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Studies on variability, heritability and genetic advance for quantitative characters in rice (*Oryza sativa* L.) germplasm

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Abstract
A study was conducted to determine the genetic variability and correlation between yield and other yield-related characteristics of rice genotypes. In an augmented design, 255 genotypes were grown during the kharif season under direct seeding conditions. The analysis of variance revealed significant differences for all of the studied characters, indicating that the genotypes have a high genetic variability. GCV and PCV estimates were high for traits such as grain yield per plant, harvest index, and seedling vigour, indicating their importance in rice yield selection. For the traits like no. of spikelets panicles^{-1}, spikelets fertility, plant height, and days of 50% flowering, high heritability was observed in conjunction with high expected genetic advance as a percentage of mean. Days to 50% flowering, biological yield plant^{-1}, seedling vigour, and number of grains panicle^{-1} are all factors to consider. Grain yield plant^{-1} was strongly related to the number of spikelets^{-1} panicles, biological yield plant^{-1}, harvest index, and test weight. Path coefficient analysis revealed that harvest-index, followed by biological yield plant^{-1}, has a positive direct effect on grain yield plant^{-1}.

Keywords: Correlation, Heritability, Genetic advance, path analysis, rice.

Introduction
Rice (*Oryza sativa* L.) is a staple food for many people around the world (Zhang, 2007). Rain fed upland rice accounts for 6.00 million hectares in India, or 13.5 percent of total rice area, with farmers mostly using traditional early rice varieties and contributing low productivity (0.6 to 1.5 t ha^{-1}). Oryza contains twenty-two wild species and two cultivated species, *Oryza sativa* and *Oryza glaberrima*. The world's sativa rice germplasm is commonly classified into three subspecies: Indica, Japonica, and Javanica, which are grown in tropical, temperate, and intermediate climates, respectively. The interaction of various characters was required to determine their contribution to yield. Under these conditions, developing high yielding genotypes necessitates a thorough understanding of existing genetic variation and the extent of association of yield contributing characters. Grain yield is a complex trait that results from the interaction of numerous variables (Singh *et al.*, 2015a) [15].

Though a wide range of genetic variability for yield traits has been reported in the past, there is still untapped genetic variability in germplasms that is critical in selecting potential parents to achieve maximum heterosis and superior recombinants (Rashmi *et al.*, 2017) [14]. The nature and amount of variability in the genetic stock, as well as the extent to which the desirable traits are heritable, all influence genetic improvement for quantitative traits (Namrata *et al.*, 2016) [12]. Knowledge of the genetic variability of yield contributing characters, their interrelationships, and their relationship with yield is required for an effective breeding programme (Nayak *et al.*, 2016) [13]. Plant breeders can use heritability knowledge to predict the nature of the next generation, make appropriate selections, and assess the magnitude of genetic improvement through selection (Tuhina Khatun *et al.*, 2015) [18]. Furthermore, high genetic advance combined with high heritability provides the most effective condition for character selection (Larik and Rajput, 2000) [11].

The interaction of various characters was critical in determining their contribution to yield. Correlation studies allow researchers to investigate the magnitude and direction of association between various traits and grain yield, as well as their direct and indirect effects on grain yield (Solanki *et al.*, 2017) [16]. An attempt was made in this context to assess genetic variability for yield characteristics and unravel the correlation of different grain yield traits among a set of thirty-eight rice germplasms.

Plant breeders have used path analysis to assist in identifying promising traits as selection criteria to improve crop yield and to detect the amount of direct and indirect effect of the causal components on the effect component (Bose *et al*., 2005; Indu Rani *et al*., 2008; Togay *et al*., 2008; Ali *et al*., 2009; Chandra *et al*., 2009; Akhatar *et al*., 2011; Cyprian and Kumar, 2011) [4, 9, 17, 3, 6, 1, 7]. A systematic evaluation and characterization of germplasm lines not only aids in the identification of superior and genetically divergent germplasm lines, but it also provides data on the utility of genetic resources. Characterization of accessions provides information on the material's morphological and agronomic aspects, which is critical for gene bank management. As a result, the current study was undertaken to investigate the genetic variability for yield and its component characters in various rice germplasm lines.

Materials and Methods

Plant material and experimental design

The material for the present investigation consists of 250 genotypes and 5 checks. These were grown in a Augumented design during wet season 2019 at CRS (Crop Research Station), Masodha, Achraya Narandra Deva University of Agriculture and Technology, Ayodhya, U.P., India. The entries were direct seeded with ten rows per entry having 25 hills per row with 20 x 15 cm spacing. The nursery was sown on 01 July, 2019 on uniform raised beds applied with a fertilizer dose of N:P:K, 80:40:40. 25-30 days old seedlings were transplanted in main research plot with one seedling hill^{-1}.

Data collection

Observations on quantitative traits like days to 50% flowering, seedling vigor, plant height, flag leaf area, panicle bearing tillers per plant, panicle length, no. of spikelet per panicle, no. of grains per panicle, spikelet fertility, biological yield per plant, harvest index, test weight, grain yield per plant were recorded on five randomly selected plants excluding the border rows from each entry while days to 50% flowering and plot yield were recorded on plot basis. The recommended agronomic practices were followed to raise a good and healthy crop.

Statistical analysis

The analysis of variance was done by Federer (1956). Co-efficient of variations were computed through Burton's method (Burton and de vane, 1953) [5]. Heritability and genetic advance were worked out as per the method of Burton and de vane (1953) [5] and Johnson *et al*. (1955). Correlation co-efficient was calculated according to the procedure suggested by Searle (1961) and path analysis was worked out following Dewey and Lu (1959) [8]. The statistical analysis was done using SAS 9.2 software.

Results and Discussion

Analysis of variance (ANOVA) shows that among the genotypes all traits were significant indicates the presence of considerable amount of genetic variation among the genotypes (Table 1). The magnitude of variations between genotypes was revealed by high values of mean and range for traits of the genotypes (Table 2). High genetic variability for different traits in rice was earlier reported (Khan *et al*., 2009; Umadevi *et al*., 2009; Akinwale *et al*., 2011; Ullah *et al*., 2011) [10, 20, 2, 19]. The results of the analysis of variance for augmented design in respect of all the 13 characters under study are presented in Table 1. The variation due to blocks was significant or highly significant for all the characters under study except non-significant means squares observed for Panicles bearing tillers per plant. The differences among the check varieties were also found to be significant or highly significant for all the characters under study.

The Estimates of mean, range, coefficient of variance (CV), genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability and genetic advance of studied traits are presented in Table 2. It is observed that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) indicating environmental effect on the expression of the characters.

The high magnitude of PCV observed for Grain yield per plant, Harvest index and Seedling Vigor. This indicates that these characters can be manipulated for breeding high yielding varieties through hybridization and selection in subsequent generations in rice improvement programme. High estimates of heritability was estimated for no. of spikelets per Panicles, spikelets fertility, plant height, days of 50% Flowering, biological yield per plant, seedling vigor and no. of grains per Panicle (Table 2). The genetic advance in percent of mean in normal condition were found to be very high for seedling vigor and spikelets fertility. Moderate to high degree of heritability estimates indicate the presence of additive genetic effects hence selection based on phenotypic performance of these character will be effective.

Table 3 gives the simple linear correlation coefficient between all the pairs of studied traits. It shows that yield is positively and significantly correlated with the traits grain yield per plant exhibited highly significant and positive correlations with no. of spikelets per Panicles, biological yield per plant, harvest index and test weight. The genotypic correlation coefficients were partitioned using path analysis to find out the direct and indirect effects of yield contributing traits towards grain yield and number in parenthesis are the direct on yield (Table 4) which reveals that the very high positive direct effects on grain yield per plant were exerted by biological yield per plant followed by harvest-index. This suggests that these traits can be manoeuvred successfully for breeding high yielding varieties for this dynamic ecology.

Table 1: Analysis of Variance for different traits

Source of variation	DF	Days of 50% Flowering	Seedling Vigor	Plant Height	Flag Leaf Area	Penicles bearing tillers /plant	Panicle Length	No of spikelets per penicles	No of grains per penicle	spikelets fertility	Biological yield per plant	Harvest index	Test Weight	Grain yield per plant
Block	9	196.28**	106.97**	366.55**	14.14*	3.26	9.44**	2434.90**	66.31**	1924.76**	475.79**	399.65**	59.13**	99.88**
CHECKS	4	659.05**	1095.04**	1139.78**	323.80**	7.58**	22.47**	875.61**	582.73**	1487.36**	504.44**	1238.11**	359.82**	141.11**
ERROR	36	6.72	7.17	8.19	6.45	2.15	3.13	9.47	6.82	16.59	4.08	30.98	11.74	2.22

*, ** significant at 5% and 1% level, respectively

Table 2: Estimates of different parameters of variability of different traits

Characters	Mean	Min	Max	var (g)	var (p)	Heritability (%)	GA	GA% mean	GA 1%	GA mean 1%	GCV (%)	PCV (%)	ECV (%)
Days of 50% Flowering	104.54	78.00	124.00	35.00	41.72	83.90	11.16	10.68	14.31	13.69	5.66	6.18	2.48
Seedling Vigor	32.09	15.20	61.60	34.12	41.29	82.63	10.94	34.08	14.02	43.68	18.20	20.02	8.35
Plant Height	118.60	68.00	178.00	72.93	81.12	89.90	16.68	14.06	21.38	18.02	7.20	7.59	2.41
Flag Leaf Area	25.32	14.30	37.50	4.12	10.57	38.95	2.61	10.30	3.34	13.20	8.01	12.84	10.03
Penicles bearing tillers / plant	9.09	5.00	12.67	0.82	2.97	27.61	0.98	10.78	1.26	13.82	9.96	18.96	16.13
Penicle Length	26.22	16.10	32.00	1.75	4.87	35.82	1.63	6.21	2.09	7.96	5.04	8.42	6.74
No of spikelets per penicles	113.16	46.38	179.69	200.97	210.44	95.50	28.54	25.22	36.57	32.32	12.53	12.82	2.72
No of grains per penicle	83.95	70.00	99.00	24.11	30.93	77.95	8.93	10.64	11.45	13.63	5.85	6.62	3.11
spikelets fertility	78.65	34.75	195.54	153.93	170.52	90.27	24.28	30.88	31.12	39.57	15.78	16.60	5.18
Biological yield per plant	29.02	9.23	54.82	21.07	25.15	83.77	8.65	29.82	11.09	38.22	15.82	17.28	6.96
Harvest index	39.27	14.63	93.56	39.73	70.72	56.19	9.73	24.79	12.47	31.76	16.05	21.41	14.17
Test Weight	23.31	12.31	35.08	4.47	16.21	27.57	2.29	9.81	2.93	12.57	9.07	17.27	14.70
Grain yield per plant	10.93	5.04	21.05	3.32	5.54	59.91	2.90	26.58	3.72	34.07	16.67	21.54	13.64

Table 3: Simple correlation of traits

Characters	Days of 50% Flowering	Seedling Vigor	Plant Height	Flag Leaf Area	Penicles bearing tillers per plant	Penicle Length	No of spikelets per penicles	No of grains per penicle	spikelets fertility	Biological yield per plant	Harvest index	Test Weight	Grain yield per plant
Days of 50% Flowering	1.000	-0.069	0.081	0.057	-0.167**	0.073	0.113	-0.002	-0.089	0.077	0.015	-0.013	0.071
Seedling Vigor		1.000	-0.005	0.017	-0.040	-0.043	0.025	-0.158*	-0.119	0.042	-0.128*	-0.053	-0.079
Plant Height			1.000	-0.086	0.067	0.578**	0.006	-0.030	0.022	0.020	0.054	-0.029	0.089
Flag Leaf Area				1.000	-0.007	-0.122	-0.016	0.110	0.049	-0.013	0.047	0.048	0.033
Penicles bearing tillers per plant					1.000	-0.039	0.034	-0.055	-0.058	0.084	-0.044	0.094	0.025
Penicle Length						1.000	0.032	-0.055	-0.009	-0.008	0.129*	-0.008	0.113
No of spikelets per penicles							1.000	0.054	-0.856**	0.244**	-0.033	-0.064	0.240**
No of grains per penicle								1.000	0.327**	-0.014	0.083	0.054	0.105
spikelets fertility									1.000	-0.253**	0.134*	0.117	-0.147*
Biological yield per plant										1.000	-0.447**	0.026	0.559**
Harvest index											1.000	0.151*	0.429**
Test Weight												1.000	0.162**
Grain yield per plant													1.000

*, ** significant at 5% and 1% level, respectively

Table 4: Path coefficient showing direct and indirect effects of trait on grain yield

Characters	Days of 50% Flowering	Seedling Vigor	Plant Height	Flag Leaf Area	Penicles bearing tillers per plant	Penicle Length	No of spikelets per penicles	No of grains per penicle	spikelets fertility	Biological yield per plant	Harvest index	Test Weight	Grain yield per plant
Days of 50% Flowering	-0.0241	0.0006	0.0029	0.0003	0.0039	-0.0003	-0.0017	-0.0001	0.0061	0.0710	0.0126	-0.0002	0.071
Seedling Vigor	0.0017	-0.0091	-0.0002	0.0001	0.0009	0.0002	-0.0004	-0.0105	0.0081	0.0386	-0.1075	-0.0009	-0.079
Plant Height	-0.0020	0.0001	0.0358	-0.0004	-0.0016	-0.0026	-0.0001	-0.0020	-0.0015	0.0186	0.0452	-0.0005	0.089
Flag Leaf Area	-0.0014	-0.0002	-0.0031	0.0043	0.0002	0.0005	0.0002	0.0073	-0.0033	-0.0116	0.0394	0.0008	0.033
Penicles bearing tillers per plant	0.0040	0.0004	0.0024	0.0000	-0.0236	0.0002	-0.0005	-0.0037	0.0039	0.0772	-0.0372	0.0016	0.025
Penicle Length	-0.0018	0.0004	0.0207	-0.0005	0.0009	-0.0045	-0.0005	-0.0037	0.0006	-0.0070	0.1085	-0.0001	0.113
No of spikelets per penicles	-0.0027	-0.0002	0.0002	-0.0001	-0.0008	-0.0001	-0.0149	0.0036	0.0581	0.2259	-0.0279	-0.0011	0.240**
No of grains per penicle	0.0001	0.0014	-0.0011	0.0005	0.0013	0.0003	-0.0008	0.0667	-0.0222	-0.0125	0.0700	0.0009	0.105
spikelets fertility	0.0022	0.0011	0.0008	0.0002	0.0014	0.0000	0.0128	0.0218	-0.0678	-0.2338	0.1124	0.0020	-0.147*
Biological yield per plant	-0.0019	-0.0004	0.0007	-0.0001	-0.0020	0.0000	-0.0036	-0.0009	0.0172	0.9246	-0.3750	0.0004	0.559**
Harvest index	-0.0004	0.0012	0.0019	0.0002	0.0010	-0.0006	0.0005	0.0056	-0.0091	-0.4131	0.8392	0.0026	0.429**
Test Weight	0.0003	0.0005	-0.0011	0.0002	-0.0022	0.0000	0.0010	0.0036	-0.0079	0.0237	0.1266	0.0171	0.162**

Resi = 0.106

*, ** significant at 5% and 1% level, respectively

Conclusion

The results of the present study show that there is adequate genetic variability in the studied material. The high magnitude of PCV observed for Grain yield per plant, Harvest index and Seedling Vigor. High estimates of heritability was estimated for no. of spikelets per Panicles, spikelets fertility, plant height, days of 50% Flowering, biological yield per plant, seedling vigor and no. of grains per Panicle. The genetic advance in percent of mean in normal condition were found to be very high for seedling vigor and spikelets fertility.

Correlation coefficient shows that yield is positively and significantly correlated with the traits grain yield per plant exhibited highly significant and positive correlations with no. of spikelets per Panicles, biological yield per plant, harvest index and test weight. The path analysis reveals that the very high positive direct effects on grain yield per plant were exerted by biological yield per plant followed by harvest-index should be considered for upland ecology.

References

1. Akhatar N, Nazir MF, Rabnawaz T, Mahmood ME, Safdar M, Asif AR *et al*. Estimation of heritability, correlation and path coefficient analysis in fine grain rice (*Oryza sativa* l.). The journal of animal & plant sciences. 2011;21(4):660-664.
2. Akinwale MG, Gregorio G, Nwilene F, Akinyele BO, Ogunbayo SA, Odiyi AC *et al*. Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* l.). African journal of plant science. 2011;5:207-212.
3. Ali MA, Nawad NN, Abbas A, Zulkiffal M, Sajjad M. Evaluation of selection criteria in *Cicer arietinum* l. Using correlation coefficients and path analysis. Australian journal of crop science. 2009;3(2):65-70.
4. Bose IK, Pradhan SK, Mohanty A, Nagaraju M. Genetic variability and association of yield attributing characters with grain yield in deepwater rice. Korean journal of crop science. 2005;50(4):262-264.
5. Burton GW, Devane EH. Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. Agron J. 1953;45:478-481.
6. Chandra BS, Reddy TD, Ansari NA, Kumar SS. Correlation and path analysis for yield and yield components in rice (*Oryza sativa* L.). Agricultural science digest. 2009;29(1):45-47.
7. Cyprian M, Kumar V. Correlation and path coefficient analysis of rice cultivars data. Journal of reliability and statistical studies. 2011;4(2):119-131.
8. Dewey DR, Lu KH. A correlation and path co-efficient analysis of components of crested wheat grass seed production. Agronomy journal. 1959;51:515-518.
9. Indurani C, Veeraragathantham D, Sanjutha S. Studies on correlation and path coefficient analysis on yield attributes in root knot nematode resistant F1 hybrids of tomato. J appl sci res. 2008;4(3):287-295.
10. Khan AS, Imran M, Ashfaq M. Estimation of genetic variability and correlation for grain yield components in rice (*Oryza sativa* l.). American-eurasian journal of agricultural & environmental sciences. 2009;6:585-590.
11. Larik AS, Rajput LS. Estimation of selection indices in *Brassica juncea* L. and *Brassica napus* L. Pakistan Journal of Botany. 2000;32(2):323-330.
12. Namrata Sharma H, Ranwah BR, Bisen P. Variability Assessment and Path Coefficient Analysis in Groundnut (*Arachis hypogaea* L.) Genotypes in Sub- Humid Southern Plains of Rajasthan. Trends in Biosciences. 2016;9:642-646.
13. Nayak R, Singh VK, Singh A, Singh PK. Genetic variability, character association and path analysis of rice genotypes. Annals of Plant and Soil Research. 2016;18(2):161-164.
14. Rashmi D, Saha S, Loitongbam B, Singh S, Singh PK. Genetic variability study for yield and yield components in rice (*Oryza sativa* L.). International Journal of Agriculture, Environment and Biotechnology. 2017;10(2):171-176.
15. Singh A, Saini R, Singh J, Arya M, Mukh Ram, Pallavi *et al*. Genetic diversity studies in rice (*Oryza sativa* L.) using microsatellite markers. International Journal of Agriculture Environment and Biotechnology. 2015;8:143-152.
16. Solanki G, Dodiya NS, Kunwar R, Bisen P, Kumar R, Singh J *et al*. Character Association and Path Coefficient Analysis for Seed Yield and Latex Yield in Opium Poppy (*Papaver somniferum* L.). International Journal of Current Microbiology and Applied Sciences. 2017;6(8):1116-1123.
17. Togay N, Togay Y, Yildirin B, Dogan Y. relationships between yield and some yield components in pea (*Pisum sativum* ssp. Arvense l.) Genotypes by using correlation and path analysis. African journal of biotechnology. 2008;7(23):4285-4287.
18. Tuhina-Khatun M, Hanafi MM, Rafii Yusop M, Wong MY, Salleh FM, Ferdous J *et al*. Genetic variation, heritability, and diversity analysis of upland rice (*Oryza sativa* L.) genotypes based on quantitative traits. BioMed research international, 2015, 7.
19. Ullah MZ, Bashar MK, Bhuiyan MSR, Khalequzzaman M, Hasan MJ. Interrelationship and cause-effect analysis among morpho-physiological traits in biroin rice of bangladesh. International journal of plant breeding and genetics. 2011;5:246-254.
20. Umadevi M, Veerabadhiran P, Manonmani S. genetic variability, heritability, genetic advance and correlation for morphological traits in rice genotypes. Madras agricultural journal. 2009;96:316-318.
21. Zhang Q. Strategies for developing green super rice. Proceeding of the national academy of sciences USA. 2007;104:16402-16409.