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Morphometric Diversity Studies in Rice Genotypes for Yield and Yield Attributing Characters under Drought

Shafina Haque

Crop Improvement Division, Central Rice Research Institute, Cuttack, Orissa, India

S. K. Pradhan

Crop Improvement Division, Central Rice Research Institute, Cuttack, Orissa, India

A. Anandan

Crop Improvement Division, Central Rice Research Institute, Cuttack, Orissa, India

O. N. Singh

Crop Improvement Division, Central Rice Research Institute, Cuttack, Orissa, India

Abstract:

Selection of parents for hybridization has widely been associated with degree of divergence among the selects. Mahalanobis D^2 analysis was carried out involving a set of 76 rice genotypes, landraces and popular variety consisting of both indigenous and exotic collection were studied for yield and yield related attributing traits under drought. Based on D^2 analysis, the genotypes were grouped into 8 clusters. Maximum number of genotypes (48 genotypes) was grouped in cluster I. The maximum inter cluster distance was observed between cluster II and VI (840.14) followed by between cluster VI and VIII (815.34) 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 (71.67) followed by cluster II (54.07). 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 11 traits studied, plot yield contributed maximum divergence (56.49%) followed by 1000 grain weight (22.28%). The traits viz., harvest index, sterility, plot yield, kernel length, kernel breadth, 1000 grain weight contributed 88.78% towards total divergence. Therefore, these characters may be used for initiating a hybridization programme to develop drought tolerant genotype.

Keywords: Rice, genetic variability, cluster analysis

1. Introduction

Presently, more than half of the world's population depends on rice as a staple food. Asia can be considered as 'Rice Basket' of the world, as more than 90 per cent of the rice is produced and consumed in Asia, a region with high population density. Due to quest for high yielding varieties, 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.

2. Materials and Methods

Seventy six rice genotypes consist of 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 Rabi season, 2013 and 2014 to identify diverse genotypes. The experiment was laid out in Randomized Block Design with three replications. The genotypes were direct seeded in plot of 5 rows with each row of 6 m length. Row to row and plant to plant spacing was maintained at 20 x 15 cm. The recommended agronomic practices were followed up to flowering stage. After flowering, irrigation was stopped. Eleven 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 and 1000 grain weight were estimated under drought stress. The genetic distances between the genotypes was worked out using Mahalanobis D^2 analysis (1936) and grouping of varieties into clusters was done following the Tochers method as detailed by Rao, 1952.

3. Results and Discussion

Via Tocher's methods, 76 genotypes were grouped into 8 clusters (Table 1). Maximum number of genotypes (48 genotypes) was grouped in cluster I. Cluster II consists of 13 genotypes followed by cluster III with nine genotypes. Cluster VI had two 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), Nayak et al. (2004) and Anandan et al. (2011). According to Bhutia *et. al.*, (2005) out of 41 high yielding and local genotypes of rice 6 clusters were found.

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 II and VI (840.14) followed by between cluster VI and VIII (815.34) and between cluster VII and VIII also indicating wider genetic diversity (737.79) 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 IV and IV (0), 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 productive result. The maximum intra cluster distance was observed in cluster III (71.67), followed by cluster II (54.07). 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 (Bose and Pradhan , 2005, Joshi et al., 2008).

A perusal of results of cluster means (Table 3) revealed that cluster VIII with one genotype (Saita) exhibited the highest mean value for plot yield (135.25), total dry matter production (117.47), panicle length (22.15), harvest index (0.23) and lowest sterility (23.95). Cluster III was characterized by the lowest days for 50% flowering (69.61) and highest ear bearing tiller (10.42). Early flowering genotypes (69.61 days) *viz.*, Dhalasaita was grouped in cluster III. The genotype *viz.*, Swarna (96.5) in cluster V and UPLRI 4 (90.5) 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 VIII recorded desirable mean value for maximum number of productive traits *viz.*, plot yield, harvest index, total dry matter production, panicle length and lowest sterility. Similar result was 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, plot yield contributed maximum divergence (56.49%) followed by 1000 grain weight (22.28%). The minimum percentage of contribution was observed in ear bearing tillers (0.66%). 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.*, harvest index, sterility, plot yield, kernel length, kernel breadth and 1000 grain weight contributed 88.78% towards total divergence. Consequently, 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 length, kernel breadth, days to 50% flowering and plant height had more contribution to total divergence.

4. Conclusion

Traits with high divergence can be used for crop improvement. The objective of measuring genetic divergence is to identify the most divergent parents. The results indicated that parental lines selected from clusters II and VI could be used in a hybridization programme, since hybridization between divergent parents is likely to produce wide variability and transgressive segregations. Crosses between unrelated lines tend to exhibit heterosis. Thus, diverse lines from different clusters should be chosen for crossing in a hybrid rice breeding programme. Also, traits contributing maximum to genetic divergence *viz.* harvest index, sterility, plot yield, kernel length, kernel breadth, 1000 grain weight 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.

5. References

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Cluster	Number of Genotypes	Name of genotypes
I	48	CR2702(IET21627),IET21692,Mayanur,CHAU, CR2707,NSICRC 9,Naveen,IR 20,Davao, RATNA,BPI RI 10,N 22,NSIC Rc 192,IET 21625(CR 2698),IR74371-46-1-1,BR 21,ASSE Y PUNG,BR 1,ZHENSHAN 2,MAGAWK DONG 269-7-7 (9),GS 529;DULAR,AI JIAO NAN TE,BROWN GORA,CO 25,IR 81896-B-B-195,KASALATH,DEE-GEO-WOO-GEN,Sahbhagi,Pyari,Dhagad deshi, BINNATOHA, PSBRC 80,M 55419-04,PSBRC 80,T 136,SARJOO 50,BLACK GORA (NCS 12),NAN TE HAO,ANNADA, KOSHIHIKARI,RD 25,ASSE Y PUNG,BR 2,JHONA 349,KU 113 1,KINASTANO,Mahulata,IR 64,MUEY NONG (WANG DIN)
II	13	DUBRAJ, Samba Masuri, BASMATI 370, RTS 4, IRR1 123, MTU1010, KALAMKATI, TAICHUNG NATIVE 1, CR2699, SATHI 34-36, CR2706, Lalat, T1
III	9	PURBACHI (CHINESE 1), CR 143-2-2, TAM CAU 9 A, DHOLI BORO, KALAKERI, JAYA, DINORADO, DHALASHAITA, Vandana
IV	1	Satyabhama
V	1	Swarna
VI	2	IR74371-70-1-1, NIAW
VII	1	UPLRI 4
VIII	1	SAITA

Table 1: Clustering pattern of 76 genotypes using Mahalanobis statistics

	I	II	III	IV	V	VI	VII	VIII
I	52.41	166.93	104.18	87.53	84.61	347.35	89.03	509.66
II		54.07	356.9	111.6	239.29	840.14	161.74	675.07
III			71.67	213.35	133.2	179.85	158.91	521.92
IV				0	45.63	514.07	123.5	536.49
V					0	298.84	143.03	542.65
VI						22.87	434.38	815.34
VII							0	737.79
VIII								0

Table 2: Intra and inter cluster average of yield in 76 genotypes

Cluster	Days to 50% flowering	Plant height	Ear bearing tiller	Panicle length	Total dry matter production	Harvest index	Sterility%	Plot yield	Kernel length	Kernel breadth	1000 grain weight
I	72.92	79.17	8.37	20.18	93.12	0.21	38.15	64.83	6.14	2.11	24.68
II	75.58	84.75	6.7	18.83	84.72	0.21	38.89	51.27	7.1	1.99	22.41
III	69.61	86.12	10.42	19.82	102.65	0.18	33.63	102	5.61	2.15	23.92
IV	97	72.1	3.6	17.15	88.91	0.17	68.6	11.47	6.34	2.15	24.05
V	96.5	86.9	6.85	19.15	88.26	0.23	78.8	10.82	5.79	2.04	29.8
VI	73.25	68.73	7.65	21.93	107.84	0.2	47.15	77.23	4.51	1.85	23.13
VII	90.5	56	7	19.5	66.05	0.16	58.6	124.1	6.4	1.4	31.45
VIII	80.5	90.75	7.15	22.15	117.47	0.23	23.95	135.25	6.1	1.15	26.25

Table 3: Cluster mean of different yield characters in 76 genotypes

Character	No. of first rank	Contribution %
Days to 50% flowering	89	3.14%
plant height	62	2.17%
ear bearing tiller	23	0.66%
Panicle length	82	2.87%
Total dry matter production	68	2.38%
Harvest index	19	5.08%
Sterility	89	3.15%
Plot yield	1610	56.49%
Kernel length	145	0.80%
Kernel breadth	28	0.98%
1000 grain weight	635	22.28%
Total	2850	100.00%

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