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## Genetic divergence and association study for grain yield in rice (*Oryza sativa* L.) genotypes

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**Abstract**

The present investigation was undertaken to obtain information on the variability and genetic divergence of the genotypes studied. Assessment of genetic diversity in crop germplasm is vital for identification of the genotypes to be used in the future breeding programme. Nature and magnitude of genetic variability, genetic diversity ( $D^2$  statistics) at the phenotypic level was estimated in 102 rice genotypes. Morphological traits *vis-a-vis*, flag leaf angle, panicle type, awing, panicle threshability and seed coat colour was characterized using standard procedure of IRRI on the basis of scale (scores 0-9). Analysis of variance revealed significant differences among genotypes for all the traits studied. The highest phenotypic and genotypic coefficients of variability were observed for leaf width (cm) followed by tillering ability, grain yield  $ha^{-1}$  (q), plant height (cm), leaf length (cm) and panicle length (cm). In general the phenotypic coefficients of variation were higher than genotypic coefficients of variation which indicates the role of environment in the expression of traits under observation. The estimates of heritability in broad sense was high for all the characters. The present investigation indicates a great scope in the improvement of these traits as these characters in general possessed high estimates of heritability coupled with high genetic advancement except for days to maturity, grain length (mm) and days to 50% flowering (high heritability but moderate genetic gain) indicating the preponderance of additive gene action for control of these traits. Estimates of divergence among 102 rice genotypes revealed that significant divergence existed among them. The genotypes under study were grouped into 8 clusters as per Mahalanobis  $D^2$  (1928) analysis employing Tochers method; with maximum number of genotypes in cluster IV (40) followed by cluster II (23), cluster VII (16), cluster VI (14) and cluster VIII (3). Maximum intercluster distance was observed between cluster VII and VIII (1146.52) while maximum intracluster distance was observed in cluster V (1271.69). The per cent contribution towards the total genetic divergence revealed that plant height (cm), days to 50% flowering, grain yield  $ha^{-1}$  (q), days to maturity, tillering ability and leaf width (cm) were the main contributing characters towards total genetic divergence.

**Keywords:** genetic diversity, heritability, correlation coefficient, yield-related traits, rice

**Introduction**

Rice (*Oryza Sativa* L.) is one of the world's most important cereal crop and is a major food grain contributor to the total world food grain basket. It belongs to the genus *Oryza* family Gramineae (*Poaceae*) and tribe *Oryzaceae*. The genus *Oryza* consists of 23 wild and two cultivated species, viz., the Asian *O. sativa* and the African *O. glaberrima*. *O. sativa* earlier domesticated in Asia has now spread to almost all the rice growing areas of the world, while *O. glaberrima*, domesticated in Western tropical Africa is confined to that part of the world alone. The basic chromosome number of the genus is  $n=12$ . The species are either diploid with  $2n=24$  chromosomes or tetraploids with  $2n=48$  chromosomes. Because of long history of cultivation and selection under diverse environments, rice has acquired a broad range of adaptability and tolerance to abiotic stresses, thereby making its cultivation possible over a wide range of water, soil and climatic conditions that include areas from even below the mean sea level to about 2100 m a.m.s.l. The world's rice production has doubled during last 25 years, largely due to the use of improved technology such as high yielding varieties and better crop management practices. Further scope of crop improvement depends on the conserved use of genetic variability and diversity in plant breeding programmes and use of new biotechnological tools. There is wide genetic variability available in rice among and between wild relatives and varieties leaving a wide scope for future crop improvement. Better understanding on the genetic diversity ensures the breeder in planning crosses for hybrid and

line development, in assigning lines to heterotic groups and in plant variety protection. Thus the success of breeding programme depends in part upon choosing breeding stocks that have sufficient variability. Classification of total variability into its heritable and non-heritable components such as phenotypic and genotypic coefficient of variations, heritability estimates and expected genetic advance is of paramount importance in understanding the genetic make-up of any breeding material under improvement.

### Materials and Methods

One hundred two rice cultivars, along with standard checks, were evaluated for maturity, yield and quality traits at geographical environments in the Kashmir valley. The experimental field was located at the main campus SKUAST-K, Shalimar, Srinagar which is 15 km away from Srinagar city on the foot hills of Mahadev. The altitude of the location is 1685 meter above mean sea level and situated 34° N of latitude and 74.89° E of longitude. The climate is temperate characterized by mild summers. June and July are the hottest months while January and February are the coldest. The maximum rain fall is received during March to April. Experiment was laid in RBD with three replications. Ten competitive plants were randomly selected for recording the observations for all the characters except for maturity traits, where whole experimental plot was considered. Mean/median values were used to compute the analysis of variance. Diagnostic plant characteristics (as per the standard method suggested by IRRI) were recorded, besides recording the other observations viz. plant height (cm), panicle length (cm), leaf length (cm), leaf width (cm), tillering ability, days to 50% flowering, days to maturity, grain length (mm), grain width (mm), 1000 seed weight (g), grain yield ha<sup>-1</sup>. Analysis of variance for all the quantitative characters was performed to estimate the magnitude of G x E interaction and get a reliable estimate of the genotypic and phenotypic variance and other related parameters.

### Results and Discussion

For estimation of diagnostic characteristics a general scale with index value of 0-9 was adopted for most of the traits as per the SES scale of IRRI. Desirable parents for a particular trait were identified if the score was 3 or less on the scale. Such varieties or cultivars having majority of the traits with a score of 3 or less are known to express full biological potential even under different levels of biotic and abiotic stresses. These cultivars are good to be used as parents for hybridization to broaden their genetic base or incorporate elite allelic resources present in these indigenous cultivars into high yielding exotic varieties to recover segregants with better quality and higher yield. Sixteen morphological traits were considered for diagnostic characterization of these varieties. Persual of the results (Table-1) revealed that genotypes with erect flag leaf angle were 45 (44.11%) and intermediate 32 (31.37%). Similarly horizontal flag leaf angle was recorded in 25 (24.50%) genotypes. Panicle type was compact in 56 (54.90%) and intermediate in 32 (31.37%) genotypes. It was open in 14 (13.72%) genotypes. Awning pattern revealed that it was absent in 87 (85.29%), short and partly awned in 9 (8.82%), short and fully awned in 3 (2.94%) and long and partially awned in 1 (0.98%). Seed coat colour was white in 23 (22.54%), light brown in 47 (39.16%) speckled brown colour in 3 (2.94%) genotypes and brown in 27 (26.47%). Panicle threshability was difficult in 7 (6.86%) genotypes. It

was moderately in 31 (30.39%), intermediate in 49 (48.03%) and loose in 15 (14.70%) genotypes. Analysis of variance revealed significant difference in the environments (locations) and G x E interaction for all the traits except 1000-seed weight (Table-2). All the characters revealed significant difference, revealing presence of substantial genetic variability. Perusal of the Table-3 revealed that mean plant height of the genotypes was recorded as 93.16±0.74 cm, with the range of variability from 120.00 to 45.66 cm. Panicle length had a population mean of 19.76±0.57 cm, with variability range of 24.66 to 14.66 cm. Leaf length and its width ranged from 50.66 to 24.00 cm and 1.43 to 0.40 cm with a population mean of 33.98±1.72 and 0.60±0.02. Tillering ability exhibited from 26.66 to 7.00, with a mean of 15.54±0.51. Days to 50% flowering revealed that on an average the mean days taken to 50% flowering were 104.46±0.55 days with the variability range of 125.00 to 87.33. Days to maturity revealed that early, medium and late maturing genotypes were present in the population studied. On an average, the mean days taken to maturity were 135.37±0.46 with the variability range of 147.66 to 124.00 days. Grain length and its width also exhibited significant variation in the genotypes. The minimum grain length recorded was 7.75 cm and grain width 2.04 cm, while maximum grain length was 8.54 cm and grain width 3.18 cm. The population mean for Grain length was 7.75±0.07 cm and for grain width 2.81±0.05 cm. 1000-seed recorded a population mean weight (g) of 28.43 ±0.55 with a variability range of 31.83 to 20.43. Grain yield qha<sup>-1</sup> revealed tremendous variability range of 131.92 to 16.85 q with a mean population grain yield of 10.22±2.76 q ha<sup>-1</sup>. Coefficient of variation (both phenotypic and genotypic) was low (>10.0) for days to maturity, grain length (mm) and days to 50% flowering. It was moderate (10.0-30.0%) for plant height (cm), panicle length (cm), leaf length (cm), grain width (mm) and 1000-seed weight (g) and high (>30%) for leaf width (cm), tillering ability and grain yield q ha<sup>-1</sup>. Similarly, Anjaneyulu *et al.*, (2010) [4] studied on 50 germplasm lines of rice revealed that high PCV and GCV were recorded for number of grains per panicle, fertility percentage and grain yield per plant. Heritability (broad sense) estimates are informative as they indicate relative importance of genotypic and environmental contribution to variability exhibited and reliance that can be placed on phenotypic value during selection. It is considered in conjunction with the predicated genetic advance as suggested by Panse and Sukhatme (1957) [18] and Johnson *et al.*, (1955) [11] as the heritability is influenced by bio-metrical method, generation of hybrid, sample size of experimental material and environment. Estimates of heritability (broad sense) were high (>60%) for all the traits in environment taken (Table 4). The estimated genetic advance and heritability (bs) was utilized to calculate expected genetic gain (% of mean). Therefore, the effect of selection is realized more quickly in those characters which have high heritability as well as high genetic gain. The expected genetic gain revealed that it was high (>30%) for plant height (cm) and grain yield (q ha<sup>-1</sup>) whereas, it was low (20.0%) for panicle length (cm), leaf length (cm), leaf width (cm), tillering ability, days to 50% flowering, days to maturity, grain length (mm), grain width (mm), 1000- seed weight (g). Most of the above results in respect of heritability and genetic advance were in agreement with reports on rice by Sarawgi and Rastogi (2000) [27], Vange (2009) and Pandey and John Anurag (2010) [17].

**Table 1:** Morphological characters recorded in the rice genotypes

S. No.	Name of the genotype	Flag leaf angle	Panicle type	Awning	Panicle Threshability	Seed coat colour
<b>Local Landraces</b>						
1	Gulbara	5	3	7	7	2
2	Tumlahaal	5	1	9	3	4
3	Gurah	5	1	5	7	2
4	Baber	1	1	0	3	2
5	Wazul krea	5	1	0	3	1
6	Mushkbudji	5	1	0	1	3
7	Niver Zag	5	3	0	7	2
8	Local Budgam 1	3	1	0	3	1
9	Local Budgam 2	3	2	0	5	4
10	Local Budgam 3	1	1	0	3	2
<b>Released Varieties/Genotypes of SKUAST</b>						
1	SKAU-429	3	2	0	7	2
2	SK-356	5	3	0	7	2
3	Shalimar Rice-1	5	2	0	5	2
4	KHD/GP/120	3	3	0	7	2
5	KHD/GP/27	5	3	0	7	2
6	Shalimar Rice-3	5	2	0	5	4
7	China-1031	5	2	0	5	2
8	SKAU-336	1	3	0	5	2
9	SKAU-2	1	1	0	5	2
10	SKAU-337	1	1	0	5	2
11	Pusa Sugand-3	1	1	0	1	2
12	SKAU-408	1	2	0	1	2
13	SKAU-389	1	1	0	5	2
14	Shalimar Rice -2	3	2	0	5	2
15	KHD/GP/150	1	1	0	3	2
16	Shalkew	3	1	0	5	3
17	K-332	3	1	1	3	1
18	K-116	5	5	5	5	2
19	Jehlum	1	1	0	5	1
20	SKAU-403	3	2	0	5	1
21	Chenab	3	1	0	1	1
22	SKAU-339	3	1	0	5	2
23	China-1039	3	1	5	7	1
24	SKAU-292	5	2	0	7	4
25	China-988	5	1	0	7	1
26	SK-338	1	1	0	3	4
27	SKAU-39	3	1	0	5	2
28	China-1007	5	1	0	7	1
29	Pusa sugand-5	1	1	0	1	1
30	SKAU-46	1	1	0	3	1
31	SKAU-402	1	1	0	3	4
32	SKAU-404	3	2	0	5	2
33	SKAU-3	1	1	0	3	1
34	SKAU-98	1	1	0	5	4
35	SKAU-405	3	2	0	5	4
36	China-972	5	1	0	7	1
37	Kamad	3	1	0	3	1
<b>Other genotypes from IRRI etc.</b>						
1	Calaro	1	1	0	5	2
2	C101A51	1	1	0	5	4
3	C101PKT	1	1	0	5	4
4	IR61728-413-2-1-1	3	1	0	5	2
5	Shai Tai Tsau	1	1	0	5	4
6	C101A51/ARBN 152	5	3	0	3	4
7	BL-122`	5	1	0	3	2
8	Rasi	1	2	0	5	2
9	IR64	5	3	7	7	2
10	IR68333-RR-B-19	5	3	0	5	2
11	Kanto-51	3	2	0	5	1
12	RIL-10	5	3	0	5	4
13	IRBL1-CL/EC 565160	5	3	0	7	4
14	IRBL 5M/EC 565166	5	3	0	5	2
15	A57-115-4/ARBN 148	5	2	0	5	2
16	B-4	3	3	0	3	1

17	IRBN KS-S/EC 565178	1	2	0	3	2
18	C104PKT	1	2	0	3	2
19	A-57	3	2	0	5	2
20	B-9	3	2	0	5	4
21	B-14	3	2	1	5	2
22	RIL-29	1	1	0	5	4
23	Usen	1	2	0	3	2
24	Raminad Str 3	1	1	0	1	3
25	BL 245	1	1	1	3	4
26	BL-42	3	2	0	3	1
27	SAFED BREZ	3	1	9	1	1
28	KHD/GP/154	1	1	0	5	4
29	T2 (71)	1	1	0	3	2
30	NP 125	1	1	0	5	4
31	IRBN 2008 V-87	5	1	0	3	4
32	Dular	5	3	0	5	4
33	CO-39	5	1	0	7	1
34	BL-122/ARBN 141	1	1	0	3	2

**Table 2:** Analysis of variance for yield and yield component traits of 102 rice (*O. sativa* L.) genotypes

S. No.	Source of variation	d. f.	Mean squares										
			Plant height (cm)	Panicle length (cm)	Leaf length (cm)	Leaf width (cm)	Tillering ability	Days to 50% flowering	Days to maturity	Grain length (mm)	Grain width (mm)	1000-seed weight (g)	Grain yield plot <sup>-1</sup> kg
1.	Replication	2	16.74**	0.421	9.558	0.005*	1.39	0.59	2.83*	0.028	0.13*	13.50**	43.01
2.	Treatment	101	944.23**	17.04**	88.65**	0.12**	77.87**	208.47**	73.19**	0.40**	0.263*	26.32**	2612.44**
3.	Error	202	1.66	0.99	9.03	0.001	0.79	0.92	0.64	0.01	0.009	0.94	23.18
S.E. Diff from Mean			0.74	0.57	1.72	0.02	0.51	0.55	0.46	0.07	0.05	0.55	2.76
CD (p≤0.05)			2.74	2.11	6.38	0.08	1.88	2.04	1.70	0.27	0.20	2.05	10.22

\*Significant at 0.05 probability level

\*\*Significant at 0.01 probability level

**Table 3:** Magnitude of variability, phenotypic and genotypic coefficient of variation for different traits in rice (*O. sativa* L.)

S. No.	Trait	95% CI	Mean	Range	PCV	GCV
1.	Plant height (cm)	91.17-95.15	93.16	45.66-120.00	19.07	19.02
2.	Panicle length (cm)	19.48-20.04	19.76	14.66-24.66	12.74	11.70
3.	Leaf length (cm)	33.31-34.64	33.98	24.00-50.66	17.55	15.16
4.	Leaf width (cm)	0.57-0.62	0.60	0.40-1.43	34.81	34.16
5.	Tillering ability	14.96-16.12	15.54	7.00-26.66	33.10	32.60
6.	Days to 50% flowering	103.52-105.40	104.46	87.33-125.00	8.01	7.96
7.	Days to maturity	134.81-135.93	135.37	124.00-147.00	3.68	3.63
8.	Grain length (mm)	7.714-7.80	7.75	6.31-8.54	4.92	4.63
9.	Grain width (cm)	2.77-2.84	2.81s	2.04-3.18	10.90	10.34
10.	100-seed weight (g)	27.76-28.45	28.10	20.43-31.83	10.90	10.34
11.	Grain yield (q ha <sup>-1</sup> )	88.99-95.67	92.33	16.85-131.92	32.24	31.81

**Table 4:** Estimates of variability, heritability, genetic advance and expected genetic gain for different traits of rice (*O. sativa* L.)

S. No.	Traits	Phenotypic variance	Genotypic variance	Heritability (broad sense)	Genetic advance	Expected genetic (% of mean)
1.	Plant height (cm)	315.85	314.18	0.99	36.41	39.08 %
2.	Panicle length (cm)	6.34	5.35	0.84	4.37	22.14 %
3.	Leaf length (cm)	35.57	26.53	0.74	9.16	26.97 %
4.	Leaf width (cm)	0.04	0.04	0.96	0.41	69.06 %
5.	Tillering ability	26.48	25.69	0.97	10.28	66.15 %
6.	Days to 50% flowering	70.10	69.18	0.98	17.02	16.29 %
7.	Days to maturity	24.83	24.18	0.97	9.99	7.38 %
8.	Grain length (mm)	0.14	0.12	0.88	0.69	8.96 %
9.	Grain width (cm)	0.09	0.08	0.90	0.56	20.22 %
10.	1000-seed weight (g)	9.40	8.46	0.90	5.68	20.22 %
11.	Grain yield (q ha <sup>-1</sup> )	886.26	863.08	0.97	59.72	64.68 %

**Table 5:** Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficient of yield and yield component traits in 102 rice (*O. sativa* L.) genotypes

\	Traits	Plant height (cm)	Panicle length (cm)	Leaf length (cm)	Leaf width (cm)	Tillering ability	Days to 50% flowering	Days to maturity	Grain length (mm)	Grain width (mm)	100-seed weight (g)	Grain yield ha <sup>-1</sup> q
1.	Plant height (cm)	<b>314.18</b>	0.37	0.08	-0.31	-0.35	-0.49	-0.41	-0.03	-0.06	-0.06	0.20*
2.	Panicle length (cm)	0.34 **	<b>5.35</b>	0.20	0.007	-0.33	-0.35	-0.25	0.04	0.29	0.29	0.21**
3.	Leaf length (cm)	0.07	0.21 **	<b>26.53</b>	0.19	-0.06	0.11	0.30	0.24	0.02	0.02	0.28**
4.	Leaf width (cm)	-0.30 **	0.01	0.16 **	<b>0.04</b>	0.07	0.53	0.48	-0.27	0.06	0.06	0.21**
5.	Tillering ability	-0.34**	-0.30 **	-0.06	0.07	<b>25.69</b>	0.29	0.56	-0.05	-0.08	-0.08	0.26**

6.	Days to 50% flowering	-0.49**	-0.32 **	0.09	0.52 **	0.29 **	69.18	0.41	-0.14	-0.06	-0.06	-0.15
7.	Days to maturity	-0.40 **	-0.22 **	0.25 **	0.47 **	0.54 **	0.41 **	24.18	-0.001	0.19	0.19	0.13
8.	Grain length (mm)	-0.03	0.03	0.18*	-0.24 **	-0.05	-0.13 *	-0.002	0.12	-0.17	-0.17	0.24**
9.	Grain width (cm)	-0.05	0.25 **	0.03	0.05	-0.07	-0.06	0.18 **	-0.14 *	0.08	1.00	0.32**
10.	100-seed weight (g)	-0.05	0.25**	0.03	0.05	-0.07	-0.06	0.18 **	-0.14 *	1.00*	8.46	0.32**
11.	Grain yield plot <sup>-1</sup> kg	0.21**	0.21**	0.23 **	0.20 **	0.23 *	-0.15 *	-0.13 *	0.23 *	0.29 **	0.29 **	863.08

\*,\*\*=Significant at 5% and 1% respectively

**Table 6:** Distribution of different rice genotypes into clusters based on D<sup>2</sup> statistics (clustering by Tocher Method)

S. No.	Cluster	No. of genotypes	Variety/Accession No. of genotypes
1.	I	2	Calaro, Kamad
2.	II	23	SKAU-429, B-11, B-24, B-4, B-26, B-3, SKAU-3, SKAU-46, Mushkbudji, B-5, China-988,China-972, B-32, Jehlum, Dular, IRBL Z-FU/EC 565188, Chenab, K-116, Shalimar Rice-2, IRBL5M/ EC565166, Shalimar Rice-3, C101A51/ARBN152, Shalimar Rice-1
3.	III	2	B-8, SKAU-356
4.	IV	40	IR64, Tumlahaal, K-225, SKAU-336, C104PKT, A57, SK-2, SKAU-337, B-9, B-14, SKAU-408, IR61728-413-2-1-1, IR68333-RR-B-19, T2(MAS 71), Raminad Str 3, CO.39, Local Budgam-3, IR63347-AL-201-1, IRBN 2008 V-87, Shalkew, BL-42, K-332, Wazul Krew, Kanto-51, RIL-10, BL-142/ARBN 142, T1, SK-339, China-1039, SKAU-338, China-1007, B-10, B-13, B-19, B-1509, SKAU-98, B-28, A3(IRRI LINE), Local Budgam-1, Local Budgam-2
5.	V	2	KHD/GP/27, Pusa Susand-3
6.	VI	14	SKAU-405, Safed Brez, C105TTP.4L23, BL-122, Shai Tai Tsau, Usen, SKAU-389, Baber, RIL-29, IRBLKS-S/EC565178, Gulbara,Rasi,C101PKT, C101A51
7.	VII	16	Niver Zag, IRBL1-CL/EC565160, Gurah, KHD/ GP/120, China-1031, A57-115-4/ARBN148, KHD/GP/150,NP 125, BL 245,Yunlen-19, KHD/GP/ 154,SKAU-403, SKAU-292,SKAU-39,SKAU-402, SKAU-404
8.	VIII	3	BL-122/ARBN 141, KHD/GP/208,Pusa Sugand-5

**Table 7:** Average inter-cluster and intra-cluster D<sup>2</sup>-values among rice (*O. sativa* L.) genotypes

S. No.	↓Cluster→	I	II	III	IV	V	VI	VII	VIII
1.	I	601.56	376.39	431.65	305.03	599.95	364.32	621.91	593.00
2.	II		74.67	177.62	193.55	505.93	545.17	187.82	874.66
3.	III			435.27	220.46	518.98	533.96	250.13	791.78
4.	IV				149.36	429.71	370.68	338.67	503.01
5.	V					1271.69	668.36	633.46	635.85
6.	VI						261.09	823.12	449.53
7.	VII							131.99	1146.52
8.	VIII								0.00

**Table 8:** Cluster means for yield and yield component traits in different clusters Of 102 rice genotypes (*O. sativa* L.)

S. No.	Cluster	Plant height (cm)	Panicle length (cm)	Leaf length (cm)	Leaf width (cm)	Tillering ability	Days to 50% flowering	Days to maturity	Grain length (mm)	Grain width (mm)	1000-seed weight (g)	Grain yield ha <sup>-1</sup> q
1.	I	77.00	16.83	31.83	0.63	20.17	104.67	138.83	7.83	2.50	24.97	120.40
2.	II	102.36	21.06	32.55	0.51	13.38	95.49	133.93	7.79	2.90	29.05	104.72
3.	III	98.67	19.83	31.50	0.50	15.33	103.00	132.83	7.90	2.84	28.38	82.20
4.	IV	91.57	20.00	35.91	0.61	16.68	107.17	137.68	7.74	2.96	29.63	86.73
5.	V	95.00	19.83	34.67	0.97	17.17	109.50	140.00	7.86	2.50	25.03	66.10
6.	VI	64.00	17.43	30.36	0.60	16.52	109.14	134.14	7.76	2.62	26.21	89.07
7.	VII	114.04	19.73	33.44	0.54	13.75	102.21	129.77	7.74	2.52	25.21	101.16
8.	VIII	74.67	19.67	41.67	1.43	18.00	125.00	147.67	7.66	2.90	28.97	45.88

**Table 9:** Contribution of different traits to total genetic divergence

S. No.	Trait	Times ranked 1 <sup>st</sup>	Contribution (%)
1.	Plant height (cm)	2120	41.16
2.	Days to 50% flowering	936	18.17
3.	Grain yield (q ha <sup>-1</sup> )	619	12.02
4.	Days to maturity	514	9.98
5.	Tillering ability	411	7.984
6.	Leaf width (cm)	296	5.75
7.	Grain length (mm)	96	9.98
8.	Grain width (cm)	58	1.13

### Correlation coefficients

Yield is an ultimate criterion which a plant breeder has always to keep in view for evolving improved cultivars of any crop. However, yield is a polygenic character and highly influenced

by environment. Knowledge of the association of quantitative characters specifically for yield and its attributes is of immense practical value during selection. Variability studies provide information on the extent of improvement possible in

different characters, but they do not throw light on the extent and nature of relationship existing between various contributing characters and economically important characters. Hence, a knowledge regarding association of various characters among themselves and with economic character is necessary for making indirect selection for improvement of economical characters. Correlation studies pave way to know the association prevailing between highly heritable characters with most economic characters and gives better understanding of the contribution of each trait in building up the genetic makeup of the crop. The phenotypic correlations indicate the extent of the observed relationship between two characters. This does not give true genetic picture of the relationship because it indicates both heritability as well as environmental influences. Genotypic correlations provide an estimate of inherent association between genes controlling any two characters. Hence, it is of greater significance and could be effectively utilized in formulating an effective selection scheme. Perusal of Table-5 indicated that in the present investigation, the estimates of phenotypic correlation were in general slightly higher than genotypic correlation. In all instances, however, more impetus may be placed on the genotypic correlations. The nature of genotypic correlation was more or less similar to phenotypic correlation under study. Correlation coefficients revealed that the economically important trait i.e. grain yield ( $\text{qha}^{-1}$ ) exhibited significant positive association with plant height ( $r_g=0.211$ ,  $r_p = 0.210$ ), panicle length ( $r_g=0.214$ ,  $r_p= 0.212$ ), leaf length ( $r_g = 0.287$ ,  $r_p= 0.232$ ), leaf width ( $r_g =0.211$ ,  $r_p0.203$ ), tillering ability ( $r_g=0.261$ ,  $r_p=0.234$ ), grain length ( $r_g=0.242$ ,  $r_p=0.230$ ), grain width ( $r_g =0.322$ ,  $r_p = 0.231$ ), 1000-seed weight ( $r_g=0.322$ ,  $r_p=0.293$ ) both at genotypic and phenotypic levels. A similar result was also reported by Sarkar (2006) [26] and Sharifi *et al.*, (2013) [30]. The finding of present investigation is agreement with the earlier worker viz., Laxmi *et al.*, 2014 [15], Deepa *et al.*, 2006 [9] and Ravindra *et al.*, 2012 [22]; they have also recorded the positive correlation of effective tiller with grain yield per plant.

Days to 50% flowering ( $r_g = -0.153$ ,  $r_p = - 0.151$ ), Days to maturity ( $r_g = -0.134$ ,  $r_p = -0.131$ ) exhibited negative and non-significant association with grain yield plant<sup>-1</sup>. It was noticed that grain length was positively and significantly associated with leaf length and leaf width and grain width with panicle length. Similar result also estimated by Sarawgi *et al.*, (1997) [28] with leaf length and leaf width on grain yield which showed positive direct effect. The harmony conclusion of negative direct effect of days to maturity on grain yield was exposed by Hasan *et al.*, (2012) [10]. The correlation between plant height and grain yield was significant and positive. The positive direct effect of plant height on grain yield also explained by Akhtar *et al.*, (2011) [3] and Ravindra *et al.*, (2012) [22].

### Genetic diversity

Analysis of genetic diversity is a platform for stratified sampling of breeding population. Involving genetically diverse parents is known to provide an opportunity for bringing together gene constellations yielding desirable transgressive segregants in advanced generations. Estimation of genetic divergence helps in reducing the large data of genotypes to manageable proportions. It is assumed that the parents showing wide genetic divergence are best suited for being used in the hybridization programme. In the process of formulating the rice improvement programme through hybridization and creating variability for the improvement of

yield and other desirable traits, it is essential to understand the nature and degree of genetic divergence present in the available germplasm. In the present study, 102 genotypes of rice were evaluated to estimate the genetic divergence for identification of potential parents using Mahalanobis  $D^2$  statistics. Analysis of variance for divergence revealed that the value of V-statistic were significant indicating substantial genetic diversity in the material. Classification of the 102 genotypes led to formation of eight clusters (Table-6) as per Mahalanobis  $D^2$  analysis employing Tochers method (Rao, 1952) [20]. Cluster IV comprised of maximum number of genotypes (40) followed by cluster II (23), cluster VII (16), cluster VI (14), cluster VIII (3) and cluster I, cluster III and cluster V (two each). Clustering together of genotypes from different sources is probably due to free exchange of germplasm among breeders of different regions and/or unidirectional selection practised by breeders while tailoring promising cultivars for different regions (Chaturvedi and Maurya, 2005; Sabesan *et al.*, 2008) [6, 25]. Similarly, genotypes from the same source of origin getting grouped into different clusters may be due to differential adaptation to varied agro-ecosystems (Kadamoorthy and Govindarasu, 2005; Senapati and Sarkar, 2005) [12, 29]. The mean inter- and intra-cluster distances was measured to identify the most divergent clusters and also the genotypes within a cluster. The maximum intra-cluster distance ( $D^2$ ) of (1271.69) was in cluster V had followed by cluster I (601.56) and the minimum intra-cluster distance ( $D^2$ ) of (0.00) was in cluster VIII. The maximum inter-cluster distances ( $D^2$ ) value was (1146.52) between cluster VIII and VII followed by cluster VII and VI (823.12), cluster VI and I (668.36), cluster V and III (599.95) (Table-7). The minimum inter- cluster distance was observed between cluster II and IV (376.39). Genotypes included in a particular cluster indicated their close relationship among themselves as compared to the other clusters. Therefore, it could be expected that genotypes within a cluster were less genetically different with each other, and were diverse from the accessions belonging to other clusters. Sohrabi *et al.* (2012) [31] clustered 35 upland rice into six clusters, cluster III contains 15 accessions and clusters I, II, IV and V comprised 6, 10, 2 and 4 accessions, respectively, and cluster VI was monogenic. Cluster mean for different traits (Table-8) revealed that the magnitude of differences among the mean of the traits for clusters was significant. The highest cluster means for plant height cm (114.04) was found in cluster VII, for panicle length (cm) was 21.06 in cluster II, for leaf length (cm) was 41.67 in cluster VIII, for leaf width (cm) was 1.43 in cluster VIII, for tillering ability was 20.17 in cluster I, for days to 50% flowering was 125.00 in cluster VIII, for days to maturity was 147.67 in cluster VIII, for grain length (mm) was 7.90 in cluster III, for grain width (mm) was 2.96 in cluster IV, for 1000-seed weight (g) was 29.63 in cluster IV and for grain yield  $\text{qha}^{-1}$  was 120.40 in cluster I. Cluster mean of different characters help in choosing the diverse parents for hybridization and these divergent parents are likely to broaden the genetic base (variability) and make available transgressive segregants with high heterotic effects (Qian and He, 1991; Rao and Gomathinayagam, 1997) [19, 21]. Sardana *et al.*, (1997) [25] observed that cluster means and genotypic coefficient variation reveal interesting picture about nature of diversity. The maximum intra cluster distance ( $D^2$ ) (cluster V) indicated high heterogeneity in genetic constitution of genotypes in that cluster while minimum intra cluster distance ( $D^2$ ) (cluster VIII) indicated homogeneity in genetic constitution of genotypes in that cluster. As well as the highest value of

intercluster distance (cluster VIII and VII) indicated also more heterogeneous genetic constitution of genotypes included in both clusters. Selection of the parents for hybridization should be done from different clusters having wide inter-cluster distance and those selected parents should have high *per se* performance for the traits contributing maximum towards divergence (Singh *et al.*, 1996) [33]. Clusters consisting of only one genotype with specific traits could be used in hybridisation programme for the exploitation of heterosis mainly as testers for expression of maximum heterosis. Singh *et al.*, (2010) [34] reported that highest mean values for days to maturity, plant height, total number of tillers per plant and panicle length and lowest mean values for test weight and kernel length.

The per cent contributions of the traits towards total genetic divergence (Table-9) revealed that plant height was the main factor contributing to divergence accounting for 41.16% followed by days to 50% flowering (18.17%), gain yield q ha<sup>-1</sup> (12.02%), days to maturity (9.98%), grain length (9.98%), tillering ability (7.98%), leaf width (5.75%), and grain width (1.13). The minimum contribution towards divergence was from grain width (1.13%) followed by leaf width (5.75%) and tillering ability (7.98%). The traits contributing maximum towards the divergence should be given great emphasis for deciding the clusters to be chosen for hybridisation and the subsequent selection of the parents from the clusters be based on their *per se* performance. In rice crop significant contribution towards divergence has been reported from plant height (Karthikeyan, 2002) [14]; and grain yield (Singh *et al.*, 1996; Ahmad and Borah, 1999; Karthikeyan, 2002; Datt and Mani, 2003) [33, 1, 14, 8].

The important characters reported by some researchers were plant height, panicle length, number of unfilled grains per panicle, 1000-grain weight (Latif *et al.*, 2011 and Sabesan *et al.*, 2009) [16, 24], grain yield, number of effective tillers (Baradhan and Thangavel, 2011) [5], harvest index (Ahmed *et al.*, 2010) [2], days to maturity (Kanwal *et al.*, 1983) [13] and number of secondary branches per panicle (Sinha *et al.*, 1991) [32].

## Conclusion

The multivariate analysis of the morphological traits clearly showed the existence of the wide variation among the genotypes. For each and every character, these variations could be exploited in improvement program. The study also suggests direct selection of the traits like plant height, days to 50% flowering, gain yield q ha<sup>-1</sup>, days to maturity, grain length, tillering ability, leaf width and grain width for future breeding program. Also the promising genotypes can be used as a reservoir of beneficial gene pool in developing high yielding varieties. Multivariate clustering pattern could also suggest the breeders about the suitability of different genotypes of rice for breeding program.

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