Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

Krishna Tandekar
Departement of Plant Breeding
and Genetics Indira Gandhi
Krishi Vishwavidyalaya, Raipur,
Chhattisgarh, India

Sandeep Bhandarkar
Departement of Plant Breeding
and Genetics Indira Gandhi
Krishi Vishwavidyalaya, Raipur,
Chhattisgarh, India

AK Sarawgi
Departement of Plant Breeding
and Genetics Indira Gandhi
Krishi Vishwavidyalaya, Raipur,
Chhattisgarh, India

Genetic divergence studies for yeild and its components in rice (*oryza sativa* l.) accession

Krishna Tandekar, Sandeep Bhandarkar and AK Sarawgi

Abstract
The hundred genotypes of rice accession were used to study the nature and magnitude of genetic divergence Mahalonobis D^2 statistics. The genotypes were grouped in to 10 cluster showing fair degree of relationship between agro-morphological variation and genetic divergence. The higher inter cluster distance was in between cluster II and cluster V followed by cluster VII and cluster I, cluster IX and cluster II and cluster III and cluster II. The lowest inter cluster distance was found between cluster III and cluster I. Thus, in the present study the better genotype were identified in respect to most of the characters on the basis of mean performance in the cluster. The inter cluster distances in the present study were higher than the intra cluster distances in all cases reflecting wider diversity among the genotypes of the distant group. The best genotypes in the present study for seed yield per plant are Veerhuli, Jaldubi and Lohandi and for harvest index the superior genotype are Kaveri, Kansari and I.T.

Keywords: Genetic divergence, D^2 statistics, clustering pattern, rice germplasm

1. Introduction
Rice (*Oryza sativa* L.) is one of the staple cereal crops of the world and it is one of the main sources of carbohydrate for nearly one half of the world population. In India 43 million hectares of total geographical area was cropped with rice but the production is very low due to the low productivity of rice in major rice growing areas of eastern region. The major constraint is lack of suitable varieties for this fragile ecosystem. The development of stable rice varieties for this fragile ecosystem should be the major thrust in present situation. Genetic diversity is one of the key factors in tailoring the effective breeding program in any crop plant. The estimate of genetic divergence in the available germplasm is important for the selection of desirable donors for breeding program. The information on genetic divergence of available genotypes will be helpful in planning hybridization program for evolving superior varieties; hence the studies on genetic divergence of rice genotype were undertaken.

2. Materials and Methods
The experiment materials consisting of 97 indegenous rice germplasm accession with three checks. These accession were collected from different regions/parts of chhattisgargh were grown in a randomized block design with two replication at research farm of Department of plant breeding and genetics IGKVV, Raipur. Detailed observations were recorded on five randomly selected plants from each genotype for days to 50% flowering, plant height, panicle length and numbers of tillers. The data on twelve characters were analyzed utilizing Mahalonobis generalized distance (D^2) to measure the genetic divergence among the test varieties and their grouping into different clusters was done by the Tocher's Method (Rao,1952)

3. Results and Discussions
The analysis of variance shows highly significant differences among the genotypes for all 12 characters studied (Table 1). The result indicated that high variances for most of the characters, which may favors selection and further utilization in future recombination breeding program. Using Tocher's method, hundred genotypes within the cluster had smaller D^2 values among themselves (Table 2). The pattern of distribution of genotype in various cluster revealed that there was considerable genetic variability within the genotypes under studies.
The hundred rice genotypes were grouped into ten clusters. Cluster III was the biggest cluster consisted of seventeen genotypes followed by cluster I containing fifteen genotypes. Fourteen in cluster VIII and IX, nine in cluster V and VII, four in cluster VI and the minimum number of two genotypes in cluster II respectively. The maximum divergence was observed in cluster III it is reported that genotypes within the cluster with high degree of divergence would

Correspondence
Krishna Tandekar
Departement Of Plant Breeding
And Genetics Indira Gandhi
Krishi Vishwavidyalaya, Raipur,
Chhattisgarh, India

produce more desirable breeding materials for achieving maximum genetic advance. Genotypes belonging to clusters separated by high genetic distance may be used in hybridization programme to obtain a wide spectrum of variation of among the segregates (Bhatt,1970) Therefore emphasis should be given on the members of cluster III for selection of parents for hybridization program.

The cluster mean for various traits of different cluster showed maximum and minimum value for different traits (Table-2). Cluster II showed highest mean performance for plant height, number of filled spikelets and number of total spikelets. Cluster VI expressed highest mean value for days to 50 percent flowering and number of unfilled spikelets, cluster IV showed highest mean value for panicle length and seed yield per plant. Cluster VIII and Cluster III showed highest mean for harvest index. (Table-5)

The contribution of all characters to the genetic divergence is presented in Table -3. The contribution towards total divergence was highest for days to 50 percent flowering (34.11%) followed by hundred seed weight (23.8%), plant height (23.40%). The contribution to total divergence was highest of days to 50 percent flowering and plant height, which is in accordance to the findings of Garg et al.(2011) while hundred grains weight is also contributor to genetic divergence which is similar to the finding of Kandamoorthy and Govindarasu (2005). In spite of low contribution towards total divergence was also shown by number of filled spikelet (8.88 %), harvest index (5.36%) and number of unfilled spikelets (4.45%).

The inter and intra cluster distance for all the traits represented by D^2 values have been presented in table 4. The highest inter cluster distance was in between cluster II and cluster V (8.370) followed by cluster VII and cluster I (8.360), cluster IX and cluster II (7.705) and cluster III and cluster II (6.873), whereas the lowest inter cluster distance was found between cluster III and cluster I (2.165). The inter cluster distances in the present study were higher than the intra cluster distances in all cases reflecting wider diversity among the genotypes of the distant group. The result was agreed with the finding of Hosan et al. (2010). The intra cluster distance varied from 1.284 to 2.652. The maximum intra cluster distance was shown by cluster VI having 4 genotype namely Lohandi (44), Gangtaichur(52), Lalat(60) and Swarna (100).

The intra cluster distance were low for all ten cluster with the range of 1.284 in cluster II and 2.652 in cluster VI that indicated the homogenous nature of the genotypes within the clusters. Clusters distance varied from 1.284 to 2.652. The maximum intra cluster distance was shown by cluster VI having 4 genotype namely Lohandi (44), Gangtaichur(52), Lalat(60) and Swarna (100).The intra cluster distance were low for all ten cluster with the range of 1.284 in cluster II and 2.652 in cluster VI that indicated the homogenous nature of the genotypes within the clusters..

Hence it can be concluded that the best genotypes in the present study for seed yield per plant are Veerhuli(23), Jaldubi(49) and Lohandi(75) and for harvest index the superior genotypes are Kaveri(73), Kansari(21) and I.T.(72) (Table-5). These varieties, which come from widely separated cluster are usually presumed to be diverse and can be utilized in hybridization program.

Genotype belonging to clusters separated by high genetic distance may be used in hybridization program to obtain a wide spectrum of variation of among the segregates (Bhat, 1970)

So, greater emphasis should be given to the above mentioned characters during the selection of cluster and parents for the hybridization program.

In present investigation diversity existed both within and between clusters. So, for yield potential and other characteristics, it is suggested that the hybridization might be carried out among the distantly related parents belonging to cluster II and V, cluster VII and I to obtain good sergeants in succeeding generations. The major divergence imparting characters like panicle length, indicated their importance during the selection of parents in crossing programme as well as selection of segregates in succeeding generations.

Table 1: Clustering pattern of 100 rice genotypes on the basis of Mahalanobis D^2 statistics

Cluster Number	Number of genotypes	Genotypes name
I	15	Teen pakhiyan dahi (7), Alsanga (14), Goda dani (15), Chingar chinga (16), Kariya (17), Bhuri dahi (18), Sikki (24), Shakar Chini(31), Surujot (39), Chhindmouri (59), Tendumudi (61), Birhuli (64), Bansbuta (80), Rajga (83), Ganga Prasad (95)
II	2	Jeeraphool (47), Jeeraphool (97).
III	17	Sikar (4), Sariya bhaya (10), Bala (22), Dhawari (29), Nunga (37), Raichuni (40), Chhinmouri (42), Baiku (46), Jhingi Paras (50), Dhouri (58), Ratuwa (77), Rathuwa (82), Kansari (87), Narpati (88), Nunga (89), Kalam (90), Barhi (93).
IV	6	Veerhuli (23), Nago (26), Bilai lungi (38), Jaldubi (49), Lahondi (75) and Bako (94).
V	9	Karhani (3), Jani jane (28), Sarya (34), Karhani (55), Jejne (56), Karhani (63), Kalinga (74), Karhani (84) and Karhani (86).
VI	4	Lohandi (44), Gargtaichur (52), Lalat (60) and Swarna (100).
VII	9	Goda dani (11), Dani goda (13), Kansari (21), Saina goda (27), Rajga (36), Goda dhan (67), Tharra lal (70), I.T. (72), Kaveri.Cluster (73).
VIII	14	Bhaya(9), Chirpoti(33), Lusari(41), Kheerasar(43), Gumarya (45), Churlai (51), Kansari (53), Birhuli (54), Khirasar (66), Bisunbhog (78), Bhatha phool (79), Birhuliya (81), Gurmariya (91), MTU 1010 (98).
IX	14	Sathiya (2), Baladani (6), Malchi dahi (8), Pode (12), Lalat (20), Nando (25), Jajne (57), Goda dhan (62), Kala-tharra (71), Sanchuriya (85), Laldhan (30), Newari (32), Sacachar (5) and Poornima (99).
X	10	Laldhan (1), Harad guhi dahi (5), Sindur Chinga (19), Jhingi (48), Bisunbhog (65), Lohandi (76), Bhulo (92), Baljer (63), Batasi (69) and Chhind Mouri (96).

Table 2: Cluster mean group for quantitative characters in rice germplasm

Characters / Clusters	Days to 50 per cent flowering	Plant height	Panicle length	No. of tillers	No. of filled spikelets	No. of unfilled spikelets	No. of Total spikelets	Hundred seed wt.	Biological yield per plant	Harvest index	Seed yield per plant
I	77.30	135.75	25.37	5.96	121.84	14.51	134.93	2.50	25.40	43.51	10.80
II	88.00	152.20	28.48	7.20	187.35	65.15	252.50	1.05	25.88	33.92	8.62
III	79.15	139.93	25.07	5.65	138.51	17.00	154.89	2.52	27.46	52.76	14.50
IV	80.67	151.34	29.88	5.58	173.55	27.37	202.58	2.08	29.35	53.10	15.57
V	70.33	112.73	21.52	8.56	75.22	11.58	86.80	2.16	19.57	49.58	9.69
VI	91.12	107.64	22.28	6.75	128.46	66.49	190.27	2.05	28.76	50.12	14.28
VII	78.50	117.68	23.63	7.88	94.58	11.76	106.33	2.48	26.24	57.92	15.17
VIII	82.14	139.84	26.14	7.63	148.63	24.23	172.86	1.88	30.35	48.96	14.54
IX	75.71	111.24	23.62	6.60	98.29	16.80	115.83	2.33	19.66	54.60	10.70
X	80.15	129.32	25.12	5.74	170.08	37.37	207.39	1.81	23.05	52.35	12.62

Table 3: Contribution of each character to Genetic divergence

Characters	Number of times appearing first Ranking	Percent contribution
Days to 50% flowering	1271	34.11
Plant height	872	23.40
Number of filled spikelets	331	8.88
Number of unfilled spikelets	166	4.45
Hundred seed weight	887	23.80
Harvest index	200	5.36
Total	3727	100.00

Table 4.10: Intra and inter cluster distances based on D^2 statistics

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	1.812									
II	6.412	1.284								
III	2.165	6.873	1.584							
IV	4.013	5.683	2.775	2.179						
V	3.751	8.370	4.734	6.785	1.864					
VI	5.149	5.838	4.638	5.204	6.246	2.652				
VII	3.460	8.360	2.783	4.915	3.382	4.997	1.888			
VIII	3.093	5.338	2.382	2.518	5.127	4.065	3.543	2.083		
IX	2.769	7.705	3.213	5.306	2.323	5.122	2.591	4.250	1.951	
X	3.464	4.927	2.896	2.974	5.265	3.664	4.408	2.641	3.770	**2.321**

Note: Bold figures are intra cluster distance

Table 5: Desirable genotypes for the important traits

Characters	I	II	III
Number of tillers	Karhani (55)	Karhani (63)	Kalinga (74)
Number of filled spikelets	Jeeraphool (47)	Jeeraphool (97)	-
Hundred seed weight	Barhi (93)	Bala (22)	Nunga (37)
Harvest index	Kaveri (73)	Kansari (21)	I.T. (72)
Seed yield per plant	Veerhuli (23)	Jaldubi (49)	Lahondi (75)
Panicle length	Lahondi (75)	Jaldubi (49)	Bilai Lungi (58)

4. References

1. Bhatt GM. Multivariate analysis approach to selection of parents for hybridization aiming at yield improvement in self-pollinated crops. Aust. J Res Agric. 1970; 4:1-7.
2. Garg P, Pandey DP, Kaushik RP. Genetic divergence for yield and quality traits in Rice (Oryza sativa L.) Journal of Rice Research. 2011; 4(1, 2).
3. Hosan SM, Sultana Nasir, Iftekharudduala KM. Nasarddin A, Mia S. Genetic divergence in landraces of Bangladesh Rice (*Oryza Sativa* L.) The Agriculturist. 2010; 8(2):28-34.
4. Kandamoorthy S, Govindarasu R. Genetic divergence in extra early rice (*Oryza sativa* L.) under two culture systems. Indian Genet. 2005; 65(1):43-44.
5. Mahalanobis PC. On the generalized distance in statistics. Proc. National Inst. Sci. 1936, 49-55.
6. Rao CR. Advanced statistical methods in biometrical research. John Willey and Sons, Inc. New York, 1952.