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## Assessment of elite and local genotypes of rice (*Oryza sativa* L.) for yield and yield components suited to eastern plain zone of Uttar Pradesh

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### Abstract

The present study consists of 26 rice genotypes including one check variety that were evaluated at Field Experimentation Centre of the Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj (Allahabad). The data was recorded on thirteen quantitative characters to study genetic variability, heritability, genetic advance and correlation coefficient analysis and path analysis. The experiment was conducted by using Randomized Block Design with three replications during *Kharif* -2019. On the basis of mean performance Burma Black Rice found to be superior in grain yield per hill followed by Chinniponni, Assami Variety, showed higher grain yield. Analysis of variance among 26 rice genotypes showed highly significant differences for all the characters under study indicated the presence of substantial amount of genetic variability. Biological yield character had the highest estimates of GCV and PCV. Test weight character also had the highest heritability coupled with high genetic advance. Grain yield per plant showed the high significant positive correlation with plant height, panicle length, number of tillers/plant, flag leaf length, flag leaf width and biological yield showed positive significant correlation with grain yield at phenotypic and genotypic levels. Path coefficient analysis revealed that days to 50% flowering, flag leaf length, flag leaf width, number of tillers/plant, number of panicles/hill, panicle length, biological yield and harvest index has positive direct effect on grain yield per plant.

**Keywords:** rice, genetic advance, variability, heritability, correlation coefficient and path analysis

### Introduction

Rice (*Oryza 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. Asia is considered to be “rice bowl” of the world, and it produces and consumes more than 90 percent of world rice. While, in newly born state Chhattisgarh is known as “rice bowl” of India. India is the largest rice growing country while, china is the largest rice producer of rice. In India, rice is cultivated in 44.13 million hectares during 2015 with production of 106.19 million tones and productivity of 2416kg per hectare (Anon., 2015). In Gujarat, rice is cultivated in 7.88 lakh hectares with production of 16.36 lakh tones and productivity of 2076 per hectare (Anon., 2015).

New era in the development of rice in India had started with the introduction of Taichung (Native) 1, the first high yielding dwarf indica variety developed Taiwan. Subsequently a large numbers of high yielding dwarf varieties have been developed under national rice research programme in almost all the Asian countries including India. Rice is the major crop in Uttar Pradesh and is grown in about 5.9 m ha. The cropping intensity is 153%. The state ranks 1st in the country in production of rice. The production is 14.63 and productivity of the state is round 2447 kg/ha thus it is understood that there is an extreme need to enhance the rice productivity in Uttar Pradesh (holds 5.9 million tonnes) which will be achieved only by developing high yielding hybrid varieties (Agriculture statistics, 2016-2017) Current population in India is 120 cores by 2025 it will be around 150 cores. So, there is need to develop high yielding varieties.

Variability refers to the presence of differences among the individuals of plant population due to their genetic composition and the environment in which they are raised. Genetic variability is the basis of plant breeding because any crop improvement depends on the amount and direction of genetic association of the traits in the base population. It provides a wide range of genotypes that can be selected to develop new varieties (Saha *et al.*, 2019) <sup>[10]</sup>. The variability and novel characters existing in the germplasm can be exploited during crossing programme to develop need-based varieties and hybrids. (Murthy and Arunachalam *et al.*, 1966).

The magnitude of heritable variation in the traits studied has immense value understanding the potential of the genotype for further breeding programme. Heritability and genetic advance are important selection parameters. Heritability estimates along with genetics advance are normally more helpful in predicting the gain under selection than heritability estimates alone. 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 trait, which helps in choosing an appropriate breeding method (Kumar *et al.*, 2014) [11].

Correlation coefficient measure the relationship between two characters and does not indicate relative importance of each factors, this study's was conducted to determine the nature of relationship between grain yield and yield components. Grain yield, being quantitative traits is a complex character of ant crop. Various morphological and physiological plant characters contribute to yield. These yield contributing components are inter-related with each other showings a complex chain of relationship and also highly influenced by the environmental conditions the genotypic correlation on the other hand is the only heritable part and represents the (Kina *et al.*, 2015). Phenotypic correlation & genotypic correlation plays a key role in the development and execution of suitable breeding programmes (Selvaraj *et al.*, 2011) [12].

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 plant breeding programs to determine the nature of relationship between yield and yield components that are useful as selection criteria to improve the crop yield.

Yield is a complex character being governed by a large number of cumulative, duplicate and dominant genes and highly influenced by environment. The success of breeding programme depends upon the quantum of genetic variability available for exploitation and the extent to which the desirable characters are heritable. Variability refers to the presence of differences among the individuals of plant population. Variation results due to difference either in genetic constitution of the individual of a plant population or in environment, they have grown. The existence of variability is essential for improvement of genetic material. Selection is also effective when their significant amount of genetic variability among the individuals in a population (Singh and Narayana, 2007).

### Materials and Methods

The experimental material consisted of 26 elite 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) [8], coefficient of variation (GCV and PCV) by Burton (1952). 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) [4]. Genetic advance was calculated by the method suggested by Johnson *et al.*, (1955) [7]. Correlation coefficient and path coefficient was worked out as method suggested by Al Jibouri *et al.* (1958) [1], Dewey and Lu (1959) [5] 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). 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 biological yield, number of tillers per plant and number of panicles per plant. Similar findings were obtained by (Dhurai *et al.*, 2014, Rashmi *et al.*, 2017, and Harsha *et al.*, 2017) [9, 6].

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; test weight followed by days to plant height, days to 50% flowering, days to maturity, spikelets per panicle, Panicle length, Flag leaf length, grain yield, number of panicles, number of tillers, biological yield per hill, flag leaf width, harvest index. High estimates of heritability were reported earlier for panicle length and test weight (Deepa *et al.* 2006).

The characters exhibiting high heritability may not be necessary to give high genetic advance. Johnson (1955) [7] 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 flag leaf length, panicle length, number of tillers, grain yield, spikelet per panicle. Genotypic and phenotypic correlation coefficients (Table 3 (a & b)) 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, number of tillers per plant, number of panicles per plant, flag leaf length, flag leaf width and biological yield showed positive significant correlation at phenotype and genotypic levels.

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). Path coefficient analysis revealed that the Days to 50% flowering, flag leaf length, flag leaf width, number of tillers, panicle length, biological yield, harvest index at both Genotypic and Phenotypic levels has positive direct effect on

grain yield per plant. Positive direct effect of these traits indicated that direct selection for these traits would be likely be effective in increasing grain yield. The direct effects of panicle Per hill were negative followed by Plant height, spikelet per panicle, days to maturity, test weight. In the

present study path coefficient revealed that number of tillers per hill, biological yield per hill and days to 50% flowering had influence on grain yield per hill. Selection of plants on these traits would certainly lead to improvement in grain yield.

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

S. no	Characters	Mean sum of squares		
		Replication	Treatment	Error
		(df=2)	(df=25)	(df=50)
1	Days to 50% Flowering	4.474*	278.318***	1.341
2	Plant height(cm)	38.278*	4983.412***	11.972
3	Flag leaf length(cm)	1.823	158.830***	7.071
4	Flag leaf width(cm)	0.007	0.223***	0.006
5	Tillers per hill	1.146	83.858***	2.281
6	Panicles per hill	1.089	71.710***	2.149
7	Spikelet's per panicle	1.38	19.122***	1.369
8	Panicle length	706.192**	12198.810***	138.486
9	Biological yield (g)	3.09	263.971***	1.85
10	Harvest Index (%)	8.049	2872.148***	77.927
11	Days to maturity	4.269	275.859***	6.213
12	Test weight (g)	0.099	89.041***	0.124
13	Grain yield per plant (g)	5.445	207.706***	9.133

Significant at 1% level \* and Significant at 5% \*\* level of significance respectively

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

S. No	Traits	GCV	PCV	h <sub>2</sub> (Broad Sense)	Genetic Advancement 5%	Gen. Adv as % of Mean 5%
1	Days to 50% flowering	9.14	9.21	98.60	19.65	18.71
2	Plant height(cm)	28.92	29.02	99.30	83.55	59.37
3	Flag leaf length(cm)	19.22	20.52	87.70	13.72	37.10
4	Flag leaf width(cm)	20.16	20.92	92.90	0.53	40.02
5	Number of tillers/ hill	45.77	47.66	92.30	10.31	90.58
6	Number of panicles/hill	44.85	46.88	91.50	9.49	88.39
7	Panicle length(cm)	8.74	9.70	81.20	4.51	16.22
8	No of Spikelets/panicle	34.56	35.15	96.70	128.42	70.01
9	Days to maturity	7.02	7.10	97.90	19.05	14.32
10	Biological yield(g)	47.75	49.71	92.30	60.393	94.51
12	Test weight (g)	25.42	25.48	99.60	11.19	52.27
13	Harvest index(%)	23.41	24.20	93.50	18.88	46.64
13	Grain yield/ hill(g)	33.65	35.89	87.90	15.71	64.98

**Table 3(a):** Estimation of Phenotypic correlation coefficient for yield and its related traits in 26 rice genotypes.

Phenotypical Correlation Matrix													
	DF (50%)	PH	FL	FW	T	P	PL	SPP	DM	BYH	HI	TW	GYPH
DF (50%)	1	0.4926***	0.0624	0.0269	0.0006	-0.0595	0.6726***	0.6860***	0.9857***	0.2473 *	-0.4993***	-0.8605***	0.0268
PH	0.4926***	1	0.6419***	0.6139***	0.3851***	0.3064**	0.5605***	0.6067***	0.4812***	0.7153***	-0.9004***	-0.7209***	0.239*
FL	0.0624	0.6419***	1	0.7021***	0.7474***	0.7255***	0.2883 *	0.1571	0.0969	0.8054***	-0.4896***	-0.214	0.655**
FW	0.0269	0.6139***	0.7021***	1	0.5080***	0.5050***	0.1857	0.2446 *	0.0327	0.7944***	-0.3847***	-0.1609	0.647**
T	0.0006	0.3851***	0.7474***	0.5080***	1	0.9876***	0.0196	-0.0207	0.0186	0.7407***	-0.3240**	-0.1921	0.783**
P	-0.0595	0.3064 **	0.7255***	0.5050***	0.9876***	1	-0.02	-0.0932	-0.0373	0.7329***	-0.2373 *	-0.1015	0.823**
PL	0.6726***	0.5605***	0.2883 *	0.1857	0.0196	-0.02	1	0.5441***	0.6933***	0.3130 **	-0.4614***	-0.5978***	0.0689
SPP	0.6860***	0.6067***	0.1571	0.2446 *	-0.0207	-0.0932	0.5441***	1	0.6465***	0.3150 **	-0.5757***	-0.7278***	-0.0194
DM	0.9857***	0.4812***	0.0969	0.0327	0.0186	-0.0373	0.6933***	0.6465***	1	0.2541 *	-0.4673***	-0.8393***	0.0583
BYH	0.2473 *	0.7153***	0.8054***	0.7944***	0.7407***	0.7329***	0.3130 **	0.3150 **	0.2541 *	1	-0.5675***	-0.4027***	0.810**
HI	-0.4993***	-0.9004***	-0.4896***	-0.3847***	-0.3240**	-0.2373 *	-0.4614***	-0.5757***	-0.4673***	-0.5675***	1	0.7648***	-0.0243
TW	-0.8605***	-0.7209***	-0.214	-0.1609	-0.1921	-0.1015	-0.5978***	-0.7278***	-0.8393***	-0.4027***	0.7648***	1	-0.0437

**Table 3(b):** Genotypical correlation coefficient for yield and its related traits in 26 rice genotypes.

Genotypical Correlation Matrix													
	DF (50%)	PH	FL	FW	T	P	PL	SPP	DM	BYH	HI	TW	GYPH
DF (50%)	1	0.498**	0.07	0.032	-0.003	-0.071	0.749**	0.703**	0.994**	0.263*	-0.519**	-0.867**	0.031
PH	0.498**	1	0.683**	0.639**	0.397**	0.317**	0.607**	0.621**	0.485**	0.743**	-0.935**	-0.725**	0.248*
FL	0.07	0.683**	1	0.810**	0.810**	0.794**	0.268*	0.179	0.099	0.858**	-0.525**	-0.228	0.718**
FW	0.032	0.639**	0.810**	1	0.555**	0.556**	0.213	0.257*	0.035	0.860**	-0.411**	-0.168	0.723**
T	-0.003	0.397**	0.810**	0.555**	1	0.992**	-0.04	-0.014	0.017	0.764**	-0.342**	-0.203	0.812**
P	-0.071	0.317**	0.794**	0.556**	0.992**	1	-0.087	-0.089	-0.046	0.761**	-0.240*	-0.108	0.866**
PL	0.749**	0.607**	0.268*	0.213	-0.04	-0.087	1	0.626**	0.758**	0.336**	-0.509**	-0.666**	0.049
SPP	0.703**	0.621**	0.179	0.257*	-0.014	-0.089	0.626**	1	0.664**	0.337**	-0.605**	-0.744**	-0.018

DM	0.994**	0.485**	0.099	0.035	0.017	-0.046	0.758**	0.664**	1	0.272*	-0.490**	-0.849**	0.064
BYH	0.263*	0.743**	0.858**	0.860**	0.764**	0.761**	0.336**	0.337**	0.272*	1	-0.591**	-0.424**	0.818**
HI	-0.519**	-0.935**	-0.525**	-0.411**	-0.342**	-0.240*	-0.509**	-0.605**	-0.490**	-0.591**	1	0.795**	-0.056
TW	-0.867**	-0.725**	-0.228	-0.168	-0.203	-0.108	-0.666**	-0.744**	-0.849**	-0.424**	0.795**	1	-0.048

**Table 4:** Estimation of path coefficient at genotypic level for 13 yield component traits with grain yield per hill in rice during *kharif*-2019

PATH matrix of GYPH													
	DF (50%)	PH	FL	FW	T	P	PL	SPP	DM	BYH	HI	TW	GYPH
DF (50%)	0.0969	0.0483	0.0068	0.0031	-0.0002	-0.0068	0.0725	0.0681	0.0964	0.0255	-0.0503	-0.084	0.031
PH	-0.2295	-0.4607	-0.3145	-0.2944	-0.1831	-0.146	-0.2795	-0.2861	-0.2236	-0.3421	0.4309	0.3341	0.248*
FL	0.0073	0.0713	0.1045	0.0846	0.0846	0.083	0.028	0.0187	0.0103	0.0896	-0.0549	-0.0238	0.718**
FW	0.0054	0.1092	0.1385	0.1709	0.0949	0.0951	0.0365	0.044	0.0059	0.147	-0.0702	-0.0288	0.723**
T	-0.0011	0.1669	0.3399	0.233	0.4198	0.4167	-0.0167	-0.0057	0.0072	0.3206	-0.1437	-0.0852	0.812**
P	0.0138	-0.0619	-0.1553	-0.1088	-0.194	-0.1955	0.0169	0.0174	0.009	-0.1488	0.0469	0.021	0.866**
PL	0.0284	0.023	0.0101	0.0081	-0.0015	-0.0033	0.0379	0.0237	0.0287	0.0127	-0.0193	-0.0252	0.049
SPP	-0.0434	-0.0383	-0.011	-0.0159	0.0008	0.0055	-0.0386	-0.0617	-0.041	-0.0208	0.0373	0.0459	-0.018
DM	-0.0094	-0.0046	-0.0009	-0.0003	-0.0002	0.0004	-0.0072	-0.0063	-0.0095	-0.0026	0.0046	0.008	0.064
BYH	0.2448	0.6898	0.797	0.7989	0.7095	0.7068	0.3122	0.3127	0.253	0.929	-0.5494	-0.3937	0.818**
HI	-0.2344	-0.4227	-0.2374	-0.1855	-0.1547	-0.1084	-0.23	-0.2733	-0.2213	-0.2673	0.452	0.3591	-0.056
TW	0.1524	0.1274	0.04	0.0296	0.0357	0.0189	0.117	0.1307	0.1491	0.0744	-0.1396	-0.1757	-0.048
GYPH	0.0311	0.2475	0.7177	0.7233	0.8116	0.8664	0.049	-0.0179	0.0643	0.8175	-0.0556	-0.0482	1

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