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Genetic divergence in aromatic rice genotype based on quantitative character

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Abstract

The present investigation entitled “study of genetic divergence in aromatic rice genotype based on quantitative character” was carried out with the 47 genotypes which were grouped into five clusters for quantitative traits. In quantitative characters, there were fifteen genotypes in clusters I, five in cluster II, eleven in cluster III, nine in cluster IV and seven in cluster V. The maximum intra cluster distance was shown by cluster IV and maximum inter cluster distance was found between cluster II and cluster V. Selection of genetically diverse parent is important to get wide range of recombinants.

Keywords: Aromatic rice, genetic divergence, quantitative characters, cluster analysis

Introduction

The diversity in crop varieties is essential for agricultural development for increasing food production, poverty alleviation and promoting economic growth. The available diversity in the germplasm also serves as an insurance against known future needs and conditions, thereby contributing to the stability of farming system at national and global levels (Singh *et al.*, 2000) [5]. In crop improvement programme, genetic variability for agronomic traits as well as quality tests in almost all the crops is important, since this component is transmitted to the next generation (Singh *et al.*, 1996) [4]. Study of genetic divergence among the plant materials is a vital tool to the plant breeders for an efficient choice of parents for plant improvement. Genetically diverse parents are likely to contribute desirable segregants and/or to produce high heterotic crosses. For the assessment of variation on multivariate scale, Mahalanobis D² statistics has proved to be powerful technique (Murty and Arumachalam, 1966) [2].

Material and methods

The experiment was carried out at the Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India. The experiment was consisting of about 47 Aromatic genotypes of rice were selected for this study including 3 popular checks viz., Kalanamak, Badshahbhog and Indira Sugandhit Dhan-1 in a Randomized Block Design (RBD) with two replications. Each genotype was grown in on plot size was 5m X 2m with row to row distance was 20 cm and plant to plant distance was 15 cm. These genotypes were received from DRR Hyderabad. Five random plants from each of the plot were taken for recording data on various quantitative characters. The mean value was considered for statistical analysis, to assess distinctness, uniformity and stability.

The D² statistics was originally developed by P.C. Mahalanabis (1928). Rao *et al.* (1952) [1, 3] suggested the application of this technique for the assessment of genetic divergence between the populations. The D² between any two populations were estimated from the sample on the of P characters by the following formula

$$D^2 = \sum_{i=1}^p \sum_{j=1}^p (\Delta_{ij}) \Delta_i \Delta_j$$

Where,

Δ_{ij} = reciprocal matrix of (ijth) the pooled common dispersion matrix (*i.e.* error matrix)

Δ_i = difference in the mean value of ith character

Δ_j = difference in the mean value of jth character

Pooled error and error + variety variance and covariance matrix was obtained by adding the sums of squares for different characters and character pairs and dividing it by pooled degree

of freedom for error and error + variety. The D^2 with such transformed variables reduces to the evaluation of simple sums of squares. The actual value of D^2 between any two cultures based on different characters was then obtained. The genotypes were grouped into a number of clusters by Tocher's method as described by Rao *et al.* (1952) [3], after forming the clusters, intra and inter cluster distances were estimated. Square roots of the average D^2 values represented the distance between and within cluster.

Result and Discussion

In hybridization programme, selection of genetically diverse parent is important to get wide range of recombinants. The analysis of variance for quantitative characters is presented in table 1.

Analysis of variance for quantitative characters

The result of analysis of variance indicated that the mean sum of squares due to the genotypes were highly significant for the quantitative characters studied *i.e.* leaf length, leaf L/W ratio, days to 50% flowering, plant height, panicle length, number of effective tillers per plant, number of grains per panicle, number of filled grains per panicle, number of unfilled grains per panicle, spikelet sterility percentage, spikelet fertility percentage, 1000 seed weight and grain yield per plant.

Mean and Range

Mean performance and range of different quantitative characters recorded in different aromatic rice genotypes, have been described below. Mean performance and range of different quantitative characters is presented in table 2.

Leaf length (cm)

Leaf length ranged from 31.02 to 57.68 with a mean performance of 43.65cm. The maximum leaf length (57.68) recorded for HUR 1307 and minimum leaf length (31.02) was recorded for PAB 9527.

Leaf width (cm)

Leaf width ranged from 0.73 to 1.42, with a mean performance of 0.95cm. The maximum leaf width (1.42) recorded for Indira Sugandhit dhan-1 and minimum leaf width (0.95) was recorded for CN1643-3.

Leaf L/W ratio (cm)

Leaf L/W ratio ranged from 29.41 to 65.55 with a mean performance of 46.99cm. The maximum leaf L/W ratio (65.55) observed for CN1643-3 and minimum leaf L/W ratio (29.41) was observed for Indira Sugandhit Dhan-1.

Days to 50% flowering

Days to 50% flowering ranged from 76 to 125 days with a mean performance of 102 days. CR 2947-1-1-5 (125 days) recorded maximum days for 50% flowering, while CSAR 10210 required 76 days for 50% flowering.

Plant height (cm)

In experimental material plant height was ranged from 92.80 to 198.90 cm with a mean plant height of 126.15 cm. The maximum plant height was recorded in Kalanamak (RC) (198.90cm) and the minimum plant height (92.80cm) was observed in R1656-1146-5-513-1.

Panicle length (cm)

The range for panicle length varied from 20.80 cm to 33.70 cm with an overall mean of 25.56 cm. The highest panicle length was recorded in Kalanamak (33.70cm). However, the minimum panicle length was recorded in HUR-917 (20.80 cm).

Number of tillers per plant

A range of 5 to 10 tillers per plant was recorded with an average of 7.46 tillers. The maximum number of tillers per plant was possessed in Indira Sugandhit Dhan-1 (10). Minimum number of tillers (5) was recorded in NDR 9720.

Number of effective tillers per plant

The range for number of effective tillers per plant varied from 3 to 9 with an overall mean of 6.74. The highest effective tillers per plant was recorded in Indira Sugandhit Dhan-1 (9) and the minimum effective tillers per plant was recorded in NDR6357 (3).

Number of grains per panicle

A range of 98 to 331 grains per panicle were recorded with a mean of 177.9 grains per panicle. The maximum grains per panicle was possessed in PAB 9527 (331), however minimum number of grains per panicle was recorded in Indira Sugandhit Dhan-1 (98).

Number of filled grains per panicle

A range of 43 to 210 filled grains per panicle were recorded with a mean of 125.99 filled grains per panicle. The maximum filled grains was possessed in NDR 6330 (210), however minimum number of filled grains was recorded in CR 2938-6 (43).

Number of unfilled grains per panicle

A range of 16 to 176 unfilled grains per panicle was recorded with a mean of 52.02 unfilled grains per panicle. The maximum unfilled grains was possessed in PAB 9527(176), however minimum number of unfilled grains was recorded in Indira Sugandhit Dhan-1 (16).

Spikelet Sterility %

In experimental material spikelet sterility % was ranged from 8.69 to 66.44 with a mean spikelet sterility of 30.04 %. The maximum spikelet sterility % was recorded in CN 1646-1-9 (66.44), however minimum spikelet sterility % was recorded in NDR 6330 (8.69).

Spikelet Fertility %

In experimental material spikelet fertility % was ranged from 33.55 to 91.30 with a mean spikelet fertility of 69.95 %. The maximum spikelet fertility % was recorded in NDR 6330 (91.30), however minimum spikelet fertility % was recorded in CN1646-1-9 (33.55).

1000 seed weight (g)

1000 seed weight ranged from 9.40 to 26.55 g with an average weight of 17.96 g. The maximum 1000 seed weight recorded in CN 1268-5-7 (26.55 g) and the minimum 1000 seed weight was recorded in Badshahbhog (9.40 g).

Grain yield per plant (g)

The range for grain yield per plant varied from 6.70 to 36.50g with a mean value of 19.43g. The highest grain yield per plant

was recorded in TTBJ 2 (36.50g) and the minimum grain yield per plant was recorded in CSAR 10210 (6.70g).

Cluster analysis of quantitative characters

The clustering pattern of 47 genotypes on the basis of cluster analysis of quantitative characters has been presented in table 3. The 47 entries were grouped into 5 clusters. The highest number of genotype appears in cluster I which contain 15 genotypes viz., CR2713-35, CN1646-5-7, CR2947-1-1-5, CR2938-6, NDR6226, CRL74-89-2-4-2, CRL16-66-18-2-PR-1, Pusa1638-07-62-2-27, HUR1309, MGD1301, R1747-4941-1-515-1, R1656-1146-5-513-1, R1630-1237-2-827-1, BRR0001 and TTBJ2. The second largest grouped was cluster III which contain 11 genotypes viz., CR2713-179, CRL-74-89-2-4-1, NLR40054, CR2713-11, PNR546 (check), R-1521-950-6-843-1, CN-1268-5-7, CN-1646-11-9, R1536-136-1-77-1, CR2945-1-1-3 and NDR9718(IR72014-8-NDR-28-1-41-B-2). The cluster IV contain 09 genotype viz., CR2713-183, CSAR10210, CR2947, HUR-917, CR2939-3, NDR6357, Indira Sugandhit Dhan-1, BRR0002 and Dubraj whereas cluster V contain 07 genotype viz., NP6137, CN1643-3, CN1646-1-9, CR2939-5-16-2-4-3-1-1, Pusa1638-07-129-2-63, NDR9720(IR2014-8-NDR-28-1-14-B-6) and PAB9527. The smallest group was cluster II which contain 05 genotypes viz., Badshahbhog, NDR6330, Kalanamak, MGD1302 and HUR1307.

Intra and inter cluster distance based on D^2 distance of quantitative character have been presented in table 4. The

highest inter cluster distance was found between cluster II and cluster V (5.735) followed by cluster I and cluster II (4.655), cluster IV and cluster V (4.573), cluster III and cluster V (4.569), cluster II and cluster IV (3.986), cluster II and cluster III (3.573), cluster I and cluster III (3.419), cluster I and cluster IV (3.102), cluster I and cluster V (3.097) and the lowest cluster distance found in between cluster III and cluster IV (2.952). The highest intra cluster distance found between cluster IV (3.311) followed by cluster V (3.094), cluster III (3.017), cluster II (2.912) and lowest intra cluster distance found in cluster I (2.763).

Conclusion

The D^2 analysis indicates the presence of appreciable genetic diversity in the material. 47 aromatic genotypes were grouped into 5 clusters. The highest number of genotype was found in cluster I, III, IV, V and II had 15, 11, 09, 07 and 05, respectively. The maximum intra cluster distance was shown by cluster IV and maximum inter cluster distance was found between cluster II and cluster V.

The inter cluster distances for both quantitative character in present study were higher than the intra cluster distance in all cases reflecting wider diversity among the genotypes of distant grouped. Hence, it is suggested that inter crossing of genotypes from diverse cluster showing high mean performance will be helpful in obtaining better recombination with higher genetic variability.

Table 1: Analysis of variance (ANOVA) for different quantitative traits in rice

Source of Variation	Mean squares for the characters		
	Replication (df = 1)	Genotype (df = 46)	Error (df = 46)
Leaf length (cm)	0.125	63.43**	0.987
Leaf width (cm)	2.720	0.033	1.699
Leaf L/W ratio	9.015	120.2**	5.475
Days to 50% flowering	13.62	246.3**	7.911
Plant height (cm)	-0.250	1296**	14.40
Panicle length (cm)	3.257	17.90**	1.384
No. of tillers/plant	0.084	1.362	1.027
No. of effective tillers/plant	0.235	2.377**	0.812
No. of grains /panicle	1555	4663**	72.39
No. of filled grains/ panicle	757.8	4146**	34.56
No. of unfilled grains/panicle	151.2	1460**	95.56
Spikelet Sterility %	0.046	376.3**	19.14
Spikelet Fertility %	0.062	376.4**	19.19
1000 seed weight (gm)	5.261	32.32**	2.968
Grain yield/plant (gm)	11.03	59.68**	26.24

**Highly significant at 1% *Significant at 5%

Table 2: Genotypic and phenotypic coefficient of variance (GCV) and (PCV), heritability (h^2_{bs}) and GA as percentage of mean for quantitative characters

S. No.	Characters	Mean	Range		PCV (%)	GCV (%)	h^2_{bs} (%)	GA% mean
			Max.	Min.				
1	Leaf length (cm)	43.65	57.68	31.02	13.00	12.80	96.90	25.95
2	Leaf width (cm)	0.953	1.18	0.73	13.86	13.17	90.30	26.31
3	Leaf L/W ratio	46.99	65.55	35.53	16.87	16.12	91.30	31.73
4	Days to 50% flowering	102.0	124.5	75.50	11.05	10.70	93.80	21.34
5	Plant height (cm)	126.1	191.40	92.80	20.30	20.07	97.80	40.88
6	Panicle length (cm)	25.56	33.40	20.80	12.15	11.24	85.60	21.43
7	No. of tillers/plant	7.462	8.50	5.00	14.65	05.49	14.00	4.28
8	No. of effective tillers/plant	6.745	8.00	3.00	18.72	13.11	49.00	18.97
9	No. of grains /panicle	177.9	330.7	97.60	27.34	26.92	96.90	54.59
10	No. of filled grains/panicle	125.9	209.5	42.80	36.29	35.99	98.30	73.51
11	No. of unfilled grains/panicle	52.02	176.6	16.00	53.63	50.23	87.70	96.90
12	Spikelet Sterility %	30.04	66.4	8.690	46.80	44.48	90.30	87.08
13	Spikelet Fertility %	69.95	91.30	33.55	20.11	19.11	90.30	37.39

14	1000 seed weight (gm)	17.96	26.55	9.60	23.39	21.33	83.20	40.08
15	Grain yield/plant(gm)	19.43	36.50	6.70	33.72	21.03	38.90	27.02

Note: GCV: Genotypic coefficient of variance; PCV: Phenotypic coefficient of variance; $h^2_{(bs)}$: Heritability; GA%: Genetic advance as percentage of mean

Table 3: Cluster analysis of quantitative characters

Cluster	Number of entries	Entries numbers
I	15	CR2713-35, CN1646-5-7, CR2947-1-1-5, CR2938-6, NDR6226, CRL74-89-2-4-2, CRL16-66-18-2-PR-1, Pusa1638-07-62-2-27, HUR1309, MGD1301, R1747-4941-1-515-1, R1656-1146-5-513-1, R1630-1237-2-827-1, BRR0001, TTBJ2
II	05	Badshahbhog, NDR6330, Kalanamak, MGD1302, HUR1307
III	11	CR2713-179, CRL-74-89-2-4-1, NLR40054, CR2713-11, PNR546(check), R-1521-950-6-843-1, CN-1268-5-7, CN-1646-11-9, R1536-136-1-77-1, CR2945-1-1-3, NDR9718(IR72014-8-NDR-28-1-41-B-2)
IV	09	CR2713-183, CSAR10210, CR2947, HUR-917, CR2939-3, NDR6357, Indira Sugandhit Dhan-1, BRR0002, Dubraj
V	07	NP6137, CN1643-3, CN1646-1-9, CR2939-5-16-2-4-3-1-1, Pusa1638-07-129-2-63, NDR9720(IR2014-8-NDR-28-1-14-B-6), PAB9527

Table 4: Average Intra and Inter Cluster Distance Based on D^2 Distance of Quantitative character

Cluster	No. of genotype	I	II	III	IV	V
I	15	2.763				
II	05	4.655	2.912			
III	11	3.419	3.573	3.017		
IV	09	3.102	3.986	2.952	3.311	
V	07	3.097	5.735	4.569	4.573	3.094

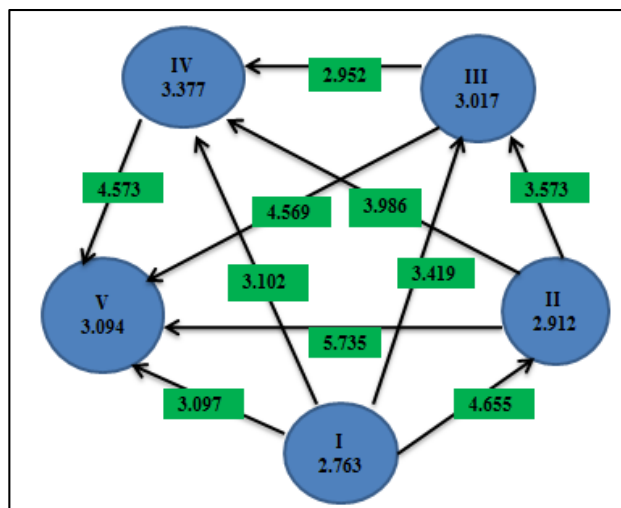


Fig 1: Cluster diagram of quantitative characters showing inter cluster distance and intra cluster distance between members

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