GENETIC DIVERGENCE FOR YIELD AND YIELD COMPONENTS IN COLD TOLERANT RICE

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ABSTRACT

Substantial genetic diversity among the 40 cold tolerant rice genotypes for components of fitness between and within the geographic regions existed. The clustering pattern indicated that geographic diversity was not a reliable criterion of genetic diversity in cold tolerant rice. The genotypes related by their origin of region or by pedigree tended to group in the same cluster in general. There was a wide range of variation in the intra-cluster mean values in respect of each of the quantitative triats studied. The yield component traits viz., number of grains per panicle and number of productive tillers contributed the most to the genetic divergence between the genotypes.

KEY WORDS: Genetic divergence, Cold tolerant rice, Grain yield.

Information about the genetic divergence is helpful in crop improvement programme since the genetically divergent parents on crossing are known to produce hybrids with high heterosis followed by desirable segregants. The present study was undertaken to determine genetic divergence among a set of 40 cold tolerant rice genotypes.

MATERIALS AND METHODS

Forty cold tolerant rice entries comprised of cultivars, local selection/varieties and breeding lines drawn from different geographic regions constituted the materials for the study. The experiment was conducted at the sub-centre for cold tolerance rice breeding at Keelagudalur situated at 500 m above MSL in Cumbum valley of Madurai district. A completely randomised block design with three replications was adopted. Observations on plant height, days to 50 per cent flowering, number of productive tillers, panicle length, number of filled grains per panicle, chaff percentage, 100 grain weight and single plant yield were recorded on five random plants per repli-

cation. The genetic diversity existing between the genotypes with respect to the set of eight correlated variables was worked out using Mahalanobis' D^2 statistics (Mahalanobis, 1936). The criterion used by Tocher (Rao, 1952) was applied for determining the group constellations. The average intra and inter-cluster distances were worked out following the methods described by Singh and Chaudhary (1977).

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant differences among the genotypes for all the eight characters studied indicating thereby the existence of genetic variability. The significance of lambda statistics showed that the differences between the mean in respect of the pooled effect of all the characters between different population were significant. Hence, further analysis to estimate D^2 values was done and on the basis of relative magnitude of D^2 values, all the 40 genotypes were grouped into eleven clusters, the composition of which in respect of the genotypes, their origin and parentage are presented in Table 1. Of the 11 clusters, three (IX, X and XI) had single genotype while the rest eight clusters

nad many genotypes. The clustering pattern indicated that genotypes from different origins clustered together in eight out of 11 cases. The cluster III composed of seven genotypes from four geographic regions. Six genotypes from three geographic regions clustered in cluster II. The trend of different genotypes from different geographic centres assembling in a cluster was a common feature in respect of other clusters.

The fact that genotypes belonging to different geographic regions got grouped in individual clusters indicated that geographic diversity was not necessarily related with genetic diversity. There was no direct relationship between geographic distribution and genetic divergence in a number of crops with variable breeding systems (Murty and Arunachalam, 1966). It was also found that there was no correspondence between geographic and genetic diversity in rice (Chatterjee et al., 1978). Free exchange of breeding materials from one place to another or a fixed selection criterion being followed in different centres could have enabled the genotypes from different geographic regions to cluster together in the same cluster.

When genotypes related by their origin in a region or by pedigree tended to group in the same cluster, there were also instances where the genotypes from the same centre of origin or pedigree were distributed in different clusters. For example, the fourteen genotypes from Tamil Nadu were scattered into seven different clusters. The genotypes from Andhra Pradesh, Kerala and Karnataka were distributed in four clusters each. Similarly, the breeding lines derived from the cross with common parents got grouped into different clusters. Six breeding lines being the derivatives of the cross involving IR 8 and Co 25 as parents were scattered in four clusters. This kind of genetic diversity among the genotypes belonging to either the same geographic region or parental combinations might be due to differential adaptation, selection criteria, selection pressure and environments (Das and Borthakur, 1973; Maurya and Singh, 1977).

Intra and inter-cluster distance analysis revealed that the genetic diversity among the varieties in custer V was minimum (7.06) pointing out to the gross genetic similarity between the three constituent genotypes, two of which viz., Phalguna and

Vikram were related by pedigree (Table 2). Unidirectional selection exercised in the past would have resulted in uniform features with the consequence of less divergence between the genotypes. The maximum intra-cluster distance (9.20) was observed in cluster VIII made of Rajumeni from Kerala and Madhu from Karnataka. This high intra-cluster distance indicative of wide genetic divergence between the partners could be made use of in yield improvement of cold tolerant rice cultivars through inter-varietal hybridisation. Angadi (1976) reported that varieties in a cluster found with high order of divergence among themselves would be the best breeding materials for achieving maximum genetic advance with regard to yield per se. Selection within a cluster might also be exercised based on the highest mean performance of the varieties for desirable traits such as number of grains per panicle and productive tillers having profound influence on yield in rice.

The minimum (10.54) and the maximum (42.51) inter-cluster distance was observed between varieties of clusters V and IX and between that of V and VIII respectively. The degree of divergence, decided

Table 1. Composition of D^2 clusters

Cluster No.	Varieties	Parentage	Origin
I	TNAU 20991	Bhavani x BC 11-6-3	Coimbatore, Tamil Nadu
	TNAU 20997	Bhavani x BC 11-6-3	-do-
	IET 6187	Vijaya x Ptb 21	Hyderabad, Andhra Pradesh
	IET 6551	Palman 579 x IET 2508	-do-
	IET 6727	IR 22 x WGL 12708	-do-
	IET 7011	Surekha x Kakatiya	-do-
	IET 7013	IR ww x WGO 12708	-do-
	Puspha	Jaya x B. Thaga	Mandya, Karnataka
II	IET 7024	Jagannatha natural cross	Cuttack, Orissa
	Adakkan 49	Pure line selection from Adakkan	Wynad, Kerala
	Wynad II	Pure line selection from Marathondi	-do-
	AMBT 2	Local collection, Wynad	-do-
	Pragathi	Jaya x S 37	Mandya, Karnataka
	Mangala	Jaya x S 37	-do-
III	TNAU 20105	IR 8 x co 25	Coimbatore, Tamil Nadu
	TNAU 15869/2	ASD 5 x T (N) 1	-do-
	TNAU 4372	Co 29 M-9 x Dawn	-do-
	IET 2938	IR 8 x Lotisail-3	Hyderabad, Andhra Pradesh
	KMP 41	Sona x W 1263	Mandya, Karnataka
	Sona	GEB 24 x T (N) 1	Hyderabad, Andhra Pradesh
	IR 20	IR 262 x TKM 6	Philippines
IV	DPI 335	Co 30 x IR 22	Paiyur, Tamil Nadu
	DPI 583	IR 22 x Co 30	-do-
	KMP 47	Sona x W1263	Mandya, Karnataka
	HR 35	Selection from Kichili sannalu	Hyderabad, Andhra Pradesh
V	Phalguna	IR 8 x Siam 29	Hyderabad, Andhra Pradesh
	Vikram	IR 8 x Siam 29	-do-
	Intan	Indonesian introduction	Indonesia
VI	TNAU 20115	IR 8 x Co 25	Coimbatore, Tamil Nadu
	TNAU 20147	Co 25 x IR 8	-do-
	Peruvaya	Local collection, Wynad	Wynad, Kerala
	Kattathondi	-do-	-do-
VII	TNAU 20107	IR 8 x Co 25	Coimbatore, Tamil Nadu
	TNAU 20112	IR 8 x Co 25	-do-
	DPI 662	Jaya x Co 18	Paiyur, Tamil Nadu
VIII	Rajumeni	Local collection, Wynad	Wynad, Kerala
	Madhu	T (N) 1 x TKM 6	Mandya, Karnataka
IX	TNAU 20114	IR 8 x Co 25	Coimbatore, Tamil Nadu
X	TNAU 1142/1	Bhavani x Ponni	-do-
XI	Gandhakasala	Local collection Wynad.	Wynad, Kerala

Table 2. Intra and inter-cluster D^2 values and distance (within parenthesis)

Cluster	I	II	III	VI	V	VI	VII	VIII	IX	X	XI
I	65.24	187.27	213.28	151.34	727.79	207.25	484.62	408.12	795.47	301.02	914.92
	(8.08)	(13.68)	(14.60)	(12.30)	(26.98)	(14.40)	(22.01)	(20.20)	(28.20)	(17.35)	(30.26)
II		56.51	626.77	219.91	1395.20	362.28	999.84	239.89	1492.79	718.35	1591.72
		(7.52)	(25.04)	(14.83)	(37.35)	(19.03)	(31.62)	(15.49)	(38.64)	(26.80)	(39.90)
III			54.52	387.21	257.69	321.67	211.59	914.37	294.86	182.80	491.57
			(7.38)	(19.68)	(16.02)	(17.94)	(14.55)	(30.24)	(17.17)	(13.52)	(22.17)
IV				68.02	979.48	187.41	544.65	181.74	912.28	298.32	862.03
				(8.25)	(31.30)	(13.69)	(23.34)	(13.48)	(30.20)	(17.27)	(29.36)
V					48.89	676.81	199.57	1807.20	111.11	452.15	334.64
					(7.06)	(26.02)	(14.13)	(42.51)	(10.54)	(21.26)	(18.29)
VI						80.69	318.13	468.44	673.91	246.26	603.60
						(8.98)	(17.84)	(21.64)	(25.96)	(15.93)	(24.57)
VII							82.13	1154.04	126.61	155.50	149.60
							(9.06)	(33.97)	(11.25)	(12.47)	(12.23)
VIII								84.13	1698.05	725.47	1557.46
								(9.20)	(41.21)	(26.93)	(39.46)
IX									-	314.99	137.96
										(17.75)	(11.75)
X										-	276.15
											(16.62)
XI											-

by the measure of distance, varied with the clusters in general. Considering cluster I as a typical case for study, it was least divergent from clusters II, III, IV and VI, moderately divergent from clusters V, VII, VIII, IX and X, and highly divergent from clus-ter XI. An overall assessment of the clusters showed that there was high divergence bet-ween clusters II and V, II and XI, V and VIII, VIII and IX, and VIII and XI that might be made use of in heterosis as well as recombination breeding pro-gramme since highly divergent

Table 3. Intra-cluster mean values for economic characters in rice

Cluster	Plant height (cm)	Days to 50% flowering	Number of productive tillers	Panicle length (cm)	Number of grains per panicle	Chaff Percentage	100 grain weight(g)	Single plant yield (g)
I	62.27	93.08	9.09	18.63	56.72	20.90	2.45	9.89
II	66.16	81.28	9.75	16.90	39.35	22.95	2.67	9.44
III	62.62	106.05	8.87	21.80	67.40	27.20	2.28	13.27
IV	94.75	90.42	8.60	22.30	59.72	16.94	2.07	10.44
V	78.47	120.78	7.84	22.11	61.11	26.96	2.68	12.00
VI	107.73	96.83	7.05	22.05	81.28	16.10	2.86	13.15
VII	108.51	114.00	7.80	21.62	86.26	20.29	2.45	15.13
VIII	102.16	78.50	7.06	22.50	60.08	18.82	1.90	11.05
IX	106.33	122.00	10.60	24.60	85.93	35.70	2.09	18.99
X	93.80	105.67	6.67	21.93	114.07	19.67	1.96	14.03
XI	131.93	120.67	6.87	27.67	105.63	11.13	2.13	13.17
Grand mean	92.70	102.66	8.20	22.01	74.23	21.51	2.32	12.78

genotypes would produce a wide spectrum of variability enabling further selection and improvement (Bhatt, 1973)

Intra-cluster mean values for all eight characters are furnished in Table 3. There was a wide range of variation in the intra-cluster mean values in respect of each of the character under study. It was found that four out of 11 clusters vis., VI, IX, X and XI, featured as those having high mean values. High means for 100 grain weight in cluster VI, days to 50 per cent flowering, number of productive tillers and single plant yield in cluster IX, grains per panicle in cluster X, and for plant yield, panicle length and least chaff percentage in cluster XI were recorded. The genotypes with high values on any cluster can either straight away be used for adoption or for hybridisation for further selection and improvement. The genotype,'Gandakasala' in cluster XI had high expression for plant height and panicle length besides moderate number of grains per panicle, low chaff percentage and low number of productive tillers. The genotype TNAU 20114 in cluster IX had high values for

days to 50 per cent flowering, number of productive tillers, single plant yield and chaff percentage. These two genotypes might be employed for crop improvement work by involving them as parents in recombination breeding method. The genotypes 'Gandakasala' might be useful as a valuable parent due to its desirable economic traits and low chaff percentage in any breeding programme for cold tolerance.

The utility of D² analysis is enhanced by its applicability to estimate the relative contribution of the various plant characters to genetic divergence. The present study revealed that number of grains per panicle, followed by number of productive tillers contributed the most to genetic divergence between the genotypes. Number of grain per panicle and number of productive tillers were already found to contribute the most to genetic divergence in the studies of Chatterjee et al. (1978)

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