"Assessment of Heritability, Genetic Advance and Correlation Analysis for Grain Yield Characters of Rice (*Oryza sativa L.*)"

ABSTRACT

An investigation was carried out on twenty one rice genotype during *kharif*, 2021 at the experimental field of Department of Genetics and Plant Breeding, SHUATS, Allahabad in Randomized Block Design with three replications to analyze heritability and genetic advance for 14 quantitative characters. A close examination of variability coefficients revealed that the differences between PCV and GCV were small indicating little influence of environment on the expression of the characters. High to moderate estimates of GCV and PCV were recorded for number of tillers per hill followed by grain yield per plant, number of filled grains per panicle and biological yield. High estimates of heritability were observed for days to maturity, number of total tillers per hill, plant height, days to 50% flowering, grain yield per hill which suggested that these traits would respond to selection owing to their high genetic variability and transmissibility and certainly lead to improvement in grain yield. Moreover, the information generated from this study, can be exploited in future rice breeding program.

Key words: - Genetic advance, heritability, Rice genotypes, variability.

INTRODUCTION

Rice (O*ryza 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. It meets the calorie requirement of 50 percent of the population and provides livelihood to 160 million of rural poor. (Santha *et al.*, 2016). The crop is cultivated round the year in one or the other parts of the country under diverse ecologies spread about 44 million hacteres. About 40 percent of the rice area in Indiais rainfed, more than 70 percent of which is in eastern India. About 23 percent of rainfed rice area is upland and 77 percent is lowland.

Cultivation of rice is important for the food security of Asia. India has a long history of rice cultivation. India stands first in area (43.78 mha) and world's second largest producer (109.32 mt) of rice after china with the productivity of 2.7 tons per hectare. The year 2016-17 recorded the highest rice production (109.32) still now. It is estimated that in India, the demand for rice will be 129.6 million tons by 2040 and 137.3 million tons by 2050 for internal consumption. (Directorate of Economics and Statistics, 2019-20).

In order to feed the increasing population, the production of rice has to match with the consumption growth, where rice is the staple food crop. . Irrigated rice production supplies 75 to 80 percent of global rice requirements. However, the yield in irrigated area has reached a plateau and it is time to break the yield ceiling in those areas to feed the growing population. As the land frontiers for many countries have been exhausted, diversification of land to other crops is taking place due to higher returns and consumer demand, and more land is being diverted for non-agricultural purposes, the growth in many countries has to come from increase in productivity of arable land.

Thus, it is understood that there is an extreme need to enhance the rice productivity which will be achieved only by developing high yielding varieties. Genetic variability is the foremost important breeding tool in order to break yield stagnation and developing high yielding varieties.

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 theenvironment in which they are grown. (Mohammad *et al.,* 2012).

Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. Hence knowledge about genetic advance coupled with heritability is most useful. Character exhibiting high heritability may not necessarily give high genetic advance. High heritability should be accompanied with high genetic advance to arrive more reliable conclusion. Expected genetic advance as per cent of mean indicates the mode of gene action in the expression of a trait, which helps in choosing an appropriate breeding method (Kumar *et* al., 2014).

A thorough knowledge of nature and magnitude of genetic variability and association of characters in a crop species is a pre-requisite for a successful breeding programme, information on direct and indirect effects contributed by each character towards yield will be an added advantage in aiding the selection process.

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).

MATERIALS AND METHODS

The present investigation was carried out in the Field Experimentation Centre of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad, U.P during *Kharif*-2021. A randomized block design was adopted with three replications and row to row spacing is 20cm and plant to plant spacing is 15cm with plot size of 5mx2m.

Replication wise data on the basis of five randomly taken competitive plants from each replication were recorded on following fourteen quantitative traits : 1) Days to 50% flowering, 2) Days to maturity, 3) Flag leaf length, 4) Flag leaf width, 5) Plant height, 6) Number of total tillers per hill, 7) Panicle length, 8) Number of spikelets per panicle, 9) Number of filled grains per panicle, 10) Number of unfilled grains per panicle, 11) Test weight, 12) Harvest index, 13)Biological yield, 14) Grain yield per hill.

The recorded for all the considered characters were subjected to analysis of variance with the formula suggested by Panse and Sukhatme (1978). Further, different components of variance i.e., phenotypic, genotypic and environmental variance were estimated and genetic parameters like genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability in broad sense, genetic advance as percent of mean and correlation analysis were conducted by following appropriate statistical procedure.

RESULTS AND DISCUSSION

Analysis of variance indicated significant difference among the genotypes for all the traits (Table 1). This indicates that there was an ample scope for selection of promising lines from the present gene pool for yield and its components traits. The presence of large amount of variability might be due to diverse source of material taken as well as environmental influence affecting the phenotypes.

In the present investigation, genetics parameters (table 2) revealed that the PCV was higher than the corresponding GCV for all the traits indicating that there was an influence of the environment. GCV (%) values ranged between least of 8.1% (Harvest index) to a highest value of 39.83% (number of tillers per hill). PCV (%) values ranged between least of 8.95% (Plant height) to a highest value of 40.29% (number of tillers per hill). The high estimates of PCV and GCV for these traits like number of total tillers per hill, biological yield per plant (g) and number of filled grains per panicle suggested that the possibility of yield improvement through selection of these traits.

In the present investigation, all traits showed the high heritability ranging from 54.13% (Number of unfilled grains) to 98.91% (Days to maturity). High heritability values (>60%) were recorded for days to maturity (98.919%), number of total tillers per hill (97.734%), plant height (97.666%), days to 50% flowering (97.615%), grain yield per hill (97.487%), biological yield (91.673%), flag leaf width (90.532%), number of filled grains per panicle (89.313%), panicle length (88.056%), number of spikelets per panicle (88.029%), test weight (86.788%), flag leaf length (75.474%) and harvest index (61.126%).

The high heritability values of the considered traits in the present study indicated that those were less influenced by the environment and thus help in effective selection of the traits based on the phenotypic expression by adopting simple selection method and suggested the scope of genetic improvement. In the present study, genetic advance for different traits revealed that it varied from 0.403 to 88.862. High genetic advance (above 20%) was observed for number of filled grains per panicle per panicle (88.862%) among all the quantitative characters followed by number of spikelets per panicle (86.681%), days to 50% flowering (28.609%), biological yield (26.929%), days to maturity (26.905%), grain yield per hill (24.507%), plant height (24.264%).

Estimates of genetic advance as a percentage of mean revealed that number of tillers per hill (81.12%) showed highest genetic advance as percentage of mean, followed by grain yield per plant (66.68%). While moderate genetic advance as a percent of mean was observed only in harvest index (13.18%). All the characters under study showed high heritability coupled with high values of genetic advance as percent mean which indicates that the characters mostly governed by additive gene action. So direct selection of these characters based on phenotypic expression by simple selection method would be effective due to accumulation of more additive genes leading to further improvement.

Correlation analysis among the yield and its contributing characters (table 3 & 4) revealed that the genotypic correlation coefficients in most cases were higher than their phenotypic correlation coefficients indicating the association was largely due to genetic reason. At both genotypic and phenotypic levels, significant positive correlations were observed for grain yield per plant with biological yield per plant, days to maturity and number of unfilled grains per panicle. From the present investigation it is concluded that among 21 rice varieties based on the mean performance RGL-2536 (63.3g) genotype was found to be superior in grain yield per plant. Number of tillers per hill had recorded with high estimates of GCV and PCV. All the characters under study showed high heritability coupled with high values of genetic advance as percent mean. At both genotypic and phenotypic levels, significant positive correlations were observed for grain yield per plant with biological yield per plant, days to maturity and number of unfilled grains per panicle. The results of the path coefficient analysis revealed that both phenotypic and genotypic level, harvest index, flag leaf width, number of filled grains per panicle and number of unfilled grains per panicle had positive direct effects on grain yield per plant. Selection of plants on these traits would certainly lead to improvement in grain yield.

Table 1 : Analysis of Variance for fourteen Quantitative Traits in Rice

Sl.No.	**Source**	**Replication**	**Treatment**	**Error**
	Degrees of freedom	**2**	**20**	**40**
1	Days to 50 flowering	5.4720	597.587**	4.829
2	Days to maturity	1.9260	519.211**	1.885
3	Flag leaf length	7.6480	136.178**	13.309
4	Flag leaf width	0.0010	0.131**	0.004
5	Plant height	1.4380	429.552**	3.395
6	Number of total tillers per hill	0.340	78.437**	0.602
7	Panicle length	1.9510	20.679**	0.895
8	Number of spikelets per panicle	256.5370	6307.536**	273.512
9	Number of filled grains per panicle	373.6610	6499.718**	249.308
10	Number of unfilled grains per panicle	19.3960	29.576**	6.513
11	Test weight	4.8210	37.11**	1.792
12	Harvest Index	30.180	58.508**	10.234
13	Biological yield	7.9920	576.153**	16.932
14	Grain yield per hill	2.7510	439.266**	3.742

** indicates 1% level of significance respectively

Table 2 : Genetic parameters for fourteen Quantitative traits in Rice

Traits	GCV	PCV	h2 (Broad Sense)	GA	GA as % of Mean
1. Days to 50 flowering	13.465	13.628	97.615	28.609	27.404
2. Days to maturity	10.197	10.253	98.919	26.905	20.892
3. Flag leaf length	14.693	16.913	75.474	11.453	26.295
4. Flag leaf width	16.409	17.246	90.532	0.403	32.162
5. Plant height	8.845	8.95	97.666	24.264	18.007
6. Number of total tillers per hill	39.833	40.293	97.734	10.373	81.122
7. Panicle length	10.196	10.866	88.056	4.964	19.71
8.Numberof pikelets per panicle	24.426	26.034	88.029	86.681	47.21
9. Number of filled grains per panicle	27.429	29.024	89.313	88.862	53.399
10.Number of unfilled grains per panicle	20.827	28.307	54.135	4.202	31.567
11. Test weight	15.069	16.176	86.788	6.585	28.919
12. Harvest Index	8.188	10.473	61.126	6.461	13.188
13. Biological yield	21.486	22.441	91.673	26.929	42.378
14. Grain yield per hill	32.788	33.207	97.487	24.507	66.689

GA = Genetic Advance, GA as % of mean = Genetic Advance as % of mean, h^2 = Heritability, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation.

Table 3 : Genotypic correlation matrix

Traits	Days to 50 flowering	Days to maturity	Flag leaf length	Flag leaf width	Plant height	Number of total tillers per hill	Panicle length	Number of spikelets per panicle	Number of filled grains per panicle	Number of unfilled grains per panicle	Test weight	Harvest Index	Biological yield	Grain yield per hill
Days to 50 flowering	1.0000	0.957**	0.1509	0.1635	0.0712	0.690**	0.0028	0.343*	0.309*	0.2190	-0.0973	0.2043	0.0407	0.2112
Days to maturity	0.957**	1.0000	0.0698	0.309*	-0.1024	0.597**	-0.0474	0.2064	0.1668	0.1078	-0.0803	0.1769	-0.0380	0.270*
Flag leaf length	0.1509	0.0698	1.0000	-0.332*	0.301*	0.0717	0.450**	-0.0773	0.0093	-0.1600	0.0638	0.269*	-0.0663	-0.1338
Flag leaf width	0.1635	0.309*	-0.332*	1.0000	-0.288*	-0.0557	-0.1338	0.1170	-0.1490	-0.1404	-0.1094	-0.269*	-0.318*	0.0475
Plant height	0.0712	-0.1024	0.301*	-0.288*	1.0000	0.0766	0.0955	-0.0924	-0.0522	-0.2003	-0.395*	0.0134	-0.1781	-0.1230
Number of total tillers per hill	0.690**	0.597**	0.0717	-0.0557	0.0766	1.0000	0.1096	0.1497	0.1007	0.324*	-0.410**	0.285*	0.256*	0.2322
Panicle length	0.0028	-0.0474	0.450**	-0.1338	0.0955	0.1096	1.0000	-0.2121	-0.332*	-0.1705	0.0985	0.269*	0.1827	-0.0671
Number of spikelets per panicle	0.343*	0.2064	-0.0773	0.1170	-0.0924	0.1497	-0.2121	1.0000	0.923**	0.639**	0.2016	0.0843	0.0315	-0.1725
Number of filled grains per panicle	0.309*	0.1668	0.0093	-0.1490	-0.0522	0.1007	-0.332*	0.923**	1.0000	0.675**	0.2280	0.1206	0.1499	-0.0523
Number of unfilled grains per panicle	0.2190	0.1078	-0.1600	-0.1404	-0.2003	0.324*	-0.1705	0.639**	0.675**	1.0000	-0.0525	0.1152	0.253*	0.352*
Test weight	-0.0973	-0.0803	0.0638	-0.1094	-0.395*	-0.410**	0.0985	0.2016	0.2280	-0.0525	1.0000	0.0379	0.0866	-0.2472
Harvest Index	0.2043	0.1769	0.269*	-0.269*	0.0134	0.285*	0.269*	0.0843	0.1206	0.1152	0.0379	1.0000	0.471**	0.275*
Biological yield	0.0407	-0.0380	-0.0663	-0.318*	-0.1781	0.256*	0.1827	0.0315	0.1499	0.253*	0.0866	0.471**	1.0000	0.473**

**** indicates 1% level of significance**

***indicates 5% level of significance**

Table 4 : Phenotypic correlation matrix

Traits	Days to 50 flowering	Days to maturity	Flag leaf length	Flag leaf width	Plant height	Number of total tillers per hill	Panicle length	Number of spikelets per panicle	Number of filled grains per panicle	Number of unfilled grains per panicle	Test weight	Harvest Index	Biological yield	Grain yield per hill
Days to 50 flowering	1.0000	0.945**	0.1247	0.1388	0.0655	0.671**	-0.0014	0.307*	0.288*	0.1559	-0.0997	0.1555	0.0401	0.2092
Days to maturity	0.945**	1.0000	0.0661	0.307*	-0.0960	0.584**	-0.0447	0.1887	0.1561	0.0866	-0.0677	0.1366	-0.0391	0.266*
Flag leaf length	0.1247	0.0661	1.0000	-0.2332	0.267*	0.0326	0.387*	-0.1012	-0.0021	-0.1438	0.0693	0.1089	-0.0598	-0.1100
Flag leaf width	0.1388	0.307*	-0.2332	1.0000	-0.253*	-0.0600	-0.0974	0.1206	-0.1166	-0.1044	-0.0854	-0.2028	-0.306*	0.0369
Plant height	0.0655	-0.0960	0.267*	-0.253*	1.0000	0.0710	0.0841	-0.0973	-0.0575	-0.1505	-0.357*	-0.0046	-0.1702	-0.1257
Number of total tillers per hill	0.671**	0.584**	0.0326	-0.0600	0.0710	1.0000	0.1052	0.1580	0.1005	0.2345	-0.371*	0.2296	0.2417	0.2294
Panicle length	-0.0014	-0.0447	0.387*	-0.0974	0.0841	0.1052	1.0000	-0.1725	-0.293*	-0.0603	0.0803	0.1878	0.1890	-0.0613
Number of spikelets per panicle	0.307*	0.1887	-0.1012	0.1206	-0.0973	0.1580	-0.1725	1.0000	0.895**	0.498**	0.1651	0.0403	0.0414	-0.1587
Number of filled grains per panicle	0.288*	0.1561	-0.0021	-0.1166	-0.0575	0.1005	-0.293*	0.895**	1.0000	0.529**	0.1952	0.0461	0.1355	-0.0533
Number of unfilled grains per panicle	0.1559	0.0866	-0.1438	-0.1044	-0.1505	0.2345	-0.0603	0.498**	0.529**	1.0000	-0.0830	0.0732	0.2045	0.261*
Test weight	-0.0997	-0.0677	0.0693	-0.0854	-0.357*	-0.371*	0.0803	0.1651	0.1952	-0.0830	1.0000	0.0382	0.0555	-0.2271
Harvest Index	0.1555	0.1366	0.1089	-0.2028	-0.0046	0.2296	0.1878	0.0403	0.0461	0.0732	0.0382	1.0000	0.364*	0.2423
Biological yield	0.0401	-0.0391	-0.0598	-0.306*	-0.1702	0.2417	0.1890	0.0414	0.1355	0.2045	0.0555	0.364*	1.0000	0.470**

**** indicates 1% level of significance**

***indicates 5% level of significance**

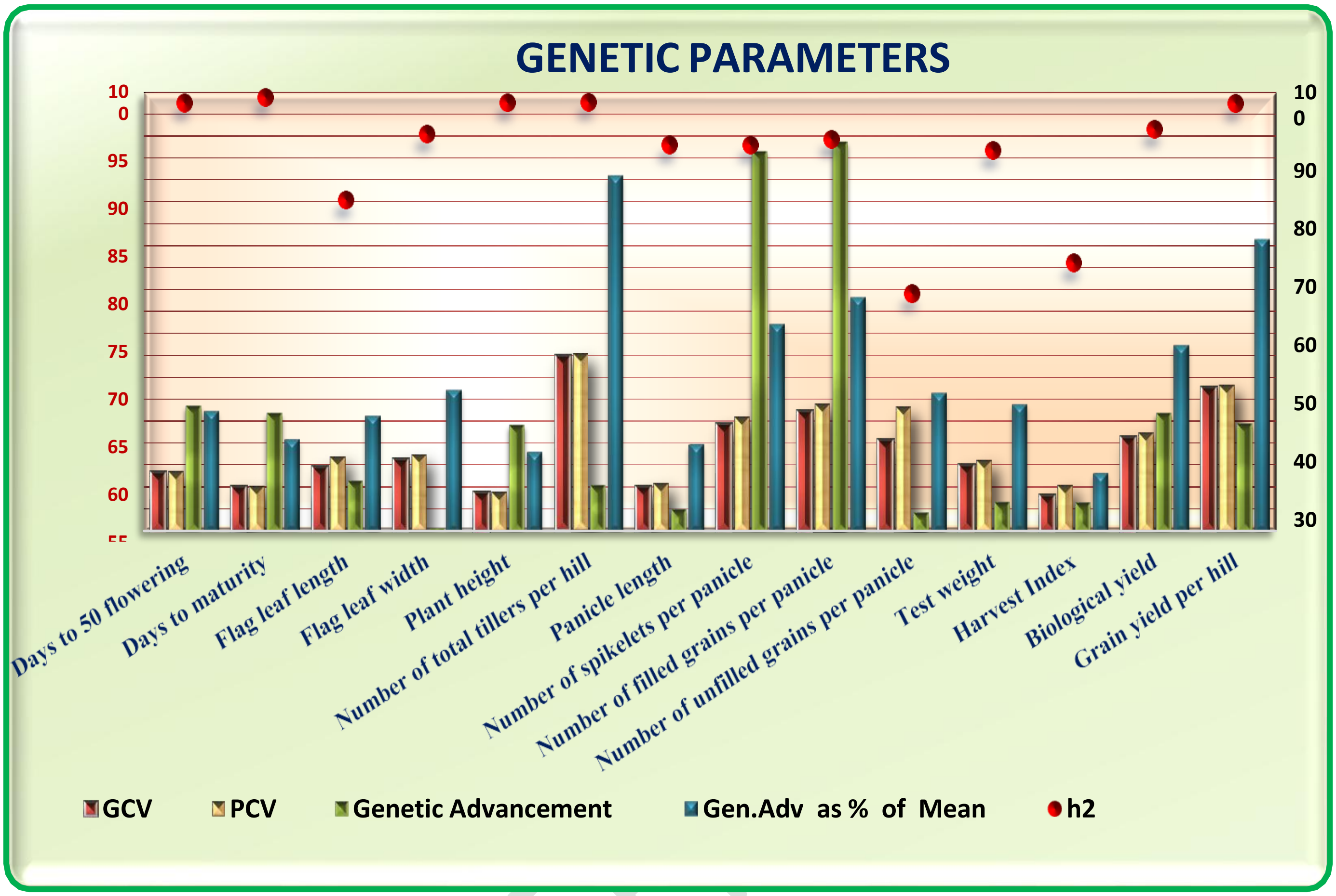

Fig 1 : Histogram depicting GCV, PCV, GA and Heritability for fourteen quantitative characters.

From the present investigation it is concluded that number of tillers per hill had recorded with high estimates of GCV and PCV. All the characters under study showed high heritability coupled with high values of genetic advance as percent mean. At both genotypic and phenotypic levels, significant positive correlations were observed for grain yield per plant with biological yield per plant, days to maturity and number of unfilled grains per panicle. Selection of plants on these traits would certainly lead to improvement in grain yield.

COMPETING INTERESTS DISCLAIMER:

Authors have declared that no competing interests exist. The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors.

REFERENCES

Aditya, J. P. and Bhartiya, A. (2013). Genetic variability, correlation and path analysis for quantitative characters in rainfed upland rice of Uttarakhand Hills. *Journal of Rice Research*, **6** (2): 24-34.

Akinwale, M. G., Gregorio, G., Nwilene, F., Ogunbayo, S. A. and Odiyi, A. C. (2011). Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). *African Journal of Plant Science*, **5** (3): 207-212.

Ashish, K. P., Bharathi, M. and Kumaravadivel, N. (2018). Genetic variability and character association studies in advanced backcross generation of rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry*, **7** (1): 2397-2400.

Bagati, S., Singh, A. K., Salgotra, R. K., Bhardwaj, R., Sharma, M., Rai, S. K and Bhat. (2016). Genetic variability, heritability and correlation coefficients of yield and its component traits in basmati rice (O*ryza sativa* L.). *SABRAO Journal of Breeding and Genetics*, **48** (4): 445-452.

Bhati, M., Suresh, B. G. and Rajput, A. S. (2015). Genetic variability, correlation and path coefficient for grain yield and quantitative traits of elite rice (*Oryza sativa* L.) genotypes at Uttar Pradesh. *Electronic Journal of Plant Breeding*, **6** (2): 586-591.

Devi, G. N., Padmavathi, G., Kota, S. and Babu, V. R. (2015). Genetic variability, heritability and correlation coefficients of grain quality characters in rice **(***Oryza sativa* L.). *SABRAO Journal of Breeding and Genetics,* **47** (4): 424-433.

Islam, M. J., Raffi, S. A., Hossain, M. A. and Hasan, A. K. (2015). Analysis of genetic variability, heritability and genetic advance for yield and yield associated traits in some promising advanced lines of rice (*Oryza sativa* L.). *Progressive Agriculture*, **26** (1): 26-31.

Kalyan, B., Radha Krishna, K. V. and Rao, S. L. V. (2017). Studies on variability, heritabillty and genetic advance for quantitative characters in rice germplasm (*Oryza sativa* L.). *International Journal of Pure and Applied Bioscience*, **5** (6): 1015-1020.

Karim, D., **Sarkar, U., Siddique, M. N. A., Khaleque, M. A and Hasnat, M. Z. (2007).** Variability and genetic parameter analysis in aromatic rice. *International Journal of Sustain and Crop Production,* **2** (5):15-18.

Ketan, R. and Sakar, G. (2014). Studies on variability, heritability, genetic advance and path analysis in some indigenous *Aman r*ice (*Oryza sativa* L.). *Journal of Crop and Weed,* **10** (2): 308-315.

Prajapati, M. K., Singh, C. M., Suresh, B. G., Lavanya, G. R. and Jadav, P. (2011). Genetic parameters for grain yield and its component characters in rice *(Oryza sativa* L.). *Electronic Journal of Plant Breeding.* **2** (2): 235-238.

Panse, V. G. and Sukhatne, P. V. (1961). Statistical methods for agricultural workers *2nd Edition* ICAR New Delhi P: 361.

Panwar, A., Dhaka, R. P. S. and Kumar, V. (2007). Genetic variability and heritability studies in rice. *Advances in Plant sciences,* **20** (1): 47-49.

Panwar, L. L. (2005). Genetic variability, heritability and genetic advance for panicle character in transplanted rice (*Oryza sativa* L.). *Agricultural Research Station Kota*, **6** (3): 505-508.