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Genetic divergence in exotic rice genotypes

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ABSTRACT

One hundred and twenty five exotic rice genotypes were assessed for the nature and magnitude of genetic divergence based on 17 quantitative traits following Mahalanobis's D^2 Statistics. Their grouping was done into different clusters following Tocher's method as described by Rao (13). The grouping showed 4 multi-genotypic and 9 mono-genotypic clusters. Cluster IV showed maximum intra-cluster D^2 value of (D^2 = 291.384) followed by Cluster XII, II and I while the inter-cluster value was maximum between Cluster VII and XI (D^2 = 3858.894). Cluster I was the largest consisting of ninety-two genotypes. The characters biological yield per plant contributed maximum towards genetic divergence followed by 1000 grain weight, plant height, panicle index, number of filled grains per panicle and days to 50 % flowering. The clustering pattern revealed that the genotypes from different sources clustered together indicating that there was no association between eco-geographical distribution of genotypes and genetic divergence.

Key words: Cluster means, D^2 analysis, genetic divergence, morphological characters, rice

Rice (*Oryza sativa* L.) is one of the most important cereals and is the main food crop to the lives of billions of people around the world as world rice consumption increased 40 percent in the last 30 years, from 61.5 kg per capita to about 85.9 kg per capita in terms of milled rice (Source: www.unctad.org). It is considered as one of the oldest domesticated grains.

The genus *Oryza* probably originated in the humid regions of the Gondwanaland supercontinents by Chang (1976). In order to feed the growing population ventures are being made in all the rice growing areas to augment the yield per hectare but the success of hybridization and there after selection of desirable segregants depends largely on the selection of parents with high genetic variability for different characters. The diversity in crop varieties is considered as a significant parameter for increasing food production, in mitigating poverty and promoting economic growth overall contributing to the development of agriculture. It serves as an insurance against unknown future needs and conditions thereby contributing to the stability of farming systems at local, national and global levels by Singh *et al.* (2000). 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. Parents identified on the basis of divergence for any breeding program would be more promising.

Grouping or classification of genotypes based on suitable scale is quite imperative to understand the usable variability existing among them. For the assessment of variation on multivariate scale, Mahalanobis's D^2-statistic has proved to be a powerful technique (Mahalanobis, 1936). Genetic variability for agronomic traits as well as quality traits in almost all the crops is important, since this component is transmitted to next generation. Hence, the present investigation was carried out on 125 exotic rice genotypes obtained from IRRI, Philippines to ascertain the value and magnitude of genetic diversity and to select suitable genotypes for further utilization in hybridization programme.

MATERIALS AND METHODS

The experiment was carried out with 39 aromatic/fine grain and 84 non-aromatic lines/materials obtained from IRRI, Philippines under INGER (International Network on Genetic Evaluation of Rice) Project along with two local checks grown in randomized complete block design with three replications at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, J.N. Agricultural University, Jabalpur (M.P.).

The experimental area occupied was quite uniform in respect of topography and fertility. Twenty-one day old seedlings were transplanted in the experimental site. Each genotype was planted in three rows of five meter length and a row to row spacing of 20 cm. was maintained with one seedling per hill. Gap filling was done within a week in order to obtain uniform plant population. Fertilizer dose of 120 kg N, 60 kg P_2O_5, and 60 kg K_2O was applied. Entire dose of P_2O_5 and K_2O along with half dose of N was applied as basal dose at the time of final field preparation, remaining amount of nitrogen was splitted in two equal splits and were applied at the time of active filling stages. The standard agronomic practices were adopted for normal crop growth.

Five competitive plants from each plot (including checks) were randomly selected and tagged for recording various quantitative characters. For the study of the character, days to 50 % flowering, the observations were recorded on plot basis under study. Observations were recorded for all the 17 quantitative characters *viz.*, plant height (cm), panicle length (cm), panicle weight per plant (g), number of tillers per plant, number of filled and unfilled grains per panicle,

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spikelet fertility and spikelet sterility %, number of grains per panicle, days to 50 % flowering, 1000 grain weight (g), spikelet density, biological yield per plant (g), grain yield per plant (g), harvest index and panicle index. The data from the present investigation was used to estimate genetic divergence among 125 genotypes using Mahalanobis's D^2 analysis and then grouping of genotypes into clusters was carried out following Tocher's method. Mean values of variables, calculated based on measurements on plants for each genotype, were used in the cluster analysis.

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for most of the characters indicating the existence of high genetic variability among the genotypes (Table 1). The analysis was done using INDOSTAT software.

On the basis of D^2 values, the 125 genotypes were grouped into 13 clusters following Tocher's method. Grouping of genotypes showed 4 multi-genotypic and 9 mono-genotypic clusters. The average intra and inter-cluster D^2 values estimated as per the procedure given by Singh and Choudhary (19). Cluster IV showed maximum intra-cluster D^2 value of (D^2 = 291.384) followed by Cluster XII (D^2 = 271.920), Cluster II (D^2 = 194.602) and Cluster I (D^2 = 189.612). Cluster III, V, VI, VII, VIII, IX, X, XII and XIII were mono-genotypic clusters consisting of one genotype each (Table 2). The inter-cluster D^2 value was minimum between Clusters V and VI (D^2 = 91.011) while it was maximum between Cluster VII and XI (D^2 = 3858.894) (Table 3 & 4). Cluster I was the largest cluster consisting of ninety-two genotypes. It was nearest to Cluster III (D^2 = 358.723) followed by Cluster VII (D^2 = 370.562). Cluster II comprised of seventeen genotypes, being nearest to Cluster VII (D^2 = 492.84) and VIII (D^2 = 594.38). Cluster II recorded the highest cluster mean value for panicle weight per plant and number of effective tillers per plant.

Cluster III was a mono-genotypic cluster comprising of only one genotype (IR 79201-49-1-1-1). It was nearest to Cluster IX (D^2 = 244.296) and IV (D^2 = 247.747). Cluster III recorded the highest cluster mean value for harvest index. It was distantly placed to Cluster II. Cluster IV comprised of five genotypes. It recorded the lowest mean value for panicle weight per plant, biological yield per plant and highest value for panicle index. It was distantly placed to Cluster II. Cluster V comprised of only one genotype namely, PSB RC2 (IR 32809-26-3-3). It was nearest to Cluster VI (91.011) and recorded the highest cluster mean value for grain yield per plant. It was distantly placed to Cluster II and IV. Cluster VI comprised of only one genotype (HO13-5-3-B4). Lowest value of cluster mean for number of effective tillers per plant was observed for this cluster.

Table 1: Analysis of variance for 17 characters in 125 exotic rice genotypes (Mean sum of square)

Characters	Sources of variation		
	Replication (2)	Genotypes (124)	Error (248)
Plant height (cm)	14.862	407.333*	3.425
Panicle length (cm)	0.518	19.868*	1.549
Panicle weight per plant (g)	72.930	413.288*	17.769
Number of tillers per plant	5.768	28.745*	2.501
Number of effective tillers per plant	14.242	20.399*	1.567
Number of filled grains per panicle	93.842	2861.070*	53.958
Number of unfilled grains per panicle	31.178	421.086*	18.600
Number of grains per panicle	232.978	3694.525*	72.752
Days to 50 % flowering	45.066	122.070*	2.284
1000 grain weight (g)	0.185	41.419*	0.072
Spikelet density	0.227	5.670*	0.203
Biological yield per plant (g)	1.205	2983.564*	6.762
Grain yield per plant (g)	260.932	517.630*	24.357
Harvest index	0.018	0.076	0.002
Panicle index	0.049	1.387*	0.266
Spikelet fertility %	4.103	98.470*	6.857
Spikelet sterility %	2.826	108.661*	22.283

** Significant at 5 % level probability*

Table 2: Distribution of rice genotypes in different clusters

Cluster	Number of genotypes	Genotypes
1.	92	IR 81168-31-2-3-2, IR 81328-74-2-2-2, IR 77533-29-2-2-2, IR 73718-26-1-2-5, IR 79525-20-2-2-2, KALIMAS, IR 79597-56-1-2-1, IR 78585-64-2-4-3, IR 79254-86-2-3-1, IR 79216-141-1-3-3, IR 74052-153-5-3-1-3, IR 77298-14-1-2, IR 81346-22-1-1-1, IR 80897-20-1-2-2, WAS 197-B-4-1-22, IR 81178-29-2-3-2, IR 77512-2-1-2-2, IR 81309-67-3-2-3, IR 74642-198-1-3-2, PEPE, IR 79504-5-3-3-2, IR 77734-93-2-3-2, IR 79203-105-1-1-3, IR 80894-66-3-2-3, IR 79247-107-1-2-1, IR 79216-141-1-3-3, IR 77498-47-2-6-2-3, IR 80705-36-1-3-3, IR 73007-44-1-2-3, IR 74288-153-5-1-1-3, IR 79246-47-1-3-3, IR 80290-74-1-5-6-3, PSB RC64(IR59552-21-3-2-2), IR 78566-1-2-1-2, IR 79200-65-2-2-1, IR 74646-96-2-3-3, IR 77495-10-2-6-2, IR 81873-31-2-2-2, M1-10-29 UL, MARO, IR 80376-51-2-2-1, IR 80375-13-3-3, IR 60080-46A, IR 79511-47-2-6-3, IR 81310-25-3-2-2, IR 79585-61-2-3-3, WAS 197-B-6-3-4, IR 79504-48-1-6-2, IR 79643-23-3-3-3, WAB 515-B-10 A 1-4, IR 79195-115-2-2-3, HO14-1-1-B2, WAS 169-B-B-4-2-9, IR79242-28-3-2-3, WAS 197-B-6-3-2, IR 80376-36-2-2-1,TOX3867-19-1-2-3-3, CIASEM, IR 80919-57-2-2-1, IR 78537-32-1-2-1, WAS 197-B-4-1-25, TOX 3226-5-2-2-2-2, IR 79228-9-2-3-1, IR 79228-67-1-1-3, IR 80658-67-2-1-2, IR 79538-1-1-1-1, IR 81166-150-2-1-3, IR 79505-51-2-2-2, IR 79201-49-1-1-1, IR 80894-8-1-1-3, IR 79254-48-2-1-1, IR 75299-94-1-2-2, IR 72164-348-6-2-2-2, IR 79246-103-2-2-4, IR 79532-21-2-2-1, IR 78126-1-2-1, IR-36, IR-74, IR 77629-72-2-1-3, IR 80707-69-1-3-3, IR-80395-97-3-3-2, IR 80901-32-3-3-2, IR 81174-83-2-1-3, IR 75287-19-3-3-3, IR78006-55-2-3-3, IR 76494-28-1-2-2, IR 79233-28-2-1-2, IR 79515-25-1-6-1, WAS 198-B-B-2, IR 72890-81-3-2-2, BATANG LEMBANG
2.	17	IR 79226-98-1-1-3, IR 80285-34-3-3-2, WAS 197-B-5-2-5, 88023-RE, WAS 197-B-5-2-16, Local Check JR-201, IR 78554-145-1-3-2, IR 77140-24--2-1-2, IR 77721-93-2-2-1, CT9882-16-4-2-3-2P-M, PSB RC18(IR51672-62-2-1-1-2-3), IR-72, IR 73546-66-1-1-1, IR-50,WAS 169-B-B-4-2-7, IR 80904-50-3-1-3, WITA 7(TOX 3440-171-1-1-1-1
3.	01	IR 79201-49-1-1-1
4.	05	CIAPUS, IR 79204-84-2-2-3, WAB 337-B-B-15-H1, IR 77736-54-3-1-2, IR 81172-140-1-3-2
5.	01	PSB RC2(IR 32809-26-3-3)
6.	01	HO13-5-3-B4
7.	01	IR 64
8.	01	WAS 197-B-6-3-16
9.	01	IR 79327-9-3-3-1
10.	01	IRYN 1068-7-1
11.	02	WAS 197-B-6-3-12, WAB 99-84
12.	01	WAB 272-B-B-5-H5
13.	01	BASMATI 370

It was distantly placed to Cluster IV, II, I. Cluster VII comprised of one genotype (IR-64). It recorded the lowest cluster mean value for plant height, number of unfilled grains per panicle and days to 50 % flowering. It was distantly placed to Clusters IV, III and VI. One genotype was occupied by Cluster VIII (WAS 197-B-6-3-16) and recorded the lowest cluster mean value for 1000 grain weight, grain yield per plant, harvest index, panicle index and placed distantly to V, III and VI. Cluster IX comprised of one genotype (IR 79327-I9-3-3-1). It recorded the highest cluster mean value for panicle length, spikelet sterility % and lowest for number of filled grains per panicle, number of grains per panicle, spikelet density and spikelet fertility %. It was distantly placed to VIII, II and VI. Cluster X was a mono-genotypic cluster. It recorded the highest cluster mean value for number of tillers per plant, number of filled grains per panicle, number of grains per panicle, days to 50 % flowering and spikelet density and placed away from Clusters IX, VI, V. Cluster XI consisted of two genotypes (WAS 197-B-6-3-12, WAB 99-84); it was nearest to Cluster XII (1582.448) and distantly placed to Cluster VII, X, II and recorded the highest cluster mean value for 1000 grain weight. Cluster XII (WAB 272-B-B-5-H5) and XIII (BASMATI 370) comprised of one genotype each. Cluster XII recorded the highest cluster mean value for number of unfilled grains per panicle and biological yield per plant and lowest cluster mean value for panicle length and number of tillers per plant and distantly placed to Clusters X, IV and VIII. Cluster XIII recorded highest value of cluster mean for panicle length, spikelet fertility % and lowest for spikelet sterility % and distantly placed to Clusters XI, XII and IX.

All the characters contributed to genetic divergence except number of grains per panicle and spikelet sterility %. The character biological yield per plant contributed maximum to genetic divergence (42.45%) followed by 1000 grain weight (36.15%), plant height (6.76%), panicle index (4.76%), number of filled grains panicle (3.97%), days to 50 % flowering (3.60%) and number of sterile grains panicle^{-1} (1.20%) whereas, magnitude of genetic divergence was <1% for number of tillers per plant, panicle weight per plant, spikelet density, panicle length, grain yield per plant, harvest index, number of effective tillers per plant and spikelet fertility % (Table 5). The results of analysis of variance indicated high variance for most of the characters, which may favour selection and further utilization in future recombination breeding programmes.

Table 3: Inter-cluster and intra-cluster average divergence $\sqrt{D}^{2}$ and D^2 values

	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**
1	**13.77** **(189.61)**	25.52 (651.27)	18.94 (358.72)	20.72 429.32)	22.58 (509.86)	22.05 (486.20)	19.25 (370.56)	24.85 (617.52)	26.20 (686.44)	22.99 (528.54)	42.02 (1765.68)	33.07 (1093.62)	26.44 (699.07)
2		**13.95** **(194.60)**	35.86 (1285.93)	38.35 (1470.72)	25.33 (641.61)	25.43 (646.68)	22.20 (492.84)	24.38 (594.38)	38.33 (1469.18)	32.46 (1053.65)	51.75 (2678.06)	23.95 (573.60)	35.89 (1288.09)
3			**0.00** **(0.00)**	15.74 (247.75)	21.59 (466.13)	21.54 (463.97)	26.26 (689.59)	37.77 (1426.57)	15.63 (244.30)	30.69 (941.88)	30.66 940.04)	36.94 (1364.56)	31.85 (1014.42)
4				**17.07** **(291.384)**	30.43 (925.98)	28.84 (831.75)	28.21 (795.80)	35.07 (1229.90)	25.11 (630.51)	29.92 (895.21)	39.32 (1546.06)	43.12 (1859.33)	30.09 (905.41)
5					**0.00** **(0.00)**	9.54 (91.01)	23.48 (551.31)	38.34 (1469.95)	17.80 (316.84)	36.77 (1352.03)	30.41 (924.76)	20.20 (408.04)	37.68 (1419.78)
6						**0.00** **(0.00)**	24.62 (606.14)	37.46 (1403.25)	17.15 (294.12)	37.74 (1424.31)	28.44 (808.83)	17.23 (296.87)	34.05 (1159.40)
7							**0.00** **(0.00)**	26.29 (691.16)	30.84 (951.11)	25.72 (661.52)	46.77 (2187.43)	33.54 (1124.93)	38.92 (1514.76)
8								**0.00** **(0.00)**	46.54 (2165.97)	20.91 (437.23)	62.12 (3858.89)	40.88 (1671.17)	26.74 (715.03)
9									**0.00** **(0.00)**	41.57 (1728.06)	19.19 (368.26)	32.91 (1083.06)	39.80 (1584.04)
10										**0.00** **(0.00)**	57.56 (3313.15)	46.18 (2132.59)	30.23 (913.85)
11											**16.49** **(271.920)**	39.78 (1582.44)	51.15 (2616.32)
12												**0.00** **(0.00)**	40.24 (1619.25)
13													**0.00** **(0.00)**

Figures in bold are intra cluster values, Figures in parentheses are (D^2) intra and inter- cluster average divergence values

Table 4: Cluster mean values of different characters

Clusters	Plant height	Panicle length	Panicle weight $plant^{-1}$	No. of tillers $plant^{-1}$	No. of effective tillers $plant^{-1}$	No. of filled grains $panicle^{-1}$
1	99.65	25.71	36.01	12.44	11.74	140.28
2	102.37	25.90	50.00	14.71	13.92	143.49
3	95.47	25.33	34.67	11.67	10.67	162.33
4	96.95	25.13	16.83	10.67	10.28	110.83
5	97.10	27.00	42.00	10.33	11.00	174.00
6	113.47	22.33	27.67	8.33	7.00	139.33
7	59.53	22.37	23.67	8.67	7.67	156.00
8	110.27	29.40	31.00	10.00	8.00	152.33
9	96.67	29.67	37.33	11.33	10.33	101.67
10	90.47	23.27	42.67	18.67	13.00	261.33
11	115.77	27.37	29.17	7.50	8.00	124.67
12	133.60	22.13	34.67	6.67	7.33	151.67
13	169.80	32.00	29.67	8.00	11.67	171.67

Clusters	No. of unfilled grains $panicle^{-1}$	No. of grains $panicle^{-1}$	Days to 50 % flowering	1000 grain weight	Spikelet density	Biological yield $plant^{-1}$
1	18.94	159.22	97.94	25.42	6.22	103.23
2	21.67	165.16	95.27	24.75	6.37	165.28
3	18.33	180.67	100.00	30.33	7.12	62.24
4	13.67	124.50	91.22	26.77	4.93	60.29
5	24.00	198.00	107.00	33.57	7.34	131.64
6	10.33	149.67	93.00	33.40	6.70	125.10
7	7.67	163.67	87.00	25.50	7.33	128.55
8	15.33	167.67	93.00	16.33	5.70	130.67
9	22.33	124.00	99.67	35.93	4.18	84.21
10	17.67	279.00	110.67	18.40	12.00	102.33
11	17.33	142.00	91.33	42.97	5.25	72.69
12	28.00	179.67	93.00	33.50	8.11	169.28
13	8.33	180.00	91.67	21.53	5.64	90.29

Table 4: Cluster means values of different characters

Clusters	Grain yield $plant^{-1}$	Harvest index (%)	Panicle index	Spikelet fertility (%)	Spikelet sterility (%)
1	41.89	42	1.25	88.33	11.79
2	48.75	29	1.00	87.20	12.78
3	52.51	84	1.51	89.84	10.15
4	30.47	56	2.49	88.68	11.40
5	64.36	48	1.53	87.87	12.12
6	32.48	26	1.17	93.07	6.92
7	30.47	24	1.29	95.35	4.64
8	19.87	15	0.64	90.90	9.09
9	37.81	44	1.04	81.98	18.01
10	62.26	60	1.46	93.69	6.29
11	42.22	57	1.42	87.96	12.03
12	37.27	21	1.10	84.40	15.59
13	42.94	47	1.45	95.39	4.60

The estimate of genetic divergence in the available germplasm is important for the selection of desirable donors for breeding programme. Several workers have emphasized the importance of genetic divergence for the selection of desirable parents by Murthy and Arunachalam (1966), Sinha *et al.* (1991) and Rahman *et al.* (1997). The assessment of divergence for a set of characters using multivariate analysis like Mahalanobis's D^2 or distance analysis has been attempted and effectively used in a number of crop species with diverse breeding systems. The use of Mahalanobis's D^2 statistic for estimating genetic divergence has been emphasized by Shukla *et al.* (2006) and Sarawagi and Binse (2007) five exotic rice genotypes were obtained from IRRI (origin being IRRI, Senegal, WARDA, CIAT, Argentina, Myanmar, Indonesia, IITA and Pakistan) under the project INGER. The D^2 values of the genotypes ranged from 91.011 to 3858.89 indicating that the material was quite diverse.

The clustering pattern of genotypes also confirmed the quantum of diversity present. Based on genetic distance, the 125 genotypes were grouped in 13 clusters. The results indicated that the characters biological yield per plant and 1000 grain weight contributed greatly towards genetic divergence however the contribution of plant height, panicle index, number of filled grains panicle and days to 50 % flowering were moderate. The rest of the characters contributed less than 1 % towards total genetic divergence. Plant height contributed moderately towards genetic divergence, followed by panicle index, number of filled grains per panicle and days to 50 % flowering. The average intra and inter-cluster distance (D^2) values revealed that the highest intra cluster distance of 291.384 was observed in Cluster IV followed by Cluster XI (271.920). It is evident from inter-cluster distance that the most divergent clusters were VIII and XI (D^2= 3858.89) followed by Clusters X and XI (D^2= 3313.15) and Clusters II and XI (D^2= 2678.06) suggesting wide diversity between them and the genotypes in these clusters could be used as parents in hybridization programme since hybridization between divergent parents is likely to produce wide variability and transgressive segregations with high heterotic effects by Rama (12). Such recommendations were also made by Murthy and Arunachalam (1966), Qian and He (1991) and Rao and Gomanthinayagam (1997). Pradhan and Ray (9), Rahman *et al.* (1997) and Bose and Pradhan (2005) have also reported that selection of parents for hybridization should be done from two clusters having wider inter-cluster distances to get maximum variability in the segregating generations. Heterosis is generally attributed to genetic divergence among the parental lines involved in the crosses. Nevertheless, the genetic divergence for the maximum expression of the heterotic effect has a limit by Moll *et al.* (1965) and Arunachalam and Bandyopadhyay (1984). On the other hand, the minimum inter-cluster distance was found between Clusters V and VI (D^2 = 91.011) followed by Clusters III and IX (D^2 = 244.296) and Clusters III and IV (D^2 = 247.747) indicating that the genotypes of these clusters were genetically similar. Such analysis was meant to avoid selection of parents from genetically homogenous clusters and to maintain a relatively broad genetic base.

Table 5: Different characters towards clustering in rice genotypes

Sl. No.	Character	Contribution towards divergence	
		D^2 value	% contribution
1.	Biological yield per plant (g)	3290	42.45
2.	1000 grain weight (g)	2802	36.15
3.	Plant height (cm)	524	6.76
4.	Panicle index	369	4.76
5.	Number of filled grains per panicle	308	3.97
6.	Days to 50 % flowering	279	3.60
7.	Number of unfilled grains per panicle	93	1.20
8.	Number of tillers per plant	25	0.32
9.	Panicle weight per plant (g)	12	0.15
10.	Spikelet density	12	0.15
11.	Panicle length (cm)	11	0.14
12.	Grain yield per plant (g)	09	0.12
13.	Harvest index (%)	08	0.10
14.	Number of effective tillers per plant	08	0.06
15.	Spikelet fertility (%)	03	0.04
16.	Number of grains per panicle	00	0.00
17.	Spikelet sterility (%)	00	0.00

Cluster I the largest cluster comprised of ninety-two genotypes which indicated that all the ninety-two genotypes were having some similar characteristics or common parent which led to their grouping followed by Cluster II with seventeen genotypes. The Clusters IV and XI contained five and two genotypes respectively. The Clusters III, V, VI, VII, VIII, XI, X, XII and XIII were mono-genotypic clusters. This indicated negligible genetic diversity among the genotypes for each character. The clustering pattern revealed that the genotypes from different sources clustered together indicated that there was no association between eco-geographical distribution of genotypes and genetic divergence. The possible reason for grouping of genotypes of different places in one cluster could be the free exchange of germplasm among the breeders of different regions or unidirectional selection practiced by breeder in tailoring the promising cultivars for different regions by Verma and Mehta (1976). Similar findings were reported by Chaturvedi and Maurya (2005) and Sabesan and Saravan (2008). This indicated that in general, selection has been towards the same goal in the different centres of origin of these genotypes and yet there is sufficient genetic variability which distinctly differentiates them into thirteen clusters. On the other hand our study has also revealed that genotypes from the same centre of origin were distributed in different clusters which may be due to differential adaptation to varied agro-ecosystems by Kandamoorthy and Govindarasu (2005) and Senapati and Sarkar (2005) except Basmati 370 which was the only genotype, origin being Pakistan was grouped in a separate Cluster XIII.

The cluster mean values showed a wide range of variation for all the traits studied. Cluster II recorded the highest cluster mean value for panicle weight per plant and number of effective tillers per plant whereas; Cluster III recorded the highest value for harvest index. Genotype of this cluster can be utilized for improvement in yield through selection for harvest index. Cluster IV recorded the lowest mean value for panicle weight per plant, biological yield per plant and highest value for panicle index while, Cluster V recorded the highest cluster mean value for grain yield per plant. Therefore, genotype belonging to this cluster can be utilized effectively for getting higher yield per plant thus increasing the overall productivity. Lowest value of cluster mean for number of effective tillers per plant was observed in Cluster VI. Cluster VII recorded the lowest cluster mean value for plant height, number of unfilled grains per panicle and days to 50 % flowering which can be utilized for developing dwarf genotypes.

Cluster VIII recorded the lowest cluster mean value for 1000 grain weight, grain yield per plant, harvest index and panicle index. Cluster IX recorded the highest cluster mean value for spikelet sterility % and lowest for number of filled grains per panicle, number of grains per panicle, spikelet density and spikelet fertility %. While, Cluster number X recorded the highest cluster mean value for number of tillers per plant, number of filled grains per panicle, number of grains per panicle, days to 50 % flowering and spikelet density. Genotypes belonging to this group recorded the highest values for most of the characters contributing towards yield; therefore they can be used in breeding programmes aimed at improving yield. Cluster XI recorded highest value for 1000 grain weight while, Cluster XII for number of unfilled grains per panicle and biological yield per plant and lowest cluster mean value for panicle length and number of tillers per plant. These traits can be utilized as parameters in selecting genetically diverse parents. Cluster XIII recorded the highest value of cluster mean for panicle length, spikelet fertility % and lowest for spikelet sterility %. The genotype falling in this cluster can be utilized for breeding plants with high panicle length and fertility %. The single genotypic clusters were quite different from the other clusters by either highest or lowest value for a particular character.

The clustering pattern in the present investigation revealed that the genotypes from different geographic origins fell in the same cluster while, those genotypes belonging to same source were grouped in different clusters, *e.g.* IR 79201-49-1-1-1 belonged to IRRI was grouped in a separate cluster, CIAPUS, IR 79204-84-2-2-3, WAB 337-B-B-15-H1, IR 77736-54-3-1-2, IR 81172-140-1-3-2 originated from IRRI, WARDA and Indonesia were grouped in one cluster. Similarly, genotypes from the same centre of origin were grouped in separate clusters exception being Basmati-370 which belonged to Pakistan was grouped in a separate Cluster XIII.

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APPENDIX: DETAILS OF AROMATIC/FINE GRAIN AND NON-AROMATIC LINES

SL. No.	Designation	Cross	Origin
	Aromatic/fine grain lines		
1.	88023-RE	-	CIAT
2.	CT9882-16-4-2-3-2P-M	-	CIAT
3.	H013-5-3-B4	-	ARGENTINA
4.	H014-1-1-B2	-	ARGENTINA
5.	IR 60080-46A	IR 47686-08-4-3/CT 6516-21-4-4	IRRI
6.	IR 74	IR 19661-131-1-2/IR 15795-199-3-3	IRRI
7.	IR 77734-93-2-3-2	NSIC RC 148/PSB RC 18/ NSIC RC 148	IRRI
8.	IR 77736-54-3-1-2	NSIC RC 148/PSB RC 64/ NSIC RC 148	IRRI
9.	IR 78006-55-2-3-3	IR 67406-6-3-2-3/IR 72860-80-3-3-3	IRRI
10.	IR 78537-32-1-2-1	IR 65610-38-2-4-2-6-3/IR 60912-93-3-2-3-3	IRRI
11.	IR 78554-145-1-3-2	IR 72861-13-2-1-2/IR 68450-36-3-2-2-3	IRRI
12.	IR 77298-14-1-2	IR 64(WH)/ADAY SEL//3 IR 64	IRRI
13.	IR 77512-2-1-2-2	IR 68726-3-3-1-2/IR 71730-51-2	IRRI
14.	IR 77629-72-2-1-3	IR 71730-51-2/IR 71742-267-3-2	IRRI
15.	M1-10-29 UL	-	MYANMAR
16.	TOX 3226-5-2-2-2-2	ITA 235/IR 9828-91-2-3//CT 19	IITA
17.	TOX 3867-19-1-2-3-3	-	WARDA
18.	WAB 272-B-B-5-H5	3290/WABC 165	WARDA
19.	WAB 99-84	ITA 257/WABUKA	WARDA
20.	WAB 337-B-B-15-H1	ITA 135/WABC 165	WARDA
21.	WAB 515-B-10 A1-4	-	WARDA
22.	WAS 169-B-B-4-2-7	JAYA/BASMATI 370	SENEGAL
23.	WAS 169-B-B-4-2-9	JAYA/BASMATI 371	SENEGAL
24.	WAS 197-B-4-1-22	IR 31851-96-2-3-2-1/IR 66231-37-1-2	SENEGAL
25.	WAS 197-B-4-1-25	IR 31851-96-2-3-2-1/IR 66231-37-1-3	SENEGAL
26.	WAS 197-B-5-2-16	IR 31851-96-2-3-2-1/IR 66231-37-1-4	SENEGAL
27.	WAS 197-B-5-2-5	IR 31851-96-2-3-2-1/IR 66231-37-1-5	SENEGAL
28.	WAS 197-B-6-3-12	IR 31851-96-2-3-2-1/IR 66231-37-1-6	SENEGAL
29.	WAS 197-B-6-3-16	IR 31851-96-2-3-2-1/IR 66231-37-1-7	SENEGAL
30.	WAS 197-B-6-3-2	IR 31851-96-2-3-2-1/IR 66231-37-1-8	SENEGAL
31.	WAS 197-B-6-3-4	IR 31851-96-2-3-2-1/IR 66231-37-1-9	SENEGAL
32.	WITA 7(TOX 3440-171-1-1-1-1)	TOX 891-212-1-201-1-105/TOX 3056-5-1	WARDA
33.	BASMATI 370	-	PAKISTAN
34.	IR 50	IR 2153-14-1-6-2/IR 2061-214-3-8-2//IR2071-625-1-252	IRRI
35.	IR 64	IR 5657-33-2-1/IR 2061-465-1-5-5	IRRI
36.	IR 72	IR 19661-9-2-3/IR 15795-199-3-3//IR 9129-209-2-2-2-1	IRRI
37.	PSB RC2(IR 32809-26-3-3)	IR 4215-301-2-2-6/BG 90-2//IR 19661-131-1-2	IRRI
38.	PSB RC18(IR51672-62-2-1-1-2-3)	IR 24594-204-1-3-2-6-2/IR 28222-9-2-2-2-2	IRRI
39.	PSB RC64(IR59552-21-3-2-2)	IR 32809-26-3-3/IR 39292-142-3-2-3	IRRI
40.	LOCAL CHECK JR-201	-	
41.	LOCAL CHECK IR-36	-	IRRI
	Non-aromatic lines		
1.	BATANG LEMBANG	SINYHA/ IR 64	INDONESIA
2.	CIAPUS	MEMBERAMO/IR 6612-52-1-2-2	INDONESIA
3.	CIASEM	IR 65/B 8203-1-17-1	INDONESIA
4.	IR 72164-348-6-2-2-2-2	IR 44962-161-2-4-4/IR 67966-44-2-3	IRRI
5.	IR 72890-81-3-2-2	IR 60912-93-3-2-3-3/IR 68058-35-2-2	IRRI
6.	IR 73007-44-1-2-3	IR 65469-161-2-2-3-2-2/IR 65629-157-3-2-3-2-1	IRRI
7.	IR 73546-66-1-1-1	IR 71025-187-1-3-3/IR 68059-137-2-1-3-3	IRRI
8.	IR 73718-26-1-2-5	IR 65469-161-2-2-3-2-2/IR 65459-73-1-2-2-3//IR 43	IRRI
9.	IR 74052-153-5-3-1-3	IR 65610-24-3-6-3-2-3/IR 67406-49-2-3-6-3-1	IRRI
10.	IR 74288-153-5-1-1-3	IR 58773-35-3-1-2/IR 68075-81-3-2-1-3-3//IR 64	IRRI
11.	IR 74642-195-1-3-2	BG 90-2/IRN68059-97-2-3-2-1	IRRI
12.	IR 74646-96-2-3-3	BG 90-2/IR 69734-38-3-3	IRRI
13.	IR 75287-19-3-3-3	IR 68440-36-2-2-3/IR 62243-41-1-3-3	IRRI
14.	IR 75299-94-1-2-2	IR 00A107/IR 64	IRRI
15.	IR 76494-28-1-2-2	IR 71459-45-2-3/IR 68058-64-1-2//IRRI 118	IRRI
16.	IR 77140-24-2-1-2	IR 68068-99-1-3-3-3/JANAKI//PSB RC 18	IRRI
17.	IR 77495-10-2-6-2	IR 68077-82-2-2-2-3/IR 5958-122-1-4-1	IRRI
18.	IR 77498-47-2-6-2-3	IR 68077-82-2-2-2-3/IR 73885-1-4-3-2-1-10	IRRI
19.	IR 77533-29-2-2-2	IR 69713-43-1-3-2-3/IRRI 115	IRRI
20.	IR 77721-93-2-2-1-2-2	IR 69020-21-3-2-2-2/IR 68068-99-1-3-3-3//BG 90-2	IRRI
21.	IR 78126-1-2-1	PSB RC 52/MATATAG 2	IRRI
22.	IR 78566-1-2-1-2	IR 72890-70-2-3-3/PSB RC 20	IRRI
23.	IR 78585-64-2-4-3	IR 73718-1-2-1-3/PSB RC 10	IRRI
24.	IR 79195-115-2-2-3	IR 72909-139-1-2-2/ IR 68059-66-2-3-3-3	IRRI
25.	IR 79200-65-2-2-1	IR 00A103/ IR 72165-63-2-3-3	IRRI

Contd..

SL. No.	Designation Aromatic/fine grain lines	Cross	Origin
26.	IR 79201-49-1-1-1	IR 67406-6-3-2-3/ IR 71700-247-1-1-2	IRRI
27.	IR 79203-105-1-1-3	IR 71676-34-1-1/ IR 73006-12-3-3-2	IRRI
28.	IR 79204-84-2-2-3	IR 71676-34-1-1/ IR 73008-138-2-2-2	IRRI
29.	IR 79216-141-1-3-3	IR 72164-348-6-2-2-2/IR 72905-49-3-2-2	IRRI
30.	IR 79226-98-1-1-3	IR 72903-6-2-2-1/IR 72158-68-6-3	IRRI
31.	IR 79228-67-1-1-3	IR 72903-6-2-2-1/IR 67966-44-2-3-2	IRRI
32.	IR 79228-9-2-3-1	IR 72903-6-2-2-1/IR 67966-44-2-3-2	IRRI
33.	IR 79233-28-2-1-2	IR 72906-32-1-3-3/IR 72158-16-3-3	IRRI
34.	IR 79242-28-3-2-3	IR 72967-12-2-3/IR 68059-66-2-3-3-3	IRRI
35.	IR 79246-105-2-2-4	IR 73006-12-3-3-2/IR 73707-45-3-2-3	IRRI
36.	IR 79246-47-1-3-3	IR 73006-12-3-3-2/IR 73707-45-3-2-3	IRRI
37.	IR 79247-107-1-2-1	IR 73013-107-3-1-2/IR 72158-116-6	IRRI
38.	IR 79254-48-2-1-1	IR 74052-297-2-1/IR 72165-63-2-3-3	IRRI
39.	IR 79254-86-2-3-1	IR 74052-297-2-1/IR 72165-63-2-3-3	IRRI
40.	IR 79327-107-2-3-3	JANAKI/IR 43//IR 73885-1-4-3-2-1-10	IRRI
41.	IR 79327-9-3-3-1	JANAKI/IR 43//IR 73885-1-4-3-2-1-10	IRRI
42.	IR 79504-48-1-6-2	IR 73707-56-5-1-2/IR 73707-45-3-2-3	IRRI
43.	IR 79504-5-3-3-2	IR 73707-56-5-1-2/IR 73707-45-3-2-3	IRRI
44.	IR 79505-51-2-2-2	IR 71700-247-1-1-2/JANAKI	IRRI
45.	IR 79511-47-2-6-3	IR 72158-11-5-2-3/JANAKI	IRRI
46.	IR 79515-25-1-6-1	IR 72158-11-5-2-3/IR 72903-121-2-1-2	IRRI
47.	IR 79525-20-2-2-2	IR 72165-63-2-3-3/IR 72903-121-2-1-2	IRRI
48.	IR 79532-21-2-2-1	IR 72967-12-2-3/IR 72903-121-2-1-2	IRRI
49.	IR 79538-1-1-1-1	IR 72985-65-3-1/IR 72903-121-2-1-2	IRRI
50.	IR 79585-61-2-3-3	IR 72887-34-2-1-3/IR 73707-45-3-2-3	IRRI
51.	IR 79597-56-1-2-1	IR 73004-34-1-3-1/IR 72225-20-3-2-3	IRRI
52.	IR 79643-23-3-3-3	IR 72904-65-1-3-3/IR 73012-137-2-2-2	IRRI
53.	IR 80285-34-3-3-2	IR 74052-297-2-1/IR 71700-247-1-1-2//MATATAG 9	IRRI
54.	IR 80290-74-1-5-6-3	IRB74271-68-3-2/IR 68552-100-1-2-2// IR 00A109	IRRI
55.	IR 80375-13-3-3	IR 73707-45-3-2-3/IR 68544-29-2-1-3-1-2	IRRI
56.	IR 80376-36-2-2-1	IR 73707-45-3-2-3/IR 68552-100-1-2-2	IRRI
57.	IR 80376-51-2-2-1	IR 73707-45-3-2-3/ IR 68552-100-1-2-2	IRRI
58.	IR 80395-97-3-3-2	IR 71676-90-2-2/JANAKI	IRRI
59.	IR 80658-67-2-1-2	IR 72967-12-2-3/IR 72225-20-3-2-3//IR 00A105	IRRI
60.	IR 80705-36-1-3-3	IR 72869-52-1-1-1/IRRI 106//IRRI 143	IRRI
61.	IR 807070-69-1-3-3	IR 72903-121-2-1-2/IR 00A117//PSB RC 82	IRRI
62.	IR 80894-66-3-2-3	IR 02A127/JANAKI	IRRI
63.	IR 80894-8-1-1-3	IR 02A127/JANAKI	IRRI
64.	IR 80897-20-1-2-2	IR 02A127/IR 64	IRRI
65.	IR 80901-32-3-3-2	IR 69021-67-2-2-2-3-2-2/IR 68058-71-2-1	IRRI
66.	IR 80904-50-3-1-3	IR 71718-59-1-2-3/IRRI 105	IRRI
67.	IR 80919-57-2-2-1	IR 72158-16-3-3/BASMATI 370	IRRI
68.	IR 81166-150-2-1-3	IR 00A109/IR 72870-19-2-2-3//IRRI 105	IRRI
69.	IR 81168-31-2-3-2	IR 00A109/PSB RC 82//JANAKI	IRRI
70.	IR 81172-140-1-3-2	IR 00A117/IR 72891-29-3-3-3//IR 73012-137-2-2-2	IRRI
71.	IR 81174-83-2-1-3	IR 72176-140-1-2-2-3/IR 00A109//IRRI 105	IRRI
72.	IR 81178-29-2-3-2	IR 72158-16-3-3/IR 01A154//IRRI 118	IRRI
73.	IR 81309-67-3-2-3	IR 72225-29-1-2-1/IR 04K102	IRRI
74.	IR 81310-25-3-2-2	IR 72225-20-3-2-3/HR 17512-11-2-3-1-4-2-3	IRRI
75.	IR 81328-74-2-2-2	IR 60912-93-3-2-3/IR 73720-36-3-3-1	IRRI
76.	IR 81336-39-3-3-3	IR 68058-71-2-1/IR 73012-15-2-2-1	IRRI
77.	IR 81346-22-1-1-1	IR 72875-94-3-3-2/IR 65450-173-2-1-1-3-3	IRRI
78.	IR 81347-10-2-3-3	IR 72890-81-3-2/IR 64	IRRI
79.	IR 81873-31-2-2-2	IR 76910-20-6(XA 5,XA 13, XA 21)/IR 72894-35-2-22//IR 72870-19-2-2-3	IRRI
80.	IRYN 1068-7-1	MANAWTHUKHA/IR BB 21	IRRI
81.	KALIMAS	PSB RC 2/IR 39292-142-3-2-3	MYANMMAR
82.	MARO	-	MYANMMAR
83.	PEPE	-	MYANMMAR
84.	CIAPUS	-	MYANMMAR