Biological Forum – An International Journal **13(4): 601-606(2021)**

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Genetic Variability and Correlation Coefficient Analysis for Yield and Grain Quality Traits in (F_8 Generation) of Elite Upland Rice (*Oryza sativa* L.) Germplasm

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(Received 31 August 2021, Accepted 04 November, 2021)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: The success of most crop improvement programs largely depends upon genetic variability and heritability and the genetic advance of desired traits. Breeders can use the degree and kind of genetic variability to establish the selection criteria and breeding plans to apply for improvement. Therefore, this research aimed to identify potential genotypes and suitable traits of upland rice germplasm for breeding programs. An experiment with 26 upland rice germplasm was done to determine the extent of genetic variability and to conduct a correlation analysis during *Kharif*-2020. All genotypes exhibited a wide and significant variation for 14 traits. The highest GCV and PCV was recorded for the grain yield per plant followed by biological yield per plant. The high heritability coupled with high genetic advance was exhibited by the number of tillers per plant and number of panicles per plant. Correlation studies revealed that grain yield per plant at genotypic and phenotypic levels was positively correlated with spikelets per panicle, panicles per plant, tillers per plant, and harvest index. According to the findings of this study, a genotype should have the following characteristics in order to increase rice output in upland ecosystem i.e., more spikelets per panicle, tillers per plant and panicles per plant, harvest index and biological yield per plant.

Keywords: Variability, broad-sense heritability, genetic advance, correlation coefficient, upland rice.

INTRODUCTION

Upland rice has been gaining appeal, because current high-yielding varieties have resulted in an increase in genetic susceptibility, a scarcity of water for irrigation, and a breakdown of resistance genes against developing races of disease due to intense farming. Increases in world rice production that have resulted from advances in research and the transfer of modern technology have primarily benefited irrigated high-yielding cultivars in recent decades. Research in upland rice has been very limited and most of the research findings have not published; therefore, these successes have had virtually no effect on upland rice production. It is a nutritious cereal crop, provides 20% of calories and 15% of the protein consumed by the world's population. Upland rice comprises 11% of the total global rice production and is cultivated on about 18 million hectares (United States, Department of Agriculture, Annual Report 2019-2020). It is also important in the cropping system, because of the lack of irrigation facilities and lower cost of production.

In India, it is cultivated on 7 million hectares of land. To boost the yield potential of upland rice, it is necessary to identify the cultivars with improved yield and other desirable agronomic characters, to overcome the global problem of hunger and starvation especially in eastern India (Mustafa *et al.*, 2012). Plant breeding is based on genetic variation, which provides a wide range of genotypes from which new varieties or breeding material can be developed (Pandey *et al.*, 2019). The development of high-yielding varieties requires a thorough understanding of existing genetic variability as well as the magnitude and direction of genetic association among the yield contributing characters. Plant breeders can use heritability information to forecast the nature of the next generation, make appropriate selections, and measure the extent of genetic improvement achieved through selection (Khutan *et al.*, 2007). Knowing the direct and indirect impacts of relationship between grain yield and other characteristics can aid in the effective selection of suitable rice cultivars for rainfed upland conditions.

MATERIALS AND METHODS

The experiment was conducted during *Kharif*- 2020 at the field experimental center of the Department of Genetics and Plant Breeding, Naini Agriculture Institute, SHUATS, Prayagraj (Allahabad), U.P., India. The experimental material consisting of 24 elite upland rice genotypes with two check varieties which were laid out as a randomized block design (RBD) with 3 replications. Under rainfed situations, the crop is direct sown. Each plot consisting of a five-row plot 2×3 m with the spacing of 20 cm between the rows. Five randomly selected plants per genotype per replication for recording observations on 14 quantitative traits and 9 quality traits. The mean value was used as the replicated data and was subjected to statistical analysis by the INDOSTAT software package. Analysis of variance was estimated following Panse and Sukhatme, (1985). The phenotypic and genotypic coefficient of variation, heritability in the broad sense, genetic advance at 5% selection intensity were computed as suggested by Johnson *et al.,* (1955). The phenotypic correlation coefficient among all the traits under study was calculated following Al-Jobouri *et al.,* (1958) and the path analysis was carried out as per the method of Dewey and Lu, (1959).

RESULTS AND DISCUSSION

In the present study analysis of variance revealed significant differences among 26 genotypes for all traits which indicates that the possibility to select promising lines from the existing genotypes (Table 2). The magnitude of variation between genotypes was reflected by high values of mean and range for genotype traits studied (Table 3).

A. Coefficients of variation

For all of the traits studied, the phenotypic coefficient of variation (PCV) estimates were slightly higher than the genotypic coefficient of variation (GCV) estimates (Table 3). The extent of the environment's influence on traits is explained by the magnitude of difference between GCV and PCV. A large difference in GCV and PCV values indicates that the expression of traits is strongly influenced by the environment.

Table 1: List of rainfed upland rice genotypes under study and their pedigree.

Sr. No.	NOTATION	PEDIGREE
1.	SHUATS UPR – 25	IR82589-B-B-121-3 × NDR-97 (P2)
2.	SHUATS UPR – 26	IR82589-B-B-121-3 × NDR-97 (P3)
3.	SHUATS UPR – 27	IR82589-B-B-121-3 × NDR-97 (P5)
4.	SHUATS UPR – 28	IR82589-B-B-121-3 × NDR-97 (P7)
5.	SHUATS UPR – 29	IR82589-B-B-121-3 × Sahbhagi Dhan (P1)
6.	SHUATS UPR – 30	IR82589-B-B-121-3 × Sahbhagi Dhan (P2)
7.	SHUATS UPR – 31	IR82589-B-B-121-3 × Sahbhagi Dhan (P3)
8.	SHUATS UPR – 32	IR82589-B-B-121-3 × Sahbhagi Dhan (P4)
9.	SHUATS UPR – 33	IR82589-B-B-121-3 × Sahbhagi Dhan (P5)
10.	SHUATS UPR – 34	IR82589-B-B-121-3 × Sahbhagi Dhan (P6)
11.	SHUATS UPR – 35	IR82589-B-B-121-3 × Sahbhagi Dhan (P7)
12.	SHUATS UPR – 36	IR82639-B-B-200-4× Vandhana (P5)
13.	SHUATS UPR – 37	IR82639-B-B-200-4× Vandhana (P8)
14.	SHUATS UPR – 38	IR82639-B-B-200-4× Sahbhagi Dhan (P1)
15.	SHUATS UPR – 39	IR82639-B-B-200-4× Sahbhagi Dhan (P2)
16.	SHUATS UPR – 40	IR82639-B-B-200-4× Sahbhagi Dhan (P3)
17.	SHUATS UPR – 41	IR82639-B-B-200-4× Sahbhagi Dhan (P5)
18.	SHUATS UPR – 42	IR82639-B-B-200-4× Sahbhagi Dhan (P8)
19.	SHUATS UPR – 43	IR83750-B-B-131-1× NDR-97 (P1)
20.	SHUATS UPR – 44	IR83750-B-B-131-1× NDR-97 (P3)
21.	SHUATS UPR – 45	IR83750-B-B-131-1× NDR-97 (P4)
22.	SHUATS UPR – 46	IR83750-B-B-131-1× NDR-97 (P5)
23.	SHUATS UPR – 47	IR83750-B-B-131-1× NDR-97 (P7)
24.	SHUATS UPR – 48	IR83750-B-B-131-1× Sahbhagi Dhan (P1)
25.	NDR – 97 (C)	
26.	SAHBHAGI DHAN (C)	

Table 2: Analysis of variance (ANOVA) among 26 Upland rice genotypes for 14 quantitative traits.

Sr.No.	CHARACTERS	Mean Sum Of Squares		
		Replications (df=2)	Treatments (df=25)	Error (df=50)
1.	Days to 50% Flowering	0.72	63.64**	15.81
2.	Plant Height (cm)	13.4	1239.16**	92.39
3.	Flag Leaf Length (cm)	0.93	202.92**	10.33
4.	Flag Leaf Width (cm)	0.001	0.019**	0.007
5.	Number of Tillers per plant	0.018	6.84**	0.13
6.	Number of Panicle per plant	0.013	5.62**	0.21
7.	Panicle Length (cm)	0.014	13.59**	5.33
8.	Number of spikelets per panicle	8.004	3797.90**	294.70
9.	Spikelet Fertility (%)	10.16	54.98**	25.49
10.	Days to Maturity	1.41	34.48**	15.98
11.	Biological yield per plant (g)	0.25	153.81**	12.65
12.	Harvest Index (%)	2.27	25.65**	11.89
13.	Test weight (g)	0.94	45.54**	5.91
14.	Grain yield per plant (g)	0.069	42.83**	4.23

** indicates significance at 1% level of significance

In this study, slight differences indicated minimum environmental influences and a consequently greater role of genetic factors on the expression of traits. However, there were close correspondence between estimates of PCV and GCV test the characters viz., plant height, flag leaf length, number of tillers per hill and number of panicles per hill indicates the fact that these characters were less influenced by the environmental factors as evidenced from the less difference in magnitude of PCV and GCV (Singh *et al.*, 2013). A wide range of PCV was observed ranging from 4.64% for days to maturity to 26.55% for grain yield per plant. GCV ranged from 2.45% for days to maturity to 23.03% for grain yield per plant.

B. Heritability

A perusal of Table 3revealed that the estimates of heritability in broad sense for fourteen characters ranged from 27.80 % for spikelet fertility, days to maturity and harvest index to 94.20 % for number of tillers per plant (Singh *et al.*, 2014). High heritability (above 60%) was observed in the following characters i.e., number of panicles per plant (89.30%), flag leaf length (86.10%), plant height (80.50%), number of spikelets per panicle (79.80%), biological yield per plant (78.80%), grain yield per plant (75.20%) and test weight (69.10%).

C. Genetic Advance

Genetic advance is the improvement in the mean of selected families over the base population (Lush, 1949 and Johnson *et al.,* 1955). It is likewise expressed because the shift in gene frequency closer to the advanced aspect on exercise choice pressure. Genetic advance when expressed as a percentage over mean is called genetic gain. The high genetic advance as percent of the mean (more than 20%) was recorded for number of tillers per plant (42.76%), number of panicles per plant (41.22%), Grain yield per plant (41.15%), biological yield per plant (39.53%), number of spikelets per panicle (38.31%), flag leaf length (34.01%), test weight (26.88%) and plant height (24.47%).

A character exhibiting high heritability may not necessarily give a high genetic advance. Johanson *et al.,* (1955) reported that high heritability should be accompanied by high genetic advance to arrive at a more reliable conclusion. The breeder should be cautious in making selections based on heritability as it includes both additive and non-additive gene actions. In the present study, high heritability along with high genetic advance was exhibited by number of tillers per plant (94.20% and 42.76%), number of panicles per plant (89.30% and 41.22%), number of spikelets per panicle (79.80% and 38.31%), biological yield per plant (78.80% and 39.53%) and grain yield per plant (75.20% to 41.15%). These characters show additive gene action that indicates ample scope of selection. As a result, phenotypic performance-based selection would be beneficial. Similar findings were reported by Sarawagi *et al.,* (2020), Singh *et al.,* (2014); Singh *et al.,* (2013); Samudin *et al*., (2010).

Table 3: Estimate of genetic parameters for 14 quantitative characters in 26 elite upland rice genotypes.

Sr. No.	Character	Mean	Range	GCV%	PCV%	Heritability (%)	GA	GA as % mean
1.	Days to 50% flowering	70.70	63.00-83.33	5.64	7.97	50.20	5.83	8.24
2.	Plant height (cm)	147.70	82.66-173.83	13.24	14.75	80.50	36.14	24.47
3.	Flag leaf length (cm)	45.04	20.96-54.64	17.79	19.17	86.10	15.32	34.01
4.	Flag leaf width (cm)	1.05	0.80-1.18	5.99	10.15	34.90	0.08	7.29
5.	Number of tillers/plant	6.99	5.13-11.85	21.39	22.04	94.20	2.99	42.76
6.	Number of panicles/plant	6.33	4.80-10.93	21.18	22.42	89.30	2.61	41.22
7.	Panicle length (cm)	24.77	19.93-28.56	6.70	11.48	34.00	1.99	8.05
8.	Number of spikelets/panicle	164.18	105.23-244.52	20.81	23.29	79.80	62.90	38.31
9.	Spikelet fertility (%)	89.23	81.37-95.68	3.51	6.66	27.80	3.41	3.82
10.	Days to Maturity	101.55	95.00-113.33	2.45	4.64	27.80	2.70	2.66
11.	Biological yield/ plant	31.73	14.53-49.89	21.61	24.35	78.80	12.55	39.53
12.	Harvest Index	48.91	42.67-55.18	4.38	8.30	27.80	2.33	4.76
13.	Test weight	23.15	17.32-28.46	15.70	18.89	69.10	6.22	26.88
14.	Grain yield/plant	15.57	6.19-24.47	23.03	26.55	75.20	6.41	41.15

D. Correlation coefficient analysis

Correlation coefficient is a statistical measure that is used to find out the degree (strength) and direction of the relationship between two or more variables. The results of phenotypic correlation coefficients between all pairs of traits as shown in Table 4 reveals grain yield had a positive and significant association with biological yield per plant (0.856***), number of spikelets per panicle (0.64***), number of tillers per panicle (0.586***), number of panicles per plant (0.580***), test weight (0.46***), harvest index (0.3204**), spikelet fertility (0.29*), flag leaf width (0.26*). The correlation shows a positive non-significant association with flag leaf length (0.20), plant height (0.09), panicle length (0.05). The correlation shows a negative non-significant association with days to maturity (-0.499), days to 50% flowering (-0.134).

Table 4: Correlation coefficient at phenotypic level between yield and its related traits in 26 elite upland rice genotypes.

Sr. No.	Traits	Days to 50% flowering	Plant height (cm)	Flag Leaf Length (cm)	Flag Leaf Width (cm)	Tillers/ plant	Panicle/ plant	Panicle Length (cm)	Spikelets/ panicle	Spikelet Fertility (%)	Days to Maturity	Biological Yield/ plant	Harvest Index (%)	Test Weight (g)	Grain Yield/ plant
1.	**DF**	**1.00**	-0.37***	-0.51***	0.168	0.128	0.106	-0.077	-0.062	-0.38***	0.468***	-0.08	-0.107	-0.06	-0.13
2.	**PH**		**1.00**	0.808***	0.205	0.022	-0.04	0.30**	0.167	0.151	-0.43***	0.213	-0.16	0.178	0.09
3.	**FL**			**1.00**	0.194	-0.049	-0.071	0.29**	0.203	0.220	-0.53***	0.26*	-0.13	0.117	0.20
4.	**FW**				**1.00**	0.141	0.135	-0.05	0.212	-0.074	-0.093	0.22*	-0.21	0.0415	0.26*
5.	**NT**					**1.00**	0.93***	0.152	0.25*	0.065	-0.033	0.50***	0.32***	0.454***	0.586***
6.	**NP**						**1.00**	0.178	0.22*	0.116	0.032	0.50***	0.34**	0.36**	0.580***
7.	**PL**							**1.00**	-0.165	0.020	-0.115	0.129	-0.16	0.0192	0.057
8.	**SPP**								**1.00**	0.1697	-0.0676	0.63***	0.13	0.268*	0.64***
9.	**SF%**									**1.00**	-0.226*	0.166	0.30**	0.0193	0.2901**
10.	**DM**										**1.00**	-0.071	-0.088	0.0141	-0.0499
11.	**BYP**											**1.00**	0.137	0.53***	0.8565***
12.	**HI**												**1.00**	0.149	0.320**
13.	**TW**													**1.00**	0.46***
14.	**GYPP**														**1.00**

Table 5: Direct and indirect effects for different quantitative characters on grain yield at the phenotypic level.

PATH matrix of GY/plant														
Traits	**DF (50%)**	**PH**	**FL**	**FW**	**NT**	**NP**	**PL**	**SPP**	**SF%**	**DM**	**BYP**	**HI**	**TW**	**GYPP**
DF(50%)	**-0.0381**	0.0143	0.0198	-0.0064	-0.0049	-0.0041	0.003	0.0024	0.0147	-0.0179	0.0031	0.0041	0.0024	0.0051
PH	-0.0232	**0.062**	0.0502	0.0128	0.0014	-0.0029	0.019	0.0104	0.0094	-0.0269	0.0132	-0.0102	0.0111	0.0057
FL	0.082	-0.128	**-0.1582**	-0.0308	0.0078	0.0112	-0.047	-0.0322	-0.0348	0.084	-0.0414	0.0208	-0.0186	-0.032
FW	0.0022	0.0026	0.0025	**0.0129**	0.0018	0.0017	-0.0007	0.0027	-0.001	-0.0012	0.0029	-0.0028	0.0005	0.0034
NT	0.0534	0.0093	-0.0205	0.0588	**0.4158**	0.3889	0.0633	0.1049	0.0271	-0.014	0.2117	0.1371	0.189	0.2439
NP	-0.0375	0.0164	0.025	-0.0479	-0.33	**-0.3528**	-0.063	-0.08	-0.0412	-0.0114	-0.1769	-0.1209	-0.127	-0.2046
PL	-0.0036	0.0142	0.0137	-0.0024	0.007	0.0082	**0.0462**	-0.0077	0.0009	-0.0053	0.006	-0.0077	0.0009	0.0027
SPP	-0.0076	0.0204	0.0248	0.0259	0.0308	0.0277	-0.0202	**0.1221**	0.0207	-0.0083	0.0775	0.0165	0.0328	0.0786
SF%	-0.0291	0.0115	0.0167	-0.0057	0.0049	0.0088	0.0015	0.0129	**0.0757**	-0.0171	0.0126	0.0234	0.0015	0.022
DM	-0.0009	0.0009	0.001	0.0002	0.0001	-0.0001	0.0002	0.0001	0.0004	**-0.002**	0.0001	0.0002	0	0.0001
BYP	-0.0401	0.1043	0.128	0.1099	0.2489	0.2451	0.0634	0.3102	0.0812	-0.0348	**0.4888**	0.0672	0.2607	0.4187
HI	-0.0088	-0.0135	-0.0108	-0.0176	0.027	0.0281	-0.0137	0.0111	0.0253	-0.0072	0.0113	**0.082**	0.0122	0.0263
TW	-0.0038	0.0105	0.0069	0.0024	0.0267	0.0212	0.0011	0.0158	0.0011	0.0008	0.0313	0.0088	**0.0588**	0.0273

DF: Days to 50% flowering, DM: Days to maturity, FL: Flag leaf length (cm), FW: Flag leaf width (cm), PH: Plant height (cm), NT: Number of total tillers per Plant, NP- Number of total Panicles per Plant, PL: Panicle length (cm), SPP: Number of spikelets per panicle, SF%: Spikelet Fertility, BYP: Biological yield per Plant (g), TW: Test weight (g), HI: Harvest index (%), GYPP: Grain yield per plant (g).

The characters, which showed a strong association with yield were biological yield per plant, test weight, number of spikelets per panicle and number of panicles per plant. This revealed that selection based on these characters bears relevance to grain yield. Similar results have been reported by Pathak and Patel (1989); Rathod *et al.,* (1995); Kishor *et al.,* (2008); Sravan *et al.,* (2012).

E. Path coefficient analysis

The correlation coefficient values do not reveal the true pattern of association between the independent and dependent variables. Path coefficient analysis, on the other hand, is a useful statistical tool for determining the qualitative interrelationships between various components and their direct and indirect effects on grain yield, as well as applying selection pressure more effectively for improved output. Therefore, the phenotypic correlation of grain yield with other characters was partitioned into components of direct and indirect effect through path coefficient analysis.

Table 5 showed that the direct effects on grain yield of other traits were directly useful for the development of yield. An indirect effect of some traits showed that traits indirectly affected the grain. The path coefficient analysis at phenotypic level with residual effect 0.395 revealed that biological yield per plant (0.4888) had the highest direct effect on grain yield followed by number of tillers per plant (0.4158), number of spikelets per panicle (0.1221), harvest index (0.082), spikelet fertility (0.0757), plant height (0.062), test weight (0.0588), panicle length (0.0462) and flag leaf width (0.0129)**.** Besides days to maturity (-0.002), days to maturity (-0.0381), flag leaf length (-0.1582) and number of panicles per plant (0.3528) had a negative direct effect on the grain yield. These findings concerning different component traits are in agreement with published work on path analysis by Amirthadevarathnam (1990); Mokate *et al.,* (1998); Kishor *et al.,* (2008); Vange (2008); Sravan *et al*., (2012).

CONCLUSION

The present investigation concluded that the existence of adequate genetic variability among the 26 upland rice genotypes. Based on mean performance SHUATS UPR-48 was found to be superior in grain yield per hill over the check variety followed by SHUATS UPR-32 and SHUATS UPR-46. High heritability coupled with high genetic advance was exhibited by number of tillers per plant, number of panicles per plant and number of spikelets per panicle. Grain yield per plant shows high positive significant phenotypic, genotypic association with number of spikelets per panicle, number of panicles per plant, number of tillers per plant and harvest index that these characters can be used as selection parameters of upland rice improvement. Path analysis revealed that number of tillers per plant, biological yield per plant, number of spikelets per panicle and harvest index exhibited a positive direct effect on grain yield per plant at both the genotypic and phenotypic level. These traits contributed the maximum to high grain yield compared to other characters, thus, selection for these characters helps in the selection of superior fine upland rice genotypes. Hence, the characters should be given more preference during selection.

FUTURE SCOPE

Based on the findings of present investigation the following suggestions are being made for future work

— The high yielding genotypes namely SHUATS UPR-48, SHUATS UPR-32 and SHUATS UPR-46 may be tested in multiplication of test their suitability and adoptability in various environments.

— Number of tillers per plant, Number of panicles per plant, Number of spikelets per panicle, Biological yield per plant and grain yield per plant these characters may be included in selection criteria for improvement of yield in upland rice cultivation.

Acknowledgement. The authors acknowledge the Department of Genetics and Plant Breeding, Naini Agriculture Institute (NAI), Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj, U.P., India is a source of genotypes.

Conflict of Interest. None.

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How to cite this article: Yadav, M.J. and Lal, G.M. (2021). GeneticVariability and Correlation Coefficient Analysis for Yield and Grain Quality Traits in (F_8 Generation) of Elite Upland Rice (*Oryza sativa* L.) Germplasm. *Biological Forum – An International Journal*, *13*(4): 601-606.