

Genetic diversity analysis of direct seeded rice genotypes under drought situation

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ABSTRACT

Genetic divergence is an efficient tool for the selection of parents used in hybridization programme. In the present study, Seventy six rice genotypes, landraces and popular varieties consisting of both indigenous and exotic collection were studied for yield and yield related traits. Based on D^2 analysis, the genotypes were grouped into eight clusters. Maximum number of genotypes (35 genotypes) were grouped in cluster I. The maximum inter cluster distance was observed between cluster VI and VII (35.02) followed by between cluster III and VII (34.68) and between cluster I and VIII possessing wider genetic diversity among the genotypes between these groups. The hybrids developed from the selected members of these clusters would produce highly variable population in the segregating generations. The maximum intra cluster distance was observed in cluster III (6.46) followed by cluster IV (6.32). Hence, selection within these clusters may be exercised based on the highest areas for the desirable traits, which would be made use of in improvement through intervarietal hybridization. Among the twelve traits studied, kernel length contributed maximum divergence (34.32%) followed by plot yield (21.02%). Hence, the traits viz., sterility, plot yield, kernel length, kernel breadth, 1000 grain weight contributed 71.52 per cent towards total divergence. Therefore, these characters should be given importance during hybridization and selection in the segregating population.

Key words: Rice, genetic diversity, D^2 analysis, clustering

The success of any breeding programme depends on the selection of parents for hybridization. The parents involved in the development of varieties should be divergent. The germplasm provides immense scope for wide variability. Genetic divergence is an efficient tool for an effective choice of parents for hybridization programme. Such study also selects the genetically divergent parents to obtain desirable combinations in the segregating generations. Drought stress is not only limited to arid or semi arid areas, but also sometimes, due to irregular distribution of rain, causes significant decrease of plant yield. Drought stress during cropping season directly affects the grain yield; particularly the stress at reproductive stage is most devastating (Venuprasad *et al.*, 2009a; Lanceras *et al.*, 2004). Information on extent of genetic divergence would help the plant breeder in choosing the right parents for the breeding programme. Keeping this in view, the present

study was focused to assess the genetic diversity 76 rice genotypes using Mahalanobis D^2 statistics.

MATERIALS AND METHODS

Seventy six rice genotypes consisting of direct seeded landraces of upland and lowland ecology and some promising cultures were acquired from Central Rice Research Institute and International Rice Research Institute. The germplasm lines were grown during dry season, 2012 & 2013 to identify diverse genotypes. The experiment was laid out in Randomized Block Design with two replications. The genotypes were direct seeded in plot of 6 rows with each row of 5 metre length. Row to row and plant to plant spacing was maintained at 20 x 15 cm. The recommended agronomic practices were followed before flowering stage. After flowering stage irrigation was stopped. Twelve yield and yield attributing characters viz., days to 50% flowering, plant height,

number of ear bearing tillers, panicle length, total dry matter production, sterility, harvest index, plot yield, kernel length, kernel breadth, 1000 grain weight were estimated under drought stress. The genetic distances between the genotypes was worked out using Mahalanobis D² analysis (1936) and grouping of varieties into clusters was done following the Tochers method as detailed by Rao, 1952.

RESULTS AND DISCUSSION

Analysis of variance showed significant differences for all the twelve characters studied in 76 genotypes. Based on D² value, 76 genotypes were grouped into 8 clusters (Table 1). Maximum number of genotypes (35 genotypes) were grouped in cluster I. Cluster III consists of 14 genotypes followed by cluster IV with twelve genotypes. Cluster II had seven genotypes, while

Cluster VI had five genotypes. The remaining clusters were represented by monogenotypic in nature. The overall composition of the clustering pattern showed that genotypes collected from the same geographic origin were distributed in different clusters. Many clusters obtained from 76 genotypes indicated that ample diversity exist in the studied materials. Similar findings of non- correspondence of geographic origin with genetic diversity were also reported by Shanmugasundaram *et al.*, (2000) and Nayak *et al.*, (2004). According to Bhutia *et. al.*, (2005) out of 41 high yielding and local genotypes of rice 6 clusters were found. Out of these clusters IV, V and VI were monogenotypic.

The intra and inter cluster distance are presented in Table 2. Inter cluster distance was higher than intra cluster distance indicating wider genetic diversity among the genotypes. The maximum inter cluster distance was observed between cluster VI and VII (35.02) followed by between cluster III and VII (34.68) and between cluster I and VIII indicating wider genetic diversity among the genotypes between these groups (Bose and Pradhan *et al.*(2005), Subudhi *et al.*, (2009). The hybrids developed from the selected members of these clusters would produce highly variable population in the segregating generations. The minimum inter cluster distance was found between cluster V and V (0), VII and VII (0) and VIII and VIII (0). These genotypes in these clusters are genetically very close and hence, hybridization among the varieties within the groups will not give fruitful result. The maximum intra cluster distance was observed in cluster III (6.46) followed by cluster IV (6.32). Hence, selection within these clusters may be exercised based on the highest areas for the desirable traits, which would be

Table 1. Clustering pattern of 76 genotypes using Mahalanobis statistics

Cluster	Number of genotypes	Name of genotypes
I	35	NSICRC9, CR2702, IET21692, IR20, Apo, Sahabhagi, CR2707, M55419 04, Satyabhama, BPI RI 10, CR2706, NSIC Rc 192, MAGAWK DONG 269-7-7 (9), Naveen, IET21625, Sariadhan, CO 25, CHAU, Vandana, Dhagad deshi, ZHENSHAN 2, RD 25, AI JIAO NAN TE, CR 143-2-2, IR 81896-B-B-195, DEE-GEO-WOO-GEN, DHOLI BORO, KASALATH, BR 1, BR 2, IR74371-46-1-1, BINNATOHA, TAM CAU 9 A, KINASTANO, PURBACHI (CHINESE 1)
II	7	TAICHUNG NATIVE 1, SARJOO 50, T 136, MTU1010, RATNA, BASMATI 370, JAYA
III	14	BLACK GORA (NCS 12), ANNADA, NAN TE HAO, BR 21, DHALASHAITA, KALAKERI, BROWN GORA, GS529;DULAR, KOSHIHIKARI, SAITA, JHONA 349, MUEY NONG (WANG DIN), UPLRI 4, Mahulata
IV	12	N 22, KALAMKATI, SATHI 34-36, PSBRC 80, IRRI 123, ASSE Y PUNG, T 1, RTS 4, CR2699, Lalat, IR 64, KU 113-1
V	1	Davo
VI	5	DINORADO, BASMATI 334, IR74371-70-1-1, NIAW, Swarna
VII	1	DUBRAJ
VIII	1	SAMBHA MAHSURI

Table 2. Intra and inter cluster average distances in 76 genotypes

	I	II	III	IV	V	VI	VII	VIII
I	5	27.59	7.54	8	6.35	8.06	34.04	24.96
II		5.57	28.32	27.43	27.48	28.82	7.99	7.94
III			6.46	9.85	9.9	10.44	34.68	25.89
IV				6.32	10.27	12.94	33.84	23.91
V					0	6.32	33.65	24.79
VI						6.39	35.02	27.01
VII							0	11.81
VIII								0

made use of in improvement through intervarietal hybridization (Bose and Pradhan, 2005, Joshi *et al.*, 2008).

Cluster III with fourteen genotypes exhibited highest mean value for plot yield (153.29), harvest index (0.27), total dry matter production (103.62), ear bearing tiller (9.47) and 1000 grain weight (27.54) (Table 3). Cluster V was characterized by lowest plant height (65.7) but with low total dry matter production (75.72), plot yield (17.05). Early flowering genotypes (65.96 days) *viz.*, Dhalasaita was grouped in cluster III . The genotype *viz.*, Sambha Mahsuri (88.5) in cluster VIII and Dubraj (92) in cluster VII had long flowering duration. None of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. However the cluster III recorded desirable mean value for maximum number of productive traits *viz.*, plot yield, harvest index, total dry matter production, ear bearing tiller. Similar results were also reported by Bose and Pradhan (2005) while studying the divergence in deep water rice genotypes, thereby underlining the fact that the hybridization between genotypes of different clusters is necessary for the development of desirable genotypes. Composition of cluster indicated the non-existence of correspondence between genetic diversity and geographical distribution. Based on the per se performance of the best genotypes within the clusters, they may be directly selected or may be used as potential parents in hybridization programme.

The contribution of each trait to total divergence is presented in Table 4. Among the traits studied, kernel length contributed maximum divergence (34.32%) followed by plot yield (21.02%). The minimum percentage of contribution was observed in ear bearing tillers (0.81%). Low variability of ear bearing tillers indicated that the sink size (ear bearing tiller) is a limitation in the commonly available materials. Hence due emphasis should be given for component of sink size under direct seeded and drought affected condition. The traits *viz.*, sterility, plot yield, kernel length, kernel breadth, 1000 grain weight contributed 71.52% towards total divergence. Hence, these characters should be given importance during hybridization and selection in the segregating population. Similar findings also reported by Chandra *et al.*, 2007, where characters like Kernel

Table 3. Cluster mean of different yield and yield contributing traits in 76 genotypes

Cluster	Days to 50% flowering	Plant height(cm)	Ear-bearing tiller	Panicle length (cm)	Total dry matter production(gm)	Harvest index	Sterility %	Plot yield(gm)	Kernel length(mm)	kernel breadth (mm)	1000 grain weight(gm)
I	75.49	77.73	8.02	20.12	90.85	0.21	39.11	56.86	6.07	2.12	25.6
II	69.07	83.29	7.14	17.44	73.74	0.19	55.43	56.58	6.2	2.01	24.35
III	65.96	84.32	9.47	20.88	103.62	0.27	26.51	153.29	6.14	2.05	27.54
IV	69.29	85.11	8.65	22.1	87.48	0.22	42.85	55.57	7.12	2.05	25.1
V	71	65.7	4.95	18.9	75.72	0.16	71.7	17.05	5.69	2.14	18.55
VI	83.1	76.27	7.64	20.42	87.69	0.19	52.55	40.27	4.99	1.94	26.6
VII	92	85.4	7.65	17.25	67.95	0.2	70.83	64.5	6.13	2.28	20.25
VIII	88.5	87.9	4.85	16.55	79.3	0.16	81.2	52.1	7.19	2.15	17.61

Table 4. Percentage of contribution of each character towards total divergence

Character	No. of first rank	Contribution %
Days to 50% flowering	52	1.82%
Plant height(cm)	27	0.95%
Ear bearing tiller	23	0.81%
Panicle length(cm)	25	0.88%
Total dry matter production(gm)	27	0.95%
Harvest index	43	1.51%
Sterility%	258	9.05%
Plot yield(gm)	599	21.02%
kernel length(mm)	978	34.32%
kernel breadth(mm)	133	4.67%
1000 grain weight(gm)	70	2.46%
Total	2849	78.44%

length, Kernel breadth, days to 50% flowering and plant height had more contribution to total divergence.

In the present investigation, it is suggested that Intervarietal hybridization programme within the divergent cluster III and IV are expected to give promising and desirable recombinants in the segregating generations. Also, traits contributing maximum to genetic divergence viz. sterility, plot yield, kernel length, kernel breadth, 1000 grain weight yield may be utilized in selecting genetically diverse parents. If breeder's intention is to improve grain yield, he can select genotypes which are highly divergent with respect to these characters.

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