



EVALUATION OF GERMPLASM FOR SOME GENETICAL STUDIES IN RICE (*ORYZA SATIVA* L.)

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Abstract

The present investigation was carried out at Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Tamilnadu under natural saline soil condition, to evaluate the collected germplasm of rice for yield and its components traits of 48 genotypes, with three replications in Randomized Block Design. The study revealed that the mean sum of squares due to genotypes were significant for all the characters, through wide range of genetic variability in the material. The higher magnitude of coefficient of variation at phenotypic and genotypic levels were observed for grain yield per plant, number of grains per panicle, number of panicles per plant which indicated the existence of non-additive gene effects whereas for other traits environmental influence was very less. High heritability coupled with high genetic advance as per cent of mean was observed in all the eight characters studied. Hence all those traits were said to controlled by additive gene action, hence direct selection based on phenotypic observations may be effective for improvement of these traits. Genotypes from clusters V, VI, VIII and IX could be used as parents for combining characters for yield and its components characters for further improvement through hybridization and selection.

Key words : PCV, GCV, h^2 , GA, Rice.

Introduction

Rice is one of the significant cereal commodities which fulfills nutrition requirement of billions of world's populations. Total rice production is increased to 490.9 million metric tons worldwide and among that 90 percent is produce and consume in developing countries. As the world's population is increases, the demand for production of rice is also rises to meet the growing demand. In recent years, the increases in rice yield have resulted from intensive research in irrigated rice varieties but as fresh water resources are declining, growing of rice under aerobic and saline condition is gaining popularity. But research finding on performance of rice under aerobic condition is very limited. Development of variety under such condition require a thorough knowledge of genetic variation of yield contributing characters. The observed variability is a combined contribution of genetic and environmental factors whereas genetic variability is heritable. Knowledge of genetic variation is the basis of selection of genotypes for development of new varieties and heritability is one of the key estimates for the selection. Heritability estimates along with genetic advance is more helpful in predicting expected genetic gain in the succeeding generation.

In this instance, Akinwale *et al.*, (2011) reported high to

medium sense of heritability for days to heading, days to maturity, plant height, number of panicles and grain yield while Abebe *et al.*, (2017) reported high to medium heritability with high genotypic coefficient of variation (GCV) and genetic advance as percent of mean (GAM) for various agronomic traits in 36 rice genotypes suggesting a high component of heritable portion of variation. Fentie *et al.*, (2014) evaluated 12 upland rice genotypes and reported existence of adequate genetic variability, heritability and genetic advance among the tested materials.

As estimation of performance of genotypes for yield attributing characters and genetic variability is important before launching a breeding programme and limited reports are available regarding performance of genotypes in aerobic and saline condition. Therefore, the present study was carried out to asses the mean performance and extent of genetic variability, heritability and genetic advance among ten rice genotypes for yield and related traits in aerobic condition.

Materials and Methods

The present day investigation was conducted at the Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Tamil Nadu, India during the year 2015 – 2017. Observations were made on 48 rice genotypes for eight

characters and the data were subjected to D^2 analysis. The experimental materials for this genetic divergence study comprised of 48 rice genotypes collected from various places. The details of the materials are presented in Table 1.

Seeds of the forty eight genotypes were sown in raised nursery beds during February, 2016. In each genotype, one seedling per hill was transplanted in the main field after 25 days with spacing of 20 cm x 20 cm. The experiments were conducted at the Experimental Farm of Plant Breeding (11°24' N latitude and 79°44' E longitude, + 5.79 MSL), Annamalai University, Tamil Nadu, India. The experiment was carried out in a Randomized Block Design with three replications. As recommended, agronomic and plant protection measures were followed during the crop period.

A uniform population of 12 plants in a row was maintained.

Eight yield characters were recorded on single plant basis in ten randomly selected plants of each genotype per replication. The mean data were utilized for the statistical studies. Observations were recorded on days to first flower, plant height, number of tillers per plant, number of panicles per plant, number of grains per panicle, panicle length, thousand grain weight and grain yield per plant.

Statistical tools like analysis of variance (Panse and Suthmate, 1967), coefficient variability (Burton, 1952), heritability (Lush, 1949), genetic advance (Robinson *et al.*, 1949) and D^2 statistics (Mahalanobis, 1936) were used for analysis.

Table 1: List of genotypes selected for D^2 analysis

SL.No.	Name of genotype	Origin of genotype
1.	ADT47	TRRI, Aduthurai, India
2.	ADT41	TRRI, Aduthurai, India
3.	ADT37	TRRI, Aduthurai, India
4.	ADT36	TRRI, Aduthurai, India
5.	ADT45	TRRI, Aduthurai, India
6.	ADT48	TRRI, Aduthurai, India
7.	ADT43	TRRI, Aduthurai, India
8.	ADT42	TRRI, Aduthurai, India
9.	ASD 16	RRS, Ambasamudram, India
10.	ASD 18	RRS, Ambasamudram, India
11.	IR66	IRRI, Philippines
12.	IR64	IRRI, Philippines
13.	IR72	IRRI, Philippines
14.	IR50	IRRI, Philippines
15.	TPS5	ARS, Tirupathisaram, India
16.	CO 51	TNAU, Coimbatore, India
17.	CO 47	TNAU, Coimbatore, India
18.	TRY 2	AnbilDharmalingam AC & RI, Trichy, India
19.	TKM9	RRS, Tirurkuppam, India
20.	MDU5	AC & RI, Madurai, India
21.	PY3	RRS, Paiyur, India
22.	PMK3	ARS, Paramakudi, India
23.	AVT 1303	Advanced Variety Trial, Annamalai University, India
24.	Dhanya Lakshmi	Non traceable

SL.No.	Name of genotype	Origin of genotype
25.	IR20	IRRI, Philippines
26.	Geetanjali	CRRI, Cuttack, India
27.	IET 14348	B.H.U., Varanasi
28.	Jaya Mathi	DRR, Hyderabad, India
29.	Samba Mashuri	A.N.G.R.A.U. RS, Marteru, India
30.	MTU 1156	A.N.G.R.A.U. RS, Marteru, India
31.	MTU 7029	A.N.G.R.A.U. RS, Marteru, India
32.	MTU 1121	A.N.G.R.A.U. RS, Marteru, India
33.	Super Amman	Non traceable
34.	AngurSelam	Non traceable
35.	ASD 1	RRS, Ambasamudram, India
36.	STBN 18	DRR, Hyderabad, India
37.	Bhavani	TNAU, Coimbatore, India
38.	PLA1100	A.N.G.R.A.U. RS, Marteru, India
39.	MTU 1010	A.N.G.R.A.U. RS, Marteru, India
40.	K. Sona	Non traceable
41.	AVT 1320	Advanced Variety Trail, Annamalai University, India
42.	AVT 1302	Advanced Variety Trail, Annamalai University, India
43.	AVT 1321	Advanced Variety Trail, Annamalai University, India
44.	Kullakar	Traditional Variety of T.N. (Tiruthuraipoondi)
45.	Pooughar	Traditional Variety of T.N. (Tiruthuraipoondi)
46.	IR36	IRRI, Philippines
47.	NLR 34449	ARS, Nellore, India
48.	Akshaya	B.H.U., Varanasi

Results

Analysis of variance for different characters is presented in Table 2. The mean sum of square due to genotypes showed significant differences for all eight characters under study at 1 per cent level of significance suggesting that the genotypes selected for the present study were genetically divergent. It indicated that there is ample scope for selection of promising varieties from the present gene pool for yield and its components.

Group constellation

Using Mahalanobis D^2 analysis, the forty eight genotypes taken for divergence studies were grouped into nine clusters. Clusters were grouped utilizing clustering technique based on the relative magnitude of D^2 values. The results are furnished in Table 3. Cluster I, the largest cluster, comprised of 19 genotypes whereas clusters II, III, IV, V, VI

and VII comprised of minimum number of genotypes namely two genotypes in each. Cluster VIII composed of 7 genotypes and cluster IX encompassed of 10 genotypes. The nine clusters with the corresponding genotypes are tabulated.

Intra and inter cluster distances

The intra and inter cluster distances among the nine clusters are provided in Table 4. The intra cluster distance ranged from 4.63 to 35.87. The maximum intra cluster distance was exhibited by cluster VIII (35.87) followed by cluster IX (32.82), cluster I (28.70) and cluster VII (12.49) and the minimum intra cluster distance was found in cluster II (4.63).

The inter cluster distance ranged from 7.06 to 54.23. The maximum inter cluster distance was found between Cluster VI and Cluster VIII (54.23) followed by Cluster VIII and IX (51.01), cluster V and VIII (50.26), cluster III and VIII (45.60) and cluster I and VI (45.09). The minimum inter

cluster distance was exhibited between Cluster II and Cluster III (7.06).

Variability Studies

Variability was measured by estimation of mean, coefficient of variation such as phenotypic coefficient of variation and genotypic coefficient of variation, heritability (broad sense) and genetic advance as per cent of mean. The estimates of PCV and GCV were studied for all the eight characters and enlisted. Heritability and genetic advance as per cent of mean were also studied and given in Table 5.

Phenotypic coefficient of variation

The phenotypic coefficient of variation (PCV) was observed to be higher than genotypic coefficient of variation for all the characters taken under study. The phenotypic coefficient of variation ranged from 12.90 to 58.28 per cent. Higher magnitude was observed in grain yield per plant (58.28 per cent) followed by number of grains per panicle (42.75 per cent), number of panicles per plant (41.61 per cent) and number of tillers per plant (37.79 per cent). Moderate PCV was perceived in thousand grain weight (17.31 per cent), plant height (16.23 per cent), days to first flower (14.86 per cent) and panicle length (13.05 per cent).

Genotypic coefficient of variation

The genotypic coefficient of variation ranged from 11.41 to 58.21 per cent. High GCV was observed in grain yield per plant (58.21 per cent), number of panicles per plant (40.36 per cent), number grains per panicle (39.56 per cent) and number of tillers per plant (37.79 per cent). Moderate GCV was recorded in thousand grain weight (17.22 per cent), plant height (16.01 per cent), days to first flower (13.93 per cent), grain L/B ratio (12.69 per cent) and panicle length (11.41 per cent).

Heritability (h^2)

Heritability is a measure of the extent of phenotypic variation caused by the action of genes. The heritability values ranged from 99.75 to 76.47 per cent. High heritability was recorded for grain yield per plant (99.75 per cent), thousand grain weight (99.00 per cent), plant height (97.30 per cent), number of tillers per plant (97.13 per cent), number of panicles per plant (94.07 per cent), days to first flower (87.86 per cent), number of grains per panicle (85.64 per cent) and panicle length (76.47 per cent). Thus all the characters taken under study for the concerned forty eight genotypes exhibited high heritability.

Genetic advance as per cent of mean

Genetic advance as per cent of mean ranged from 20.56 to 119.76 per cent. High genetic advance as per cent of mean was observed for grain yield per plant (119.76 per cent), number of panicles per plant (80.64 per cent), number of tillers per plant (75.60 per cent), number of grains per panicle (75.41 per cent), thousand grain weight (35.30 per cent), plant height (32.54 per cent), days to first flower (26.90 per cent) and panicle length (20.56 per cent). As in heritability, all the characters considered for experiment also exhibited high genetic advance as per cent of mean. Thus high heritability

coupled with high genetic advance as per cent of mean was recorded for all the characters studied.

Discussion

Analysis of variance revealed significant differences for all the characters in respect of the genotypes under present study (Table 2) indicating the presence of considerable amount of variability among the genotypes. Similar findings were reported by Chandramohan *et al.* (2016).

Genetic divergence studies revealed that, 48 genotypes were grouped into nine clusters based on their D^2 values. Among the nine clusters, cluster I accommodated maximum of 19 genotypes followed by cluster IX of 10 genotypes and cluster VIII of 7 genotypes. The remaining clusters i.e. II, III, IV, V, VI and VII were accommodated with two genotypes.

The genotypes included in cluster I originated from different origins indicating that there was no parallelism between clustering pattern and geographic distribution of genotypes (Nayak *et al.*, 2004). Therefore the kinds of genetic diversity found among the genotypes belonging to same geographic origin might be due to differences in adoption, selection criteria, and selection pressure in environmental conditions (Maurya and Singh, 1977).

The grouping of genotypes into so many clusters suggested the presence of high degree of diversity in the material evaluated. Earlier workers have also reported presence of substantial genetic diversity in rice (Sandhya *et al.*, 2015).

The highest intra cluster distance was registered in cluster VIII (35.87) followed by cluster IX (32.82) and cluster I (28.70). Thus the genotypes from those clusters had high degree of divergence that would produce more desirable sergents for achieving greater genetic advance. The least intra cluster distance was revealed in cluster II (4.63) followed by cluster III (7.75) and cluster IV (9.22) indicating homogenous nature of the genotypes with less deviation between the genotypes. Parallel findings were found by Hossain *et al.*, (2015).

Highest inter cluster distance (54.23) was found between cluster VI and VIII followed by cluster VIII and IX (51.01), cluster V and VIII (50.26), cluster III and VIII (45.60) and cluster I and VI (45.09) indicating the wider genetic diversity among the genotypes between these clusters. This indicated that the genotypes in these clusters are having broad spectrum of genetic diversity and could very well be used in hybridization programme. Similar results were reported by Sandhya *et al.* (2015).

The minimum inter cluster distance was found between cluster II and III (7.06). The inter cluster distances were greater than intra cluster indicating wide genetic diversity among genotypes. Similar results were reported by Nirosha *et al.* (2016). The overall clustering pattern indicated that genotypes developed in same geographical region were distributed in different clusters. Shanmugam and Rangasamy (1982) reported that grouping of material of same geographical origin into different clusters was an indication

of the broad genetic base of genotypes belonging to that origin. Similar results of non-association of geographical region with the genetic diversity were reported by Thippeswamy *et al.* (2016).

Variability Studies

The relative values of genotypic and phenotypic coefficient of variation provide important information on the magnitude of variation. Genotypic coefficient of variation measures the variability of any character. The extent of the environmental influence on any character is indicated by the magnitude of the differences between the genotypic and phenotypic coefficients of variation. Large differences reflect high environmental influence, while small differences reveal high genetic influence.

High phenotypic variations composed of high genotypic variations and less of environmental variations, indicates the presence of high genetic variability for different traits and less influence of environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits. Similar results were observed by Sao (2002). Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all the traits studied indicating that the characters were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits.

High PCV and GCV were recorded for grain yield per plant, number of 'grains per panicle, number of panicles per plant and number of tillers per plant. The high magnitude of GCV and PCV for the above traits suggested the presence of high degree of variability and so better scope for the improvement through simple selection. Similar results were drawn by Tuhina - Khatun *et al.* (2015) for number of tillers per plant, number of panicles per plant and grain yield per plant, Chanbeni *et al.* (2012) for number of tillers per plant, number of panicles per plant, number of grains per panicle and grain yield per plant, Singh *et al.* (2013) for number of panicles per plant, number of grains and grain yield per plant, Thippeswamy *et al.*, (2016) for number of grains per panicle and Akhtar *et al.*, (2011) for number of grains per panicle.

Moderate GCV and PCV were recorded for thousand grain weight, plant height, days to first flower, panicle length. This indicates the existence of comparatively moderate variability for these traits, which could be exploited for improvement through selection in advanced generations. Similar findings were reported by Tuhina - Khatun *et al.*,

(2015) for days to first flower and plant height, Chanbeni *et al.*, (2012) for plant height, panicle length and thousand grain weight and Thippeswamy *et al.*, (2016) for grain yield per plant.

Narrow differences between PCV and GCV were observed for plant height, number of tillers per plant, thousand grain weight, grain L/B ratio and grain yield per plant which suggested that these traits were less influenced by environmental forces. Hence they could be improved through simple selection, whereas relatively more difference between PCV and GCV for days to first flowering, number of panicles per plant, number of grains per panicle and panicle length indicated the sensitive nature of these traits to environmental fluctuations. Similar conclusions were drawn by Mohan *et al.*, (2015).

Genetic analysis

Knowledge of heritability of a character to a breeder is important as it indicates the possibility and extent to which improvement is possible through selection. Heritability in broad sense includes both fixable (additive) and non -fixable (dominant and epistatic) variances and also provides a good indication about the repeatability of the traits. All the characters recorded high estimates of heritability, hence indicated that expression of these traits is less influenced by the environment and could be improved through mere selection.

Although, the presence of high heritability values indicates the effectiveness of selection on the basis of phenotypic performance, it does not show any indication to the amount of genetic progress. High heritability does not always indicate high genetic gain. Burton (1952) pointed out the heritability in combination with intensity of selection and amount of variability present in the population influences gains to be obtained from selection. Therefore heritability and genetic advance should be considered together in selection process for obtaining the best segregants.

Since high heritability along with high genetic advance was observed for all the characters taken under study, it conveyed the predominance of additive gene affects in controlling the traits and hence strong selection forces could improve these traits. Similar findings were reported by Tuhina -Khatun *et al.* (2015) for days to first flowering, plant height, number of tillers per plant, number of panicles per plant and grain yield per plant, Santhosh Kumar *et al.* (2015) for number of tillers per plant and number of grains per panicle, Chandramohan *et al.* (2016) for number of grains per

Table 2: Analysis of variance for nine characters in rice genotypes

Sl. No.	Source	df	Days to first flower (days)	Plant height (cm)	No. of tillers per plant	No. of panicles per plant	No. of grains per panicle	Panicle length (cm)	Thousand grain weight (g)	Grain yield per plant (g)
			MSS							
1.	Replication	2	75.55	4.98	4.32	3.31	297.28	1.77	0.36	0.46
2.	Genotype	47	448.13**	788.95**	292.72**	146.37**	17721.09**	24.31**	29.30**	45.35**
3.	Error	94	19.73	7.23	2.85	3.01	938.31	2.26	0.10	0.37

** significant at 1% level.

Table 3: Distribution of rice genotypes in different clusters based on D² analysis

Cluster No.	Number of genotypes	List of the genotypes
I	18	ADT 47, ADT 41, ADT 37, ADT 36, ADT 45, ADT 48, ADT 43, ADT 42, ASD 16, ASD 18, IR 66, IR 64, IR 72, IR 50, TPS 5, CO 51, CO 47, Jaya Mathi, MTU
II	2	IET 14348, MTU 7029
III	2	STBN 18, Bhavani
IV	2	MDU 5, PY 3
V	2	Geetanjali, SamaMashuri
VI	2	AVT 1320, AVT 1321
VII	2	MTU 1121, MTU 1010
VIII	7	TRY 2, TKM 9, PMK 3, AVT 1303, Dhanya Lakshmi, IR 20, Super Amman
IX	10	AngurSelam, ASD 1, PLA 1100, K. Sona, AVT 1302, Kullakar, Pooughar, IR 36, NLR 34449, Akshaya

Table 4: Intra (bold) and inter cluster (unbold) D² values of various clusters in rice

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX
I	823.66	1296.21	1345.02	667.38	1760.43	2033.09	1166.63	1138.41	1998.20
II		21.40	49.83	329.83	155.52	426.51	71.33	1988.60	615.30
III			59.98	407.21	175.14	334.87	141.25	2079.67	662.27
IV				85.08	736.41	918.62	267.05	1194.36	997.33
V					122.00	440.03	275.38	2526.30	638.02
VI						144.65	564.37	2940.36	846.72
VII							156.11	1791.71	699.23
VIII								1286.55	2602.09
IX									1076.80

Table 5: Estimates of mean, range, coefficient of variation, heritability and genetic advance as per cent of mean in rice genotypes

S. No.	Characters	Grand mean	Range	PCV	GCV	Heritability (%) h ²	Genetic advance as percent of mean
1	Days to first flower (days)	85.77	134.55 – 71.01	14.86	13.93	87.86	26.90
2	Plant height (cm)	100.81	141.78 – 70.70	16.23	16.01	97.30	32.54
3	Number of tillers per plant	26.40	63.43 – 14.57	37.79	37.24	97.13	75.60
4	Number of panicles per plant	17.13	44.57 – 9.45	41.61	40.36	94.07	80.64
5	Number of grains per panicle	189.07	415.02 – 72.51	42.75	39.56	85.64	75.41
6	Panicle length (cm)	23.75	30.31 – 17.27	13.05	11.41	76.47	20.56
7	Thousand grain weight (g)	18.12	23.57 – 9.43	17.31	17.22	99.00	35.30
8	Grain yield per plant (g)	21.04	49.83 – 5.79	58.28	58.21	99.75	119.76

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