



P-ISSN: 2349-8528

E-ISSN: 2321-4902

[www.chemijournal.com](http://www.chemijournal.com)

IJCS 2021; 9(1): 2768-2772

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Received: 08-10-2020

Accepted: 19-11-2020

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## Genetic diversity and correlation studies in rice (*Oryza sativa* L.)

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DOI: <https://doi.org/10.22271/chemi.2021.v9.i1am.11643>

### Abstract

The present investigation consists of 26 germplasm used for the experiment was conducted during Kharif-2019 in Randomized Block Design with three replications at Field Experimentation Centre, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj (Allahabad). The data were recorded on thirteen quantitative characters to study genetic variability, heritability, genetic advance, correlation coefficient, path coefficient and genetic divergence. On the basis of mean performance highest grain yield per plant was exhibited by SHIATS DHAN-2 (38.4 g), followed by SHIATS DHAN-1 (38.0 g), SHIATS DHAN- 3 (37.60 g). Analysis of variance among 26 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 higher estimates of GCV and PCV were for Spikelets per panicle followed by tillers and number of panicles. High heritability was recorded for days to maturity followed by Days to flowering 50%. High heritability coupled with high genetic advance is recorded for spikelets per panicle. Correlation study revealed that grain yield per plant showed the high positive significant association for all the characters plant height, flag leaf width, number of tillers, number of panicles, panicle length, biological yield per plant and spikeslets per panicle at both phenotypic and genotypic levels. Path coefficient analysis revealed that plant height, flag leaf width, number of panicles, panicle length, days to maturity, biological yield per hill and harvest index had positive direct effect on yield at phenotypic level for improvement of grain yield in rice. Based on the relative magnitude of D2 values, the genotypes were grouped into seven clusters by Euclidean methods of divergence study. Cluster I consist of a maximum of eight genotypes, followed by cluster II with six genotypes, cluster III with three genotypes, cluster IV with three genotypes, cluster V with two genotypes, cluster VI with one genotype, cluster VII with three genotypes. The maximum inter-cluster distance was observed between cluster VII and V followed by cluster V and IV. Thus, the genotypes from the clusters having maximum inter-cluster distance can be selected and used as parents for hybridization programme to develop desirable lines. Maximum genetic divergence was exhibited by grain yield per hill and test weight contributed to 78.77% of total divergence which is needed to be focused while selecting parents for hybridization programme.

**Keywords:** Genotype, GCV, PCV, heritability, genetic advance and D2 analysis

### Introduction

Rice (*Oryza sativa* L.) is a staple and most important security food crop consumed by almost half of the world's population. Rice is nutritious crop and it is an important source of proteins providing the substantial amount of recommended nutrient intake of zinc and niacin. However, rice is very low in calcium, iron, thiamine and riboflavin and nearly devoid of beta-carotene. Rice protein is biologically the richest by virtue of its high true digestibility (88%) among cereal proteins and also provides minerals and fibre. Rice is Life. Globally rice is cultivated on 167.13 million hectares with annual production of around 769.9 million tones and average productivity of 4.6 tons per hectare (FAO, 2018-19) [15]. More than 90% of rice is produced and consumed in Asian countries.

Rice is grown in almost all the states in the country however the major states in rice production are West Bengal, Uttar Pradesh, Andhra Pradesh, Punjab and Tamil Nadu. In India, rice is grown in 43 million ha, the production level is 115 million tons and the average productivity is about 2700kg/ha during 2018-19 (Annual Report, NRRI-2019). It is grown under diverse soil and climate conditions the productivity level of rice is low compared to the productivity level levels of many countries in the world.

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Also, about 90% of the cultivated land belongs to marginal, small and medium farmers, which is another constrain in increasing the productivity of rice in the country. It is, therefore there is ample scope to increase the productivity of rice in the country. The highest productivity is 7030kg/ha of China followed by Vietnam (5913kg/ha), Indonesia (4680kg/ha) etc. in comparison of India (2700kg/ha).

In India, West Bengal stands top in the production of rice with an area of 5.12 million hectares with the production of 14.97 million tonnes and productivity of 2926kg/ha. Whereas in Uttar Pradesh rice is grown in 5.91 million hectares with the production of 13.27 million tonnes with productivity 2.2 t/ha. Uttar Pradesh ranks second in the production of rice. Correlation is the measure of the mutual relationship between two variables. The study of correlations may help the plant breeder to know how the improvement of one character will bring simultaneous improvement in other characters. Path coefficient analysis is a standardized regression coefficient and measures the direct influence of one variable upon the other. Direct selection for yield is not a reliable approach since it is influenced by the environment. Therefore, it is essential to identify the component characters through which yield can be improved. Selection would be more effective for the trait, which has got high genetic advance and high correlation with grain yield. The use of correlation coefficient is to establish extent of association between yield and yield component and other character, which are having decisive role in influencing the yield (Singh, 2009) [16]. However, it is only genetic variation which is heritable and hence important in any selection programme. Path coefficient analysis is a standardized regression coefficient and measures the direct influence of one variable upon the other. It is statistical technique of partitioning the correlation coefficient into its direct and indirect effects, so that the contribution of each character to yield could be estimated. Direct selection for yield is not reliable approach since it is influenced by the environment. It is used in the plant breeding programmes to determine the nature of relationship between yield and yield components that are useful as selection criteria to improve crop yield.

Genetic diversity is the foundation of the genetic improvement of crops. The diversity in crop varieties is essential for agricultural development for increasing food production, poverty alleviation and promoting economic growth. The available diversity in the germplasm also serves as an insurance against unknown future needs and conditions, there by contributing to the stability of farming systems at local, national and global levels (Singh *et al.*, 2000) [25].

Study of genetic divergence among the plant materials are an important tool to the plant breeders for an efficient selection of the diverse parents for their potential use in a rice breeding programme for the improvement of the rice production. Parents identified on the basis of divergence for any breeding programme would be more promising (Kwon *et al.*, 2002) Grouping or classification of genotypes based on suitable scale is quite imperative to understand the usable variability existing among them. For the assessment of variation on multivariate scale, Mahalanobis D<sup>2</sup> statistics has proved to be a powerful technique.

## Materials and Methods

The experimental material consisted of 26 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*-2019. Twenty-one days old seedlings were transplanted in  $2 \times 1$  m<sup>2</sup> 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) [22], coefficient of variation (GCV and PCV) by Burton (1952) [9]. 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) [10]. Genetic advance was calculated by the method suggested by Johnson *et al.*, (1955) [17]. Correlation coefficient and path coefficient was worked out as method suggested by Al Jibouri *et al.* (1958) [4], Dewey and Lu (1959) [13]. Genetic divergence was calculated based on Mahalanobis (1936) D<sup>2</sup> statistics respectively.

## Results and 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) [12], 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 Spikelets per panicle followed by tillers and number of panicles. Similar findings were obtained by Aditya *et al.* 2013 [2], Dinesh *et al.* 2011 [14], Kishore *et al.* 2015 [18], Abdul *et al.* 2011 [1].

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; days to maturity followed by Days to flowering 50%, flag leaf width, panicle length, spikelets per panicle, biological yield per hill, plant height, number of tillers, flag leaf length, number of panicles and whereas, characters like; grain yield per hill, test weight depicted moderate estimate of heritability and harvest index of the characters showed low estimates of heritability. Similar results are reported by Kumar *et al.* (2012) [19], Allam *et al.* (2015) [5], Abdul *et al.* (2011) [1], Rashmi *et al.* (2017) [12], Dinesh *et al.* (2011) [14], Aditya *et al.* (2013) [2], Kishore *et al.* (2015) [18], Ogunbayoa *et al.* (2014) [23], Shiva *et al.* (2018) [24] recorded high heritability for grain yield per hill.

The characters exhibiting high heritability may not be necessary to give high genetic advance. Johnson (1955) [17] 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 spikelets per panicle. Similar results were reported earlier in rice by Abdul

*et al.* (2011) [1]. 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 plant height, flag leaf width, number of tillers, number of panicles, biological yield per plant and spikeslets per panicle showed positive significant correlation at phenotype and genotypic levels. The positive correlation of grain yield with various traits was supported by the Abdul *et al.* (2011) [1], Rashmi *et al.* (2017) [12], Aditya *et al.* (2013) [2], Shiva *et al.* (2018) [24]. 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). The path analysis at phenotypic level of the characters like plant height, flag leaf width, number of panicles, panicle length, days to maturity, biological yield per hill and harvest index had positive direct effect on grain yield per hill. whereas, days to 50% flowering, flag leaf length, number of tillers, spikes per panicle and test weight showed negative direct effect on grain yield per hill. Similar results were reported earlier by Abdul *et al.* (2011) [1] for spikelets per panicle, biological yield per hill, harvest index, test weight; Rashmi *et al.* (2017) [12] for days to maturity, plant height, panicle length, Days to maturity; Aditya *et al.* (2013) [2] for Day to 50% flowering, Plant height, flag leaf width, panicle length, Days to maturity, test weight and Kishore *et al.* (2015) [18] for Plant height, flag leaf length. The path analysis at genotypic level of the characters like plant height, flag leaf length, number of panicles, spikes per panicle, harvest index and biological yield per hill had positive direct effect on grain yield per hill whereas, days to 50% flowering, flag leaf width, number of tillers, panicle length days to maturity and test weight showed negative direct effect on grain yield per hill. Similar results were reported earlier by Abdul *et al.* (2011) [1] for Plant height, number of tillers per hill, panicle length, biological yield per hill, harvest index, test weight; Kishore *et al.* (2015) [18] for Plant height, panicle length and Bhandari *et al.* (2019) for Day to 50% flowering.

On the basis of Mahalanobis D2 statistics, 26 genotypes were grouped into seven clusters (table no. 5). The maximum inter cluster distance was observed between cluster VII and V, followed by cluster V and IV and Cluster V and III. The minimum inter cluster distance was observed between cluster

VI and II. The maximum intra-cluster distance was registered for cluster IV, followed by cluster VII and cluster III. While, the minimum intra cluster distance was registered in cluster VI followed by cluster I and cluster V. Pradhan and Roy, (1990), Mishra *et al.* (2003) and Chaturvedi and Maurya (2005) [11] recommended that parents should be selected from two clusters having wider inter-cluster distance.

Selection of genotype from cluster IV and cluster VII has recorded high mean value for grain yield and its components traits were suggested for utilization in hybridization programme and aimed at improvement of these traits. Therefore, hybridization between selected genotypes from divergent clusters is essential to judiciously combined all the target traits.

The genotypes with high mean values may be directly used for adaptation or may be used as parents in the future breeding programme. In the present study, cluster I have low mean values for plant height, flag leaf length, flag leaf width, number of tillers per hill and grain yield per hill. Cluster II shows low mean values for Panicle Length, biological yield per hill. Cluster III shows high mean values for days to maturity and low mean value for number of panicles per hill. Cluster IV shows high mean value for Flag leaf length, flag leaf width, panicle length, spikelets per panicle, harvest index and grain yield per hill and low mean value for Days to 50% flowering and days to maturity. Cluster V shows high mean value for days to 50% Flowering and test weight and low mean value for spikelets per panicle and harvest index. Cluster VI shows high mean values for number of tillers per hill, number of panicles per hill and biological yield per hill. Cluster VII shows high mean value for plant height.

The selection and choice of parents mainly depend upon the contribution of characters towards divergence. Among 13 characters studied panicle length followed by plant height, spikelets per panicle, harvest index and flag leaf length contributed maximum to the total genetic divergence.

The present investigation revealed that grain yield per hill and test weight were the major contributors towards divergence and accounted for about 78.77% of contribution towards total divergence (table.6). Number of panicles per hill and harvest index had zero contribution towards divergence. Oving *et al.* (2012) [21] also reported a maximum contribution of plant height and spikelets per panicle. Singh and Singh (2008) reported the minimum contribution of days to 50% flowering, tillers per plant and grain yield among all characters.

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

Mean squares	Characters		Days to 50% Flowering	Plant Height	Flag leaf length	Flag leaf width	Tillers per hill	Panicles per hill	Panicle Length	Spikelet's per Panicle	Days to Maturity	Biological Yield	Harvest index	Test Weight	Grain Yield per hill
	Replication	(d.f=2)	10.5	18.91	3.16	0.06	6.6	3.85	0.032	92.39	18.93	65.1	13.8	32.74	16.15
Treatments	(d.f=25)	67.65	175.41	57.54	0.11	19.42	14.2	16.95	4233.59	75.96	342.42	40.4	23.91	70.82	
Error	(d.f=50)	2.31	15.36	6.56	0.008	1.95	1.74	1.33	362.61	1.82	29.92	16.02	5.35	9.19	

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

	Days to 50% Flowering	Plant Height	Flag leaf length	Flag leaf width	Tillers per hill	Panicles per hill	Panicle Length	Spikelet's per Panicle	Days to Maturity	Biological Yield	Harvest index	Test Weight	Grain Yield per hill
GCV	4.676	6.239	11.617	14.488	21.992	21.241	8.930	22.577	3.861	14.343	6.509	11.038	14.608
PCV	4.918	7.080	13.678	15.912	25.414	25.311	10.011	25.554	4.001	16.273	11.222	15.077	17.575
h <sup>2</sup> (Broad Sense)	90.400	77.600	72.100	82.900	74.900	70.400	79.600	78.100	93.100	77.700	33.600	53.600	69.100
Genetic Advancement 5%	9.141	13.258	7.212	0.361	4.302	3.523	4.193	65.379	9.881	18.531	3.406	3.751	7.760
Gen. Adv as % of Mean 5%	9.159	11.324	20.325	27.174	39.205	36.722	16.409	41.092	7.674	26.041	7.777	16.647	25.011

**Table 3(a):** Correlation coefficient between yield and its related traits in 26 rice genotypes at genotypic level

Character	Days to 50% Flowering	Plant Height	Flag leaf length	Flag leaf width	Tillers per hill	Panicles per hill	Panicle Length	Spikelet's per Panicle	Days to Maturity	Biological Yield	Harvest index	Test Weight	Grain Yield per hill
Days to 50% flowering	1	-0.0497	-0.0735	0.0572	-0.026	0.063	-0.420**	-0.135	0.979**	0.059	-0.493**	-0.168	-0.199
Plant height (cm)		1	0.585**	0.568**	0.418**	0.315*	-0.03	0.299*	-0.0157	0.207	0.189	0.199	0.307*
Flag leaf length (cm)			1	0.636**	0.331*	0.277*	-0.01	0.313*	0.006	0.287*	-0.116	0.280*	0.146
Flag leaf width (cm)				1	0.696**	0.680**	-0.109	0.533**	0.111	0.494**	0.015	-0.1503	0.508**
Tillers/ hill					1	0.993**	0.056	0.618**	0.019	0.573**	-0.062	-0.045	0.582**
Panicles/ hill						1	0.051	0.609**	0.093	0.614**	-0.163	-0.15	0.568**
Panicle length (cm)							1	0.454**	-0.468**	0.261*	0.601**	-0.232*	0.547**
Spikelets/ panicle								1	-0.148	0.166	0.553**	-0.373**	0.446**
Days to maturity									1	0.103	-0.553**	-0.111	-0.186
Biological yield/hill (g)										1	-0.350*	-0.037	0.892**
Harvest index											1	-0.079	0.099
Test weight(g)												1	-0.088

**Table 3(b):** Correlation coefficient between yield and its related traits in 26 rice genotypes at phenotypic level

	DF (50%)	PH	FL	FW	T	P	PL	SPP	DM	BYH	HI	TW	GYPH
DF (50%)	1	-0.0417	-0.0805	0.0509	-0.0216	0.0421	-0.3722***	-0.0672	0.9710***	0.0731	-0.3428**	-0.1538	-0.1815
PH		1	0.4706***	0.4256***	0.3528**	0.2695*	0.0721	0.2173	-0.0028	0.1461	0.1507	0.165	0.241*
FL			1	0.5276***	0.2995**	0.2553*	0.0654	0.2281*	-0.0091	0.1705	0.0142	0.2155	0.1238
FW				1	0.5915***	0.5505***	-0.0627	0.4670***	0.0876	0.4440***	0.0377	-0.0938	0.411**
T					1	0.9716***	0.1068	0.4323***	0.0182	0.4588***	0.0931	-0.0073	0.474**
P						1	0.0748	0.4059***	0.0746	0.4675***	0.0685	-0.0852	0.468**
PL							1	0.3407**	-0.4103***	0.2005	0.3048**	-0.1097	0.394**
SPP								1	-0.1042	0.1734	0.2869*	-0.2867*	0.317*
DM									1	0.1132	-0.3613**	-0.1041	-0.1499
BYH										1	-0.2303*	-0.0156	0.771**
HI											1	-0.0677	0.377**
TW												1	-0.0887
GYPH													1

**Table 4:** Correlation coefficient between yield and its related traits in 26 rice genotypes at genotypic level

	DF (50%)	PH	FL	FW	T	P	PL	SPP	DM	BYH	HI	TW	GYPH
DF (50%)	1	-0.0497	-0.0735	0.0572	-0.026	0.063	-0.420**	-0.135	0.979**	0.059	-0.493**	-0.168	-0.199
PH		1	0.585**	0.568**	0.418**	0.315*	-0.03	0.299*	-0.0157	0.207	0.189	0.199	0.307*
FL			1	0.636**	0.331*	0.277*	-0.01	0.313*	0.006	0.287*	-0.116	0.280*	0.146
FW				1	0.696**	0.680**	-0.109	0.533**	0.111	0.494**	0.015	-0.1503	0.508**
T					1	0.993**	0.056	0.618**	0.019	0.573**	-0.062	-0.045	0.582**
P						1	0.051	0.609**	0.093	0.614**	-0.163	-0.15	0.568**
PL							1	0.454**	-0.468**	0.261*	0.601**	-0.232*	0.547**
SPP								1	-0.148	0.166	0.553**	-0.373**	0.446**
DM									1	0.103	-0.553**	-0.111	-0.186
BYH										1	-0.350*	-0.037	0.892**
HI											1	-0.079	0.099
TW												1	-0.088
GYPH													1

**Table 5:** Intra and Inter-cluster average distances in rice germplasm

Cluster Distances							
	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Cluster 1	21.91	83.27	45.81	58.12	278.94	90.44	193.8
Cluster 2		25.99	91.94	120.84	110.63	44.21	319.8
Cluster 3			40.59	76.82	308.38	107.26	144.19
Cluster 4				48.29	365.34	91.64	133.39
Cluster 5					24.25	149.37	716.51
Cluster 6						0	286.28
Cluster 7							45.97



**Table 6:** Percent contribution of 13 characters to genetic divergence

	Source	Contribution %	Times ranked 1st
1	DF (50%)	0.92	3
2	PH	0.62	2
3	FL	0.62	2
4	FW	1.54	5
5	T	3.08	10
6	P	0	0
7	PL	5.23	17
8	SPP	2.77	9
9	DM	3.69	12
10	BYH	2.77	9
11	HI	0	0
12	TW	9.54	31
13	GYPH	69.23	225

## References

1. Abdul Fiyaz R, Ramya KT, Chikkalingaiah, Ajay BC, Gireesh C, Kulkarni RS. Genetic variability, correlation and path coefficient analysis studies in rice (*Oryza sativa* L.) under alkaline soil condition Electronic Journal of Plant Breeding 2011;2(4):531-537.
2. Aditya JP, Bhartiya A. Genetic variability, correlation and path analysis for quantitative characters in rainfed upland rice of Uttarakhand Hills. Journal of Rice Research 2013;6(2):24-34.
3. Agricultural statistics at A glance. Ministry of Agriculture & Farmers welfare, Department of Agriculture, Cooperation & Farmers welfare, Directorate of Economics and Statistics, Government of India 2018.
4. Al-Jibouri HA, Muller PA, Robinson HF. Genetic and environmental variances and co-variances in an upland cotton cross of inter specific origin. Agronomy J 1958;50:633-636.  
<http://dx.doi.org/10.2134/agronj1958.00021962005000100020x>
5. Allam CR, Jaiswal HK, Qamar A. Character association and path analysis studies of yield and quality parameters in basmati rice (*Oryza sativa* L.). The Bioscan 2015;9(4):1733-1737.
6. Bhandari K, Poudel A, Sharma S, Kandel BP, Upadhyay K. Genetic Variability, correlation and path analysis of rice genotypes in rainfed 2015.
7. Bhandari K, Poudel A, Sharma S, Kandel BP, Upadhyay K. Genetic variability, correlation and path analysis of rice genotypes in rainfed 2015.
8. Bharadwaj CH, Mishra Rajesh, Satyavathi Tara C, Rao SK, Kumar KS. Genetic variability, heritability and genetic advance in some new plant type-based crosses of rice (*Oryza sativa* L.). Indian Journal of Agricultural Research 2007;41(3):189-194.
9. Burton GW. Quantitative inheritance in grasses. Proceeding of 6th International Grassland Congress 1952;1:277-283.
10. Burton GW, Devane EH. Estimating heritability in tall fescue (*Restuca arundian*) from replicated clonal material. Agronomy Journal 1953;(1):478-481.
11. Chaturvedi HP, Maurya DM. Genetic divergence analysis in rice (*Oryza sativa* L.). Advances in Plant Sciences 2005;18(1):349-353.
12. Deep Rashmi, Shoumik S, Bapsila L, Sakshi S, Singh PK. Genetic Variability Study for Yield and Yield Components in Rice (*Oryza sativa* L.) International Journal of Agriculture, Environment and Biotechnology Citation: IJAEB 2017;10(2):1-6.
13. Dewey DR, Lu KH. Genetic variability, correlation and path coefficient analysis of components of crested wheat grass seed production. Agronomic Journal 1959;51:515-518.
14. Dinesh KT, Praveen P, Sachchidanand T, Prasad Giri S, Jawahar LD. Studies on genetic variability for yield components in rice (*Oryza sativa* L.) International Journal of the Bioflux Society 2011.
15. FAO. Food and Agricultural organization. Online Interactive Database on Agriculture 2019.
16. Hossain MS, Singh AK, Fasih-uz-Zaman. Cooking and eating characteristics of some newly identified inter subspecies (indica/japonica) rice hybrids. Science Asia 2009;35:320-325.
17. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agronomy Journal 1955;47:314-318.
18. Kishore NS, Srinivas T, Nagabhushanam U, Pallavi M, Sameera SK. Genetic variability, correlation and path analysis for yield and yield components in promising rice (*Oryza sativa* L.) genotypes. SAARC Journal of Agriculture 2015;13(1):556-560.
19. Kumar S, Singh D, Satyendra Sirohi A, Kant S, Kumar A, Pal K, Kumar M. Variability, heritability and genetic advance in rice (*Oryza sativa* L.) under Aerobic condition. Environment and Ecology 2012;30(4):1374-1377.
20. Nath S, Singh SP. Study of genetic variability in rice (*Oryza sativa* L.). Progressive Research 2013;8(Special):52-54.
21. Ovung CY, Lal GM, Rai PK. Studies on genetic diversity in Rice (*Oryza sativa* L.). Journal of Agricultural Technology 2012;8(3):1059-1065.
22. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. 2nd Edn ICAR, New Delhi 1961, 361.
23. Ogunbayoa SA, Sié M, Ojo DK, Sanni KA, Akinwale MG, Toulou B *et al.* Genetic variation and heritability of yield and related traits in promising rice genotypes (*Oryza sativa* L.) Journal of Plant Breeding and Crop Science 2014;6(11):153-159.
24. Shiva A, Abhisek S, Narayan A, Ankur P, Suvarna A. Genetic Variability, Heritability and Correlation Analysis In Quantitative Traits of Irrigated Rice (*Oryza Sativa* L.) Biosciences biotechnology research Asia 2018;15(3):729-735.
25. Verma OP, Santhoshi U, Singh Dwivedi JL, Singh PP. Genetic variability, heritability and genetic advance for quantitative traits in rice. *Orzya* 2000;37(2):38-40.