freedom. The 'V' statistic was found highly significant which indicates that the genotypes differed significantly when all the characters were considered simultaneously.

The 55 rice genotypes used in present study were grouped into eight clusters (Table-2). Cluster I was the largest comprising of forty eight genotypes followed and remaining clusters were only one genotype. The distribution pattern of the genotypes from different eco-geographical regions into various clusters was all at random indicating that there is no parallelism between geographical diversity and genetic diversity. This infers that the forces like exchange of breeding material, natural and artificial selection, genetic drift, migration, gene flow and variation in environment may be responsible for this diversity. Hence, the choice of suitable diverse parents selected on the basis of genetic diversity analysis would be more rewarding than the choice made on geographic diversity basis. These findings were found to be in agreement with the reports of Vennila *et al.* (2011) [14], Yadav *et al.* (2011) [16], Bupesh Kumar *et al.,* (2014) [2].

Table 2: Clustering pattern for fifty five parental lines of rice under differential soil P level by using Tocher's method

Sl. No	Clusters	Genotypes
1	Cluster 1	AYT-21, 50-13, AR 7-65R, AR 7-75R, AR 9-21R, AR 19-42R, PSV-15, PSV-18, P SV-41, PSV-49, NH-12-124R, NH-12-144R, ATR-224, ATR-226, ATR-253, MTP-5, MTP-7, APMS-6B, RASI, KMR-3, RPHR-1005, BK-36-167, BK-39-179, 50-10, SG-25-74, 612-1, BCW-56, RPHR-1096, RPHR-517, 619-2, RP-BIO4919-363-5, TCP963 TCP951, TCP950, TCP795, PUSA-5B, DR 714-1R, IR-68897B, ATR-256, ATR-304, L-2182, ATR-305, AR 19-18R, TCP-960, IR-58025B, SG-26-120, BK-49-80, IBL-57.
2	Cluster 2	BK-52-104
3	Cluster 3	TCP964
4	Cluster 4	BK-49-42
5	Cluster 5	CRMS-32B
6	Cluster 6	IR-79156B
7	Cluster 7	BK-35-155
8	Cluster 8	KASALATH

Intra cluster D^2 values ranged from 0.00 to 4.47. Maximum intra cluster distance was observed in cluster I (4.47) and remaining clusters shows 0.00 indicating that only considerable genetic divergence existed among the genotypes within the same cluster I (Table-3). This could be made use of for yield improvement through recombination breeding. Based on values of inter cluster distance was ranged from 4.63 to 14.49. it was found that highest divergence occurred between cluster II and VII (14.49) followed by cluster IV and V (14.34), cluster IV and III (14.11) and cluster V and VIII (13.79) indicating wider genetic diversity between genotypes

of these groups. On the other hand, lowest divergence was noticed between the clusters V and II (4.63) indicating close relationship and similarity for most of the traits of the genotypes in this cluster. Greater the distance between two clusters, wider the genetic diversity among the genotypes of those clusters. The crosses involving genotypes from these clusters would give wider and desirable recombinants. Chand *et al.* (2005) [3] and Chaturvedi and Maurya (2005) [4] also have recommended selection of the parents from two clusters, having wider inter cluster distance in order to realize much variability and high heterotic effect.

Table 3: Average intra (diagonal) and inter cluster distances for fifty five parental lines of rice based on morphological traits under differential soil P level

Cluster distances	Cluster-1	Cluster-2	Cluster-3	Cluster-4	Cluster-5	Cluster-6	Cluster-7	Cluster-8
Cluster-1	4.47	7.08	6.67	7.43	7.11	6.51	6.89	8.51
Cluster-2		0.00	12.14	10.41	4.63	10.65	4.74	14.49
Cluster-3			0.00	14.11	8.89	11.41	11.73	7.24
Cluster-4				0.00	14.34	6.94	6.70	12.31
Cluster-5					0.00	7.39	12.26	13.79
Cluster-6						0.00	9.49	11.04
Cluster-7							0.00	13.09
Cluster-8								0.00

It is observed that 1000 seed weight, days to 50% flowering, plant height, total tiller per plant and spikelet fertility (%) are the important traits contributing nearly 84.30% towards divergence and for discriminating the genotypes (Table- 4). Similar results were reported by Surender Raju (2002) [13], Shukla *et al.* (2006), Banumathy *et al.* (2010) and Nibedita Mohanty *et al.* (2010) [8].

Table 4: Relative contribution (%) of each character to the genetic diversity for yield and it's components in fifty five parental lines of rice

Source	Times ranked 1st	Contribution %
Days 50% to Flowering	289	19.46%
Plant Height	318	21.41%
Panicle Length	129	8.69%
Total tillers per plant	202	13.6%
Productive tillers per plant	34	2.29%
Spikelet Fertility (%)	234	15.76%
1000 Seed weight	209	14.07%
Yield Per Plant	70	4.71%

The clusters means for each of eight characters are furnished in Table 5. From the data, considerable differences existed for

all the characters under study. For days to 50 percent flowering cluster mean was highest in cluster VII (123.67 days) while lowest in cluster III (88.17 days). Plant height was highest in cluster VIII (101.42 cm) while lowest in cluster V (71.72 cm). Panicle length was highest in Cluster IV (19.39 cm) and lowest in cluster V (14.16 cm). Number of total tillers per plant was highest in cluster VI (16.03) while lowest in cluster II (10.83). Number of productive tillers was highest in cluster VI (14.91) and lowest in cluster II (9.26). Spikelet fertility (%) was highest in cluster IV (77.34) and lowest in cluster II (53.49). 1000 grain weight was highest in cluster VI (20.72 g) and lowest in cluster IV (15.62 g). Yield per plant was highest in cluster VII (14.70 g) and lowest in cluster V (4.42 g). The result indicates that selection of genotypes having high values for particular trait could be made and used in the hybridization programme for improvement of that particular character.

The cluster VI was having highest mean value for total tillers per plant, productive tillers per plant and 1000 seed weight. Likewise desirable means in cluster IV for panicle length and spikelet fertility (%). The genotypes from the clusters having high mean values may be directly used for adaptation or may be used as parents in hybridization programme.

Table 5: Cluster means for seed yield and yield attributing characters among the fifty five parental lines of rice under differential soil P level

Cluster means; Tocher method	Days 50% to flowering	Plant height	Panicle length	Total tillers per plant	Productive tillers per plant	Spikelet fertility (%)	1000 Seed weight	Yield per plant
Cluster-1	105.40	88.42	17.49	12.51	10.90	70.23	18.86	9.63
Cluster-2	121.00	88.84	16.33	10.83	9.26	53.49	16.55	7.66
Cluster-3	88.17	75.93	17.67	11.56	9.95	72.13	18.78	13.59
Cluster-4	114.33	95.72	19.39	15.22	14.04	77.34	15.62	7.96
Cluster-5	101.67	71.72	14.16	12.26	10.34	55.45	18.86	4.42
Cluster-6	102.00	82.89	18.04	16.03	14.91	63.10	20.72	6.13
Cluster-7	123.67	97.39	18.95	13.72	12.13	64.03	17.44	14.70
Cluster-8	88.67	101.42	18.33	12.39	11.47	67.77	18.50	11.98

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