

GENETIC DIVERGENCE IN RICE GENOTYPES UNDER IRRIGATED CONDITIONS

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ABSTRACT

Sixty nine genotypes of rice (*Oryza sativa* L.) were evaluated to know the extent of genetic divergence with respect to thirteen yield attributing characters viz. days to 50% flowering, plant height, number of tillers per hill, number of panicles per hill, panicle length, flag leaf length, flag leaf width, number of spikelets per panicle, days to maturity, biological yield, test weight, harvest index and grain yield per hill. The analysis of variance revealed highly significant differences for all the characters under studied, indicating that there is an ample scope for isolation of promising lines from present gene pool for yield improvement. On the basis of D^2 values the genotypes were grouped into nine clusters. Cluster I, V and VIII was the largest containing 12 genotypes followed by cluster III with 9 genotypes. The composition of clusters indicated non existence of correspondence between genetic diversity and geographical distribution. The highest inter cluster distance was observed between cluster II and VII therefore the genotypes from cluster II and VII may be used in hybridization programme to achieve desired segregants with high yield. Traits like spikelets per panicle, plant height and biological yield were the major contributors to genetic divergence.

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

INTRODUCTION

Rice is the unique grain that is nearly entirely used as human food, unlike other cereals, which are also used extensively as feed (Swaminathan, 1999). Therefore, evaluation of rice germplasm is an important step for the fulfillment of human demand and options. 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 unknown future needs and conditions, thereby contributing to the stability of farming systems at local, national and global levels (Singh *et al.*, 2000). Genetic diversity determines the inherent potential of a cross for heterosis and frequency of desirable recombinants in advanced generations. For the same, genetic distance plays a vital role, as parental diversity in optimum magnitude is required to obtain superior genotypes in segregating population. To initiate hybridization, the genotypes are to be classified into cluster distance, based on the genetic diversity and the extent of genetic divergence between them needs to be estimated. The D^2 statistics is one of the powerful tools to assess the relative contribution of different component traits to the total diversity, it helps to quantify the degree of divergence between populations and to choose genetically diverse parents for obtaining desirable recombination.

MATERIALS AND METHOD

The experimental material for the study comprised of 69 genotypes 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 analysis of variance was carried out for all the characters and then data was analyzed following multivariate analysis of Mahalanobis (1936) and genotypes were grouped into different clusters following Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

A wide range of variation was observed among 69 rice (*Oryza sativa* L.) genotypes for thirteen quantitative characters. The perusal of data revealed that variance due to treatment was highly significant for all the characters exhibited by the genotypes. Significant genetic variation in various component characters might be effective. Phenotypic variance was higher than genotypic variance for all the characters thus indicated the influence of environment factor on these traits. Similar findings were earlier reported by Mishra *et al.* (2003), Devi *et al.* (2006), Prajapati *et al.* (2011). Among coefficient of variation, phenotypic coefficient of variation

(PCV) estimates highest for harvest index (32.71) followed by biological yield (29.98) and number of panicles per hill (29.68). Lowest estimation of phenotypic coefficient of variance was observed for days to 50% flowering (7.25 %) and days to maturity (6.20 %). And highest genotypic coefficient of variation (GCV) was estimated for biological yield (27.34) followed by harvest index (26.10) and number of panicle per hill (24.40). Lowest estimates of genotypic coefficient of variance was observed for flag leaf width (7.90 %), days to 50% flowering (5.36%) and days to maturity (4.55 %). The coefficient of variation doesn't offer the full scope of heritable variation. It can be find out with greater degree of accuracy when heritability is conjunction with genetic advance study. Heritability and genetic advance were determined to study the scope of improvement in various characters through selection. Heritability and genetic advance are important selection parameters. High heritability estimates

along with high genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johanson *et al.*, 1955). Heritability is a good index of transmission of characters from parents to its progeny. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic population. High estimates of heritability in broad sense were recorded for all the thirteen characters under study, which ranges from 21.39 % (flag leaf width) to 84.31 % (plant height). High heritability was observed for plant height (84.31 %), biological yield (83.13 %), number of tillers per hill (74.76 %) grain yield per hill (69.72 %), test weight (68.21 %) number of panicle per hill (67.58%), flag leaf length (64.96 %) and harvest index (63.66 %), which suggested that these traits would respond to selection owing is their high genetic variability and transmissibility. Similar

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

Sl. No	Characters	GCV	PCV	h^2 (bs)%	GA
1.	Days to 50% flowering	5.36	7.25	54.44	8.06
2.	Plant height	15.71	17.11	84.31	30.09
3.	No. of tillers per hill	20.30	23.48	74.76	6.10
4.	No. of panicles per hill	24.40	29.68	67.58	5.94
5.	Panicle length	11.04	14.42	58.60	4.17
6.	Flag leaf length	13.44	16.68	64.96	7.53
7.	Flag leaf width	7.90	17.09	21.39	0.11
8.	No. of spikelets per panicle	17.05	24.13	49.86	31.94
9.	Days to maturity	4.55	6.20	53.98	9.06
10.	Biological yield	27.34	29.98	83.13	36.70
11.	Test weight	12.13	14.68	68.21	4.33
12.	Harvest index	26.10	32.71	63.66	14.84
13.	Grain yield per hill	23.57	28.44	68.72	9.54

GCV = Genotypic coefficient of variation

PCV = Phenotypic coefficient of variation

h^2 (bs) = Heritability (broad sense)

GA = Genetic advance

finding was earlier reported by Anandrao *et al.* (2011). While moderate estimates were observed for panicle length (58.60 %), days to 50 percent flowering (54.44 %) and days to maturity (53.98 %), and lowest estimates of heritability was observed for spikelet per panicle (49.86 %) and flag leaf width (21.39 %). A perusal of genetic advance for all the quantitative characters under study ranged from 0.12% (flag leaf width) to 36.70% (biological yield). High genetic advance was observed for biological yield (36.70), spikelet per panicle (31.94) and plant height (30.09). Harvest index (14.84) show moderate genetic advance. Lowest genetic advance was observed for flag leaf width (0.11) followed by grain yield per hill (9.54), days to maturity (9.06), days to

50% flowering (8.06), flag leaf length(7.53), number of tillers per hill (6.10), number of panicle per hill(5.94), test weight (4.33) and panicle length (4.17). Vivek *et al.* (2005) also reported similar findings.

High heritability coupled with high genetic advance was registered for biological yield and plant height suggesting predominance of additive gene action in the expression of these traits. Similar findings were reported by Tandekar *et al.* (2010). The sixty nine genotypes under study were grouped into nine clusters using Mahalanobis D^2 analysis (Table 2). Cluster I, V and VIII consist of 12 genotypes forming the largest cluster followed by cluster III (9 genotypes), clusters VI (8 genotypes),

Cluster IV and VII with 5 genotypes each, cluster IX (4 genotypes), and cluster II constitutes of 2 genotypes. The pattern of group constellation proved the existence of significant amount of variability.

Table 2: Distribution of the 69 rice genotypes into different clusters

S. No	Cluster numbers	Number of genotypes	Genotypes included
1.	I	12	ZR73885-1-4-3-2-1-6(MATATAG9)43, K-2009 (27), ZR82098 -113-13-114, K2009(12), K2009(13), PSBRC-64(ZR5955-21-3-2-2)65, ZR30(24), K2009(20), K2009(42), PSBRC-64(ZR5955-21-3-2-2)65, IR32(14), K2009(63)
2.	II	2	ZR8(38), ZR74(37)
3.	III	9	ZR61920-313-22-2-1(NSICRC106)46, ZR22(8), ZR54(26), ZR81063-13-9903-4, ZR26(10), ZR43(19), ASGON 3809, ASGON 3816, ASGON 3817
4.	IV	5	PSBRC60(2R), K-2009 (11), ZR40(21), NDR9542, ZR52(25)
5.	V	12	ZR81025-13-327-3, K2009(13), 2R-46(22), K2009 53, KJI-4-4-36-12-13-29(R ₁ 09), ZR82098-13-23-13(2), AAIS-2, ASGON 3821, RNR 2465-1, KJT 4-4-36-12-13-29, RNR 2465-1-(R ₂ 08), RNR 24-65-1
6.	VI	8	IR7160-1-1-4-2-3-1-2(NSICRC110)47, KJT-4-436-12-13-29, RNR 24657, AAIS-3, AAIS-4, NDR 9542 (ASG2VT), NDR 4542, ASGON-3808
7.	VII	5	ZR79913-13-176-13-4, AAIS-1, ARGON2009(31), ZR55423-01(MS2CRC9), ZR44(20)
8.	VIII	12	AAIS-7, AAIS-8, AAIS-6, AAIS-5, ZR38(16), ZR 61979-138-1-3-2-3(ANGELICA), KJT-4-4-36-12-13-29, 13PZ76(NS)(3), NDR9542, ZR78875-207-13-1-13(58), K2009(57), AAIS-9
9.	IX	4	ZR62(30), K2009(52), ZR69726-29-1-2-2-2(MATATAG2), NDR359

The inter and intra average distances among nine clusters were computed and have been given in Table 3. The intra cluster distance ranged from 28.98 (cluster I) to 39.85 (cluster IV). The inter cluster distance was maximum between cluster II and VIII (218.02) and minimum inter cluster distance was

observed between cluster IV and cluster V (50.15). 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	28.98	108.37	60.21	58.25	57.81	55.06	99.07	71.30	79.51
II		36.95	123.11	104.11	132.39	135.01	218.02	198.24	213.06
III			37.04	64.34	61.11	50.80	111.81	75.82	103.03
IV				39.85	50.15	61.02	94.41	82.14	117.65
V					34.65	61.10	86.11	55.95	74.10
VI						30.66	53.77	60.75	110.60
VII							32.1	74.12	141.24
VIII								32.35	54.13
IX									39.38

The cluster mean values showed a wide range of variations for all the characters undertaken in the study (Table 4). Cluster VII exhibited highest mean value for tillers per hill, plant height and flag leaf length, while cluster V contained genotypes with highest mean value for panicles per hill and flag leaf width. Cluster III recorded highest value for days to 50% flowering and days to maturity while highest mean value for spikelets per panicle and panicle length was recorded by cluster II. Cluster I had highest value for test weight and harvest index, while cluster IX recorded highest mean values for biological yield and grain yield per hill. 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 plant height (22.63%) followed by biological yield (21.57), tillers per hill (11.85%) and test weight (10.61%). Ovung *et al.* (2012) also reported that the characters plant height and biological contributed maximum to divergence and should form the basis of selection for genotypes. In other words, selection for these characters may be rewarding.

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	97.00	87.33	105.70	99.53	98.00	97.08	98.80	99.44	101.75	3.88
Plant height	91.78	77.95	92.49	94.63	92.28	114.87	135.23	113.09	90.88	22.63
Tillers per hill	15.59	12.63	13.32	18.06	19.37	13.94	19.94	18.82	18.13	11.85
Panicles per hill	11.67	8.53	12.51	14.19	18.79	12.59	17.57	14.81	15.02	4.18
Panicle length	24.42	37.18	22.94	23.87	23.65	23.15	23.14	22.86	24.92	5.12
Flag leaf length	31.27	37.43	34.42	33.54	33.46	37.48	40.77	31.27	30.28	4.39
Flag leaf width	1.29	1.24	1.39	1.44	1.60	1.41	1.55	1.43	1.53	0.21
Spikelets per panicle	126.91	146.88	126.70	127.67	136.35	128.19	120.87	126.93	125.37	3.24
Days to maturity	126.86	115.33	137.70	133.73	130.61	130.21	131.27	134.14	131.17	0.64
Biological yield	61.28	44.00	63.81	55.27	71.78	59.08	61.07	96.89	113.92	21.57
Test weight	23.92	19.38	17.47	21.96	20.26	20.05	21.24	20.83	23.78	10.61
Harvest Index	43.71	31.15	34.69	25.55	32.75	38.24	40.87	28.52	28.76	5.97
Grain yield per hill	26.17	16.17	21.93	13.87	22.48	21.92	23.93	27.33	32.33	5.71

The results concluded that genotype ZR44 (20) recorded best performance for grain yield per hill followed by ZR69726-29-1-2-2(MATATAG2) III. Characters like biological yield, harvest index and grain yield per hill show high heritability coupled with genetic advance as percent of mean therefore should be given top priority during selection. Further cluster II [ZR8 (38), ZR74 (37)] and cluster VII

[ZR79913-13-176-13-4, AAIS-1, ARGON2009 (31), ZR55423-01(MS2CRC9), ZR44 (20)] were most diverse to each other. These clusters are suggested to provide a broad spectrum of variability in segregating generations and the genotypes present in them may be used as parents for future hybridization programme to develop desirable types.

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