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Assessment of genetic variability, correlation and path analysis for yield and related traits in elite rice (*Oryza sativa* L.) germplasm

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Abstract

Studies on genetic variability, heritability, genetic advance and correlation coefficient analysis and path analysis. Analysis of variance among 26 elite rice germplasm showed highly significant differences for all the characters under study indicated the presence of a substantial amount of genetic variability. Higher estimates of GCV and PCV were for number of panicles per plant followed by number of tillers per plant followed by spikelets per panicle indicating that these characters could be used as selection for crop improvement. High heritability coupled with high genetic advance is recorded for number of spikelets per plant. Correlation study revealed that Grain yield per plant showed the high significant positive correlation with number of tillers per plant, number of panicles, panicle length, number of grains per panicle, biological yield showed positive significant correlation at phenotype and genotypic levels. Path coefficient analysis revealed that days to 50% flowering, plant height, number of tillers per plant, number of panicles per plant, flag leaf length, number of grains per panicle, biological yield and harvest index has positive direct effect on grain yield per plant.

Keywords: Rice, genetic variability, heritability, genetic advance, correlation coefficient, path analysis

Introduction

Rice is the most important food grain crop of the world and forms the staple diet of 2.7 billion peoples. Rice provides 75% of the calories and 55% of the protein in the average daily diet of the peoples. Rice contributes the 43% of total food grain production and 46% of total cereal production. (FAO [Food and Agriculture Organization]. India stands first in area and second in production. India is a major rice growing country of the world with an area 43.97 m ha, production 104.32 million tones and productivity of 2.4 t/ha (Agricultural Statistics at a glance, 2016) [1]. Genetic variability for quantitative traits is the key component of breeding programme for broadening the gene pool of rice and other crops. High magnitude of variability in a population provides the opportunity for selection to evolve a variety having desirable characters. The genetic coefficient of variation together with heritability estimate would give the best picture of the amount of advance to be expected from the selection. The amount of genetic advance under selection mainly depends on the amount of genetic variability. The systematic breeding Programme involves the steps like creating genetic variability practicing selection and utilization of selected genotypes to evolve promising varieties. Knowledge of the nature and magnitude of genetic variance present in the breeding material is the most important pre requisite for successful breeding Programme. Parameters such as genotypic and phenotypic variances, as well as co-efficient of variation are useful in detecting the variability present in the germplasm. The success of plant breeding depends on the extent of genetic variability present in a crop. Understanding the nature and magnitude of genetic variation governing the inheritance of quantitative characters like yield and its components is essential for genetic improvement. Genetic variability refers to the presence of difference among the individuals of plant population results due to the difference either in the genetic constitution of the individuals of a population. Heritability is the transmission of characters from one generation to another generation. Moreover, knowledge of heritability is essential for selection of yield related component traits for crop yield improvement. Genetic advance measures the difference between mean genotypic values of the selected population and the original population from which these were selected.

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Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful to identify the amount of variability present in germplasm. Heritability along with high genetic advance would be useful tool in estimating the resultant effect in selection of best genotypes for yield and its attributing traits. It helps in determining the influence environment on the expression the genotypic and reliability of characters.

The use of correlation coefficient is to establish the extent of association between yield and yield component and the other character, which are having decisive role in influencing the yield. However, it is only genetic variation which is heritable and hence important in any selection Programme. Path coefficient analysis is a statistical technique of partitioning the correlation coefficients into its direct and indirect effects, so that the contribution of each character to yield could be estimated. Yield is a complex character being governed by a large number of cumulative, duplicate and dominant genes and highly influenced by environment.

Materials and Methods

The experimental material consisted of 26 elite rice germplasm and present investigation was carried out at the field experimentation center, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom Institute of Agriculture Technology and Sciences, Allahabad (UP) during Kharif 2018-19. Twenty-one days old seedlings were transplanted in 2×1 m² plot in randomized block design with three replications. Distance between plant to plant and row to row were 20 cm and 15cm respectively. Standard agronomic practices were followed throughout the crop growth period to obtain good harvest. Observations were recorded on five randomly selected plant from each progeny row for 13 biometrical characters *viz*, days to 50% flowering, plant height, flag leaf length, flag leaf width, tillers per hill, panicles per hill, panicle length, spikelet per panicle, days to maturity, biological yield, harvest index, test weight and grain yield per hill. The Analysis of variance was estimated as per procedure suggested by Panse and Sukhatme (1961) [16], coefficient of variation (GCV and PCV) by Burton (1952) [5], Heritability for the grain yield and yield components in rice were worked out in broad sense by adopting formula suggested by Burton and Devane (1953) [6]. Genetic advance was calculated by the method suggested by Johnson *et al.*, (1955) [13]. Correlation coefficient and path coefficient was worked out as method suggested by Al Jibouri *et al.* (1958), Dewey and Lu (1959) [7] respectively.

Results & Discussion

The success of plant breeding Programme depends on genetic variability and the relationship between characters. Analysis of variance shown highly significant difference among the genotypes for all the traits studied indicating the presence of considerable genetic variation among the study materials (Table 1). High genetic variability for different traits in rice was reported by Rashmi *et al.* (2017) [18], Yadav *et al.* (2018) and Tiwari *et al.* (2019). Coefficient of variance is the measure of variance among the different traits (Table 2). The estimates of phenotypic coefficient of variation (PCV) were slightly higher than those of the genotypic coefficient of variation (GCV) for all the traits studied. In this study slight differences are indicated minimum environmental influence. The higher magnitude of genotypic (GCV) and phenotypic

coefficients of variation (PCV) was recorded for traits like biological yield per hill, grain yield per hill, number of spikelets per panicle and number of tillers per hill, number of panicles per hill. Similar findings were obtained by Anjaneyulu *et al.* (2010).

Heritability plays an important role in deciding the strategy for selection of the character. In the present study high heritability was observed for the traits like; grain yield per hill, number of spikelets per panicle, test weight, number panicles per hill, days to maturity, number of tillers per hill, days to 50% flowering, plant height, panicle length, flag leaf width and whereas, characters like; flag leaf length, for harvest index, flag leaf length depicted moderate estimate of heritability and none of the characters showed low estimates of heritability. Similar results are reported by Nath and Singh (2013) [15] recorded high heritability for grain yield per hill.

The characters exhibiting high heritability may not be necessary to give high genetic advance. Johnson (1955) [13] reported that high heritability should be accompanied with high genetic advance. The breeder should be cautious during the heritability. In the present study high heritability along with the high genetic advance was exhibited by grain yield per hill, number of spikelets per panicle. Similar results were reported earlier in rice by Shilpa *et al.* (2014) [19]. Genotypic and phenotypic correlation coefficients (Table 4) indicate the genotypic and phenotypic correlation coefficients were of higher in magnitude than the phenotypic correlation coefficient which might be due to the modified effect of environment at the genetic level.

Grain yield per plant showed the high significant positive correlation with number of tillers per plant, number of panicles, panicle length, number of grains per panicle, biological yield showed positive significant correlation at phenotype and genotypic levels. The positive correlation of grain yield with various traits was supported by the Bagati *et al.* (2016) [4] for number of tillers per plant, Gopikannan and Ganesh (2013) [9] for panicle length, Paul *et al.* (2011) [17] for number of panicles, Dhurai *et al.* (2014) for number of grains per panicle, Rai *et al.* (2014) for biological yield. The correlation showed non significant correlation with harvest index both at the genotypic and phenotypic level. In the present study path coefficient analysis has been conducted taking grain yield per hill as the depended variable and the other characters as independent is presented in (Table 4). Path coefficient analysis revealed that the days to 50% flowering, plant height, number of tillers per plant, number of panicles per plant, flag leaf length, number of grains per panicle, biological yield and harvest index has positive direct effect on grain yield per plant. Positive direct effect of these traits indicated that direct selection for these traits would be likely be effective in increasing grain yield. Similar results were also reported by Gyanendra *et al.* (2011) [10] for days to 50% flowering and number of tillers per plant, Kiani *et al.* (2012) [14] for number of panicles per plant, Jan *et al.* (2017) [11] for harvest index, Ekka *et al.* (2011) for flag leaf length. The direct effects of panicle Per hill were negative followed by flag leaf width, panicle length, days to maturity, plant height. In the present study path coefficient revealed that number of tillers per hill, biological yield per hill and days to 50% flowering had influence on grain yield per hill. Selection of plants on these traits would certainly lead to improvement in grain yield.

Table 1: Analysis of variance for different quantitative characters in 26 genotypes of rice

Source of Variations	D F	DF (50%)	PH	FL	FW	T	P	PL	SPP	DM	BYH	HI	TW	GYPH
Replication	2	2.808	30.397	34.485	0.006	13.015***	6.043**	1.929	3.231	1.282	25.375	13.067*	0.81	0.403
Treatments	25	50.673***	327.964***	71.787***	0.101***	31.102***	26.023***	23.394***	4953.695***	65.055***	661.855***	8.655**	27.290***	148.730***
Error	50	2.634	21.745	16.337	0.01	1.532	0.98	1.999	62.284	2.869	12.014	3.782	0.562	1.184

Significant at 1% level * and Significant at 5%** level of significance respectively

Table 2: Variability parameters for 13 traits in 26 genotypes of rice

Parameter	DF (50%)	PH	FL	FW	T	P	PL	SPP	DM	BYH	HI	TW	GYPH
GCV	3.891	7.847	10.745	10.725	34.753	38.488	10.355	26.639	3.473	24.353	1.098	13.149	24.531
PCV	4.199	8.643	14.749	12.339	37.356	40.685	11.716	27.143	3.706	25.965	6.135	13.557	25.654
h ² (Broad Sense)	85.900	82.400	53.100	75.500	86.600	89.500	78.100	96.300	87.800	94.700	30.000	94.100	97.600
Genetic Advancement 5%	7.639	18.897	6.453	0.312	6.017	5.630	4.862	81.636	8.790	28.396	0.195	5.964	14.030
Gen. Adv as % of Mean 5%	7.428	14.678	16.127	19.203	66.604	75.003	18.851	53.858	6.706	47.052	0.405	26.271	48.323

Table 3: Correlation coefficient at genotypic and phenotypic level between Yield

Character	Plant height	Flag leaf length (cm)	Flag leaf width (cm)	Tillers/hill	Panicles/hill	Panicle length (cm)	Spikelets/panicle	Days to maturity	Biological yield/hill (g)	Harvest index	Test weight(g)	Grain yield/hill	
Days to 50% flowering	G	0.099	0.0855	0.309**	-0.565**	-0.4301***	-0.3420**	-0.4525***	0.8172***	-	-0.1509	-0.2534*	-0.544**
	P	0.0501	0.0207	0.2142*	0.4372***	-0.522**	-0.403**	-0.520**	0.865**	0.5016***	-0.133	-0.273*	-0.598**
Plant height(cm)	G		0.575**	0.500**	-0.412**	-0.3675***	0.1347	-0.1664	0.1327	-0.1498	0.1003	0.4096***	-0.1299
	P		0.4488**	0.4169**	-0.3567**	-0.431**	0.111	-0.179	0.131	-0.18	0.213	0.454**	-0.1569
Flag leaf length(cm)	G			0.478**	-0.420**	-0.2965**	0.1262	-0.1468	0.0026	-0.2299**	-0.1052	0.2625*	-0.236*
	P			0.3580**	-0.2653	-0.428**	0.217	-0.208	0.025	-0.325**	-0.243*	0.360**	-0.326**
Flag leaf width(cm)	G				-0.341**	-0.2810*	-	-0.0918	0.4068***	-0.2234*	0.0757	0.0568	-0.2190
	P				-0.2258*	-0.373**	0.3759***	-0.126	0.438**	-0.303**	0.343**	0.064	-0.265*
Tillers/ hill	G					0.9794	0.2163	0.6924***	-	0.8632***	-0.0737	-0.3066**	0.847**
	P					0.963**	0.226*	0.748**	0.3915***	0.934**	-0.008	-0.342**	0.921**
Panicles/ hill	G						0.2382*	0.6955**	-	0.8678***	-0.1061	-0.3324**	0.849**
	P						0.239*	0.746**	0.3950***	0.935**	-0.096	-0.379**	0.913**
Panicle length(cm)	G							0.2942**	-	0.2689*	0.0237	0.2728*	0.279*
	P							0.347**	0.3916***	0.305**	0.078	0.306**	0.317**
Spikelets/ panicle	G								-0.2990**	0.6822***	0.0606	-0.3140**	0.691**
	P								-0.344**	0.703**	0.115	-0.330**	0.707**
Days to maturity	G									-0.2990**	-0.0397	-0.1891	-0.475**
	P									-0.529**	0.134	-0.211	-0.515**
Biological yield/hill (g)	G										-0.0775	-0.2882*	0.979**
	P										0.08	-0.312**	0.987**
Harvest index	G											0.0633	0.1124
	P											0.115	0.133
Test weight(g)	G												-0.277*
	P												-0.293**

Table 4: Direct and indirect effect between yield and its relates traits in 26 rice genotypes at genotypic level

	DF (50%)	PH	FL	FW	T	P	PL	SPP	DM	BYH	HI	TW	GYPH
DF (50%)	0.6895	0.0679	0.059	0.2132	-0.3894	-0.3599	-0.2781	-0.3582	0.5966	-0.4001	-0.0919	-0.1883	-0.598**
PH	-0.009	-0.0909	-0.0523	-0.0454	0.0375	0.0392	-0.0101	0.0162	-0.0119	0.0164	-0.0193	-0.0413	-0.1569
FL	0.0472	0.3178	0.5524	0.2643	-0.232	-0.2362	0.1198	-0.1147	0.0136	-0.1794	-0.1344	0.1987	-0.326**
FW	-0.211	-0.3409	-0.3264	-0.6823	0.2327	0.2544	0.3424	0.0862	-0.2991	0.2064	-0.2338	-0.0439	-0.265*
T	-0.7097	-0.5182	-0.5277	-0.4285	1.2566	1.2574	0.284	0.9402	-0.6013	1.173	-0.0095	-0.4293	0.921**
P	0.7497	0.6193	0.6141	0.5355	-1.4373	-1.4364	-0.3438	-1.0718	0.6634	-1.3426	0.1381	0.5446	0.913**
PL	0.2566	-0.0705	-0.1379	0.3193	-0.1438	-0.1523	-0.6363	-0.2205	0.3111	-0.1939	-0.0498	-0.1949	0.317**
SPP	-0.2465	-0.0847	-0.0985	-0.0599	0.355	0.3541	0.1644	0.4745	-0.1633	0.3336	0.0547	-0.1566	0.707**
DM	-0.2981	-0.0451	-0.0085	-0.151	0.1649	0.1591	0.1685	0.1186	-0.3446	0.1823	-0.0461	0.0728	-0.515**
BYH	-0.734	-0.2281	-0.4108	-0.3827	1.1807	1.1822	0.3854	0.8892	-0.6693	1.2648	0.1015	-0.3943	0.987**
HI	-0.052	0.0829	-0.0948	0.1335	-0.0029	-0.0375	0.0305	0.0449	0.0521	0.0313	0.3897	0.0449	0.133
TW	-0.0804	0.1337	0.1058	0.0189	-0.1005	-0.1116	0.0901	-0.0971	-0.0622	-0.0917	0.0339	0.2943	-0.293**
GYPH	-0.5975	-0.1569	-0.3256	-0.2653	0.9213	0.9126	0.3169	0.7074	-0.5148	1.0001	0.133	-0.2933	1

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