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## Genetic variability, heritability and association analyses for yield and related characters in rice germplasm (*Oryza sativa* L.)

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### Abstract

The purpose of this research was to determine the variability, heritability, correlation and path coefficient analyses of 48 rice genotypes. The experiment was carried out in a RCBD with two replications. All 13 characters mean sum of squares were significant, which shows that there is a lot of genetic variation in these variables. The high magnitude of PCV and GCV have been estimated for number of unfilled grains per panicle followed by grain yield per plant, biological yield per plant, number of filled grain per panicle and number of effective tillers per plant. High magnitude of heritability along with high genetic advance as percent of mean was observed for plant height followed by number of unfilled grains per panicle, biological yield per plant, grain yield per plant, spikelet fertility %, flag leaf length, harvest index, number of filled grain per panicle and 1000 seed weight. The results showed that biological yield, harvest index, number of effective tillers per panicle, number of filled grains per panicle, spikelet fertility percent and harvest index were all positively and significantly associated with grain yield per plant. Days of 50% flowering, plant height, number of filled grains per panicle, flag leaf length, biological yield per plant and harvest index all had a direct positive effect on yield per plant at the genotypic level, indicating their significance during selection in the yield improvement program. Additionally, the knowledge gained from this study can be used in upcoming rice breeding programs.

**Keywords:** Rice, genetic variability, heritability, correlation and path coefficient

### Introduction

Rice (*Oryza sativa* L.) is a member of the tribe *Oryzae*, a family of the Poaceae in rice (Gramineae). The number of chromosomes is  $2n = 24$ . It is one of the ancient sources of nutrients that has been farmed and can develop in a variety of environments (Kanwar *et al.*, 2015) [5]. Approximately half of the world's population consumes rice (*Oryza sativa* L.), which is grown on 162.05 million hectares (Mha) and yields 755.45 million tonnes of milled rice at a productivity of 4.64 metric tons/hectare (FAO STAT, 2019) [7]. The largest rice-growing region is in India, which covers 43.78 million hectares and produces 118.43 million tonnes of rice at a productivity of 2705 kg per hectare (Anonymous, 2020) [1].

Variability has developed to play a major part in any breeding program that starts with selection and is followed by an evaluation of effectiveness. Before starting any varietal development experiment, the material's genetic variability is correctly utilized (Prasad *et al.*, 2001) [23]. Genetic metrics like genotypic and phenotypic coefficients of variation can be used to quantify the level of variability present in any condition. When selecting attributes that will contribute to yield, heritability and genetic advance are as essential selection criteria. Heritability analyses combined with genetic advance typically perform better at predicting the outcome of selection than heritability estimates alone (Paul *et al.*, 2006) [22].

The improvement of yield is the major breeding objective of the rice breeding program. Correlation and path coefficients play an important role in selecting superior genotypes and pertinent features for rice. The correlation coefficient reveals the strength or weakness of the correlation between two variables, as well as whether there is a positive or negative correlation. The relationship between yield and its constituent attributes provides information that can be used to optimize for a greater yield. Wright (1921) [37] used a statistical tool for path analysis that divided the correlation coefficient into the direct and indirect impacts of experimental conditions on the direct variable. Selection based on simple association without accounting for the component features is worthless since grain yield is a complicated trait that is highly influenced by other traits. Each plant breeding program must therefore incorporate path analysis.

Understanding the immediate and long impacts of traits on yield can help with crop improvement selection methods.

### Materials and Methods

The current experiment will be conducted at Research cum Instructional farm, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur (C.G.) during *Kharif*, 2021. The experimental material consisted of 48 genotypes along with four checks namely Swarna, Mahsuri, Pooja and Jaldubi. In *Kharif*, 2021, the experiment was conducted in a RCBD with two replications to evaluate 48 rice genotypes. Each genotype will be raised in plot size of  $4.50 \times 1.40 \text{ m}^2$  and intra row spacing of  $45 \times 35 \text{ cm}$ . Five plants were chosen at random from each plot in each replication to record observations on different attributes.

### Results and Discussion

The experiment was conducted on 48 rice genotypes, including four checks. The experiment was conducted in a RCBD with two replications. To clearly understand the genetic parameters of variability, correlation and path analyses were investigated. For the various analyses, 13 yield characters were taken into consideration. Five plants were randomly chosen from each replication to be observed.

### Analysis of variance

The results of the analysis of variance, which was used to evaluate how much the observed characteristics varied among rice genotypes, are shown in table 1. The analysis of variance's findings shows that every characteristic under study

was found to be highly significant (at 1% level of significance) was also found by Singh *et al.* (2021) [31]. The 13 quantitative traits substantial mean sum of square values suggest that there is a lot of variation among genotype traits.

### Genotypic and phenotypic coefficient of variance

The phenotypic and genotypic coefficients of variance of all the observed quantitative traits varied in the range of days of maturity (PCV = 5.06%, GCV = 4.88%) to (number of unfilled grains per panicle), (PCV = 52.55%, GCV = 49.77%), respectively (Table 2). The (number of unfilled grains per panicle) grain yield per plant (biological yield/plant) number of filled grains per panicle) and (number of effective tillers per plants) have been observed to have a higher value of the phenotypic coefficient of variance% (52.55, 29.75, 26.15, 25.61, 20.15), respectively and genotypic coefficient of variance% (49.77, 27.36, 24.53, 21.46, 15.49) respectively. Similarly, result was found by Ekka *et al.* (2015) [5] for grain yield per plant and (number of effective tillers per plant) and Singh *et al.* (2018) [33] for (grain yield per plant). Therefore, PCV and GCV revealed low levels of (days of 50% flowering), (5.58%, 5.39%) and (days of maturity), (5.06%, 4.88%), respectively.

The estimates of PCV for all traits in the present investigation were larger than the GCV, which might be related to genotype-environment association. Similarly, result was found by Lingaiah *et al.* (2015) [17], Iqbal *et al.* (2018) [12] and Saha *et al.* (2019) [28]. The current study's higher value of genetic coefficient of variance for the number of (unfilled grains per panicle) agrees with the results of Padmaja *et al.* (2008) [20] and Singh *et al.* (2021) [31].

**Table 1:** Analysis of variance (ANOVA) for different quantitative traits

S. No.	Traits	Mean sum of square (MSS)		
		Replication	Genotype	Error
	DF	1	47	47
1.	Days of 50% flowering	3.375	74.426**	2.609
2.	Days of maturity	5.510	98.037**	3.617
3.	Plant height (cm)	10.74	719.761**	31.288
4.	Panicle length (cm)	2.056	9.075**	3.779
5.	No. of effective tillers per plant	0.882	3.323**	0.856
6.	No. of filled grains per panicle	4.293	1972.134**	345.112
7.	No. of unfilled grains per panicle	2.870	936.784**	50.782
8.	Spikelet fertility%	1.342	184.646**	20.563
9.	Flag leaf length (cm)	10.687	31.211**	4.566
10.	1000 seed weight (g)	2.727	28.103**	5.056
11.	Biological yield / plant (g)	1.023	229.774**	14.672
12.	Harvest index (%)	13.209	99.048**	15.248
13.	Grain yield / plant (g)	1.175	47.917**	4.01

\*\*Significant at 1% level

### Heritability and Genetic advance

Breeders that want to successfully select for desirable traits and produce the most genetic gain with the least amount of work and resources do so by estimating heritability. In a broad sense, according to Johnson *et al.* (1955), heritability was categorized as low (30%), medium (30-60%), and high (> 60%). The heritability of all the observed quantitative traits varied in the range of panicle length (41.20%) to days of 50% flowering (93.23%). The characters with the highest heritability had the corresponding heritability values. Days of 50% flowering showed highest heritability was 93.23%, followed by days of maturity (92.88%), plant height (91.88%), number of unfilled grains per panicle (89.72%),

biological yield per plant (88.00%), grain yield per plant (84.56%), spikelet fertility (79.96%), flag leaf length (74.45%), harvest index (73.32%), number of filled grains per panicle (70.21%) and 1000 seed weight (69.50%) (Table 2). Similarly, result was found by Jadhav *et al.* (2020) [13], Gupta *et al.* (2021) [10], and Palaniyappan *et al.* (2020) [21] also reported high heritability for these traits.

The genetic advance as% of mean of the highest value has been observed for the number of unfilled grains per panicle (97.1%), grain yield per plant (51.8%), biological yield per plant (47.40%), number of filled grains per panicle (37.05%), plant height (30.23%), harvest index (27.83%), number of effective tillers per plant (24.51%), 1000 seed weight

(23.44%), spikelet fertility (21.92%) and flag leaf length (20.53%). Similarly, result was found by Dhidhi *et al.* (2021)<sup>[4]</sup> for unfilled grains per panicle and Bhor *et al.* (2020)<sup>[2]</sup> for grain yield per plant and plant height.

High value of heritability along with high genetic advance as percent of mean was revealed for plant height, flag leaf length, number of filled grains per panicle, number of unfilled grains per panicle, spikelet fertility%, 1000 seed weight, biological yield per plant, harvest index, and grain yield per plant. It showed that heritability would be most likely due in

part to additive gene effects and selection be useful. Similar, results were found by Singh *et al.* (2011) for number of filled grains per panicle and grain yield per plant, Dhanwani *et al.* (2013)<sup>[3]</sup> for number of filled grains per panicle, Limbani *et al.* (2017)<sup>[16]</sup> for number of filled grains per panicle, grain yield per plant and harvest index, Prasad *et al.* (2017)<sup>[24]</sup> for plant height, number of filled and unfilled grains per panicle, 1000 seed weight and grain yield per plant, Bhor *et al.* (2020)<sup>[2]</sup> for plant height and grain yield per plant, Ganpati *et al.* (2020)<sup>[8]</sup> and Priyanka *et al.* (2020)<sup>[26]</sup> for plant height.

**Table 2:** Genetic parameters for different yield and its related characters

S. No.	Traits	Range			PCV%	GCV%	h <sup>2</sup> (bs)%	GA	GA as% of Mean
		Mean	Min	Max					
1.	Days of 50% flowering	111.25	95.00	123.00	5.58	5.39	93.23	11.92	10.71
2.	Days of maturity	140.80	121.00	153.00	5.06	4.88	92.88	13.64	9.69
3.	Plant height (cm)	121.06	79.95	188.13	16.01	15.33	91.67	36.59	30.23
4.	Panicle length (cm)	24.87	18.62	30.12	10.19	6.54	41.20	2.15	8.65
5.	No. of effective tillers per plant	7.17	5.00	10.45	20.15	15.49	59.04	1.76	24.51
6.	No. of filled grains per panicle	132.89	73.60	225.60	25.61	21.46	70.21	49.23	37.05
7.	No. of unfilled grains per panicle	42.29	11.30	115.40	52.55	49.77	89.72	41.07	97.11
8.	Spikelet fertility%	76.11	48.58	91.82	13.31	11.90	79.96	16.69	21.92
9.	Flag leaf length (cm)	31.61	24.03	40.11	13.38	11.55	74.48	6.49	20.53
10.	1000 seed weight (g)	24.88	15.49	30.98	16.37	13.65	69.50	6.49	23.44
11.	Biological yield /plant (g)	42.28	27.40	86.95	26.15	24.53	88.00	20.04	47.40
12.	Harvest index (%)	41.02	22.01	56.53	18.43	15.78	73.32	11.42	27.83
13.	Grain yield / plant (g)	17.13	10.63	41.71	29.75	27.36	84.56	8.88	51.83

### Correlation coefficient analysis

The related genotypic correlations are higher than the corresponding phenotypic correlations (Table 3). This is caused by the enhanced genetic impact of the environment on character association. At both the genotypic and phenotypic levels, grain yield per plant showed high positive correlations with biological yield, harvest index, number of effective tillers per panicle, number of filled grains per panicle, spikelet fertility percent, and harvest index. Similarly, result was found by Yadav *et al.* (2010)<sup>[36]</sup> for harvest index, Ekka *et al.* (2011)<sup>[6]</sup>, Kiani (2012)<sup>[14]</sup>, Sahe *et al.* (2019)<sup>[28]</sup> and Salhe *et al.* (2020)<sup>[30]</sup> for number of effective tillers/plant and number of filled grain/plant.

### Path coefficient analysis

Grain yield per plant was used as the dependent variable in the path coefficient analysis for the current study (Table 4). Path coefficient analysis revealed that biological yield/plant has highest positive direct effect on grain yield per plant, followed by harvest index, plant height, day to 50% flowering, length of flag leaf, and number of filled grains per

panicle. Similarly, results were found by Rokonuzzaman *et al.* (2008)<sup>[27]</sup>, Solomon and Wegary (2016)<sup>[35]</sup> and Priya *et al.* (2017) for plant height, Ekka *et al.* (2011)<sup>[6]</sup> for days of 50% flowering, Priya *et al.* (2017)<sup>[25]</sup> for days of 50 percent flowering, Kumar *et al.* (2018)<sup>[33]</sup> for harvest index and Singh *et al.* (2019) and Gupta *et al.* (2020)<sup>[11]</sup> for number of filled grains per panicle.

The current studies indicated a suitable correlation between biological yield per plant, harvest index, and number of filled grains per panicle. These attributes also appeared to have positive direct effects and a substantial positive correlation with grain production per plant. Similarly, results were found by Yadav *et al.* (2010)<sup>[36]</sup> and Mohammad *et al.* (2013)<sup>[18]</sup> for biological yield per plant and number of filled grains per panicle, Singh *et al.* (2019)<sup>[34]</sup> and Gupta *et al.* (2020)<sup>[11]</sup> for number of filled grains per panicle, Sahu *et al.* (2017)<sup>[29]</sup> for harvest index. Also, grain yield per plant showed a significantly positive correlation with a negative direct effect on traits such as number of effective tillers per plant, and spikelet fertility%. Similarly, results were found by Naik *et al.* (2021)<sup>[19]</sup> for number of effective tillers per plant.

**Table 3:** Correlation coefficient analysis for yield and its contributing traits in rice (Kharif, 2021)

		2	3	4	5	6	7	8	9	10	11	12	13
1.	G	0.997**	0.221*	0.039	0.043	-0.010	0.452**	-0.513**	0.237*	-0.192	0.176	-0.719**	-0.249*
	P	0.994**	0.194	-0.007	0.049	0.004	0.412**	-0.436**	0.199	-0.18	0.152	-0.573**	-0.218*
2.	G		0.217*	0.005	0.056	0.016	0.439**	-0.491**	0.192	-0.199	0.175	-0.708**	-0.236*
	P		0.186	-0.024	0.054	0.017	0.393**	-0.412**	0.168	-0.196	0.15	-0.574**	-0.213*
3.	G			0.867**	-0.487**	0.381**	-0.059	0.184	0.629**	-0.004	0.206*	-0.361**	-0.025
	P			0.549**	-0.324**	0.328**	-0.027	0.142	0.519**	-0.011	0.189	-0.270**	0.000
4.	G				-0.574**	0.284**	0.034	0.036	0.794**	0.264**	0.293**	-0.202*	0.134
	P				-0.262**	0.116	0.063	-0.062	0.474**	0.196	0.153	-0.085	0.079
5.	G					-0.114	-0.200	0.116	-0.486**	-0.368**	0.414**	0.063	0.484**
	P					0.051	-0.140	0.134	-0.367**	-0.219*	0.367**	0.083	0.435**
6.	G						0.095	0.337**	0.143	-0.580**	0.233*	0.021	0.259*
	P						0.056	0.421**	0.038	-0.328**	0.303**	0.181	0.406**

7.	G								-0.877**	0.121	-0.305**	-0.107	-0.362**	-0.330**
	P								-0.842**	0.114	-0.228*	-0.096	-0.306**	-0.301**
8.	G									-0.105	0.041	0.137	0.427**	0.401**
	P									-0.135	0.057	0.178	0.425**	0.445**
9.	G										0.258*	0.203*	-0.335**	-0.081
	P										0.186	0.142	-0.304**	-0.122
10.	G											0.014	0.313**	0.173
	P											0.074	0.237*	0.196
11.	G												-0.295**	0.798**
	P												-0.266**	0.776**
12.	G													0.323**
	P													0.380**

\*, \*\* Significant at 5% and 1% level, respectively Note- 1=Days of 50% flowering, 2= Days of maturity, 3=Plant height, 4=Panicle length, 5=No. of effective tillers per panicle, 6=No. of filled grains per panicle, 7=No. of unfilled grains per panicle, 8=Spikelet fertility%, 9=Flag leaf length, 10=1000 seed weight, 11=Biological yield / plant, 12=Harvest index, 13=Grain yield / plant.

**Table 4:** Path analysis for different yield contributing traits on grain yield per plant (dependent character) in rice

	1	2	3	4	5	6	7	8	9	10	11	12	Correlation with grain yield per plant
1.	0.318	-0.339	0.104	-0.023	-0.015	0.000	-0.257	0.368	0.007	0.051	0.236	-0.699	-0.249*
2.	0.317	-0.340	0.102	-0.003	-0.020	0.000	-0.249	0.352	0.006	0.053	0.236	-0.689	-0.236*
3.	0.070	-0.074	0.470	-0.521	0.174	0.009	0.034	-0.132	0.019	0.001	0.277	-0.352	-0.025
4.	0.012	-0.002	0.408	-0.602	0.205	0.006	-0.019	-0.026	0.024	-0.070	0.395	-0.197	0.134
5.	0.014	-0.019	-0.229	0.345	-0.357	-0.003	0.114	-0.083	-0.014	0.098	0.558	0.062	0.484**
6.	-0.003	-0.005	0.179	-0.171	0.041	0.023	-0.054	-0.242	0.004	0.154	0.313	0.021	0.259*
7.	0.144	-0.149	-0.028	-0.021	0.071	0.002	-0.568	0.629	0.004	0.081	-0.144	-0.352	-0.330**
8.	-0.163	0.167	0.086	-0.022	-0.041	0.008	0.498	-0.717	-0.003	-0.011	0.184	0.415	0.401**
9.	0.076	-0.065	0.296	-0.478	0.174	0.003	-0.069	0.075	0.030	-0.069	0.273	-0.326	-0.081
10.	-0.061	0.068	-0.002	-0.159	0.132	-0.013	0.173	-0.029	0.008	-0.266	0.018	0.305	0.173
11.	0.056	-0.059	0.097	-0.177	-0.148	0.005	0.061	-0.098	0.006	-0.004	1.346	-0.287	0.798**
12.	-0.229	0.241	-0.170	0.122	-0.023	0.000	0.206	-0.306	-0.010	-0.083	-0.397	0.972	0.323**

\*, \*\* Significant at 5% and 1% level, respectively  
Residual are 0.01813  
Note- 1=Days of 50% flowering, 2= Days of maturity, 3=Plant height, 4=Panicle length, 5=No. of effective tillers per panicle, 6=No. of filled grains per panicle, 7=No. of unfilled grains per panicle, 8=Spikelet fertility%, 9=Flag leaf length, 10=1000 seed weight, 11=Biological yield / plant, 12=Harvest index.

**Reference**

- Anonymous. Agricultural Statistics at a Glance 2020, Ministry of Agriculture & Farmers Welfare Department of Agriculture, Govt. of India, New Delhi; c2020.
- Bhor TJ, Kashid NV, Kadam SM. Genetic variability, character association and path analysis studies for yield components traits in promising rice (*Oryza sativa* L.) genotypes. Journal of Pharmacognosy and Phytochemistry. 2020;9(4):1953-1956.
- Dhanvani RK, Sarawgi AK, Solanki A, Tiwari JK. Genetic variability analysis for various yield attributing and quality traits in rice (*O. sativa* L.). Int. Quarterly J. of life Sci. 2013;8(4):1403-1407.
- Dhidhi S, Gauraha D, Sarawagi AK, Sao A. Genetic variability studies for yield and yield componenets in rice (*Oryza sativa* L.). The Pharma Innovation J. 2021;10(10):1057-1059.
- Ekka, Ruth Elizabeth, Sarawgi AK, Kanwar RR. Genetic variability and inter-relationship analysis for various yield attributing and quality traits in traditional germplasm of rice (*Oryza Sativa* L.). Plant Archives, 2015;15(2):637-645.
- Ekka, Ruth Elizabeth, Sarawgi AK, Kanwar, Raja R. Correlation and Path Analysis in Traditional Rice Accessions of Chhattisgarh. Journal of Rice Research. 2011;4:1-2.
- FAOSTAT. Food and Agricultural Organisation; c2019.
- <http://www.fao.org/faostat/en/#data/QC>
- Ganapati RK, Rasul MG, Sarker Singha U, Ashutus, Faruquee, Muhiuddin. Gene action of yield and yield contributing traits of submergence tolerant rice (*Oryza sativa* L.) in Bangladesh Bull. Natl. Res. Cent. 2020;44:8.
- Gopalan C, Rama Sastri BV, Balasubramanian SC. Nutritive value of Indian foods. National Institute of Nutrition, Indian Council of Medical Research; c1971. p. 47.
- Gupta S, Gauraha D, Sao A, Chaudhary PR. Assessment of genetic variability, heritability and genetic advance in accessions of rice (*Oryza sativa* L.). The Pharma Innovation J. 2021;10(6):1231-1233.
- Gupta S, Upadhyaya S, Koli GK, Rathi SR, Bisen P, Loitongbam B, et al. Trait Association and Path Analysis Studies of Yield Attributing Traits in Rice (*Oryza sativa* L.) Germplasm. IJBSM. 2020;11(6):508- 517.
- Iqbal T, Majeed A, Khattak SI, Ali F, Malik SN, Ahmed N, et al. Genetic Variability and Interrelationship Studies in "Green Super Rice". Research in Plant Biology. 2018;8:37-41.
- Jadhav SP, Kunkerkar RL, Thorat BS, Gawai MP, Keluskar MH. Variability and genetic parameters studies in rice (*Oryza sativa* L.). J Pharmacogn. Phytochem. 2020;9(1):1375-1377.
- Kiani G. Character association and path coefficient analysis of yield components in rice varieties. Research

- on Crops. 2012;13(2):552-555.
15. Kumar S, Chauhan MP, Tomar A, Kasana RK, Kumar N. Correlation and path coefficient analysis in rice (*Oryza sativa* L.). J Pharm. Innov. 2018;7(6):20-26.
  16. Limbani PL, Gangani MK, Pandya MM. Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.). Int. J. Pure App. Biosci. 2017;5(6):1364-1371.
  17. Lingaiah N. Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.). Asian J. Environ. Sci. 2015;10(1):110-112.
  18. Mohammad N, Kumar P, Singh S. Character association and path coefficient analysis for productivity traits in basmati rice (*Oryza sativa* L.). Pant Nagar J Res. 2013;11(3):332-336.
  19. Naik MVK, Pillai MA, Saravanan S. Assessment of Correlation and Path Coefficient Analysis for Yield Attributing and Quality Traits in promising rice varieties cultivated in Tamil Nadu. The Journal of Phyto-pharmacology. 2021;10(2):139-143.
  20. Padmaja D, Radhika K, Subba Rao LV, Padma V. Studies on variability, heritability and genetic advance for quantitative characters in 118 rice (*Oryza sativa* L.). The Indian Journal of Plant Genetic Resources. 2008;21(3):196-198.
  21. Palaniyappan S, Arunachalam P, Banumathy S, Mini ML, Muthuramu S. Genetic parameters and character association studies in rice (*Oryza sativa* L.). J. of Pharmacognosy and Phytochemistry. 2020;9(3):1652-1657.
  22. Paul AKMA, Islam MJ, Hasan MMH, Chowdhury AZMKA. Genetic variation of some morpho-physiological characters in Triticum durum wheat. Int. J. Sustain. Agric. Tech. 2006;2(8):11-14.
  23. Prasad BA, Patwary K, Biswas PS. Genetic variability and selection criteria in fine rice. (*Oryza sativa* L.). Pakistan J. Biol. Sci. 2001;4:1188-1190.
  24. Prasad KR, Radha Krishna KV, Bhawe MHV, Subba Rao LV. Genetic variability, heritability and genetic advance in boro rice (*Oryza sativa* L.) germplasm. International Journal of Current Microbiology Applied Sci. 2017;6(4):1261-1266.
  25. Priya CS, Sunnetha Y, Babu DR, Rao VS. Inter-relationship and path analysis for yield and quality characters in rice (*Oryza sativa* L.). Int. J. Sci. Env. Tech. 2017;6:381-90.
  26. Priyanka Sao A, Gauraha D. Genetic variability studies for yield and quality parameters in aromatic breeding lines of rice (*Oryza sativa* L.). J Pharmacogn. Phytochem. 2020;9(6):1637-1640.
  27. Rokonzaman M, Zahangir MS, Hussain I, Hossain S. Genotypic variability of the components and their effects on the rice yield: Correlation and path analysis study. Ital. J. Agro. 2008;3(2):131-134.
  28. Saha SR, Hassan L, Md Haque A, Islam MM, Md. Rasel. Genetic variability, heritability, correlation and path analyses of yield components in traditional rice (*Oryza sativa* L.) landraces. J Bangladesh Agril. Univ. 2019;17(1):26-32.
  29. Sahu H, Saxena RR, Verulkar SB. Genetic variability and character association study for different morphological traits and path analysis for grain yield of rice under irrigated and rainfed condition. Elec. J Pl. Breed. 2017;8(1):38-45.
  30. Saleh MM, Salem KFM, Elabd AB. Definition of selection criterion using correlation and path coefficient analysis in rice (*Oryza sativa* L.) genotypes. Bulletin of the National Res. Centre. 2020;44:143.
  31. Singh B, Gauraha G, Sao A, Nair SK. Assessment of genetic variability, heritability and genetic advance for yield and quality traits in advanced breeding lines of rice (*Oryza sativa* L.). The Pharma Innovation J 2021;10(8):1627-1630.
  32. Singh SK, Singh CM, Lal GM. Assessment of genetic variability for yield and its component characters in rice (*Oryza sativa* L.). Research in Plant Biology. 2011;1(4):23-26.
  33. Singh SK, Singh M, Vennela PR, Singh DK, Kujur SN, Kumar D. Studies on Genetic Variability, Heritability and Genetic Advance for Yield and Yield Components in Drought Tolerant Rice (*Oryza sativa* L.) Landraces. Int. J. Curr. Microbiol. App. Sci. 2018;7(03):299-305.
  34. Singh TVJ, Mohan YC, Raju CH, Jagadeswar R, Balram M. Character association and path coefficient studies in rice (*Oryza sativa* L.). J Pharmacognosy and Phytochemistry. 2019;8(3):383-387.
  35. Solomon H, Wegary D. Phenotypic Correlation and Path Coefficient Analysis of Yield and Yield Component in Rice (*Oryza Sativa* L.). Int. J Res. Rev. 2016;3(7):1-5.
  36. Yadav SK, Suresh BG, Pandey P, Kumar B. Assessment of genetic variability, correlation and path association in rice (*Oryza Sativa* L.). J Bio Sci. 2010;18:1-8.
  37. Wright S. Correlation and causation. J Agric. Res. 1921;20:557-585.