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Genetic variability for seed yield component characters and grain yield in elite breeding lines of rice (*Oryza sativa* L.)

Meghana Devi Devineni, Suresh B G
Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh, India

Abstract
Rice (*Oryza sativa* L.) is one of the staple cereal crops of the world and it is one of the main sources of carbohydrate for nearly one half of the world population. Variability may be a greater need for initiating a breeding program for yield and yield contributing traits. The present investigation was carried out with 27 Advanced Breeding Lines (ABL'S) including 2 check varieties of rice germplasm in Randomized Block Design during *kharif-2019*. The data was recorded for 13 quantitative and 07 quality traits to study Analysis of variance, assessment of variability, Heritability, Genetic advance, Correlation coefficient analysis and Path coefficients for yield, yield component traits. It is concluded from the results of the present investigation, that significant differences were observed for all the characters among the rice germplasm. A detailed analysis revealed SHUATS DHAN (ABL)-02 (36.83g) followed by SHUATS DHAN (ABL)-04 (34.33 g), SHUATS DHAN (ABL)-07 (31.90 g), SHUATS DHAN (ABL)-11 (31.60g) which had equal grain yield per hill as compared to CHECK SHIATS DHAN-1. High estimates of genotypic and phenotypic coefficient of variation were recorded for number of grains per panicle, test weight and number of tillers per plant indicating that these characters could be used as selection for crop improvement. High heritability coupled with genetic advance as percent of mean were recorded for traits test weight, number of grains per panicle, number of tillers per plant, number of panicles per plant and biological yield, indicating ample scope for their improvement through selection. Correlation study revealed that grain yield per plant showed the positive significant association with plant height, number of tillers per plant, number of panicles per plant, flag leaf length, flag leaf width, biological yield at phenotype and genotypic level. Path coefficient analysis revealed that days to 50% flowering, plant height, number of tillers per plant, flag leaf length, biological yield and test weight has positive direct effect on grain yield per plant at phenotype and genotypic level.

Keywords: advance breeding lines (ABL), genetic variability, heritability, correlation and path analysis

Introduction

Rice is the major crop in Uttar Pradesh and is grown in about 5.81 m ha (accounting for 13.28% of entire area). The state ranks second in the country in production of rice. The production is 13.27 million tons (accounting for 11.75% of entire area) and productivity of the state is around 2.2 t/ha. Thus, it is understood that there is an extreme need to enhance the rice productivity in Uttar Pradesh, which will be achieved only by developing high yielding hybrid varieties. (Agriculture statistics at a glance – 2018, DAC & FW, GoI).

Genetic variability refers to the presence of difference among the individuals of the plant population. The large spectrum of genetic variability in segregating population depends on the amount of the genetic variability among genotypes and offer better scope for selection. The magnitude of heritable variation in the traits studied has immense value in understanding the potential of the genotype for further breeding programme. Variability results due to difference either in the genetic constitution of the individuals of a population or in the environment in which they are grown. (Mohammad *et al.,* 2002).

The estimates of genotyping coefficient of variance (GCV) reflect the total amount of genetic variability present in the germplasm. However, the proportion of the genotyping variability which is transmitted from parents to the progeny is reflected by heritability. Broad sense heritability determines the efficiency with which genotypic variability in a breeding program. Correlation coefficient studies helps in determination of interrelationship between various plant characters. The path coefficient is a standardized partial regression coefficient and as such it measures the direct influence of variable upon another and partitioning correlation coefficient into components of direct and indirect effects. To improve the production potential of this crop breeding programme should be aimed at development of high yielding varieties by combining genes from diverse sources. These breeding strategies may be made more effective by gathering adequate information on genetic architecture, heterosis, inbreeding depression, correlation and path coefficient analysis for yield and its components. This helps the plant breeder in designing an ideotype and in isolation of superior genotypes from early segregating populations leading to success in crop improvement for various ecological conditions. Therefore, the present investigation was carried out to assess the genetic variability, association of different traits towards yield and selection of high yielding genotypes.

Materials and Methods

The experimental material comprised of twenty-seven advanced breeding lines of rice were sown at Field Experimentation Centre of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, U.P during Kharif-2019. The experiment was laid in Randomized Block Design. The data was recorded for 13 quantitative and 07 quality traits *viz*; Days to 50% flowering, Plant height, Flag leaf length, Flag leaf width, Number of tillers per hill, Number of panicles per hill, Panicle length, Number of spikelet's per panicle, Days to maturity, Biological yield per plant, Test weight, Harvest index, Grain yield per plant, Hulling percentage, Kernel length before cooking, Kernel width before cooking, Kernel length after cooking, Kernel width after cooking, L/B ratio and Elongation ratio. Recommended package of practices were followed to raise a healthy chickpea crop. Biometrical methods were followed to estimate genotypic and phenotypic coefficient of variation, heritability in broad sense, genetic advance and correlation and path coefficient analysis.

Results and Discussion

For all of the examined traits, analysis of variance revealed significant differences for all the characters indicating sufficient variability among the genotypes. The examination of data revealed that the mean sum of squares due to genotype showed highly significant for all the 13 quantitative characters. The performances of genotype with respect to these characters were statistically different indicating ample scope for selection of different qualitative and quantitative characters for rice improvement. The results from analysis of variance for 13 quantitative characters are presented in Table 4.1.

The presence of large amount of variability might be due to diverse source of materials taken as well as environmental influence affecting the phenotypes. High genetic variability for different quantitative traits in rice was also reported earlier by Mustafa *et al.* (2007), Vivek *et al.* (2005) [16].

The studies on GCV and PCV indicated that the presence of high amount of variation and role of the environment on the expression of these traits. The magnitude of PCV was higher than GCV for all the characters which may due to higher degree of interaction of genotype with the environment (Senapati and Kumar, 2015). High GCV were found for number of tillers per plant followed by test weight and number of grains per panicle. This indicates that certain variables are less susceptible to environmental variations, and hence, greater focus should be placed on these characters when breeding cultivars from the current material. High phenotypic coefficient of variation were found in grain yield per hill followed by biological yield test weight, number of panicles per plant, number of tillers per plant and number of grains per panicle. Environmental influences had a greater influence on the traits with a high phenotypic coefficient of variation. As a result, attention must be given during the selection process, as environmental fluctuations are highly unpredictable and may cause results to be affected.

In the present study, the heritability in broad sense (h^2) ranges from 42.8 % to 99.9%. High estimate of heritability recorded for test weight, days to 50% flowering, days to maturity, plant height, flag leaf length, panicle length, number of tillers per plant, flag leaf width, number of panicles per plant, biological yield and number of grains per panicle suggested that environmental influences had the least impact on the features, as well as phenotypic expression, which shows the genotypic ability of cultivars to pass genes to their offspring.

High genetic advance was found in test weight, number of grains per panicle, number of tillers per plant, number of panicles per plant and biological yield. High genetic advance as percent of was observed for test weight, number of grains per panicle, number of tillers per plant, number of panicles per plant, biological yield and selection may be effective for these characters. High estimates of heritability does not always mean high genetic advance. Johnson *et al*. (1955) suggested that heritability estimates and the genetic advance as percent of mean together would provide a better judgment rather than heritability alone in predicting the resultant effect of selection. Evaluation of genetic advance helps in interpreting the type of gene action involved in the expression of various polygenic traits. High values and low values genetic advance are indicative of additive gene action and non-additive gene action respectively.

Genotypic correlation coefficient analysis revealed that grain yield per plant showed highly significant and positive association with biological yield (0.862**), number of panicles per plant (0.570**), number of tillers per plant (0.543**), flag leaf width (0.503**), plant height (0.486**) and flag leaf length (0.469**). Phenotypic correlation coefficient analysis revealed that grain yield per plant showed significant and positive association with days to maturity (0.819**), number of tillers per plant (0.479**), test weight (0.441**), plant height (.375**), flag leaf length.

Table 1: Genetic parameters of yield and yield components in rice

Characters	GCV	PCV	Heritability	Genetic Advance	Genetic Advance as percent Mean
D50%F	8.33	8.45	97.3	15.71	16.93
PH	8.53	8.83	93.3	19.94	16.97
NTPP	20.40	23.44	75.8	3.43	36.58
NPPP	19.48	22.84	72.8	2.91	34.24

PL	6.77	7.63	78.7	3.02	12.37
FLL	13.28	14.63	82.5	8.33	24.86
FLW	8.05	9.39	73.6	0.18	14.24
NGPP	27.03	34.71	60.6	70.67	43.35
DM	4.86	4.96	96.2	12.06	9.82
BY	16.86	21.55	61.3	14.55	27.19
HI	8.35	26.67	57.26	7.23	13.75
TW	21.89	21.91	99.9	10.22	45.07
GYPP	13.99	20.99	44.5	5.40	19.23

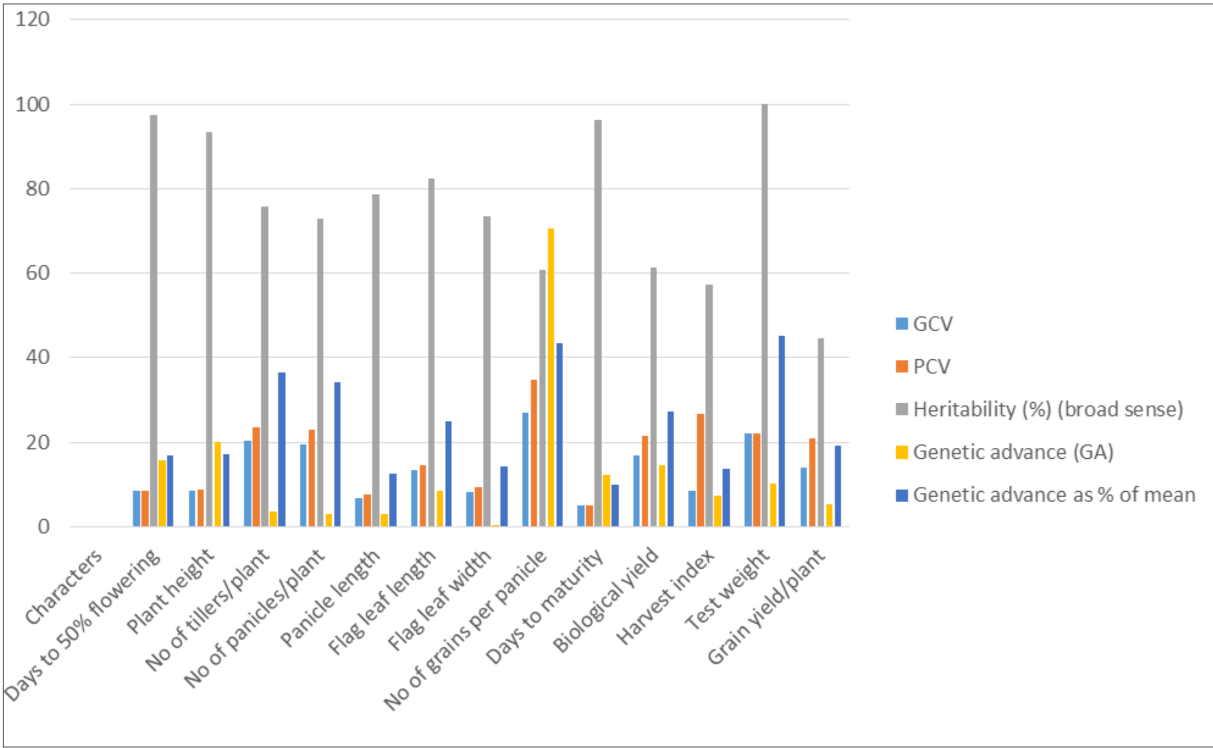

Fig 1: Genetic summary of 27 Advance Breeding Lines of Rice

Table 2: Phenotypic and Genotypic Correlation between grain yield and its components in rice

	D50%F	PH	NTPP	NPPP	PL	FLL	FLW	NGPP	DM	BY	HI	TW	GYPP
D50%F	1	0.055	0.352**	0.430**	-0.179	0.192	0.711**	0.131	0.817**	0.446**	-0.696**	-0.396**	0.181
PH	0.060	1	-0.034	-0.058	0.276*	0.891**	0.277*	0.131	-0.186	0.262*	0.366**	0.179	0.486**
NTPP	0.317**	0.038	1	0.967**	-0.177	0.096	0.197	0.014	0.330**	0.771**	-0.698**	-0.244*	0.543**
NPPP	0.373	-0.035	0.902**	1	-0.177	0.065	0.273*	0.082	0.386**	0.794**	-0.725**	-0.276*	0.570**
PL	-0.169	0.250*	-0.093	-0.80	1	0.037	-0.006	-0.317**	-0.263*	-0.007	0.008	0.420**	-0.004
FLL	0.166	0.827**	0/082	0.077	0.018	1	0.249*	0.043	-0.025	0.253*	0.346**	0.119	0.469**
FLW	0.630**	0.272*	0.151	0.195	0.023	0.213	1	0.436**	0.729**	0.683**	-0.492**	-0.264*	0.503**
NGPP	0.099	0.102	-0.011	-0.036	-0.268*	0.038	0.293**	1	0.252*	0.177	0.056	-0.785**	0.179
DM	0.794**	-0.184	0.278*	0.314**	-0.252*	-0.025	0.596**	0.190	1	0.500**	-0.688**	-0.441**	0.197
BY	0.360**	0.259	0.661*	0.638**	-0.025	0.250*	0.596**	0.133	0.362**	1	-0.616**	-0.040	0.862**
HI	0.426**	0.231*	-0.398**	0.440**	0.011	0.193	-0.233*	0.118	-0.466**	-0.257*	1	0.318**	-0.085
TW	-0.392**	0.173	-0.207	0.231*	0.375**	0.107	-0.230*	-0.613**	-0.432**	-0.030	0.205	1	0.166
GYPP	0.134	0.375**	0.479**	-0.026	0.352**	0.357**	0.140	0.080	0.819	0.176	0.112	0.441**	1

D50F=Days to 50% Flowering, PH=Plant Height, NTPP=No. of Tillers per plant, NPPP= No. of Panicles per plant, FLL= Flag Leaf Length, FLW= Flag Leaf Width, NGPP= NO. of Grains per plant, DM= Days to Maturity, HI= Harvest Index, TW= Test Weight, GYPP= Grain Yield Per Plant.

Table 3: Genotypic direct (in bold) and indirect effects of 13 traits on grain yield in rice.

	D50F	PH	NTPP	NPPP	PL	FLL	FLW	NGPP	DM	BY	HI	TW	GYPP
D50F	0.314	0.017	0.110	0.135	-0.056	0.060	0.223	0.041	0.257	0.140	-0.218	-0.124	0.181
PH	-0.001	-0.033	0.001	0.002	-0.009	-0.029	-0.009	-0.004	0.006	-0.008	-0.012	-0.006	0.486**
NTPP	-0.073	0.007	-0.209	-0.213	0.037	-0.020	-0.041	-0.003	-0.069	-0.161	0.146	0.051	0.543**
NPPP	0.374	-0.051	0.889	0.871	-0.154	0.056	0.238	0.071	0.336	0.692	-0.632	-0.240	0.570**
PL	-0.005	0.008	-0.005	-0.005	0.031	0.001	-0.000	-0.01	-0.008	-0.002	0	0.013	-0.004
FLL	0.061	0.285	0.030	0.020	0.011	0.320	0.079	0.013	-0.008	0.081	0.110	0.038	0.469**

FLW	-0.415	-0.162	-0.115	-0.159	0.003	-0.145	-0.585	-0.255	-0.426	-0.399	0.287	0.154	0.503**
NGPP	0.213	0.214	0.0229	0.133	-0.513	0.069	0.707	1.621	0.408	0.288	0.091	-1.273	0.179
DM	0.291	-0.066	0.117	0.137	-0.093	-0.008	0.259	0.089	0.356	0.177	-0.245	-0.156	0.197
BY	0.012	0.007	0.022	0.022	-0.002	0.007	0.019	0.005	0.014	0.028	-0.017	-0.001	0.862**
HI	0.108	-0.05	0.108	0.112	-0.001	-0.053	0.076	-0.008	0.107	0.095	-0.155	-0.044	-0.085
TW	-0.697	0.315	-0.430	-0.486	0.739	0.210	-0.465	-1.382	-0.775	-0.071	0.559	1.760	0.166

D50F=Days to 50% Flowering, PH=Plant Height, NTPP=No. of Tillers per plant, NPPP= No. of Panicles per plant, FLL= Flag Leaf Length, FLW= Flag Leaf Width, NGPP= NO. of Grains per plant, DM= Days to Maturity, HI= Harvest Index, TW= Test Weight, GYPP= Grain Yield Per Plant.

Table 4: Phenotypic direct (in bold) and indirect effects of 13 traits on seed yield in rice.

	D50%F	**PH**	**NTPP**	**NPPP**	**PL**	**FLL**	**FLW**	**NGPP**	**DM**	**BY**	**HI**	**TW**	**GYPP**
D50%F	0.0358	0.0022	0.0113	0.0134	-0.0061	0.0060	0.0226	0.0035	0.0285	0.0129	-0.0153	-0.0140	0.1349
PH	-0.0003	-0.0048	0.0000	0.0000	-0.0012	-0.0040	-0.0013	-0.0005	0.0009	-0.0012	-0.0011	-0.0008	0.375**
NTPP	0.0148	0.0004	0.0467	0.0421	-0.0044	0.0039	0.0071	-0.0005	0.0130	0.0309	-0.0185	-0.0097	0.479**
NPPP	0.0233	-0.0003	0.0564	0.0625	-0.0050	0.0048	0.0122	-0.0023	0.0196	0.0399	-0.0275	-0.0145	-0.0269
PL	0.0088	-0.0129	0.0048	0.0041	-0.0518	-0.0010	-0.0010	0.0139	0.0130	0.0013	-0.0006	-0.0194	0.352**
FLL	0.0053	0.0265	0.0026	0.0025	0.0006	0.0321	0.0068	0.0012	-0.0008	0.0080	0.0062	0.0034	0.357**
FLW	0.0372	0.0160	0.0089	0.0115	0.0012	0.0126	0.0590	0.0173	0.0352	0.0298	-0.0138	-0.0136	0.1409
NGPP	0.0033	0.0034	-0.0004	-0.0012	-0.0089	0.0013	0.0098	0.0334	0.0064	0.0045	0.0039	-0.0205	0.0803
DM	-0.0936	0.0218	-0.0327	-0.0370	0.0296	0.0030	-0.0702	-0.0225	-0.1179	-0.0427	0.0549	0.0509	0.819**
BY	0.3017	0.2171	0.5534	0.5344	-0.0217	0.2091	0.4232	0.1116	0.3032	0.8371	-0.2151	-0.0258	0.1766
HI	-0.1633	0.0885	-0.1521	-0.1687	0.0042	0.0742	-0.0893	0.0453	-0.1786	-0.0985	0.3834	0.0787	0.1122
TW	-0.0381	0.0168	-0.0201	-0.0225	0.0365	0.0104	-0.0224	-0.0596	-0.0420	-0.0030	0.0200	0.0973	0.441**

D50F=Days to 50% Flowering, PH=Plant Height, NTPP=No. of Tillers per plant, NPPP= No. of Panicles per plant, FLL= Flag Leaf Length, FLW= Flag Leaf Width, NGPP= NO. of Grains per plant, DM= Days to Maturity, HI= Harvest Index, TW= Test Weight, GYPP= Grain Yield Per Plant.

0.357**) and panicle length (0.352**). The study of interrelationships among various traits in the form of correlation is one of the most significant parts of a selection program for the breeder to make an efficient selection based on correlated and uncorrelated responses.

In the present investigation, results showed that the genotypic correlation coefficient in general were higher than the phenotypic correlation coefficient. The interrelationships were therefore, strongly inherent and low phenotypic expression were due to environmental factors. The phenotypic expression of correlation coefficient, however appeared to be depressed in some cases due to environmental influence thus selection based on phenotype may be effective Path coefficient analysis reveals that the association of the characters with yield is due to their direct effect on yield or is a result of their indirect effects via other components characters. It measures the direct and indirect contribution of independent variables on dependent variable and helps breeder in determining the yield components. Therefore, selection based on these traits will be effective in improving grain yield indicated that there may be few more characters which could have been included for estimation of direct and indirect contributors.

The yield related traits displaying positive and significant association with grain yield per plant suggested that grain yield can be improved through simultaneous selection for these traits. Selection is generally based on phenotypic expression of traits. Hence selection for the traits exhibiting positive significant genotypic and positive significant phenotypic correlation would be of major use in indirect and direct selection for grain yield respectively. Phenotypic path coefficient analysis indicated that, the traits having direct effects on grain yield are understood to be strongly associated with it. The path analysis results showed that positive and direct on grain yield was exhibited by test weight, biological yield, number of panicles per plant, flag leaf width, number of tillers per plant, harvest index, number of grains per plant, and flag leaf length. It means a slight increase in any one of the above traits may directly contribute towards seed yield. Breeding strategies to improve yield in rice should aim in selection of above traits in further crop improvement programme.

Conclusion

It is concluded from the present results is High to moderate estimates of GCV and PCV are recommended for number of tillers per plant, number of panicles per plant, number of grains per panicle, biological yield, test weight and grain yield per hill. High estimates of Heritability coupled with high values of Genetic advance as per cent mean was observed for biological yield, number of panicles per plant, number of tillers per plant, number of grains per panicle and test weight respectively suggesting that there was preponderance of additive gene action for the expression of these characters.

Grain yield per plant showed the high significant positive correlation with plant height, number of tillers per plant, number of panicles per plant, flag leaf length, flag leaf width, biological yield at phenotype and genotypic levels. Path coefficient analysis revealed that days to 50% flowering, plant height, number of tillers per plant, flag leaf length, biological yield and test weight has positive direct effect on grain yield per plant. Selection of plants on these traits would certainly lead to improvement in grain yield.

Since these results are based on one-year evaluation, which is not sufficient to conclude experimental results hence further experimentation is needed to confirm the result. This Advanced Breeding Lines have been studied for one year i.e., kharif-2019. The investigation should be carried out forward for better results.

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