SHORT COMMUNICATIONS

Assessment of Genetic Divergence in Relation to Hybrid Breeding in Rice

SK Singh[1], Manoj Kumar[2], VK Sharma[2], N Kumari[2], VK Shah[2] and PB Jha[1]
[1]*Department of Plant Breeding,* [2]*Department of Genetics, Rajendra Agricultural University, Pusa-848 125, Bihar*

Key Words: Rice, Restorer, Maintainer, Cluster Analysis, Divergence

Genetic diversity is considered as an important criterion while choosing the parents for realizing heterosis and recombination in breeding programmes. Within a limit, inclusion of more diverse parents in hybridization is believed to increase the chances of obtaining stronger heterosis in hybrids. In the present communication, an attempt has been made to ascertain the magnitude of diversity among some maintainer and elite restorer lines in order to provide a rational basis for the selection of suitable parental lines to develop heterotic combinations.

The experimental materials comprised 29 fertility restorers and 17 sterility maintainers of wild abortive cytosterility system (personal communication) in rice. The restorer lines IR 23352-7R, IR 33509-26-2-2R, IR 42266-29-4-4-4R, IR 43342-10-1-1-3-3R, IR 55838-B2-2-3R, IR 56381-139-2-2R, IR 58082-126-1-2R, IR 58103-62-3R, IR 59624-34-2-2R, IR 59669-93-1-3R, IR 59682-132-1-1-2R, IR 60819-34-2-1R, IR 60919-150-3-3-2R, IR 60997-16-2-3-2R, IR 61614-38-19-3-2R, IR 62030-59-1-2-2R, IR 62036-222-3-3-1-2R, IR 62037-12-1-2-2R, IR 62037-129-2-3-3-3R, IR 62161-184-3-1-3-2R, IR 62171-122-3-2-3-3R, IR 63870-123-2-2-2-2R, IR 63870-7-3-2-3-3R, IR 63875-196-2-2-1-3R, IR 63877-43-2-1-3-7R, IR 63879-195-2-2-3-2R, IR 65849-H-AC2-2R, IR 65514-5-1-2-19R, IR 65515-56-1-3-19R, (hereafter designated as R-1 to R-29, respectively) and the maintainer lines IR 58025B, IR 67684B, IR 68275B, IR 68280B, IR 68885B, IR 68888B, IR 68892B, IR 68897B, IR 68899B, IR 68902B, IR 69161B, IR 69626B, IR 69628B, IR 70362B, IR 70369B, IR 70372B and IR 70959B (hereafter designated as B-1 to B-17, respectively) were evaluated in randomized block design with three replications at the research farm of Rajendra Agricultural University, Pusa, Bihar during *kharif,* 2002. Seedlings of each entry were transplanted to the field in three rows spaced at 20 cm and inter-plant distance within a row was maintained at 10 cm. Observations for plant height, panicles per plant, panicle length, spikelets per panicle, branches per panicle, panicle exsertion, grains per panicle, spikelet fertility, panicle density, 100-seed weight and grain yield per plant were recorded on five random competitive plants from each entry in each replication, while days to 50% flowering was recorded on plot basis. Multivariate analysis was used to quantity genetic diversity and the entries were grouped into clusters (Rao, 1952). For numerical classificatory analysis (Sokal and Sneath, 1963), an average taxonomic distance (Sokal, 1961) was computed as a measure of dissimilarity. The method for tree building involved sequential agglomerative hierarchical nested clustering based on taxonomic distance. Dendrogram was constructed by unweighted pair group method using arithmetic average and the clusters were identified at the appropriate phenon levels.

Significant differences among the restorers and maintainers were observed for all characters. Using D^2 value obtained for each pair wide combination of entries, the restorer and maintainer lines were grouped into five clusters, Cluster A comprised 20 restorer and 7 maintainer lines (Table 1). Its intra-cluster distance was only next to the largest intra-cluster distance in cluster D, which had two restorer and two maintainer lines. Cluster C with the lowest intra-cluster distance accommodated only three maintainer lines. While Cluster B consisted of six restorer and five maintainer lines, cluster E was found to be monogenotypic and consisted of a maintainer line. Interestingly, the first two clusters comprised 38 entries, reflecting narrow genetic diversity among the lines under evaluation in the present study. The close genetic relationship was more apparent in the case of restorers as 26 lines were included in the first-two clusters. While the restorer lines were observed to be genetically more closely related, the maintainer lines were relatively more diverse. The similarity in parentage and fixed selection criteria might be the cause of less genetic diversity in these parental lines in general and restorer lines in particular.

Table 1. Composition of cluster based on generalized distance for twelve characters among restorers and maintainers

Cluster A: R1, R6, R7, R8, R9, R10, R11, R14, R16, R17, R18, R19, R20, R21, R23, R25, R26, R29, B2, B6, B7, B8, B9,B10, B12
Cluster B: R5, R13, R15, R24, R27, R28, B1, B3, B11, B13, B17
Cluster C: B4, B5, B14
Cluster D: R2, R4, B15, B16
Cluster E: R3

Average inter-cluster distances were greater than intra-cluster distances. The inter-cluster distance was maximum between clusters D and E. It was closely followed by a distance of cluster C and cluster B from cluster D. The greater inter-cluster distances indicated greater genetic diversity of the entries belonging to cluster D from those belonging to cluster B, cluster C or cluster E. A perusal of cluster means for different characters, indicated the superiority of cluster D over the others in respect of panicle length, panicle exsertion, spikelet fertility, 100-grain weight and grain yield per plant. Similarly, it was evident that cluster B had the highest cluster mean value for spikelets per panicle, branches per panicle, grains per panicle and panicle density. But for days to 50% flowering and panicles per plant, cluster C had the lowest and the highest mean value, respectively. While cluster C recorded the lowest cluster mean for a majority of the yield contributing characters, cluster B, D and E had higher cluster means for most of these characters. Considering inter-cluster distances in conjunction with cluster means and clustering pattern, crossing of B15 and B16 with R3 is suggested as it may give high heterotic rice hybrids. Similarly, the crosses involving B15 and B16 with R5, R24, R27 and R28, in addition to the crosses involving B1, B3, B11 and B13 with R2 and R4 could be predicated as superior heterotic combinations.

Basically the entries, were classified into one multigenotypic and one monogenotypic groups. While truncation at 60 dissimilarity units created four diverse groups (Table 2). At this phenon level, clusters A, B, C and D consisted of 22, 20, 3 and 1 entries, respectively. Cluster A was divided into sub-clusters AI and AII at 50 units of dissimilarity with 19 and 3 entries, respectively. Similarly, cluster B got divided into sub-clusters BI, BII and BIII with 18, 1 and 1 entries, respectively. While, cluster C split into CI and CII with two and one entries, respectively. An increase in phenon level

Table 2. Composition of clusters based on dissimilarity coefficients for twelve characters among restorers and maintainers

No. of clusters identified at phenon levels*			Entries included in each cluster
60%	**50%**	**40%**	
A	AI	Aia	R1, R6, R7, R8, R9, R16, R17, R18, R19, R20, R22
(22)	(19)	(16)	R25, B6, B8, B9, B12
		AIIIb	B2, B14, R11
	AII	AIIa	B5, R10
	(3)	(2)	
		AIIb	B4
		(1)	
B	BI	BIa	R2, R5, R12, R13, R14, R21, R23, R26, R27, R28
(20)	(18)	(14)	R29, B3, B13, B17
		BIVb	R15, R24, B10, B11
	BII	BII	R3
	(1)	(1)	
	BIII	BIII	B1
	(1)	(1)	
C	CI	CI	B15, R4
(3)	(2)	(2)	
	CII	CII	B16
	(1)	(1)	
D	D	D	B7
(1)	(1)	91)	

Figures in parentheses indicate number of entries in respective clusters
*Phenon levels indicate 60, 50 and 40 units of dissimilarity coefficients

by drawing the phenon line at 40 dissimilarity units, which allowed only increasingly similar entries to be clustered together, further enhanced the number of constellation of entries. It was thus possible to discern subtle differences between genotypes grouped in different clusters and/ or sub-clusters at different phenon levels. While the grouping of genotypes in different clusters through dendrogram was fairly in good agreement with the clustering through D^2 analysis, the discrepancy for some of the entries could be attributed to the difference in the methods of analysis. A further comparison of clustering patterns based on different methods showed that dendrogam clustering gave an additional advantage of distinctly discriminating the genotypes and identifying sub-clusters of the major groups at different phenon levels.

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