Genetic Divergence Studies in Drought Promising Rice Genotypes based on Quality Characters

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Grain quality characteristics of 24 drought promising genotypes were evaluated under irrigated and drought conditions for studying variability and genetic divergence. Differences among the genotypes are observed to be highly significant for all the characters; between the environments head rice recovery, alkali spreading value, water uptake, kernel length after cooking and yield are significant, while genotype x environment interaction is only significant for hulling, milling, head rice recovery and water uptake. Water uptake, alkali spreading value and head rice recovery are governed by additive gene action and contributed maximum towards divergence with kernel length after cooking. The D^2 analysis revealed that genotypes exhibited considerable diversity and were grouped into seven clusters, where cluster I was the largest and contained 18 genotypes while, rest of the clusters contained single genotypes. Based on clustering pattern and *per se* performance five genotypes were identified, which may be used in breeding programme to obtain improved genotypes with desirable attributes for stress environments.

Key Words: Drought tolerance, D^2 analysis, Variability, Quality characters, Rice

Introduction

India has the largest area under rice production in the world (47 million ha). Rice environments in India are extremely diverse with rainfed lowland being predominant across 15 million ha in eastern India where the water supply is unpredictable and droughts are common (Wade *et al*., 1999). Drought resistance appears to be the most important single factor in increasing and stabilizing of rice production in rainfed areas (Chaudhary and Rao, 1982). In recent times, there is increasing demand for good grain quality in national as well as in international market. In order to develop genotypes with desirable traits, it is needful to collect, evaluate and utilize the available diversity to suit specific need with regard to specific ecosystem. D^2 statistics are expected to provide reliable basis for selecting desirable elite and diverse parents for hybridization and exploitation of variability. Keeping this in view, the present investigation was carried out with 24 drought promising rice genotypes to obtain wide array of cross combinations.

Materials and Methods

Field screening experiments for large number of entries (72 from AYT 100-120 days, 38 from AYT > 120 days and 216 from OYT under IRRI-India Drought Breeding Network) were conducted to identify drought tolerant genotypes during dry season of 2007 and 2008 at Central Rice Research Institute, Cuttack. The experiments were laid out in randomized block design with three replications under both control irrigated (E_1) and drought stress (E_2) conditions. Plants were grown under adequate soil moisture for 30 days after germination under both the conditions. The irrigation was withdrawn for 30 days and beyond, till the susceptible check shows permanent wilting in the stress field, subsequently the plot was re-watered for recovery. Soil moisture content (SMC) during stress period was monitored through periodical soil sampling at 0–15, 15–30 cm soil depth after suspension water. The drought scores and recovery observations were taken as per SES method, 1 to 9 scales (IRRI, 1996). In the control field plants were grown under normal irrigated condition maintaining water level for 5±2 cm till dough stage. Observations were recorded on five competitive plants of the middle row of each plot for yield and 12 quality parameters. The 24 genotypes in the present study were selected on the basis of their drought tolerance and yield potential under severe stress condition, and carried out for quality analysis.

Seed samples were collected after harvest with 14% moisture from both the treatments were analyzed for

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hulling (H), milling (M), head rice recovery (HRR), amylose content (AC), alkali spreading value (ASV) and elongation ratio (ER) as per method given by Govindswamy and Ghosh, 1969. The kernel length (KL) and kernel width (KW) of the grains were measured with dial micrometer. Water uptake (WU) and volume expansion ratio (VER) were determined (Beachell and Stansel, 1963). Pooled analysis of variance (ANOVA) was used to quantify the genetic differences among the genotypes. Multivariate analysis of genetic divergence among varieties was done using Mahalanobis D^2 statistics (1936) and grouping of varieties into clusters by Tochers method (Rao, 1952). The character-wise rank totals were used to calculate the per cent contribution of each character to the total divergence. Averages inter- and intra-cluster distance, ANOVA, coefficient of variation and heritability in broad sense and genetic advance were estimated as per the method given by Singh and Chaudhary (1985).

Results and Discussion

The analysis of variance for the design of experiment indicated the existence of significant variability among the 24 genotypes of rice for all the characters under study (Table 1). The presence of large amount of variability is due to diverse source of the materials as well as environmental influence, which predominantly governed the phenotype. The analysis of variance for pooled data showed that genotype x environment interaction is significant for hulling, milling, head rice recovery and water uptake. This suggested that broad range of diversity existed among genotypes and locations for above said characters and that the performance of genotypes was differential over location. Overwhelming effect of environment on genetic performance along with G x E interaction suggests that rice varieties bred for one region may not do well in other regions. These findings call for widening the genetic base used in breeding programmes. High genotypic and phenotypic coefficient of variation and high heritability along with genetic advance were found for WU, ASV and HRR while low value of same selection parameters were recorded for rest of the characters (Table 2). These results are in accordance with the findings of Bose *et al*. (2007) and Vanaja and Babu (2006).

Based on D^2 values the genotypes were grouped into 7 distinct non-overlapping clusters (Fig. 1). Cluster I contained approximately 75% of total genotypes under study. Interestingly, only one genotype each constituted the rest of the clusters (Table 3). These monogenotypic clusters included different genotypes from different regions of different countries, indicating that clustering of the genotype did not follow their geographic distributions. Absence of correlation between genetic diversity and geographic diversity suggests that forces other than geographic origin, such as exchange of breeding material, genetic drift, and selection are responsible for diversity, as reported earlier (Murthy and Arunachalam, 1966). A noteworthy observation was that all the check varieties MTU 1010, Swarna and Sambha Mahsuri grouped into different clusters without any genotype indicates their high degree of heterogeneity.

The statistical distances represent the extent of genetic diversity amongst clusters. The average D^2 value within

Table 1. Pooled analysis of variance for quality characters in drought promising lines

	Pooled analysis				
Characters	Environment (1)	Genotype (23)	Replication (1)	Genotype x Environment (G x E) (23)	Error (47)
Hulling (%)	13.50	16.37**	2.34	13.01**	8.67
Milling (%)	3.41	23.48**	15.76**	12.80**	4.25
HRR (%)	58.59**	432.30**	6.51*	52.36**	4.71
KL (mm)	0.01	0.69**	0.02	0.03	0.01
KB (mm)	0.02	0.12**	0.01	0.04	0.01
L/W	0.01	0.33**	0.01	0.05	0.01
ASV	3.96**	13.41**	0.21	0.61	0.19
WU (ml/100/gm)	77748.1**	22399.8**	450.67**	2922.30**	700.14
VER	0.02	0.03**	0.09	0.02	0.01
KLAC (mm)	0.41**	1.96**	0.01	0.13	0.04
ER	0.01	0.05**	0.01	0.01	0.01
AC (%)	1.96	49.81**	1.44	1.59	0.67

*, **, Significant at 5% and 1% levels, respectively.
HRR: Head Rice Recovery, KL: Kernel Length, KW: Kernel Width, L/W: Kernel Length/ Kernel Width, ASV: Alkali Spreading Value, WU: Water uptake, VER: Volume expansion ratio, KLAC: Kernel Length after Cooking (mm), ER: Elongation Ratio & AC: Amylose Content

Table 2. Estimates of mean, range, coefficient of variation, heritability and genetic advance for 12 characters in drought promising rice

Characters	Mean ± SE m	Range		Coefficient of Variation		Heritability h^2 (b)	Genetic advance	Genetic advance (% of mean)
		Min.	Max.	GCV	PCV			
Hulling (%)	73.57 ±1.07	69.33	78.17	2.46	4.33	32.3	2.72	3.69
Milling (%)	62.56 ±1.16	58.25	66.00	2.43	5.14	22.4	1.90	3.03
HRR (%)	31.00 ±3.28	21.00	51.83	24.30	35.56	46.7	13.59	43.84
KL (mm)	5.62 ±0.15	4.87	6.07	3.90	7.45	27.4	0.30	5.39
KB (mm)	2.18 ±0.07	1.98	2.41	3.72	8.70	18.3	0.09	4.20
L/W	2.60 ±0.12	2.39	2.85	2.36	11.66	4.1	0.03	1.26
ASV	5.17 ±0.46	3.00	7.00	29.35	36.79	63.6	3.20	61.82
WU (ml/100/gm)	227.42 ±19.29	117.50	360.00	31.77	37.96	70.0	159.65	70.20
VER	4.06 ±0.05	3.94	4.25	1.74	3.30	28.0	0.10	2.44
KLAC (mm)	9.67 ±0.19	8.63	10.52	5.90	7.57	60.7	1.17	12.14
ER	1.73 ±0.04	1.61	1.81	2.53	6.27	16.3	0.05	2.69
AC (%)	24.48 ±1.22	18.62	29.57	8.81	15.03	34.4	3.33	13.63

HRR: Head Rice Recovery, KL: Kernel Length, KW: Kernel Width, L/W: Kernel Length/ Kernel Width, ASV: Alkali Spreading Value, WU: Water uptake, VER: Volume expansion ratio, KLAC: Kernel Length After Cooking (mm), ER: Elongation Ratio, AC: Amylose Content

Table 3. Distribution of 24 drought promising rice genotypes in different clusters

Cluster No.	Number of genotypes	Genotypes included
I	18	ARB 7, ARB 8, ARB 3, IR 78937-B-4-B-B-B, Trpuradhan, IR 70844-10-SRN-43-1-B-B-1-1, IR 55419-04, IR 70215-70-CPA-3-4-1-3, IR 69515-6-KKN-4-UBN-4-2-1-1-1, IR 78875-53-2-2-2, CBO-15-24, DGI 307, IR 74371-46-1-1, IR 83614-503-B, IR 74371-54-1-1, IR 74371-3-1-1, IR 78875-131-B-1-4 and IR 78877-181-B-1-2
II	1	MTU-1010
III	1	IR 55423-01
IV	1	Swarna
V	1	Sambha Mahsuri
VI	1	IR 72667-16-1-B-B-3
VII	1	IR 74371-70-1-1

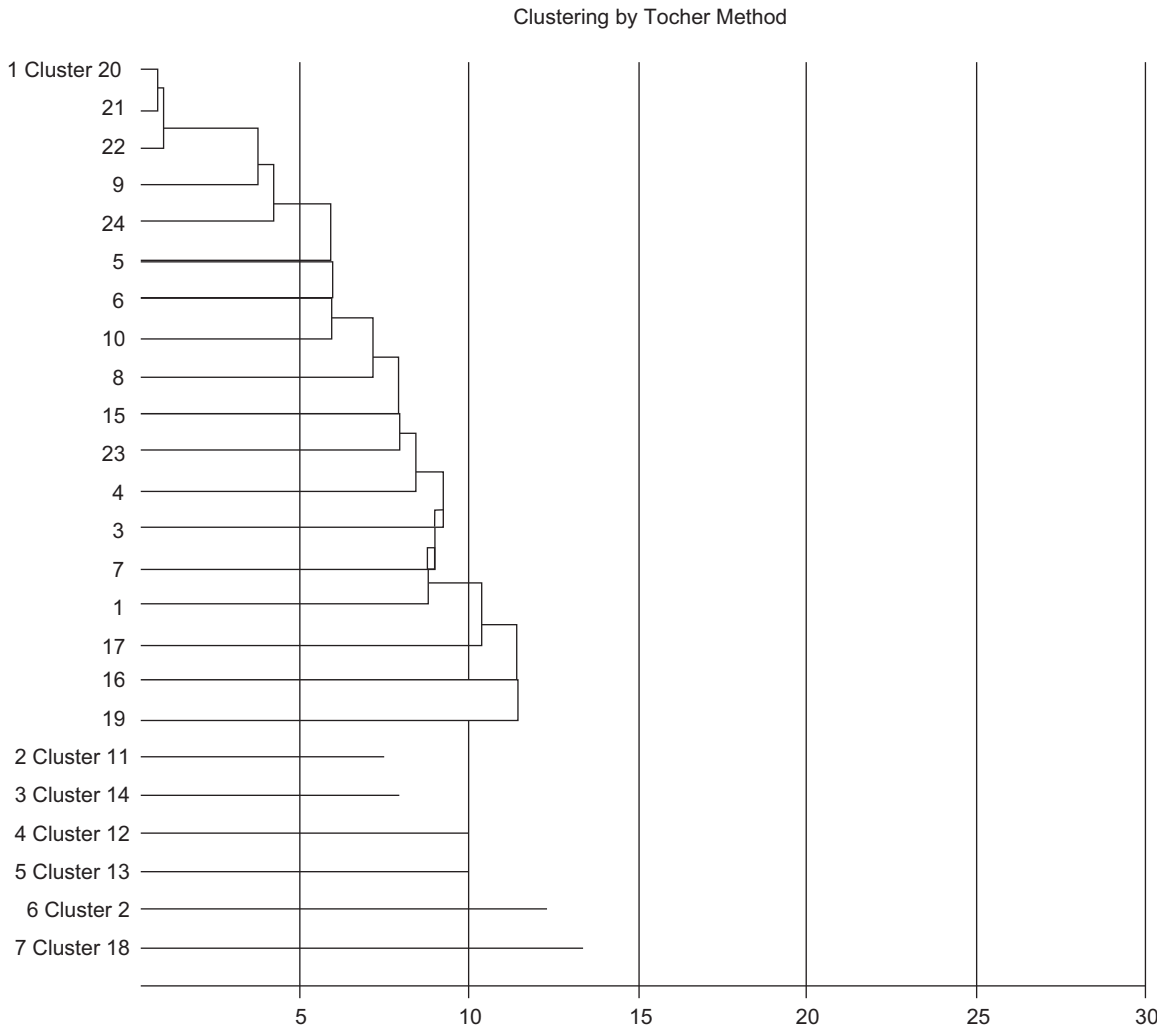

Fig. 1. Different Clusters showing the position of drought promising genotypes (mentioned by serial number)

and between clusters revealed that intra-cluster divergence was possessed by cluster I only (D^2=3.06) which included 18 genotypes because rest of the cluster included only one genotype (Table 4). The inter-cluster distance was maximum between cluster IV and VI (6.48). The closest into cluster distance was between cluster III and VI (3.16) which indicated that genotypes of these clusters had maximum number of common gene complexes. High statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates.

The genetic differences between the clusters were reflected in cluster means (Table 5). The highest average cluster mean was reported for milling and AC in cluster IV, for HRR and VER in cluster V and for ER in cluster III while, cluster VII possessed highest mean for KW and KL after cooking. All the above-said clusters had single genotype. The cluster I with 18 genotypes exhibited highest mean value for hulling. It is observed that the genotypes desirable for different traits belonged to different clusters. The genotype IR 72667-16-1-B-B-3 in cluster VI registered the highest mean value for KL, L/W, and ASV and WU. The clusters contributing maximum to D^2 values are to

Table 4. Intra- and inter-cluster D^2 among seven clusters

Clusters	I	II	III	IV	V	VI	VII
I	3.06	3.77	4.06	4.21	5.08	4.53	4.36
II		0.00	5.19	3.89	5.59	6.09	4.77
III			0.00	4.77	3.16	4.60	4.60
IV				0.00	5.11	6.48	4.72
V					0.00	4.81	5.79
VI						0.00	5.17
VII							0.00

Table 5. Cluster mean for 11 characters

Cluster No.	H (%)	M (%)	HRR (%)	KL (mm)	KW (mm)	L/W	ASV	WU (ml/100/gm)	VER	KLAC (mm)	ER	AC (%)
I	74.58**	62.85	30.72	5.70	2.21	2.59	5.35	276.39	4.08	9.92	1.75	25.09
II	73.33	61.33	14.67	5.61	2.10	2.67	3.00*	275.00	4.00	9.67	1.72	21.18
III	67.67*	63.00	47.33	5.11	2.27	2.25*	3.00*	153.33	4.25**	9.27	1.82**	19.13*
IV	74.33	64.67**	46.00	5.10	2.16	2.36	3.00*	136.67*	3.92*	7.87*	1.54*	28.25**
V	71.00	61.50	56.33**	4.63*	1.69*	2.75	3.00*	140.00	4.25**	8.07	1.74	24.96
VI	72.17	59.33*	33.33	6.17**	1.84	3.35**	7.00**	301.67**	4.00	10.10	1.63	27.58
VII	73.00	63.33	14.50*	6.08	2.68**	2.36	3.33	153.33	4.17	10.43**	1.72	19.91
No. of times ranked 1st	9	0	28	21	4	27	58	38	1	69	0	21
Contribution (%)	3.26	0.00	10.14	7.61	1.45	9.78	21.01	13.77	0.36	25.00	0.00	7.61

be given greater emphasis for deciding the clusters for the purpose of further selection and hybridization (Table 5). The characters contributing towards genetic divergence showed that maximum genetic divergence was observed for KLAC (25.00%) followed by ASV (21.01%), WU (13.77%) and HRR (10.14%). Hence, above said characters were considered to be important traits and may be used as selection parameters in segregating generations. The least and negligible contribution towards divergence was observed for milling and ER (0.00%). Similar results were earlier reported by Subudhi *et al.* (2009).

Intercrossing of divergent genotypes with desirable traits would lead to greater opportunity for maximum amount of heterosis and utilize them for multiple crossing programmes to accumulate favorable genes in single genotypes. In the view of above discussion, variation in ASV, WU and HRR offers great potential in selecting better genotype for stress environment. There is need to develop rice varieties that will produce acceptable yields in both water-limited and favourable environments with better quality traits, hence, on the basis of inter-cluster distance and *per se* performance, the genotypes *viz.*, Swarna, MTU 1010, Sambha Mahsuri, IR 72667-16-1-B-B-3 and IR 74371-70-1-1 grouped in to different clusters could be used in breeding programme to obtain improved genotypes for water limiting conditions.

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