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GENETIC DIVERGENCE IN EARLY RICE UNDER TWO SITUATIONS

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ABSTRACT

Genetic divergence was studied for yield and its eleven component traits in 28 early rice varieties (*Oryza sativa* L.) under direct seeded and transplanted conditions. The strains were grouped into five and six clusters in direct seeded and transplanted conditions, respectively. There is no relationship between geographical distribution and genetic divergence. Stable genotype like RP 1670-6-36-14 having wider genetic distance with cluster II and RAU 4045-2A are desirable to use as donor parents in hybridization programme for improvement of both direct seeded and transplanted conditions.

Key words: Genetic divergence, early rice, direct seeding, transplanting.

Improvement over existing varieties is a continuous process in plant breeding. Any successful hybridization programme for varietal improvement depends mainly on the selection of the parents having high genetic variability so that the desirable character combinations may be selected for higher grain yield. Thus, the genetic diversity in breeding for high yielding varieties has obvious importance as evidenced by earlier workers [1, 2]. Multivariate analysis by means of Mahalanobis D^2 statistic is a powerful tool in quantifying the degree of divergence among biological population. Change in environments alters clustering pattern due to genotype–environment interactions [3, 4]. Study, therefore, was undertaken to identify suitable stable donors having wider genetic distance among early rice varieties for both direct seeded and transplanted conditions through genetic divergence studies.

MATERIALS AND METHODS

Twenty eight early duration (100 days maturity) genotypes of rice were grown under direct seeded as well as transplanted conditions during rabi (dry) season in two replications. For both experiments, the crop was raised in rows with the spacing of 20 and 15 cm between rows and hills, respectively. Dibbling method was followed for direct seeded crop and 3–4 seedlings/hill were maintained by thinning operation within 10 days of germination. Under transplanted condition, 3–4 seedlings/hill were planted. In both experiments, the fertilizer was applied at the rate of 30 N and 30 P_2O_5 as basal dose. The recommended agronomic practices were followed to raise a normal crop. Observations were recorded on ten randomly selected competitive hills from each replication for twelve quantitative characters and the data from direct seeded and transplanted crops were subjected to analysis of variance separately. Mahalanobis D^2 statistic was employed to estimate genetic divergence. The genotypes were grouped in different clusters following Toucher's method as described by Rao [5].

RESULTS AND DISCUSSION

The analysis of variance showed significant differences among the 28 strains for all the 12 characters for both direct seeded and transplanted conditions, indicating the existence of genetic variability. The simultaneous test of significance based on Wilk's criteria for the pooled effect of all the characters also showed significant differences among the varieties in both direct seeded (725.4 at 324 degrees of freedom) and transplanted (811.5 at 324 degrees of freedom) conditions.

Based on the relative magnitude of the D^2 values, all the 28 strains were grouped into 5 and 6 clusters for direct sowing and transplanting, respectively (Table 1). Cluster I was comprised 57% of the total varieties under transplanting and 78% under direct sowing. Interestingly, only one variety each constituted clusters IV and V in direct sowing and IV, V and VI in transplanting. In both environments, clusters I, II and III included strains from different centres and states of India, indicating that clustering of the varieties did not follow their geographic or location distributions. Moreover, the groupings of varieties in the clusters were also different under direct seeded and transplanted conditions. This may be due to the application of directional selection pressure for realising high yield. Genetic drift and human selection in different environments have caused greater genetic diversity than geographical distances, as was suggested earlier by some workers[1, 3, 6, 7].

Among all the genotypes, RP 1670-6-36-14 (M 63-83 x Cauvery), a strain from the Directorate of Rice Research, Hyderabad, maintained its separate identity by not mixing with any other strains under both conditions. This single strain constituted clusters IV and V under transplanting and direct seeding, respectively. This could be due to its different genetic make-up as compared to other genotypes. The choice of such stable genotype as donor in hybridization is more important for varietal improvement of upland rice suited for both direct seeded and transplanted conditions.

Table 1. Clustering pattern among 28 upland rice varieties/strains

Cluster	Direct seeded		Transplanted	
	No. of genotypes	variety or strain	No. of genotypes	variety or strain
I	22	RP 2199-84-2, RP 1714-111--7-3-2, RAU4004-105, RAU 4004-109, RAU151-6, NDR112, NDR119, NDR311, NDR312-1, TNAU81804, TNAU83108, TNAU83134, NRL507, NRL502, RTN32, CR404-47, CRH4060, OR377-85-6, ADT85001, ADT25723, Cauvery and Neela	16	RP2199-84-2, RAU4004-105, RAU156-6, NDR112, NDR119, NDR311, NDR312-1, TNAU83804, NRL502, CR404-47, ADT85001, ADT25723, Pusa578, Akashi, Cauvery and Neela
II	2	RAU 4045-2A and Akashi	3	RP1714-111-7-3-2, CRH4060 and OR377-85-6
III	2	RP2466-17-40-48 and Pusa 578	6	RP2235-18-16-2, RAU4004-109, TNAU81804, TNAU83134, NRL507 and RTN 32
IV	1	RP2235-18-16-2	1	RP1670-6-36-14
V	1	RP1670-6-36-14	1	RP2466-17-40-48
VI	—	—	1	RAU4045-2A

The strains RAU 4045-2A (Fine Gora x IET 2832) and RP 2466-17-40-48 (Rasi x Gajgour) also displayed their separate genotypic identity by constituting clusters VI and V, respectively, under transplanting, while under direct sowing cluster II consisted of RAU 4045-2A and Akashi, and cluster III included RP 2466-17-40-48 and Pusa 578.

The statistical distances represent the index of genetic diversity amongst clusters. Under direct seeded condition, cluster II showed the highest intercluster distance (Table 2) with cluster V (31.1), followed by cluster IV (30.3). The highest intercluster distance was recorded under transplanted condition (Table 3) between clusters II and IV (33.8), followed by clusters II and III (28.8) and IV and VI (27.1). The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates.

Table 2. Intra- (in bold) and intercluster average D values of five clusters under direct seeding of rice

Clusters	I	II	III	IV	V
I	**10.39**	19.68	13.31	14.92	24.65
II		**5.90**	19.99	30.33	31.11
III			**11.87**	18.56	17.84
IV				**0.00**	27.11
V					**0.00**

Table 3. Intra- (in bold) and intercluster average D values of six clusters under transplanting of rice

Clusters	I	II	III	IV	V	VI
I	**10.05**	17.68	14.69	22.27	14.43	19.30
II		**11.15**	28.82	33.84	20.49	20.11
III			**12.81**	19.86	18.57	26.02
IV				0.00	17.63	27.06
V					0.00	22.36
VI						0.00

Considering the cluster means (Table 4) for different characters under direct seeded situation, it was observed that cluster II possessed dwarf plant stature with shortest maturity duration, lowest sterility, and higher number of grains/panicle and grain breadth, while cluster V had only one stable culture, RP 1670-6- 36-14, with the highest values for panicle length, secondary branches/panicle, 100-grain weight, grain length, and plant height. Cluster IV comprising only one culture, RP 2235-18-16-2, possessed highest panicle number/hill, primary branches/panicle, grains/panicle, and grain yield/hill, with longer duration, dwarf plant stature, and fine long grain. However, under transplanted condition, cluster II had the shortest duration, dwarf plant stature, maximum grains/panicle, and lowest sterility, while cluster IV had highest values of panicle length, primary and secondary

Table 4. Cluster means for 12 characters in rice under direct seeded and transplanted conditions

Cluster	Panicle per hill	Panicle length (cm)	Primary branches per panicle	Secondary branches per panicle	Grains per panicle	Chaffs per panicle	100-grain weight (g)	Grain yield per hill (g)	Day to 50% flowering	Plant height (cm)	Grain length (mm)	Grain breadth (mm)
					Direct seeding							
I	16.8	18.5	6.03	9.0	45.6	10.7	2.16	13.08	79.9	72.3	8.62	2.63
II	13.0	16.5	5.88	11.7	53.0	5.9	2.71	10.55	69.2	71.7	7.24	3.03
III	13.0	19.1	7.40	11.7	41.9	21.0	2.45	9.94	76.0	76.6	8.87	2.79
IV	17.4	20.2	7.55	11.9	55.6	15.3	1.95	14.05	89.0	70.1	9.27	2.27
V	5.6	21.9	6.85	13.9	41.5	37.2	2.84	7.30	73.0	99.2	9.45	2.94
					Transplanting							
I	10.0	18.8	6.32	9.7	48.5	11.3	2.11	8.52	78.1	70.9	8.64	2.63
II	8.9	18.9	6.42	8.6	49.0	10.0	2.18	7.25	71.5	68.4	8.43	2.86
III	10.2	18.5	6.40	10.2	47.5	13.5	2.20	8.55	82.0	70.4	8.80	2.56
IV	6.5	20.5	7.15	15.0	48.6	39.9	2.55	5.60	82.5	89.2	9.18	2.98
V	7.1	20.0	6.35	10.5	35.5	19.8	2.95	8.76	78.0	79.9	9.65	2.89
VI	7.1	14.5	4.95	10.7	43.2	11.8	1.80	4.04	75.5	67.8	6.81	2.97

branches/panicle, flowering duration, and plant height, and also higher value of grain number/panicle and grain length.

Considering the wider intercluster distance and cluster means under both situations, the genotype RP 1670-6-36-14 (cluster V under direct seeding and IV under transplanting) is recommended as one of the best parents for hybridization owing to its stability for genotype–environment interactions under both situations and maximum genetic distance from cluster II. The other parent may be chosen from cluster II of direct seeded or transplanted situation as per requirement. However, RAU 4045-2A from cluster II of direct seeding is the best choice in varietal improvement programme for both the management conditions because it has a wider genetic distance with RP 1670-6-36-14 under both the situations and formed a separate cluster in itself under transplanting.

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