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Assessment of genetic variability and correlation studies in rice (*Oryza sativa* l.) for grain yield and quality traits suited for eastern plain zone of "UP"

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Abstract

The present investigation consists of 25 genotypes of rice including 1 check, which were grown in the field experimentation centre of the Department of Genetic and Plant Breeding, SHUATS, Prayagraj during 2019-20 following RBD with three replications. The data were recorded on 13 characters to study the amount of genetic variability, heritability, genetic advance, correlation association of yield contributing components with yield and direct and indirect effects of yield contributing components in the rice genotypes. Analysis of variance among 25 rice germplasm showed highly significant differences for all the characters under study indicates the presence of a substantial amount of genetic variability. High to moderate estimates of GCV and PCV were recorded for number of tillers per hill, number of panicles per hill, test weight, biological yield and number of spikelets per panicle indicating that these characters could be used as selection for crop improvement. High estimates of heritability, broad sense revealed that characters like test weight exhibited highest heritability followed by plant height, number of spikelet's per panicle, number of tillers per hill, number of panicles per hill and panicle length. Estimates of genetic advance revealed that number of spikelets per panicle exhibited highest genetic advance followed by plant height and biological yield. Correlation coefficient analysis phenotypic level revealed that flag leaf length, flag leaf width, biological yield and test weight showed positive significant correlation with grain yield per plant at both genotypic and phenotypic level. Path coefficient analysis revealed that the flag leaf width, number of panicles per plant, panicle length, days to maturity, biological yield and harvest index has positive direct effect on grain yield per plant.

Keywords: rice (*Oryza sativa* l.), gcv, pcv, variability, heritability, genetic advance, correlation and path coefficient analysis

Introduction

Rice *Oryza sativa* L. (2n=24) belongs to family poaceae (Gramineae). Rice is a short day self-pollinated crop. Rice is one of the world's most important cereal food crops. It is the primary source of food and protein for about half of the mankind with an enormous nutritional and economic impact. (Kush, 2005) Before initiating any breeding programme, the knowledge of variability is a basic pre-requisite for improving the character. Rice grain contains 75-85% starch, 12% water and 7% protein. (Oko *et al.*, 2012; Hossain *et al*., 2015) It is the crucial dietary and food security source of many Asian countries. (Kumar *et al.*, 2020) [6] It contributes 43% of caloric requirement and 20-25% of agricultural income. Over 90 percent of the world's rice is produced and consumed in the Asian region (Pathak *et al.*, 2011) [10] comprising 80% of the world's production and consumptions. Rice is the only cereal crop which is consumed mainly after cooking whole grains and hence, the quality considerations are more important (Hossain *et al.*, 2009). The area under rice cultivation is estimated to be 162.76 million hectare with global production 495.87 million metric tons. The total food grain production for the year 2018-2019 was places at 275.7 million tons. The highest productivity is 7030kg/ha of China followed by Vietnam (5913kg/ha), Indonesia (4680kg/ha) etc. in comparison of India (3960kg/ha) SOURCE: (Directorate of Economics and Statistics, Department of Agriculture, Cooperation and Farmers Welfare, Ministry of Agriculture and farmers Welfare, GOI, 2018-2019)

Rice plays an important role in Indian economy being the staple food of two-third of the population. India has the largest area under rice crop and ranks second in production next to china, knowledge on the genetic architecture of genotypes is necessary to formulate efficient breeding methodology.

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. 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 25 rice genotypes and present investigation was carried out at the field experimentation centre, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom Institute of Agriculture Technology and Sciences, Allahabad (UP) during kharif 2019-2020. Twenty-one days old seedlings were transplanted in 2×1 m^2 plot in randomized block design with three replications distance between plant to plant and row to row were 20cm and 15cm respectively. Standard agronomic practices were followed throughout the crop growth period to obtained 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 length width, number of tillers per hill, number of panicle per hill, panicle length, spikelets 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), coefficient of variation (GCV and PCV) by Burton (1952). 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). Genetic advance was calculated by Johnson *et al,* (1955) [4]. Correlation coefficient and path coefficient was worked out as method suggested by Al Jibouri*et al*, (1958). Dewey and Lu (1959) respectively.

Results and Discussion

The success of plant breeding programme depend 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 Saha et al. (2019) [12], Kishore et al. (2020) and Nusrat et al. (2020) [8].

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 coefficient of variation (PCV) was recorded for the traits like number of tillers per hill, number of panicles per hill, grain yield per plant. Similar findings were obtained by Singh et al, (2011) [15]

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 test weight, plant height, number of spikelets per panicle, number of panicle per hill, number of tillers per hill, panicle length, flag leaf length, days to 50% flowering flag leaf width, days to maturity, biological yield. Whereas characters like harvest index and grain yield per plant. Depicted moderate estimate of heritability and none of the characters showed low estimates of heritability. Similar results are reported by Dhurai *et al*, (2014) [3] recorded high heritability for grain yield per hill.The characters exhibiting high heritability may not be necessary to give high genetic advance.

Johnson (1955) [4] reported that high variability 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 panicle length, number of tillers per hill. Similar results were reported earlier in rice by Shilpa et al. (2014) [13]. Genotypic and phenotypic correlation coefficients (Table-4) indicate the genotypic and phenotypic correlation coefficients where 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 flag leaf length, flag leaf width, biological yield, test weight showed positive significant correlation at phenotypic and genotypic levels.

The positive correlation of grain yield with various traits were supported by the Pandey et al, (2017) [9] for flag leaf length, Reddy et al, (2013) [11] for flag leaf width, Vinoth et al. (2016) [18] for biological yield, Bhati et al, (2015) [2] for test weight. The correlation showed non-significant correlation with days to maturity both at phenotypic and genotypic level. In the present study path coefficient analysis has been conducted taking grain yield per hill as the depended variable and the other character as independent is presented in (Table-5). Path coefficient analysis revealed that the flag leaf width, number of panicles per plant, panicle length, days to maturity, biological yield and harvest index has positive direct effect on grain yield per plant. Positive direct effect of these traits indicates that direct selection for these traits would be likely be effective in increasing grain yield. Similar results were also reported by Srilakshmi et al. (2021) for number of panicles per plant, Singh et al. (2018) [14] for panicle length, Srikanth et al. (2017) [16] for days to maturity, Nandan et al. (2018) [7] for harvest index, Bhati et al. (2015) [2] for biological yield. The negative direct effect followed days to 50% flowering, flag leaf length, plant height, number of tillers per hill, number of spikelets per panicle and test weight. 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 25 rice genotypes

Source of Variations	DF	DF (50%)	DM	FLL	FLW	PH	NT	NP	PL	NSP	TW	BY	HI	GYP
Replicate	2	2.902	2.48	13.005	0.005	400.801 **	0.461	0.256	1.779	44.114	0.025	70.06	34.708 **	0.452
Treatments	24	238.676 ***	277.888 ***	155.065 ***	0.150 ***	705.215 ***	22.862 ***	16.036 ***	28.171 ***	4607.717 ***	81.156 ***	447.011 ***	48.391 ***	44.652 ***
Error	48	30.895	60.441	6.809	0.006	78.828	0.579	0.321	4.014	230.078	2.299	34.885	5.048	6.651

Significant at 1% level* Significant at 5%** level of significant respectively

Table 2: Variability parameters for 13 traits in 25 genotypes of rice

Parameter	DF (50%)	DM	FLL	FLW	PH	NT	NP	PL	NSP	TW	BY	HI	GYP
GCV	8.694	6.790	16.434	16.270	10.889	31.160	28.793	10.201	21.423	24.368	22.240	8.989	16.239
PCV	10.455	9.195	17.529	17.285	12.780	32.353	29.662	12.488	23.050	25.412	24.905	10.442	20.054
h^2 (Broad Sense)	69.200	54.500	87.900	88.600	72.600	92.800	94.200	66.700	86.400	92.000	79.700	74.100	65.600
Genetic Advancement 5%	14.257	12.951	13.576	0.425	25.362	5.407	4.577	4.775	73.136	10.128	21.562	6.741	5.937
Gen.Adv as % of Mean 5%	14.894	10.329	31.737	31.547	19.112	61.824	57.577	17.167	41.016	48.138	40.914	15.941	27.088

Table 3: Correlation coefficient between yield and related traits in 25 rice genotypes at phenotypic level.

		DF 50%	DM	FLL	FLW	PH	NT	NP	PL	NSP	TW	BY	HI	GYP
DF 50%	p	1.000	0.2395 *	0.106	0.062	-0.040	-0.184	-0.018	0.4112 ***	0.6997 ***	-0.008	0.039	-0.218	-0.213
	g	1.000	0.305**	0.148	0.095	-0.046	-0.223	0.049	0.513**	1.226	0.017	-0.013	-0.265*	-0.292*
DM	p		1.000	0.6414 ***	-0.014	-0.177	-0.4235 ***	0.2821 *	-0.3359 **	0.210	0.211	0.191	-0.071	0.018
	g		1.000	0.721**	-0.063	-0.208	-0.458**	0.392**	-0.418**	0.236*	0.250*	0.263*	-0.022	0.039
FLL	p			1.000	0.4790 ***	0.075	-0.106	0.5116 ***	-0.3637 **	0.134	0.4713 ***	0.4389 ***	-0.037	0.276*
	g			1.000	0.498**	0.077	-0.137	0.644**	-0.424**	0.097	0.513**	0.533**	-0.005	0.316**
FLW	p				1.000	0.3293 **	0.2553 *	0.3417 **	0.055	0.105	0.3222 **	0.2885 *	0.020	0.294*
	g				1.000	0.343**	0.279*	0.376**	0.047	0.170	0.340**	0.360**	0.057	0.332**
PH	p					1.000	0.7179 ***	0.2929 *	0.063	-0.029	0.136	0.129	0.3153 **	0.031
	g					1.000	0.751**	0.367**	0.071	-0.072	0.143	0.147	0.347**	0.035
NT	p						1.000	0.3801 ***	0.157	-0.166	-0.112	-0.112	0.4895 ***	-0.104
	g						1.000	0.435**	0.154	-0.262*	-0.132	-0.133	0.538**	-0.121
NP	p							1.000	-0.3252 **	0.062	0.106	0.068	0.4950 ***	-0.123
	g							1.000	0.428**	-0.041	0.096	0.120	0.635**	-0.155
PL	p								1.000	0.3790 ***	-0.2688 *	-0.2585 *	-0.130	-0.109
	g								1.000	0.594**	-0.315**	-0.322**	-0.165	-0.140
NSP	p									1.000	-0.048	-0.026	-0.191	-0.202
	g									1.000	-0.040	-0.056	-0.276*	-0.303**
TW	p										1.000	0.9132 ***	-0.211	0.500 **
	g										1.000	1.050	-0.244*	0.525**
BY	p											1.000	-0.215	0.545**
	g											1.000	-0.242*	0.500**
HI	p												1.000	-0.272*
	g												1.000	0.296**
GYP	p													1.000
	g													1.000

Table 4: Direct and indirect effects of 13 traits on grain yield in rice evaluated in *kharif* 2020 at Phenotypic Level

	Days to 50% flowering	Days to Maturity	Flag leaf length (cm)	Flag leaf width (cm)	Plant height (cm)	Number of total tillers per hill	Number of panicle per hill	Panicle length (cm)	Number of spikelets per panicle	Test weight (g)	Biological yield (g)	Harvest index (%)	Grain yield per plant (g)
DF 50%	-0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	-0.001	0.000	0.000	0.000	-0.213
DM	0.006	0.026	0.017	0.000	-0.005	-0.011	0.007	-0.009	0.006	0.006	0.005	-0.002	0.018
FLL	-0.003	-0.021	-0.032	-0.016	-0.002	0.003	-0.017	0.012	-0.004	-0.015	-0.014	0.001	0.276*
FLW	0.002	0.000	0.014	0.029	0.009	0.007	0.010	0.002	0.003	0.009	0.008	0.001	0.294*
PH	0.000	0.000	0.000	-0.001	-0.002	-0.002	-0.001	0.000	0.000	0.000	0.000	-0.001	0.031
NT	0.002	0.005	0.001	-0.003	-0.009	-0.012	-0.005	-0.002	0.002	0.001	0.001	-0.006	-0.104
NP	0.000	0.001	0.002	0.001	0.001	0.001	0.004	-0.001	0.000	0.000	0.000	0.002	-0.123
PL	0.009	-0.007	-0.008	0.001	0.001	0.003	-0.007	0.022	0.008	-0.006	-0.006	-0.003	-0.109
NSP	-0.031	-0.009	-0.006	-0.005	0.001	0.007	-0.003	-0.017	-0.044	0.002	0.001	0.008	-0.202
TW	0.002	-0.048	-0.108	-0.074	-0.031	0.026	-0.024	0.062	0.011	-0.229	-0.209	0.048	0.500**
BY	0.010	0.051	0.117	0.077	0.035	-0.030	0.018	-0.069	-0.007	0.244	0.267	-0.057	0.545**
HI	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	-0.272*
GYP	-0.213	0.018	0.276*	0.294*	0.031	-0.104	-0.123	-0.109	-0.202	0.500**	0.545**	-0.272*	1.000

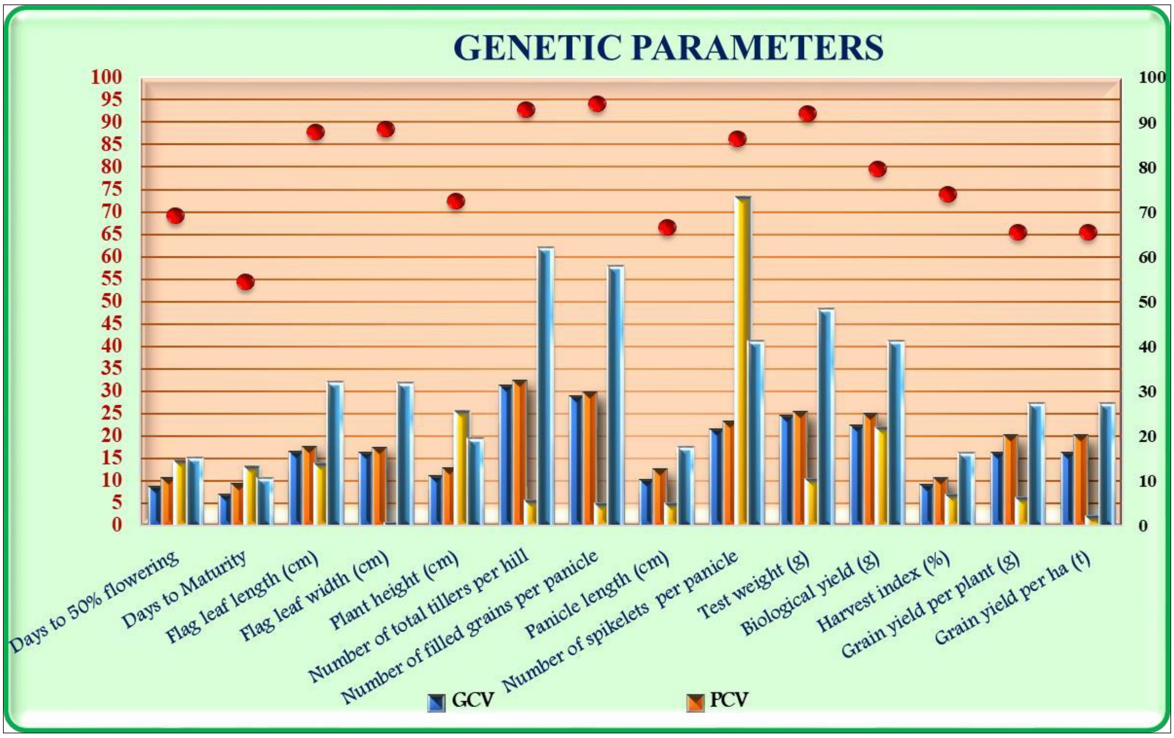

Fig 1: Histogram depicting ECV, GCV, PCV, Genetic advance and h^2 for rice genotype

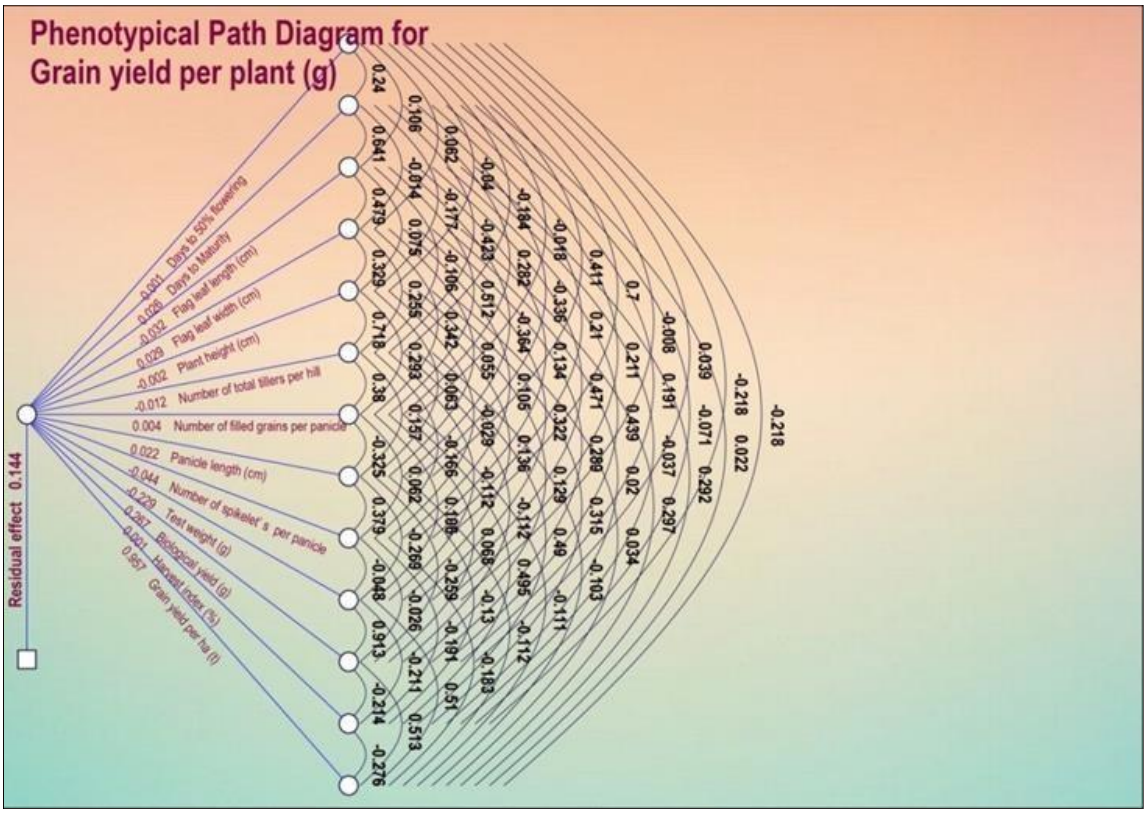

Fig 2: Phenotypic Path Diagram for Grain Yield per Plant of Rice

Conclusion

It is concluded from experimental results that among 25 genotypes of rice, on the basis of mean performance IRRI-08 (8.95t/ha) was founded to be superior for grain yield followed by RNR-11718, JGL-18047 and IRRI-30. Number of tillers per hill, number of panicles per hill and grain yield per plant exhibited high GCV and PCV. Genetic parameters revealed that heritability and genetic advance as % mean values are high for panicle length, test weight, number of tillers per hill, flag leaf width and flag leaf length. Correlation coefficient analysis revealed that seed yield per plant exhibited positive and significant association with flag leaf length, flag leaf width, biological yield and test weight at both genotypic and phenotypic levels. Path coefficient analysis revealed that characters; days to 50% flowering, flag leaf length, number of tiller, number of spikelet's per panicle, biological yield, harvest index and test weight have positive direct effect on seed yield per plant at genotypic level. Hence utmost importance should be given to these characters during selection for seed yield per plant.

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Reference

1. Agriculture statistics. Ministry of Agriculture & Farmers welfare, Department of Agriculture, Cooperation & Farmer welfare, Directorate of Economics and Statistics, Government of India, 2018.
2. Bhati M, Suresh BG, Rajput AS. Genetic variability, correlation and path coefficient for grain yield and quantitative traits of elite rice (Oryza sativa L.). Genotypes at Uttar Pradesh. ElectronicJournal of Plant Breeding,2015:6(2):586-591.
3. Dhurai SY, Bhati PK, Saroj SK. Studied on Genetic Variability for Yield and Quality Characters in Rice (Oryza sativa L.). Under Integrated Fertilizer Management. The Bioscan,2014:9(2):745-748.
4. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variabilityinsoyabean. Agronomy Journal,1955:47:314-318.
5. Kishore NS, Srinivas T, Nagabhushanam U, Pallavi M. Genetic variability, correlation and path analysis for yield and yield components in promising rice (Oryza sativa L.) SAARC. J. Agri,2015:13(1):99-108.
6. Ku kumar Saurabh Singh, Suneetha Y, Vinay Kumar G, Srinivasa Rao V, Sandeep Raja D, Srinivas T. Variability, Correlation and Path Studies in Coloured Rice, 2020.
7. Nandan R, Shravan KS. Character association and path analysis in rice (Oryza sativa L.) genotypes. Agricultural Science Digest,2018:37(3):1012-1017.
8. Nusrat Jan, Subhash C Kashyap. Studies on variability, heritability and genetic gain for quality traits in rice. Journal of Pharmacognosy and Phytochemistry,2020:9(3):537-540.
9. Pp pandey, Sonalikar. Study of morphological and yield attributing characters in indigenous rice (Oryza sativa L.) of bastar. International Journal of Agricutural ScienceandResearch,2017:7(4):537-546.
10. Pp pathak H, Tewari AN, Sankhyan S, Dubey DS, Mina U, Singh VK et al. direct-seeded rice: potential, performance and problems: A review. Current Advances in Agriculture Sciences,2011:3(2):77-88.
11. Reddy GE, Suresh BG, Sravan T, Reddy A. Inter relationship and cause effect analysis of rice genotypes in north east plain zone. The Bioscan,2013:8(4):1141-1144.
12. Saha L, Hassan MD, Ashraful Haque M, Mofazzal Islam, Rasel MD. Genetic variability, heritability, correlation and path analysis of yield components in traditional rice (Oryza sativa L.) landraces. Journal of Bangladesh Agricultural Universit,2019:17(1):26-32.
13. Shilpa HB, Shivakumar N, Patroti P, Prasad T, Hittalmani S, Lohithaswa HC et al. Genetic variability, heritability and character association studies for grain yield and yield attributing traits in segregating population of rice (Oryza sativa L.). Progressive Research,2014:9(1):1125-1128.
14. Singh L, Singh gh M, Hausila PS, Rana S, Prabhudutt S, Koutu GK. Genetic analysis of green super rice (Oryza sativa L.) for yield and quality traits. International Journal of Current Microbiology and Applied Sciences,2018:7(2):345-350.
15. Singh SK, Singh CM, Lal GM. Assessment of genetic variability for yield and its components characters in rice (Oryza sativa L.). Research in Plant Biology,2011:1(4):73-76.
16. Srikanth T, Sudheer KS, Senguttuvel P, Seshu MM. Correlation analysis for yield components in rice (Oryza sativa L.). Intrenational Journal of Pure and Applied Bioscience,2017:5(4):1412-1415.
17. Sri Lakshmi M, Suneetha Y, Srinivas T. Genetic variability, correlation and path analysis for grain yield and yield components in rice genotypes. Journal of Pharmacognosy and Phytochemistry,2021:10(1):1369-1372.
18. Vinoth R, Shivramakrishnan R, Sivaji M, Tamil kumar P, Kumar B, Marker S et al. Genetic analysis and correlation studies for grain yield in rice (Oryza sativa L.). under the Allahabad agro climatic region. International Journal of Forestry and Crop Improvement,2016:7(1):93-100.
19. Nasr ME, Zinhoum RA, Lotfy K. Efficacy of cold plasma against three of stored grain insects. Int J Entomol Res. 2020;5:113-7.