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Genetic Divergence of Aromatic Rice Genotype

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Abstract **: The present investigation entitled "Genetic divergence of aromatic rice genotype" was carried out in the Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur (C.G.) during 2013. In the present study the 47 genotypes were grouped into five clusters for both quantitative and quality characters. 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. On the basis of quality characters, 47 aromatic rice genotypes have again grouped into 5 clusters. The highest number of genotypes was found in cluster II, I, IV, III and V had 13, 12, 10, 06 and 06, respectively. The maximum intra cluster distance was shown by cluster II and maximum inter cluster distance was found between cluster II and cluster III.**

Key words: 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).

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, 1996). 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 sergeants and/or to produce high heterotic crosses. For the assessment of variation on multivariate scale, Mahalanobis D^2 statistics has proved to be powerful technique (Murty and Arumachalam, 1966).

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 during 2013. 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 Hydrabad.

Five random plants from each of the plot were taken for recording data on various quantitative and quality characters. The mean value was considered for statistical analysis**,** to assess distinctness, uniformity and stability.

The D^2 statistics was originally developed by P.C. Mahalanabis (1928). Rao (1952) suggested the application of this technique for the assessment of genetic divergence between the populations. The D^2 between any two populations were estimated from the sample on the of P characters by the following formula

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

Where,

1. Δ_{ij} = reciprocal matrix of (ij) the pooled common dispersion matrix
   (i.e. error matrix)
2. Δ_i = difference in the mean value of i^{th} character
3. Δ_j = difference in the mean value of j^{th} 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). 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.

(A) 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 1.

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 2

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).

(B) Cluster analysis of quality characters:

The clustering pattern of 47 genotypes on the basis of cluster analysis of quality characters has been presented in table 3

The 47 entries were grouped into 5 clusters. The highest number of genotypes appears in cluster II, which contain 13 genotype *viz.*, CN-1646-11-9, NP6137, CN1643-3, CN1646-1-9, CN1646-5-7, CR2947-1-1-5, CR2945-1-1-3, CR2939-3, CR2939-5-16-2-4-3-1-1, CR2938-6, NDR6226, HUR1309 and R 1747-4941-1-515-1. The second largest group was cluster I which contain 12 genotypes *viz.*, CRL-74-89-2-4-1, NLR40054, CR2713-183, CSAR10210, CR2947, NDR6330, CR2713-11, PNR 546 (check), CN-1268-5-7, Kalanamak, R1536-136-1-77-1 and Pusa1638-07-129-2-63. The third largest cluster IV contains 10 genotypes *viz.*, HUR-917, NDR6357, CRL74-89-2-4-2, CRL16-66-18-2-PR-1, Pusa1638-07-62-2-27, MGD1301, R1630-1237-2-827-1, BRR0001, BRR0002 and HUR1307. The cluster III contain 06 genotypes *viz.*, CR2713-35, Badshahbhog, CR2713-179, R-1521-950-6-843-1, MGD1302, PAB9527 and cluster V also contain 06 genotypes *viz.*, Indira Sugandhit Dhan-1, NDR9718 (IR72014-8-NDR-28-1-41-B-2), NDR9720 (IR2014-8-NDR-28-1-14-B-6), R1656-1146-5-513-1, TTBJ2 and Dubraj.

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

The highest inter cluster distance found between cluster II and cluster III (6.843) followed by cluster III and cluster V (6.202), cluster I and cluster V (5.317), cluster I and cluster II (5.048), cluster II and cluster V (4.536), cluster III and cluster IV (4.514), cluster I and cluster III (4.016), cluster II and cluster IV (3.749), cluster IV and cluster V (3.748), and the lowest cluster distance found in between cluster I and cluster IV (3.129). The highest intra cluster distance found between cluster II (2.771) followed by cluster III (2.570), cluster I (2.502), cluster IV (2.466) and lowest intra cluster distance found in cluster V (2.037). The intra cluster distances were low almost all clusters, indicating that the homogenous nature of the genotypes belonging to these clusters. Hence, it suggested that intercrossing of genotypes from diverse clusters showing high mean performance will be helpful in obtaining better recombinants with higher genetic variability.

Table 1. Cluster analysis of quantitative character.

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 2. 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

Table 3. Cluster Analysis of Quality Characters.

Cluster	Number of entries	Entries numbers
I	12	CRL-74-89-2-4-1, NLR40054, CR2713-183, CSAR10210, CR2947, NDR6330, CR2713-11, PNR546(check), CN-1268-5-7, Kalanamak, R1536-136-1-77-1, Pusa1638-07-129-2-63
II	13	CN-1646-11-9, NP6137, CN1643-3, CN1646-1-9, CN1646-5-7 , CR2947-1-1-5, CR2945-1-1-3, CR2939-3, CR2939-5-16-2-4-3-1-1, CR2938-6, NDR6226, HUR1309, R1747-4941-1-515-1
III	06	CR2713-35, Badshahbhog, CR2713-179, R-1521-950-6-843-1, MGD1302, PAB9527
IV	10	HUR-917, NDR6357, CRL74-89-2-4-2, CRL16-66-18-2-PR-1, Pusa1638-07-62-2-27, MGD1301, R1630-1237-2-827-1, BRR0001, BRR0002, HUR1307
V	06	Indira Sugandhit Dhan-1, NDR9718 (IR72014-8-NDR-28-1-41-B-2), NDR9720 (IR2014-8-NDR-28-1-14-B-6, R1656-1146-5-513-1, TTBJ2, Dubraj

Table 4: Intra and Inter Cluster Distance Based on D^2 Distance of Quality Character

Cluster	No. of genotypes	I	II	III	IV	V
I	12	2.502				

II	13	5.048	2.771			
III	6	4.016	6.843	2.57		
IV	10	3.192	3.749	4.514	2.466	
V	6	5.317	4.536	6.202	3.748	2.037

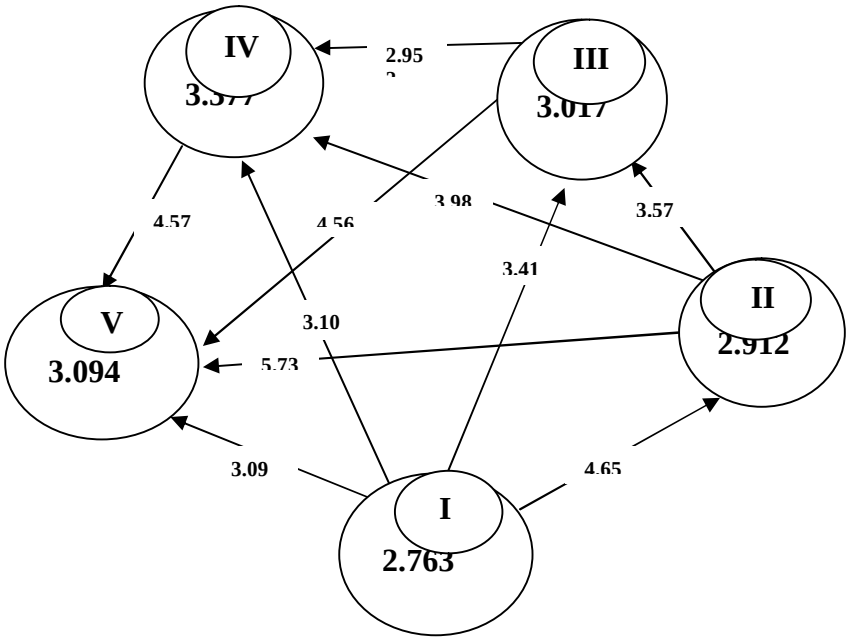

Figure 1. Cluster analysis of quantitative characters

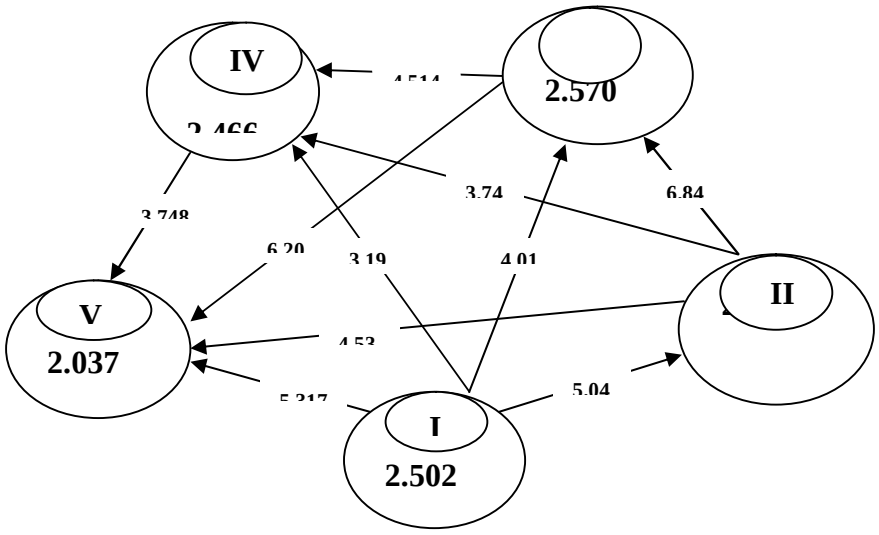

Figure 2. Cluster analysis of quality characters

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. On the basis of quality characters, 47 aromatic rice genotypes were grouped into 5 clusters. The highest number of genotypes was found in cluster II, I, IV, III and V had 13, 12, 10, 06 and 06, respectively. The maximum intra cluster distance was shown by cluster II and maximum inter cluster distance was found between cluster II and cluster III. The inter cluster distances for both quantitative and quality 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.

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