STUDIES ON GENETIC VARIABILITY IN RICE

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Genetic divergence was assessed in 32 varieties of rice (*Oryza sativa* L.) using D^2 statistic for six characters related to yield. The population was grouped into nine clusters. The geographic distribution was not related to genetic diversity. Genotypes chosen from the same eco-geographic region were found scattered in different clusters. Intra-cluster D^2 value was highest for cluster V. Maximum intercluster D^2 value was observed between clusters III and IX. Cluster III had high mean value for panicle bearing tillers, cluster V for grains/panicle and grain yield/plant, and cluster VI for panicle length. The cluster VIII had the lowest mean for sterile grains/panicle. Plant height contributed Maximum role in total genetic diversity followed by sterile grains and grains/panicle. Utilizing the genotypes of clusters which are highly divergent is likely to result in wide spectrum of variabilty through hybridization.

In earlier days various geographical sources were also regarded as a primary criterion for genetic diversity. But at present it is observed that genetic materials from the one and same eco-geographic origin also possess diverse genetic make up and it is also not uncommon that the genetic materials of different eco-geographic origin possess similar genetic architecture. Further, the more diverse the parents, the greater are the chances of obtaining higher amount of heterotic expression in F_1s and broad spectrum of variability in further generation. The diverse genetic collection in rice were not utilized fully in these aspects and so for less work has been reported. Hence as a primary to genetic improvement a study wasundertaken to estimate the genetic diversity through multivariate analysisand the results are presented hereunder.

MATERIAL AND METHODS

Thirty two cultures of rice were grown in a randomized block design with three replications at college Farm during the *Kharif* season of 1976 under saline alkali soil conditions with pH. of 10.15. Twenty five days old seedlings were transplanted on 12th July in 3 rows of 5.0 m length, having 20 cm distance between the rows and 15 cm between plant to plant. Observations were recorded on ten randomly taken plants from each plot for six metric traits namely plant height, panicle bearing tillers, panicle length, number of grains/panicle, number of sterile grains/panicle, and grain yield/plant. Multivariate analysis of genetic divergence was carried out as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the strains for all the characters indicating thereby the existence of genetic variability among the varieties The computed D^2 values varied substantially from 1.11 to 98 58 showing high divergence among the different strains. By the application

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of clustering technique, the thirty two types were grouped into nine different clusters (Table 3). Among the nine, cluster I was the largest consisting of ten types followed by II, III and IV clusters which had six, five and four types, respectively. Clusters V and VI had two types each and VII, VIII and IX consisted of only one each.

The cluster V comprised types from same geographic region (Uttar Pradesh) indicating identical genetic architecture among them. Such a parallelism was also reported by Ram and Panwar (1970) in rice. The clusters I, II, III, IV and VI were either bivarietal or multivarietal clusters and had types from different geographic regions. This leads to the inference that factors other than geographic diversity may be responsible for such grouping and there is no parallelism between geographical distribution and genetic diversity. It may perhaps be due to (a) free exchange of breeding materials from one place to other (Verma and Mehta, 1976), (b) varieties involved under similar selection pressure will cluster together irrespective of their geographic origin (Singh and Bans, 1968) and (c) interaction of some similar genotypes at different places (Singh et al 1980). Besides, the twelve types of Andhra Pradesh were found to be one or more components of four of the nine clusters. This suggests the presence of wide genetic variability among the materials though they belong to same eco-geographic region. It may also be due to the hybridization programme taken for different objectives in the same region. Singh et al. (1971) pointed out that even the temperature and rainfall

pattern respectively could influence plant characters of the same races and Murty and Arunachalam (1966) explained that such a wide adaptability could be possible due to reasons such as heterogeniety, genetic architecture of the populations, past history of the selection, developmental factors and degree of general combining ability. Hence for pedigree breeding, intercrossing these groups of parents from the same geographic region which are divergent among themselves are more desirable than choosing the parents from other region.

Intra-and inter-cluster distance are given in Table 3. Intra-cluster D values ranged from 0.00 to 10.09, Cluster V had the highest intra-cluster D^2 value whereas clusters VII, VIII and IX involving single treatment in each had zero D^2 value and were most diverse clusters. Inter-cluster D^2 value was observed to be highest between clusters III and IX (108.83), indicating wide diversity between two groups Minimum distance occurred between I and II (12.24), showing close relationship. In general, VIII and IX had higher intracluster D^2 values with all the clusters which indicated that Shyamjeera and Sarjoo-50 belonging to cluster IX and VIII respectively, were the most diverse than others. The types involved in these clusters on one hand and the types of the other clusters on the other hand may serve as potential parents in heterosis breeding if possible. Adequate relationship between the extent of heterosis and genetic divergence is also reported in tomato by Rajanna et al. (1977).

The cluster means for the different characters are presented in Table 4. Cluster VIII showed the lowest mean value for plant height, panicle length and grains/panicle but had the highest mean for panicle bearing tillers. Cluster V revealed the highest value for grains/panicle and grain yield/plant. The highest value were observed for panicle length by cluster IV and lowest for sterile grains/panicle in cluster VIII. Besides, plant height, contributed maximum role in total genetic diversity followed by sterile grains/panicle and grains/panicle. The lowest contribution was recorded for panicle bearing tillers followed by panicle length and grain yield/plant (Table 4).

Merely presence of high amount of genetic diversity in population may not be adequate to effect improvement over best existing variety because of the fact that the selection towards uniformity could cause an eroding effect on genetic diversity and genetic variation is reduced in course of selection. Therefore, it will be desirable to suggest that selection for better genotypes with desirable pre-requisites mentioned above, could be obtai-

ned from clusters, VII, VIII, V and VI, hybridization programme may be initiated by involving the best individuls and the new genot obtained by improvement in characters at high level of expression in saline alkail soil conditions.

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Table 1 Geographical origin of genotypes

Origin	Name of variety	Origin	Name of Variety
Andhra Pradesh	1. RP 319-34-8-7,	Andhra Pradesh	17. Sona,.
	2. RP 6-615-35,		18. IET-400,
	3. RP 79 23,	Orissa	19. CR 4248-183,
	4. RP 4-19,		20. Ratna,
	5. RP 6-516-29-1,		21. CR 10-432-179.
	6. RP 9-4,		
	7. RP 260-750-3,	China	22. China 4.
	8 RP 6-590-2./,	Bangala Desh	23. BR 12,
Philippines	9. IR 644,		24. BR 13.
	10. IR 28.		25. BR 14,
	11. IR 22.		26. BR 284.
		Andhra Pradesh	27. MTU 6368,
Uttar Pradesh	12. T 9,		28. Getu;
	13. T 26,	Tamil Nadu	29. C.O. 36.
	14. Sarjoo-50,	Punjab	30. PR 106,
	15. Shyamjreea.	Uttar Pradesh	31. Sudha,
Bihar	16. Bihat local.		32. Karanga.

Table 2 Composition of D² cluster

Cluster	component vaners
I.	5,7,8,9,16,17,18, 26,27,31.
II	1,3,4,11,19,28.
III	2,20 29,30,32.
IV	22,23,24,25.
V	12, 13.
VI	6,21.
VII	10.
VIII	14.
IX	15,

Table 3 : Intra-and Inter-cluster D² values among 9 clusters in rice.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	6.83	12.24	15.84	20.21	22.19	30.16	28.68	42.21	67.39
II		7.01	15.04	33.54	28.20	37.03	16.20	46.64	85.11
III			5.84	35.95	37.08	65.85	45.48	39.27	108.83
IV				7.71	18.68	45.40	57.57	36.49	29.44
V					10.09	37.15	51.17	23.25	49.16
VI						- - -	20.24	86.24	58.90
VII							0.00	95.54	94.97
VIII								0.00	75.59
IX									0.00

Table 4: Cluster means for six characters in rice

Clesters	plant height	Panicle bearing tillers	Panicle length	No. of grains/panicle	No. of sterile grains/panicle	Grain yield Plant
I	83.0	6.9	19.4	84.8	9.9	7.5
II	53.2	7.2	16.6	91.9	14.7	7.8
III	50.3	8.6	15.9	72.9	5.3	7.5
IV	90.1	8.2	19.5	85.8	8.6	9.0
V	74.7	7.6	21.0	139.2	11.0	10.6
VI	69.8	5.3	22.1	112.0	23.7	5.2
VII	52.7	6.7	17.0	94.6	23.7*	10.1
VIII	72.7	4.6a	17.3	125.1	3.5a	4.1
IX	121.4*	5.1	20.7	98.2	15.5	7.1
Total Genetic diversity in per cent	32.0	9.2	13.0	14.3	27.0	14.0

* Highest value,   (a) Lowest value.