Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

J P P Journal of Pharmacognosy and Phytochemistry

E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2017; 6(6): 510-513
Received: 15-09-2017
Accepted: 17-10-2017

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Genetic divergence among rice genotypes for drought tolerance

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Abstract
Rice (*Oryza sativa* L.) 2n=24, Family- Poaceae is the world's most important staple food crop, which not only provide food but also influenced traditions, religions, culture and life style since Vedic period. Rice is grown over an area of 153.76 m. ha with production of 598.85 m.t. in the world (FAO, 2012). Drought stress is the major constraint to rice production and yield stability in the rainfed regions, affecting 19 million ha of upland and over 14 m ha of rainfed lowland rice. In drought prone environment breeding programme must combine selection under stress condition with selection for yield potential because farmers want cultivars that are both drought-tolerant and have high yield potential in favourable years Evidence indicates that these goals are not mutually exclusive. There is a moderate to large positive correlation between yield under drought stress and yield potential under favourable condition. To achieve such goals the investigation was conducted at Experimental Farm, College of Agriculture, Rewa (M.P.) under Rice Improvement Project with 65 genotypes in D^2 statistics with three replications during Kharif 2014. Findings revealed that highest contribution towards the genetic diversity of rice genotypes was contributed Under control condition by panicle weight, grain yield per hectare, days to 50% heading, sterility per cent, no. of panicles per meter, no. of grains per panicle and biological yield, whereas in rainfed stress condition the characters like sterility per cent followed by grain yield per meter, days to 50% heading, test weight, panicle weight, biological weight per meter and no. of grains per panicle.

Keywords: Drought Stress, D^2 Statistic, Genetic Diversity, Cluster.

Introduction
Rice (*Oryza sativa* L.) 2n=24, Family- Poaceae is the world's most important staple food crop, which not only provide food but also influenced traditions, religions, culture and life style since Vedic period. Rice is grown over an area of 153.76 m. ha with production of 598.85 m.t. in the world (FAO, 2012) [6]. Drought stress is the major constraint to rice production and yield stability in the rainfed regions, affecting 19 m ha of upland and over 14 m ha of rainfed lowland rice (Evenson *et al.*, 1996; Pandey *et al.*, 2000) [5, 10]. There is high probability that a genotype performing well under non-stress conditions will also perform well under drought, even if the relative yield reduction is large, because of spill over effects of yield potential (Blum, 1988; Babu *et al.*, 2003) [4, 2]. However, stable genotypes which perform better under stress as well as under non-stress conditions are desirable in rainfed upland condition for sustainable rice production. In drought prone environment breeding programme must combine selection under stress condition with selection for yield potential because farmers want cultivars that are both drought-tolerant and have high yield potential in favourable years Evidence indicates that these goals are not mutually exclusive. There is a moderate to large positive correlation between yield under drought stress and yield potential under favourable condition (Atlin *et al*. 2004) [1]. To achieve such goals the investigation was conducted.

Material and Methods
The present investigation entitled "Genetic divergence among rice genotypes for drought tolerance" was carried out during the *Kharif* season 2013-14. The experiment was carried out at Experimental Farm, College of Agriculture, Rewa (M.P.). In this experiment 64 genotypes were used for the evaluation. There were two environments viz. Controlled and Rainfed stress condition using the D^2 experimental design.

Methodology
a) Genetic diversity through Mahalanobis D^2 analysis
Mahalanobis D^2 statistic (Mahalanobis, 1928) [7] was used for assessing the genetic divergence between different populations. The D^2 analysis was carried out using the observations made during the *kharif* 2013. Mahalanobis generalized distance (D^2) between any two populations is

given by the formulae.

$$D^2 = \delta_i \delta_j r^{ij}$$

Where,

D^2 = square of the generalized distance

Vij = reciprocal common dispersion matrix

$\delta_i = (\mu i1 - \mu i2)$

$\delta_j = (\mu j1 - \mu j2)$

Where,

μ = vector of mean value for all the characters.

The formula for estimates of D^2 for the samples is given by,

$$D^2 p = d^{is-1} d$$

Where,

$D^2 p$ = square of distance considering 'P' variables

d = vector of observed difference of mean values of all the characters

$= (xi1 - xi2)$

X_{i1} = vector of mean values of the character

S^{-1} = Inverse of variance and covariance matrix.

Since inversion matrix is complicated, the original correlation variable (xi) was transformed to non-correlated variable (Yi). So, computation of D^2 values reduces the simple summation of the square of the difference between the values of the transformed variables of two populations. The transformation was done by pivotal condensation method. These newly transformed un-correlated variables were used to calculate the square of the distance using the formulae.

$$D^2 = (Y_{i1} - Y_{i2})^2$$

Where,

Y = vector of transformed mean values.

The square of these D^2 values give the generalized distance between the two populations. The D^2 values were arranged in a matrix form.

The significance of D^2 values between two populations is tested using the formulae.

$$T^2 = \frac{N_1 \times N_2}{N_1 + N_2} \times D^2$$

Using, T^2 the F values was calculated using the formulae

$$F = \frac{(N_1 + N_2 - P - 1)}{(N_1 + N_2 - 2)P} \times T^2$$

This computed F value was compared with the table 'F' value at 5 per cent and one per cent level of probability at P and $(N1 + N2 - P - 1)$ degrees of freedom.

b) Clustering of D^2 values

All the n (n-1)/2 D^2 values were clustered during Tocher's method as described by Rao (1952) [11].

The dissimilarity coefficients were estimated by using D^2 value as suggested by Sneath and Sokal (1973) [13]. Dissimilarity coefficient between the genotypes can be arranged into reasonable hierarchal system and the diagram called Dendrrogram representing the genotypes that connect the most similar entries was constructed. By this procedure we obtain objectively delimited group of which some are right at higher ranks than others.

i) Intra cluster distance

The intra cluster distance was calculated by the following formulae (Singh and Chaudhary, 1977) [12].

$$\text{Square of intra cluster distance} = \frac{\sum D i^2}{n}$$

Where,

$\sum Di^2$ Is the sum of the distance between all possible combinations of the entries included in a number?

n = Number of possible combinations.

ii) Inter cluster distance

The inter cluster distance was calculated by the formulae given by the Singh and Chaudhary (1977) [12].

$$\text{Square of inter cluster distance} = \frac{\sum D i^2}{n_i n_j}$$

Where,

$\sum Di^2$ =Sum of distance between all possible combinations of the entries included in the cluster.

n_i = Number of entries in cluster i

n_j = Number of entries in cluster j

Result and Discussion

A clear understanding of the extent of variability prevalent for each of the character in the germplasm collection would just imply the scope for improving the character studied through selection. But, the success of any crop improvement programmes mainly depends on amount of diversity available in the crop. Improvement of yield in rice is attributed to increased use of genetically diverse parents in breeding programme. However, in case of rice varieties, a narrow genetic base has been observed. This is probably due to use of same parents for evolving new varieties. Hence, knowledge of genetic divergence in the available cultivars is of immense importance for selecting the parents to be used in hybridization programme for obtaining desirable genetic recombination's.

Mahalanobis D^2 statistic is a powerful tool used to quantify the degree of genetic divergence between the genotypes and relate cluster pattern with geographic origin. The success and usefulness of multivariate technique is quantification of genetic diversity has been demonstrated by earlier workers Bhatt, (1970) [3] and Narayanan and Macfield, (1976) [9].

In the present investigation, 65 rice lines were considered for the assessment of nature of genetic diversity by adopting Mahalanobis (1936) [8] concept of generalized distance (D^2). Sixty five genotypes used in the study representing diverse agro-climatic conditions were distributed at random among the clusters formed based on their genetic distance. The genotypes belonging to diverse ecological regions clustered together, while those of same region entered separate groups. The absence of relationship between genetic diversity and geographical origin suggests a similarity in their genetic constitution.

a) Clustering pattern of characters

A method suggested by Ward's (1936) minimum variance dendrogram was used to group into different clusters based on

the D^2 values.

Under controlled condition 65 genotypes were grouped into 14 clusters, among 14 clusters, clusters I was biggest with 42 genotypes followed by cluster III with 2 genotypes. The remaining cluster II, IV, V, VI, VII, VIII, IX, X, XI, XII, XIII and Cluster XIV contained solitary single genotype. Whereas in rainfed drought stress condition 65 genotypes were grouped into 6 clusters. Cluster I was the biggest cluster with the 58 genotypes followed by the cluster IV with 3 genotypes. The remaining cluster II, III, V, and cluster VI each contained solitary single genotype.

- **Intra and Inter cluster D2 values**

In the control condition intra cluster distances ranged from 0 (cluster II, IV, V, VI, VII, VIII, IX, X, XI, XII, XIII and XIV), which are solitary clusters to 7.27 (cluster III) indicating poor diversity. The inter cluster D^2 values exhibited a highest value of 25.70 (cluster X and XIII) and lowest value of 5.41 (cluster II and III) suggesting only a little diversity among genotypes.

Under the rainfed condition intra cluster distances ranged from 0 (cluster II, III, V, and VI) which are solitary clusters to 68.77 (cluster I) indicating poor diversity. The inter cluster D^2 values exhibited a highest value of 520.78 (cluster V and VI) and lowest value of 49.03 (cluster II and IV) suggesting only a little diversity among genotypes.

b) Percent contribution of individual character towards the total divergence

Contribution of each character towards genetic divergence has been estimated from the number of times that each character appeared in the first rank. Under control condition it was observed that grain yield per hectare (21.25), days to 50% flowering (12.5), sterility percent (11.25), no. of panicle per meter (8.95), no. of grains per panicle (7.02), biological yield per meter (1.44), test weight (0.72), harvest index and plant height (0.1) and panicle harvest index and grain yield per meter (0.05). Whereas under rainfed condition it was observed that sterility index (36.88) was highest contributor towards the divergence followed by the grain yield (13.41), days to 50% flowering (13.03), test weight (10.77), panicle weight (8.61), grain yield per hectare (5.82), biological yield per meter (5.82), no. of grains per panicle (2.82), no. of panicle per meter (1.92), plant height (0.77), panicle harvest index (0.67), panicle length (0.05) and harvest index (0).

c) Cluster mean analysis

Analysis of cluster means indicates diversity demonstrated by different clusters for a character. Based on the means, it is possible to know the character influencing divergence. The variation observed in cluster mean also points to the degree of variability.

Under the control condition for days to 50% flowering the genotypes induced in the cluster VII showed early flowering types and genotypes in cluster IX comprised of late flowering types, whereas in rainfed condition genotype induced in cluster V and genotypes in cluster IV comprised of late flowering.

Under control condition for plant height the genotypes of cluster XIV were dwarf in height while the cluster IX was taller and remaining having a intermediate height, whereas in rainfed condition the genotypes of cluster III were dwarf in height while the cluster VI was taller and remaining having a intermediate height.

Under control condition for panicles per meter the genotypes in cluster X having minimum panicles in average and cluster VI having maximum panicle in average, whereas in rainfed condition the cluster IV havening minimum panicle and cluster III having maximum panicles per meter.

Under control condition for panicle length the genotypes in cluster IX having minimum length and cluster XIII having maximum panicle length whereas in rainfed condition the cluster II having a maximum panicle and cluster V having the maximum panicle length.

Under control condition for panicle weight the genotypes in cluster XII having minimum weight and cluster XII having a maximum weight, whereas in rainfed condition the cluster V having minimum weight and cluster Vi having maximum weight.

Under control condition for grain yield per meter the genotypes in cluster XII have minimum yield and cluster XIII have maximum yield, whereas in rainfed condition the cluster V having minimum yield and cluster VI having the maximum yield.

Under control condition for panicle harvest index the genotypes in the cluster XII having minimum recovery of grain and cluster X having maximum recovery whereas in rainfed condition the cluster IV having minimum recovery of grain and cluster V having maximum recovery.

Under control condition for biological yield per meter the genotypes in cluster VI have the minimum yield and cluster VII having maximum yield whereas in the rainfed condition cluster III has a minimum yield and cluster VI having a maximum yield.

Under control condition for the harvest index the genotypes in cluster XII having minimum mean value and cluster IX having maximum whereas in rainfed condition cluster IV having minimum and cluster VI having maximum mean value for harvest index.

Under control condition for test weight the genotypes in the cluster IX having minimum mean value and cluster II has maximum mean value, whereas in rainfed condition cluster III having minimum mean value and cluster VI has maximum mean value.

Under control condition for no. of grains per panicle the genotypes in the cluster VI having a minimum mean value and cluster VII having a maximum mean value, whereas in the rainfed condition the cluster V has minimum mean value and cluster VI having a maximum mean value.

Under control condition for grain yield per hectare the genotypes in the cluster XIV having minimum mean value and cluster XI has maximum mean value whereas in rainfed condition cluster III having the maximum mean value and cluster VI has minimum mean value.

Under control condition for sterility index the genotypes in the cluster XIII having minimum mean value and cluster XIV having maximum mean value whereas in rainfed condition the genotypes cluster V having minimum mean value and cluster III having a maximum mean value.

The cluster means analysis for the 13 characters for 14 clusters in control condition and 6 clusters for rainfed drought condition presented in Table 1 and Table 2.

Table 1: Cluster mean of control condition

	DTH	PH	PPM	PL	PW	GY	PHI	BW	HI	TW	GNPP	GYPHA	S %
I	79.66	132.84	50.4	23.53	110.23	81.04	73.12	248.85	35.14	20.49	86.17	1683.6	12.18
II	78.67	127	92.67	22.33	160.67	125.1	77.89	292.03	42.9	23.4	61	2172.7	8.36
III	79.09	127.18	74.33	25.09	185.09	147.37	79.38	274.52	57.81	19.65	102.18	1907.8	13.84
IV	83.33	153.67	85.67	25	106.21	69.59	65.6	273.79	25.36	20.07	111	3072.7	17.32
V	68.67	148.33	52	27	143.17	110.17	76.94	313.43	35.34	18.53	126.33	3011	11.96
VI	83.67	160.67	112.67	23.33	116.33	92.6	78.79	162.14	58.45	19.1	59.33	2596.3	11.74
VII	68.33	121	45	24.33	118.23	98.35	82.54	447.77	21.79	23	175.67	1620.7	16.44
VIII	84.67	153	62.67	23.33	122.56	86.86	72.16	362.85	23.88	13.7	103.67	2514.7	31.61
IX	86.67	165.33	77.33	21.67	252.44	185.11	73.3	219.58	84.21	10	144.67	2055	11.07
X	76	129	40.67	24	103.5	90.63	87.31	422.37	21.46	18.97	82	4394	10.45
XI	83.33	118.33	70.67	26.33	189.06	151.7	80.21	287.64	52.74	20.23	102	4516.7	12.76
XII	74	136.33	47.67	23	81.73	53.4	65.53	356.98	14.96	20.77	83	3309.7	34.6
XIII	86	122	91.33	27.33	279.67	237.67	85.02	346.59	68.59	22.87	100	1654.3	7.31
XIV	74	99	57.67	24.67	102.73	79.36	77.27	358.55	22.18	17.27	140	1036.3	38.97

Table 2: Cluster mean of rainfed condition

	DTH	PH	PPM	PL	PW	GY	PHI	BW	HI	TW	NGPP	GYPHA	S%
I	76.28	121.98	38.39	21.82	55.59	39.23	70.89	188.7	21.5	14.8	59.83	1184.6	31.8
II	72	121.33	30.33	21.33	40.46	29.94	74.03	176.6	17	10.6	75.33	1128.3	83
III	72	102.33	42	23.67	44.73	36.17	81.24	133.8	27.1	7.4	89.67	672.33	87.5
IV	87.33	113.67	28.78	22.67	46.13	31.06	65	188.7	16	8.02	75.22	1166.9	80.6
V	70	118.67	37.33	24.67	17.87	22.68	131.5	143	16.1	12.7	51.33	1411	12.7
VI	77.67	134.67	35	23.33	125.56	116.77	92.88	211.2	61	15.7	125	1486	24.1

Conclusion

It was also found that highest contribution towards the genetic diversity of rice genotypes was contributed Under control condition by panicle weight, grain yield per hectare, days to 50% heading, sterility per cent, no. of panicles per meter, no. of grains per panicle and biological yield, whereas in rainfed stress condition the characters like sterility per cent followed by grain yield per meter, days to 50% heading, test weight, panicle weight, biological weight per meter and no. of grains per panicle.

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