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Studies on genetic diversity in Rice (*Oryza sativa* L.)

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The nature and magnitude of genetic divergence were estimated in 70 rice genotypes using Mahalanobis D^2 – statistics by considering 13 quantitative characters. ANOVA revealed the presence of considerable amount of variability among the genotypes. High estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for grain yield per hill followed by tillers per hill and harvest index. High heritability coupled with high genetic advance was recorded for spikelets per panicle. Mahalanobis D^2 analysis revealed considerable amount of diversity in the material. The genotypes were grouped into nine clusters. Cluster I and cluster III constituted maximum number of genotypes (12 each). The genotypes falling in cluster VII (2907) had the maximum divergence, which was closely followed by cluster V (2027) and cluster I (1762). The inter cluster distance was maximum between cluster VI and VII (18054) followed by cluster III and IX (12520), suggesting that the genotypes constituted in these clusters may be used as parents for future hybridization programme. Traits like spikelets per panicle; plant height and biological yield were the major contributors to genetic divergence.

Key words: Rice, GCV, PCV, heritability, genetic advance, D^2 analysis and genetic divergence.

Introduction

Knowledge about germplasm diversity and genetic relationships among breeding materials could be an invaluable aid in crop improvement strategies. Genetic diversity determines the inherent potential of a cross for heterosis and frequency of desirable recombinants in advanced generations. For

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the same, genetic distance plays a vital role, as parental diversity in optimum magnitude is required to obtain superior genotypes in segregating population.

Hybridization programme involving genetically diverse parents belonging to different clusters would provide an opportunity for bringing together gene constellations of diverse nature, promising hybrid derivatives resulted probably due to complementary interaction of divergent genes in parents. Several workers have emphasized the importance of genetic divergence for the selection of desirable parents (Murthy and Arunachalam, 1996 and Rahman, 1997). The use of Mahalanobis D^2 statistics for estimating genetic divergence has been emphasized by many workers (Roy and Panwar, 1993; Ramya and Senthilkumar, 2008). Hence, in this study 70 genotypes of rice were evaluated to assess the nature and magnitude of genetic diversity among the genotypes for further utilization in breeding programmes.

Material and methods

The experimental material for the present study comprised of 70 genotypes of rice laid in randomized block design (RBD) with three replications at the Field Experimentation Centre of Department of Genetics and Plant Breeding, Allahabad School of Agriculture, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Allahabad, U.P., during *kharif,* 2010. Standard agronomic practices and plant protection measures were taken as per schedule. Observations were recorded on five randomly selected plants per replication for plant height (cm), number of tillers per hill, number of panicles per hill, panicle length (cm), spikelets per panicle, flag leaf length (cm), flag leaf width (cm), biological yield (g), harvest index (%), test weight (g), grain yield per hill (g) and observations on days to 50% flowering and days to maturity were recorded on plot basis. The data was subjected to Mahalanobis D^2 statistics to measure the genetic divergence as suggested by Rao (1952).

Results and discussions

Analysis of variance showed significant differences for all the characters studied except for flag leaf width, suggesting the existence of high genetic variability among the genotypes. The presence of large amount of variability might be due to diverse source of materials as well as environmental influence affecting the phenotypes. Similar findings were reported by Mishra *et al.* (2003). Both PCV and GCV estimates were highest for grain yield per hill followed by tillers per hill and harvest index. The results are in confirmation to the findings of Deosarkar *et al.* (1989). High estimates of heritability (above 60%) in broad sense were recorded for all the thirteen characters under study, which ranged from 94.90% (days to 50% flowering) to 99.90% (number of spikelets per panicle). Johnson (1955) reported that high heritability should be accompanied by high genetic advance to arrive at more reliable conclusion.

Therefore, genetic advance was also computed. A perusal of genetic advance for all the quantitative characters under study ranged from 0.41% (flag leaf width) to 63.85 % (spikelets per panicle). These findings were in agreement with Bihari *et al.* (2004). High heritability coupled with high genetic advance was registered for spikelets per panicle, suggesting predominance of additive gene action in the expression of these traits. Similar findings were reported by Krishna *et al.* (2010).

Table 1. Estimation of component of variance and genetic parameters for 13 quantitative characters in rice genotypes under study

S. No	Characters	GCV	PCV	h^2(bs)%	GA
1.	Days to 50% flowering	5.74	5.89	94.90	11.64
2.	Plant height	18.90	18.92	99.80	39.39
3.	No. of tillers per hill	27.65	27.92	98.10	7.77
4.	No. of panicles per hill	23.65	24.06	96.60	5.28
5.	Panicle length	12.13	12.34	96.50	5.57
6.	Flag leaf length	18.08	18.19	98.80	10.73
7.	Flag leaf width	15.65	16.04	95.20	0.41
8.	No. of spikelets per panicle	23.05	23.06	99.90	63.85
9.	Days to maturity	4.65	4.74	96.30	12.52
10.	Biological yield	21.30	21.33	99.70	41.72
11.	Test weight	17.28	17.45	98.10	7.82
12.	Harvest index	25.85	26.02	98.70	17.46
13.	Grain yield per hill	30.73	30.87	99.10	19.54

GCV = Genotypic coefficient of variation
PCV = Phenotypic coefficient of variation
h^2 (bs) = Heritability (broad sense)   GA = Genetic advance

The seventy genotypes under study were grouped into nine clusters using Mahalanobis D^2 analysis (Table 2). Cluster I and cluster III constitutes of 12 genotypes each, forming the largest cluster followed by cluster V (11 genotypes), cluster II (8 genotypes), cluster VII and VIII (7 genotypes), clusters VI (6 genotypes), cluster IV (5 genotypes) and cluster IX (2 genotypes). The pattern of group constellation proved the existence of significant amount of variability. The clustering pattern of the genotypes revealed that the clustering did not follow any particular patterning clustering with respect to the origin (Ushakumari and Rangaswamy, 1997).

Table 2. Distribution of the 70 rice genotypes into different clusters

S. No	Cluster numbers	Number of genotypes	Genotypes included
1.	I	12	NDR-8834-2, IR 42, IR 69726-116-1-3 (MATATAG1), NDR-359 (check 1), ZR 66, JGL 17025, ADO5017, HKR 06-59, CR 2703, PSB RC 68, KMP-105, TTD 122-33-1.
2.	II	8	CR 2699, CR 2702, CR 2707, IR 40, CRR 614-IR 74371-46-1-1, ZR 52713-2B-1-2 (PSB RC-88), IR 51500-AC-11-1 (PSB RC-50), TMO 7280.
3.	III	12	PNP-208, PSB RC1, ZR 64683-87-2-2-3-3 (PSB RC 82), NP-107-4, ZR 65, PSB RC 28 (ZR56382-139-2-2), UPR 3281-9-1-1, R 1566-2577-2-1530-1, R 2039-RF-23, 608-3B-20-2-2-1-1(PSB RC-88) ZR 61, ZR25976-12-2-2-2-1-1 (PSB RC46), ZR 65195-3B-B-2-3 (PSB RC86).
4.	IV	5	DV 85, IR 72102-4-159-1-3-3-3 (NSTCRC112), ZR 70, IR 65185-3B-8-3-2 (PSB RC84), UPR 3305-25-1-1.
5.	V	11	CRR 451-2921-1-1-1, PHB- 71, NDR 1135, Govind N. Narendra, CR 2968, NWGR 4009, RPHR 516-2-4-5-6-1, CR 2617, PSB RC5 (IR47686-30-3-2), ZR 55423-01 (NSICRC 97), CRR 614-IR 71371-54-1-1.
6.	VI	6	NDR 1134, PSB RC-30 (ZRS8099-41-2-3), CRR 616-B-2-75-1, WC 1240 (ACC 13742), CR 2075-4, ZR 36.
7.	VII	7	JGL 17204, KJT 1-11-15-23-26-22, ZR 64, KJT 48, CB-06-535, ZR 62141-114-3-2-2-2 (PSB RC80), CB-05-501.
8.	VIII	7	CB-O6-112, CR 2705, CR 2708, UPR 3281-7-2-1, CR 2042-2-2, ANNODA (NC), KJT 8-1-25-13-20-24.
9.	IX	2	NDR 1133, CR 2618.

The inter and intra average distances among nine clusters were computed and have been given in Table 3. The intra cluster distance ranged from 643(cluster IV) to 2907(VII). The inter cluster distance was maximum between cluster VI and VII (18054) and minimum inter cluster distance was observed between cluster III and cluster IV (1826). To realize much variability and high heterotic effect, Mishra *et al.* (2003) and Chaturvedi and Maurya (2005) recommended that parents should be selected from two clusters having wider inter cluster distance.

Table 3. Intra (diagonal) and inter cluster average distances for different quantitative characters in rice

CLUSTERS	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**
I	1762	1952	3001	3133	5882	11689	7719	4627	10578
II		797	1971	2352	3125	7486	7678	3318	7534
III			1300	1826	4128	7401	11524	5140	12520
IV				643	3673	6391	8245	3093	10239
V					2027	3873	10364	3802	6187
VI						1135	18054	8711	10550
VII							2907	4265	6312
VIII								1499	4755
IX									1093

The cluster mean values showed a wide range of variations for all the characters undertaken in the study (Table 4). Cluster III exhibited highest mean value for tillers per hill while cluster V contained genotypes with highest mean value for panicles per hill. Cluster VI recorded highest value for plant height; biological yield and panicle length while highest mean value for spikelets per panicle and harvest index was recorded by cluster VII. Cluster VIII had highest value for grain yield per hill while cluster IX recorded highest mean values for flag leaf length, flag leaf width, test weight and lowest values for days to 50% flowering and days to maturity. The selection and choice of parents mainly depends upon contribution of characters towards divergence (Nayak *et al.*, 2004). Contribution towards genetic divergence is presented in table 4. The highest contribution in manifestation of genetic divergence was exhibited by spikelets per panicle (40.95%) followed by plant height (29.86 %) and biological yield (21.16%).

Table 4. Cluster mean values of 9 clusters for different quantitative characters in rice and their contribution to total divergence

Clusters / Characters	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**Contribution (%)**
Days to 50% flowering	99.77	98.91	102.77	106.13	100.36	98.00	104.33	100.09	95.50	0.00
Plant height	84.48	99.62	90.58	88.09	121.64	136.87	88.29	100.12	134.60	29.86
Tillers per hill	11.53	12.30	16.77	15.16	15.63	14.70	11.32	13.51	8.26	1.16
Panicles per hill	9.15	10.19	12.39	12.27	12.61	10.79	9.64	12.08	7.48	0.00
Panicle length	21.25	21.91	23.10	22.76	22.26	25.72	22.78	22.76	24.26	0.12
Flag leaf length	25.28	27.05	26.81	28.67	31.85	35.36	28.81	29.41	37.41	2.28
Flag leaf width	1.20	1.30	1.35	1.43	1.31	1.28	1.40	1.36	1.76	0.04
Spikelets/ panicle	128.65	123.49	106.56	130.40	126.82	109.05	200.02	163.84	178.96	40.95
Days to maturity	132.19	131.62	134.13	138.46	133.24	129.44	136.76	131.00	125.16	0.58
Biological yield	72.55	77.90	93.77	111.52	105.63	128.48	88.29	108.01	89.81	21.16
Test weight	18.80	24.40	24.12	19.57	23.01	21.99	20.78	22.76	27.39	1.08
Harvest Index	28.79	38.06	33.03	25.85	33.35	19.09	42.53	39.25	39.70	1.57
Grain yield / hill	20.62	29.54	30.83	28.87	35.44	24.63	37.86	42.54	35.80	1.20

It is well known that crosses between divergent parents usually produce greater heterotic effect than between closely related ones. Considering the importance of genetic distance and relative contribution of characters towards total divergence, the present study indicated that parental lines selected from cluster VI (NDR 1134, PSB RC-30 (ZRS8099-41-2-3), CRR 616-B-2-75-1, WC 1240 (ACC 13742), CR 2075-4, ZR 36) for plant height, biological yield and panicle length and cluster VII (JGL 17204, KJT 1-11-15-23-26-22, ZR 64, KJT 48, CB-06-535, ZR 62141-114-3-2-2-2 (PSB RC80, CB-05-501) for spikelets per panicle and harvest index could be used in crossing programmes to achieve desired segregants.

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