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Genetic variability studies among rice (*Oryza sativa* L.) genotypes under Kashmir conditions

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Abstract
The present investigation was undertaken to obtain information on the variability and genetic divergence with respect to various quantitative traits among 42 genotypes of rice. The experiment was laid out in the Randomized Complete Block Design with three replications. The observations were recorded on 28 characters. Analysis of variance revealed significant differences among genotypes for all the traits studied. The maximum range was recorded for grains per panicle followed by biological yield, plant height, flag leaf area and days to maturity. The highest phenotypic and genotypic coefficients of variability were observed for yield followed by harvest index, biological yield and flag leaf area. In general, the phenotypic coefficients of variation were slightly higher than genotypic coefficients of variation, which indicates the minor role of environment in the expression of traits under observation. The estimates of heritability in broad sense were high for all the characters. Correlation coefficients revealed that the grain yield per plant exhibited significant positive association with no. of grains per panicle, 1000 grain weight, panicle length and number of tillers per plant. The characters biological yield per plant contributed maximum towards genetic divergence followed by 1000 grain weight, plant height, panicle length number of filled grains per panicle and days to 50% flowering. Correlation coefficient of seed and seedling related traits revealed significant differences for all the characters among different genotypes. The present investigation indicated a great scope of in the improvement of these traits as these characters in general possessed high estimates of heritability coupled with high genetic advance except panicle length,1000 grain weight and days to maturity (high heritability but moderate genetic gain) indicating the preponderance of additive gene action for control of these traits.

Keywords: Correlation, genotypes, rice (*Oryza sativa* L.), genetic, variability, Kashmir

Introduction
Rice (*Oryza sativa* L.) is the most important food crop of the world, next only to wheat in terms of both area and production. Globally the area, production and productivity of rice is 158 million hectares, 700 million tonnes and 4.1 tonnes per hectare, respectively (Anonymous, 2013a) [1]. It is the staple diet of nearly one-half of the world population. Rice is considered as the first cultivated crop of Asia, where more than 90% of global rice is produced and consumed. India is the largest rice growing country of world in terms of area and second in production. The area, production and productivity of rice in India is 43.9 million hectares, 106.3 million tonnes and 2.42 tonnes per hectare, respectively. It accounts for more than 40% of food grain production and provides direct employment to 70% people in rural areas (Anonymous, 2013b) [2].

To sustain the high productivity level of rice, genetic variability existing in nature or created through crop breeding is of immense value. Genetic uniformity within a crop is readily brought about by using the same gene or gene complexes during breeding programmes. When uniformity becomes the cause of genetic vulnerability, genetic diversity is the only insurance against it. To overcome the menace of this uniformity, it is essential that genetic variability, present in both the cultivated and wild species, is systematically exploited and used to generate new gene complexes for higher grain yield and tolerance to biotic and abiotic stresses. The effectiveness of selection depends upon the range of genetic variability already existing in the population in respect of important economic characters. The progress of breeding is conditioned, primarily by the magnitude, nature and inter relationships of genetic variation for various plant characters in such a population. In any crop, the germplasm serves as a valuable source of base population and provides scope for wide variability. Information on the nature and degree of genetic divergence would help the plant breeder in choosing the right parents for

breeding programme (Vivekanad and Subramanian 1993) [10]. It is well known that all plant breeding programmes involve selection at one stage or other. Genetic variances serve as a basis for major plant breeding decision; they provide a greater array of genotypes among which selection can be practiced to develop still new varieties or breeding materials. Success in recombination breeding depends on the suitable exploitation of genotypes Success in recombination breeding depends on the suitable exploitation of genotypes as parents for obtaining high heterotic crosses and transgressive segregants. For this, the presence of genetic variability in a base population is essential. Heritability and genetic advance are other important selection parameters. The estimates of heritability help the plant breeder in determining the character for which selection would be rewarding. The breeders are interested in selection of superior genotypes based on their phenotypic expression. The major function of heritability estimates is to provide information on transmission of characters from the parents to the progeny. In view of the above facts the study was aimed to evaluate the Rice (*Oryzea sativa*) genotypes through genetic variability, heritability, and genetic advance estimation and correlation analysis.

Materials and Methods

The present experiment was conducted at Mountain Research Centre for Field Crops (MRCFC), SKUAST-Kashmir, Khudwani, Anantnag 70 km away from Srinagar towards south kharif 2018. The altitude of the location is 1685 meter above mean sea level and situated 34º N of latitude and 74.89º 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 and April. Forty-two genotypes of rice (*Oryza sativa* L.) were characterized based on qualitative and quantitative agro-morphological descriptors. The name of the varieties genotypes along with their source are given in Table-1. The rice genotypes were grown in a randomized block design with three replications. The 25 days old seedling from each entry were planted in 13.2 m × 8.5 m plot with 40 cm × 15 cm spacing using single seedling per hill. The plot size was kept 2.2×1.32 (2.904 m²), each plot consisted of 3 rows of each genotype in each replication at spacing of 40 × 15 cm. All necessary cultural operations and management practices were employed as and when necessary. Observations were recorded on various quantitative traits *viz*., Days to 50% flowering, Flag leaf area (cm²), Plant height (cm), Number of tillers per plant, Panicle length (cm), Biological yield per plant (g), Yield per plant (g), Harvest index percentage, Number of grains per panicle, Grain length (mm), Grain width (mm), L:B ratio, 1000-grain weight (g), and Days to maturity in order to study the magnitude of genetic variability existing in the materials under study. Each observation was made from five randomly taken plants and accessions were characterized according to descriptors established by the International Rice Research Institute (IRRI) and standard rice evaluation system.

Results and Discussion

The presence of variability in any crop population is essential improvement in breeding program of a crop (Hasan *et al*., 2006) [11]. The analysis of variance revealed that all the 14 characters exhibited highly significant differences among the genotypes (Table 2). The estimates of phenotypic and genotypic coefficients of variation of all the characters studied are presented in Table 2. In general, the phenotypic and genotypic coefficients of variation were almost similar with slight higher phenotypic coefficients of variation, which indicates the role of environment in the expression of traits under observation. This was in agreement with the study of Bandale *et al*. (2006) [31]. It is evident from the data presented in Table 3 that yield (31.19 and 29.17%), biological yield (28.059 and 27.80%) and harvest index (31.020 and 28.140%) recorded high phenotypic and genotypic coefficients of variation, indicating that genotypes had broad genetic base for these characters. Flag leaf area (25.464 and 22.036%), tillers per plant (20.740 and 17.525%), grains per panicle (17.618 and 17.618%) and plant height (15.18 and 15.176%) exhibited moderate phenotypic and genotypic coefficients of variation suggesting the existence of moderate variability in the genotypes studied. Rest of the traits such as days to 50% flowering (9.930 and 4.720%), panicle length (7.777 and 7.179%), grain length (9.495and 8.704%), grain width (8.165 and 7.989%), L: B ratio (12.714 and 11.913%), 1000 grain weight (11.358 and 7.856%) and days to maturity (8.370 and 7.850%) showed low phenotypic and genotypic coefficients of variation. Thus, these characters were less amenable for improvement through selection. Characters recording moderate to high coefficients of variation have better potential for improvement through selection. A wide range of variability along with high estimates of phenotypic and genotypic coefficients of variation further indicate that these attributes would respond to selection.

Heritability was high for most of the characters ranging from 70 to 99 percent (Except grains per panicle, grain width and days to 50% flowering) indicating that the characters were less influenced by environmental effects and the characters are effectively transmitted to the progeny, suggesting major role of genetic constitution in the expression of a character and thus selection based on phenotypic expression could be relied upon. Similar results were observed by Verma *et al*. (2004) [9]. High heritability accompanied with moderate genetic advance were observed in tillers per plant and plant height which indicated that these traits might be governed considerably by additive gene action (Panse, 1957) [7].

High estimate of heritability along with genetic gain (percent of mean) is more reliable than heritability alone for predicting the effect of selection (Johnson *et al*., 1955) [5]. The characters *viz*., grain yield, flag leaf area, biological yield and harvest index recorded high estimates of heritability coupled with high genetic advance as percent of mean (GAM), indicating the preponderance of additive gene action for control of these traits. This suggests that real progress in improvement through selection could be made for yield. Grain yield plant^{-1} is an important character, which decides the commercial viability of the hybrid/variety. Thus, the trait deserves the highest priority in any breeding programme. This was supported by Singh *et al*. (2005) [8], Verma *et al*. (2004) [9], Mallikarjun *et al*. (2003) [6] and Jabeen *et al*. (1998) [4]. High heritability along with high genetic advance as percent of mean for this trait suggested the possibility of selecting high yielding cultivars from the present collection.

The most economically important trait i.e. grain yield exhibited significant and positive association with, number of grains per panicle (r=0.265**), and grain weight (r=0.266**) that directly contributed to the yield of the rice genotypes. Other traits such as plant height, tillers per plant, panicle

length, flag leaf area, days to 50% flowering and days to maturity were also important with respect to the yield of the plants. In this study, plant yield was positively and significantly correlated with panicle length (r= 0.265**), grains per panicle (r= 0.266**), tillers per plant (r=0.594**) and grain weight (r= 0.339**). On the other hand, panicle length was positively and significantly associated with flag leaf area (r= 0.302**), seeds per panicle (r=0.365**), and days to 50% flowering (r= 0.321**).The grains per panicle were having positive and significant correlation with seed weight (r= 0.770**) but negative and significant correlation with days to 50% flowering and days to maturity (r=-0.537**) and (r=-0.236**) respectively. These results suggested that selection for these characters may be useful for improvement in grain yield of rice. (Table 4).

Table 1: List of rice (*Oryza sativa* L.) genotypes used in the study

S. No.	Genotypes	Source
1.	K1313-24-3	SKUAST-K
2.	K1329-16-2	SKUAST-K
3.	K1329-16-3	SKUAST-K
4.	SR-1	SKUAST-K
5.	SR-2	SKUAST-K
6.	SR-3	SKUAST-K
7.	K1331-3-1	SKUAST-K
8.	K1356-6-4	SKUAST-K
9.	K1313-51-3	SKUAST-K
10.	K1329-10-4	SKUAST-K
11.	K1331-1-2	SKUAST-K
12.	K08-2-11-3	SKUAST-K
13.	k08-3-10-7	SKUAST-K
14.	K08-4-1-8	SKUAST-K
15.	K08-5-6-2	SKUAST-K
16.	K08-12-4-2	SKUAST-K
17.	K08-17-1-3	SKUAST-K
18.	K08-17-5-2	SKUAST-K
19.	K08-17-3-2	SKUAST-K
20.	K08-20-6-4	SKUAST-K
21.	K08-24-5-8	SKUAST-K
22.	K08-28-7-9	SKUAST-K
23.	K08-43-7-3	SKUAST-K
24.	K08-49-8-2	SKUAST-K
25.	K08-62-2-7	SKUAST-K
26.	K1416-23-5	SKUAST-K
27.	SKAU-417	SKUAST-K
28.	K1416-20-2	SKUAST-K
29.	K1416-1-4	SKUAST-K
30.	K1416-21-5	SKUAST-K
31.	K1416-26-2	SKUAST-K
32.	K1416-14-3	SKUAST-K
33.	K1416-8-1	SKUAST-K
34.	SKAU419	SKUAST-K
35.	SKAU420	SKUAST-K
36.	SKAU422	SKUAST-K
37.	SKAU423	SKUAST-K
38.	K09-1-6-1-5	SKUAST-K
39.	K08-2-18-1-5	SKUAST-K
40.	K08-5-41-2-4	SKUAST-K
41.	KO8-8-25-2-1	SKUAST-K
42.	K08-11-8-1-4	SKUAST-K

Table 2: Analysis of variance for various agro-morphological traits in rice

Source of variation	DF	Days to 50% flowering	No. of tillers per plant	Plant height (cm)	Biological yield (g)	Yield (g)	Harverst index	Panicle length (cm)
Replication	2	32.88	3.007	15.267	0.377	55.382	8.372	80.094
Genotypes	41	60.88	15.110	762.60	762.280	947.440	68.434	175.964
Error	82	32.47	1.78	20.467	0.115	5.777	3.119	11.776
p-value		0.0008**	0.0001**	0.0001**	0.0001**	0.0001**	0.0001**	0.0001**

Level of significance $p<0.01=$ **

Source of variation	DF	No. of grains per panicle	Grain length (mm)	Grain width (mm)	L:B ratio	1000 grain weight	Days to maturity
Replication	2	406.543	0.988	0.003	0.153	1.944	21.198
Genotypes	4`	1474.53	1.625	0.150	0.391	11.278	239.02
Error	82	23.806	0.096	0.002	0.017	3.006	10.515
p-value		0.0001**	0.0001**	0.0001**	0.0001**	0.0001**	0.0001**

Table 3: Estimates of mean, range, phenotypic variance, genotypic variance, phenotypic and genotypic coefficients of variation, heritability (bs) and genetic advance (as% of mean) for different growth characters in rice (*Oryza sativa*)

Character	Mean	Range	Genotypic coefficient of variation (GCV)	Phenotypic coefficient of variation (PCV)	Genotypic variance (gv)	Phenotypic variance (pv)	Heritability (bs)	Genetic advancement as percent of mean
Days to 50% flowering	65.15	61-73.66	4.720	9.930	9.470	41.940	22.59	5.930
Tillers per plant	12.031	7-16.33	17.525	20.740	4.446	6.226	71.40	39.096
Flag leaf area (cm²)	35.455	24.32-64.93	22.036	25.464	61.046	81.513	74.80	50.346
Plant height (cm)	105.027	74.07-131.53	15.176	15.75	254.06	254.17	78.54	40.056
Biological yield (g)	63.719	33.36-112.29	27.804	28.059	313.89	319.66	98.90	72.737
Yield (g)	15.994	8.14-30.21	29.172	31.192	21.771	24.89	87.40	72.026
Harvest index	26.289	9.7-48.4	28.140	31.020	54.729	66.50	82.20	67.392
Panicle length (cm)	22.784	18.46-25.50	7.179	7.777	2.676	3.139	85.20	17.500
Grains per panicle	127.854	79.66-179	17.199	17.618	483.57	507.38	45.30	44.328
Grain length (mm)	8.201	6.36-9.40	8.704	9.495	0.509	0.606	84.00	21.062
Grain width (mm)	2.785	2.066-3.10	7.989	8.165	0.049	0.051	44.80	20.639
L:B ratio	2.965	2.27-3.923	11.913	12.714	0.125	0.142	87.80	29.472
1000 grain weight(g)	21.135	12.66-24	7.856	11.358	2.757	5.763	47.80	14.345
Days to maturity	111.182	95.33-128.33	7.850	8.370	76.170	86.680	87.80	19.426

Table 4: Estimates of genotypic correlation coefficients among different growth characters in rice (*Oryza sativa*)

Character	Days to 50% flowering	Tillers per plant	Flag leaf area (cm²)	Plant height (cm)	Biological yield (g)	Yield (g)	Harvest index	Panicle length (cm)	Grains per panicle	Grain length (mm)	Grain width (mm)	L:B ratio	1000 grain weight	Days to maturity
Days to 50% flowering		0.171*	0.352**	-0.049	0.237**	-0.052	-0.267**	0.321**	-0.537**	0.288**	0.397**	-0.151*	-0.124*	-0.612**
Tillers per plant			-0.035	0.134*	0.313	0.157*	-0.114	0.190	-0.039	0.019	0.234*	-0.176*	-0.179*	0.043
Flag leaf area (cm²)				-0.046	0.172*	-0.206*	-0.376**	0.302**	-0.229*	0.255*	0.035	0.175*	-0.104	0.059
Plant height (cm)					-0.324**	-0.408**	0.030	-0.032	0.305**	-0.316**	0.378**	-0.532**	-0.036	0.059
Biological yield (g)						0.427**	-0.568**	-0.026	-0.173*	0.246**	0.054	0.122	0.193*	0.0252
Yield (g)							0.465**	0.265**	0.266**	-0.071	-0.051	-0.035	0.266**	0.151
Harvest index								-0.107	0.127	-0.345**	-0.029	-0.237**	-0.395**	0.0017
Panicle length (cm)									0.365**	0.267**	0.043	0.164	0.129	-0.207
Grains per panicle										0.044	0.255*	-0.234	0.770**	-0.236**
Grain length (mm)											0.111*	0.651**	0.222*	-0.183*
Grain width (mm)												-0.676**	-0.254**	-0.059
L:B ratio													0.343**	-0.076
1000 grain weight														-0.078
Days to maturity														

Level of significance $p<0.05$=* and $p<0.01$=**

Conclusion

Analysis of variance revealed significant differences among genotypes for all the traits studied. On the basis of mean performance of the genotypes K08-43-7-3 recorded the highest yield of 30.21 g per plant followed by K1313-24-3 (27.73 g), K1416- 8-1 (26.40 g), KO8-8-25-2-1 (24.10 g) and K09-1-6-1-5 (22.22 g). The phenotypic and genotypic coefficients of variability ranged from 7.77-31.192 and 4.720-29.172, respectively. The highest phenotypic and genotypic coefficients of variability were observed for grain yield. In general, the phenotypic and genotypic coefficients of variation were almost similar with slight higher phenotypic coefficients of variation, which indicates the minor role of environment in the expression of traits under observation. The present investigation indicates a great scope of fast improvement in all the traits as these characters in general possessed high estimates of heritability coupled with high genetic advance except for days to 50% flowering, grain weight, grain length, grain width and days to maturity which recorded high heritability but low genetic advance (As percent

of mean). Grain yield exhibited significant and positive association with grains per panicle and grain weight that directly contributed to the yield of the rice genotypes. Other traits such as plant height, tillers per plant, panicle length, flag leaf area, days to 50% flowering and days to maturity were also important with respect to the yield of the plants.

The study revealed considerable amount of genetic variability among the genotypes with respect to the selected traits studied.

The genotypes proved to be superior with respect to grain yield and most of its contributing traits hence these genotypes can be used in rice improvement program as elite germplasm lines and may be recommended for commercial cultivation after testing them over years and locations.

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