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Study on genetic variability, heritability, and genetic advance for seed yield and component traits in rice (*Oryza sativa* L.)

Rohit Kumar, SS Rao, Anjali Manhar, Deepak Saran, Vivek Kumar Sandilya, Deepak Gauraha and Sanjay Sharma

Abstract

The experiment was laid out at Research cum-Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur Chhattisgarh, India during *khariif* 2021-22. The experimental material comprised of five generations each cross of pair parents i.e. P₁, P₂, F₁, F₂ and F₃ of nine different crosses were conducted in Randomized Complete Block Design (RCBD) with three replications during *khariif* 2022. The highest phenotypic and genotypic variances were obtained for yield/plant, 1100-grain weight, and number of grains/panicles. The GCV ranged from 0.37% (days to maturity) to 51.01% (yield/plant). The small differences between GCV and PCV for days to 50% flowering, panicle length, number of tillers/plant, number of panicles/plant, number of grains/panicle, 100-grain weight, and yield/plant, represented some degree of environmental influence on the phenotypic expression of these characters. High heritability estimate coupled with high genetic advance as percentage of the mean obtained in cross PKVHMT x Vasumati for Yield/plant (98.90, 114.96), in cross IR-64 X TARORI BASMATI for 100 grain weight (97.30, 93.02), in cross PKVHMT x Tarori Basmati for days to 50% percent flowering (94.80, 11.58) in cross PKVHMT x Vasumati for panicle length (89.30, 20.29), in cross PKVHMT x Tarori Basmati for plant height (82.00, 28.47 and in cross IR64 x Tarori Basmati for days to maturity (70.50, 2.97). The character which have high heritability coupled with high genetic advance as percentage of mean along with governed by additive gene action and these types of characters indicates that direct selection could be effectively be made for yield improvement.

Keywords: Rice, broad sense heritability, genetic advance as percentage of mean, genotypic coefficient of variation, phenotypic coefficient of variation

Introduction

Rice is one of the most significant food crops of the world's population. It belongs to the family Poaceae and the genus *Oryza* (Gross and Zhao 2014 and Singh *et al.*, 2018) [14, 41]. The genus *Oryza* consists of 22 wild species (2 n=24, 48) and two cultivated species i.e. *O. sativa* (2 n=24=AA) and *O. glaberrima* Stued (2 n=24=AA) (Singh *et al.*, 2015) [42]. The primary center of origin of Asian rice is originated can be traced back to the river valleys of Yangtze and Mekong in China (Gross and Zhao 2014) [14]. African rice is originated in the upper valley of the Niger River and it is cultivated in western tropical Africa (Ansari *et al.*, 2015) [3]. "Cultivated rice (*O. sativa*) is predominantly self-pollinating and has lower out crossing ability. A cross pollination rate of *O. sativa* is less than one percent (Messeguer *et al.*, 2001) [26]." However, the estimated out crossing rates among wild rice populations ranges from 4.3% to 55.9% (Oka, 1988) [30]. Rice is a highly diverse crop species with wide geographic dispersal from sea level up to 3000 mean sea level. in both temperate and tropical climates (Oka, 1988 and Mickel *et al.*, 1990) [30, 27]. "Rice is the second most-produced cereal in the world after wheat and assists as a chief food basis for more than half of the world's population. (Luz *et al.*, 2016 and Dejen, 2020) [24, 10]. Most of the world's rice is cultivated and consumed in Asia (Chakravarthi and Naravaneni, 2006) [6]. Although Asia is the main place of rice cultivation, rice is also produced in other continents like Latin America, Europe, USA and Africa (Zibae, 2013) [45]." Asia accounts for the largest portion (about 144.25 million tons), whereas Africa produces approximately 11.58 million tons (FAO, 2015) [12]. China, India, and Indonesia are the largest rice producing countries in the world, with percent share of 32.9 %, 24.4% and 11.0 %, respectively. Worldwide the area covered by rice exceeds 163.1 million hectares with a production of 748 million tons (FAO, 2017) [13]. "The world's average productivity (kg/ha) has doubled during the last 25 years, largely due to the use of improved technologies such as

high yielding varieties (Rahman *et al.*, 2012) [35].” High average yields of rice was found in 2014 from Japan, China, Egypt, Vietnam, Indonesia and USA with productivity of 6.69, 6.75, 9.52, 5.75, 5.13 and 8.48 tons ha⁻¹, respectively (FAO, 2015) [12].

The success of plant breeding research relies upon at the availability of genetic variation. However, complete data is missing on the genetic variability of these days brought low land rice genotypes in the examiner location. Genetic improvement specially relies upon on the amount of genetic variability present in the populace that's a established property of all species in nature (Dutta, and Borua, 2013) [11]. Variability in genotypes for yield and yield component trends paperwork is the primary issue to be taken into consideration whilst making choice (Biodiversity International 2007) [4]. The individual yield reflects the overall performance of all plant components and might be taken into consideration as the very last result of many other traits. *i.e.* Every plant consists of an inherent physiological production capability that operates on electricity required for ordinary plant performance. Not all genotypes have the same inherent physiological potential to yield (Welsh, 1981) [44]. Heritability and genetic advance are important selection parameters while selection is made based on yield contributing traits. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Paul *et al.*, 2006) [32]. Therefore, the objective of this have a look at was to evaluate the genetic variability, heritability, and genetic advance (GA) of yield and yield associated developments in a few promising rice genotypes to help the future breeding programmers for yield improvement.

Materials and Methods

All genotypes were planted in randomized complete block design with 3 replications, plot size 3.0 m x 2.0 m consisting of 15 lines, one line -P₁, one line-P₂, one line-F₁, six lines-F₂ and six lines-F₃ planted with 20 cm x 10 cm spacing during *kharif* season of 2021 and 2022. All standardized agronomic practices adopted to maintain the good rice crop. Raised nursery seed bed was prepared for sowing of seeds. Nurseries were raised by taking seeds of all the 5 generations (P₁, P₂, F₁, F₂ and F₃) each cross. Twenty one day's old seedlings were subsequently transplanted into the field with randomized complete block design. The experimental material was planted in fifteen rows in three replications of each family.

Table 1: Cross combination of six genotypes in rice used for the study

S.N.	Crosses	
1.	PKV HMT x Pusa 1121	7. IR 64 x Pusa 1121
2.	PKV HMT x Vasumati	8. IR 64 x Vasumati
3.	PKV HMT x Tarori Basmati	9. IR 64 x Tarori Basmati
4.	MTU 1010 x Pusa 1121	
5.	MTU 1010 x Vasumati	
6.	MTU 1010 x Tarori Basmati	

Results and Discussion

Analysis of Variance: “The analysis of variance showed highly significant differences among genotypes for all evaluated traits at level of 5% and 1% respectively.” This significance difference indicates the presence of acceptable amount of variability among rice genotypes in growth

parameters, in grain yield and yield components. “This provides a great opportunity for breeders to improve desired traits through selection and hybridization.” Similar finding was previously described by (Rashid *et al.*, 2017) [37] in nine cross combinations of rice for all the traits they studied. (Konate *et al.*, 2016) [20] reported significant differences among nine cross combinations of rice evaluated in different years. (Khare *et al.*, 2014) [19] also found similar results among the genotypes for all studied traits.

Among the traits, days to 50% flowering varies from 88.05 (MTU1010 x PUSA 1121) to 102.25 (IR64 x Tarori Basmati) days while days to maturity 122.26 (IR64 x Vasumati) to 130.61 (PKVHMT x Tarori Basmati), and plant height varies from 106.65 (PKVHMT x Vasumati) to 157.11 (IR64 x Tarori Basmati) cm. The panicle length varies from 21.81 (PKVHMT x Tarori Basmati) to 32.12 (IR64 x Tarori Basmati) cm and the number of tillers/plant varies from 6.25 (IR64 x Vasumati) to 12.00 (MTU1010 x Vasumati). Number of panicles/plant varies from 5.45 (MTU1010 x Tarori Basmati) to 10.62 (MTU1010 x Vasumati) and number of grains/panicle varies from 72.85 (IR64 x Vasumati) to 228.47 (PKVHMT x Vasumati). Spikelet fertility varies from 55.39 (PKVHMT x Tarori Basmati) to 93.92 (PKVHMT x Vasumati) (%) while Harvest index varies from 28.14 (PKVHMT x Tarori Basmati) to 57.77 (MTU1010 x PUSA1121) (%). 100 grain weight varies from 1.63 (PKVHMT x Tarori Basmati) to 4.71 (IR64 x Tarori Basmati) (g) and yield/plant varies from 5.97 (IR64 x Tarori Basmati) to 21.03 (PKVHMT x PUSA1121). As a wider variation was observed among the genotypes for all the characters hence these traits can be effectively used for the selection of better perform genotypes type in nine cross combinations of rice. (Kumar *et al.*, 1999) [23] observed all eleventh considerable differences for yield attributing traits in both early and medium maturing rice genotypes, indicating a wider variability and opportunity for improvement through selection similar findings were reported by (Chauhan and Chauhan 1194, Nandeshwar *et al.*, 2010, Sala 2012, Sangeetha 2013, Das *et al.*, 2015 and Kumar *et al.*, 2015) [7, 29, 38, 39, 9, 22].

Phenotypic and genotypic variability

Phenotypic variance was higher than the genotypic variances for all the characters indicating the influence of the environmental factors on these traits. The higher phenotypic and genotypic variances were obtained from yield/plant for (PKVHMT x Tarori Basmati), 100 grain weight for (MTU1010 x Tarori Basmati) and number of grains/panicle for (PKVHMT x Tarori Basmati), high influence of the environment on the traits. Yield/plant, 100 grain weight and number of grains/panicle had high phenotypic coefficient of variation (PCV) values. The PCV values for harvest index, spikelet fertility, number of tillers/plant, and panicle length were medium. Days to 50% flowering, days to maturity and plant height had low values. The characters as yield/plant, 100 grain weight and number of grains/panicle gave comparatively higher values of genotypic coefficient of variation. The high level of genotypic and phenotypic coefficients of variation was recorded for traits like yield/plant, 100-grain weight and number of grains/panicle. However, moderate estimates were observed for harvest index, spikelet fertility, number of tillers/plant, and panicle length. “The rest of the traits showed low estimates of genotypic and phenotypic coefficients of variation. In the

present study, phenotypic coefficients of variation were slightly higher than the genotypic coefficients of variation for all the traits studied. This indicates the presence of slight environmental influence to some degree in the phenotypic expression of the characters." (Pandey *et al.*, 2010 and Mulugeta *et al.*, 2012) [31, 28] also observed similar findings.

Estimation of Broad-sense Heritability and genetic advance

The coefficient of variation does not provide complete scope of heritable variation; it gives a degree of assessment of variability and offers some indication of validity of trait for selection. The more diploma of accuracy for the selection of trends is acquired while estimates of high heritability in coupled with high genetic advance research collectively. "Both heritability and genetic advance are important direct selection parameters therefore high heritability along with high genetic advance is more useful in predicting the gain under selection than heritability estimates alone." (Johnson *et al.*, 1955) [17] also suggested that without genetic advance the estimates of heritability will not be of practical value and emphasized the concurrent use of genetic advance along with heritability. In the present investigation heritability and genetic advance have been worked out for all the quantitative characters and are brief described in below

Heritability

In this study, high category of heritability was recorded in cross MTU1010 x Vasumati for number of panicles/plant (99.30%), in cross PKVHMT x Vasumati (98.90%) for yield/plant, in cross IR-64 x PUSA 1121 for number of grains per panicle (98.50%), in cross IR-64 x Tarori Basmati (97.30%) for 100 grain weight, and in cross IR-64 x Vasumati for harvest index (96.30%) given as in Table 3. Similar findings are seen in the works of (Singh *et al.*, 2014 and

Prasad *et al.*, 2017) [33].

Genetic advance

Genetic advance as percentage of mean gives information on the improvement required in the genotypic value of the new population over original population. The value of genetic advance as percent of mean (GAM) were calculated high in cross PKVHMT x Vasumati for yield/plant (114.96%), in cross IR-64 x Tarori Basmati for 100 grain weight (93.02%), in cross PKVHMT x Tarori Basmati for number of grains/panicle (67.21%), in cross PKVHMT x Tarori Basmati for harvest index (58.10%), in cross IR-64 x PUSA 1121 for number of tillers/plant (54.84%) and cross IR-64 x Tarori Basmati for number of panicles/plant (54.28%). High genetic advance as percentage of means were reported in the works of (Abebe *et al.*, 2017 and Rahman *et al.*, 2014) [34, 1]. The estimates of genetic advance as a percent of mean provide more reliable information regarding the selection in improving the traits.

In the present study, high heritability estimate coupled with high genetic advance as percentage of mean obtained in cross PKVHMT x Vasumati for Yield/plant (98.90, 114.96), in cross IR-64 x TARORI BASMATI for 100 grain weight (97.30, 93.02), in cross PKVHMT x Tarori Basmati for days to 50% percent flowering (94.80, 11.58),) in cross PKVHMT x Vasumati for panicle length (89.30, 20.29), in cross PKVHMT x Tarori Basmati for plant height (82.00, 28.47 and in cross IR64 x Tarori Basmati for days to maturity (70.50, 2.97). The character which have high heritability coupled with high genetic advance as percentage of mean along with governed by additive gene action and these types of characters indicates that direct selection could be effectively be made for yield improvement. Similar findings were also reported by (Allam *et al.*, 2015, Kumar *et al.*, 2015, Kamboj *et al.*, 2016 and Kumar *et al.*, 2016) [2, 22, 18, 21].

Table 2: Analysis of variance for each cross and five populations

Source of Variations	df	1	2	3	4	5	6	7	8	9	10	11
PKVHMT X PUSA 1121												
Replications	2	10.80	7.15	7.82	0.25	2.88	2.21	6.10	12.38	26.29	0.05	0.71
Generations	4	69.21**	7.68*	397.94**	27.73**	1.24*	2.11*	6514**	639.65**	110.67**	0.17*	44.21**
Error	8	1.79	2.33	15.22	1.71	0.47	0.31	18.62	10.72	29.29	0.02	0.11
PKVHMT X Vasumati												
Replications	2	2.84	2.84	2.51	0.01	0.24	0.02	0.14	1.99	10.94	0.07	0.39
Generations	4	48.26**	11.46*	195.76**	24.01**	3.91**	3.22*	5214.25*	499.03**	172.46**	0.34*	77.21**
Error	8	2.69	4.44	5.45	2.11	0.52	1.07	5.34	2.36	2.69	0.01	0.53
PKVHMT X Tarori Basmati												
Replications	2	2.86	0.82	0.21	0.81	0.59	0.17	10.53	2.65	0.51	0.02	1.82
Generations	4	93.10**	5.58**	1115.01**	21.50**	1.48**	0.71*	6692.82*	659.99**	225.73**	0.55*	144.08**
Error	8	1.66	1.67	7.25	1.01	0.43	0.16	5.06	1.85	5.93	0.01	2.50
IR-64 X PUSA 1121												
Replications	2	0.27	0.39	8.32	0.16	1.04	2.09	75.98	19.64	26.45	0.10	1.07
Generations	4	9.02**	5.36**	137.41*	4.64**	2.46*	1.67**	1533.93*	245.40**	186.99**	0.31**	44.73**
Error	8	3.43	1.59	3.02	0.41	0.37	0.16	23.71	23.71	28.17	0.12	0.63
IR-64 X Vasumati												
Replications	2	2.95	0.72	4.22	0.14	0.63	0.17	13.73	21.42	0.34	0.01	4.45
Generations	4	9.45**	6.79**	242.06**	11.70*	5.77**	5.19*	2413.53*	213.26**	134.90**	0.25*	215.61**
Error	8	3.27	1.71	3.53	0.70	0.24	0.58	49.92	21.86	5.70	0.01	0.82

*, ** Significant at 5% Significant at 1% level correspondingly

df= Degree of freedom, 1. Days to 50% flowering, 2. Days to maturity, 3. Plant height (cm), 4. Panicle length (cm) 5. Number of tillers/plant 6. Number of panicles/plant, 7. Number of grains/panicle, 8. Spikelet fertility (%), 9. Harvest index (%), 10. 100-grain weight (g) and 11. Yield/plant (g).

Source of Variations	df	1	2	3	4	5	6	7	8	9	10	11
IR-64 x Tarori Basmati												
Replications	2	1.26	10.22	3.11	0.27	1.48	1.26	38.52	5.95	2.58	0.01	2.23
Generations	4	63.06**	16.32*	398.69*	5.89**	5.71**	4.88**	2783.31**	65.11*	114.51*	4.12**	83.42**
Error	8	2.04	1.99	4.43	0.92	0.28	1.21	87.76	11.21	4.10	0.01	2.76
MTU1010 x PUSA 1121												
Replications	2	7.92	2.89	5.89	0.31	0.15	0.09	36.18	3.14	49.11	0.12	1.24
Generations	4	32.04*	6.05*	205.84**	9.38*	1.35**	0.44*	381.53*	325.16*	44.58**	0.44*	35.62**
Error	8	0.72	2.27	9.76	2.84	0.25	0.69	39.83	3.84	14.11	0.21	4.49
MTU1010 x Vasumati												
Replications	2	0.07	0.36	2.38	0.55	1.17	1.09	188.02	2.61	12.32	0.01	0.96
Generations	4	10.70*	5.81**	26.59**	7.46**	4.42*	3.11**	1102.72**	251.75*	34.74**	0.21**	23.99**
Error	8	3.89	2.24	2.87	2.05	0.23	0.25	120.54	2.52	9.49	0.21	2.28
MTU1010 x Tarori Basmati												
Replications	2	2.96	7.08	1.29	0.46	0.26	0.17	78.55	0.67	11.43	0.23	0.93
Generations	4	5589.92*	12.42*	608.51**	11.44**	4.32*	1.99**	1029.76**	201.71*	75.95**	3.32**	43.59**
Error	8	3.08	1.84	10.94	1.32	0.60	0.15	68.79	3.97	2.02	0.01	0.67

*, ** Significant at 5% Significant at 1% level correspondingly

df= Degree of freedom, 1. Days to 50% flowering, 2. Days to maturity, 3. Plant height (cm), 4. Panicle length (cm) 5. Number of tillers/plant 6. Number of panicles/plant, 7. Number of grains/panicle, 8. Spikelet fertility (%), 9. Harvest index (%), 10. 100 grain weight (g) and 11. Yield/plant (g).

Table 3: Genetic variability parameters for yield and yield attributing traits in rice

Crosses	Min.	Max.	GCV (%)	PCV (%)	h ²	Genetic advance	Genetic advance as % over F ₂ mean
Days to 50% flowering							
PKVHMT x PUSA 1121	90.08	101.34	5.04	5.24	92.60	9.40	9.73
PKVHMT x Vasumati	91.20	100.33	4.13	4.48	85.00	7.40	7.85
PKVHMT x Tarori Basmati	88.41	101.24	5.72	5.87	94.80	11.08	11.58
IR-64 x PUSA 1121	91.17	95.67	1.47	2.47	35.20	1.67	1.74
IR-64 x Vasumati	91.20	94.59	0.96	2.34	16.60	0.74	0.78
IR-64 x Tarori Basmati	91.67	102.25	4.80	5.03	90.90	8.86	9.63
MTU1010 x PUSA 1121	88.05	96.37	3.50	3.62	93.50	6.44	6.68
MTU1010 x Vasumati	91.20	95.74	1.62	2.67	36.80	1.88	1.96
MTU1010 x Tarori Basmati	91.23	102.24	4.02	4.48	80.70	7.16	7.43
Crosses	Min.	Max.	GCV (%)	PCV (%)	h ²	Genetic advance	Genetic advance as % over F ₂ mean
Days to maturity							
PKVHMT x PUSA 1121	123.38	126.62	1.06	1.61	43.30	1.81	1.42
PKVHMT x Vasumati	122.46	125.69	1.22	2.08	34.50	1.85	1.47
PKVHMT x Tarori Basmati	127.55	130.61	0.47	1.34	12.10	0.43	0.32
IR-64 x PUSA 1121	122.34	124.47	0.59	1.52	15.20	0.59	0.48
IR-64 x Vasumati	122.26	124.87	0.39	1.50	6.70	0.26	0.20
IR-64 x Tarori Basmati	123.39	129.36	1.74	2.07	70.50	3.78	2.97
MTU1010 x PUSA 1121	123.38	125.15	0.59	1.30	20.70	0.69	0.55
MTU1010 x Vasumati	122.93	124.49	1.00	1.66	36.40	1.55	1.24
MTU1010 x Tarori Basmati	126.25	127.35	1.48	1.83	65.70	3.14	2.48
Crosses	Min.	Max.	GCV (%)	PCV (%)	h ²	Genetic advance	Genetic advance as % over F ₂ mean
Plant height (cm)							
PKVHMT x PUSA 1121	106.66	138.05	9.47	12.76	55.10	17.69	15.66
PKVHMT x Vasumati	106.65	128.97	6.27	9.47	43.80	10.19	8.95
PKVHMT x Tarori Basmati	108.66	156.12	14.75	16.30	82.00	36.58	28.47
IR-64 x PUSA 1121	117.65	130.99	3.82	6.03	40.00	6.20	4.99
IR-64 x Vasumati	107.14	124.26	4.92	6.88	51.20	8.51	6.97
IR-64 x Tarori Basmati	119.65	157.11	11.18	12.01	81.70	28.07	22.51
MTU1010 x PUSA 1121	117.63	130.65	4.74	6.39	55.00	8.82	7.02
MTU1010 x Vasumati	106.52	124.26	4.53	8.34	29.50	6.02	5.65
MTU1010 x Tarori Basmati	110.31	156.12	12.49	15.66	63.60	26.22	20.70
Crosses	Min.	Max.	GCV (%)	PCV (%)	h ²	Genetic advance	Genetic advance as % over F ₂ mean
Panicle length (cm)							
PKVHMT x PUSA 1121	22.81	29.23	10.76	12.47	74.50	5.05	19.88
PKVHMT x Vasumati	21.82	28.70	10.39	10.99	89.30	5.34	20.29
PKVHMT x Tarori Basmati	21.81	30.12	9.28	12.68	53.50	3.73	12.38
IR-64 x PUSA 1121	24.96	28.70	0.82	9.65	0.70	0.04	0.15
IR-64 x Vasumati	24.96	28.70	1.46	9.99	-2.10	-0.12	-0.45
IR-64 x Tarori Basmati	26.42	32.12	2.46	6.42	-14.70	-0.53	-1.64
MTU1010 x PUSA 1121	25.21	29.69	4.22	7.15	34.90	1.42	5.29
MTU1010 x Vasumati	25.02	28.70	4.19	8.24	25.90	1.17	4.67
MTU1010 x Tarori Basmati	25.58	30.45	5.02	9.14	30.10	1.54	5.05

Crosses	Min.	Max.	GCV (%)	PCV (%)	h ²	Genetic advance	Genetic advance as % over F ₂ mean
Number of tillers/plant							
PKVHMT x PUSA 1121	9.61	11.86	16.49	17.90	84.80	3.25	42.42
PKVHMT x Vasumati	7.34	11.73	16.25	17.47	86.50	2.96	40.32
PKVHMT x Tarori Basmati	7.61	16.02	15.81	17.92	77.80	2.83	37.18
IR-64 x PUSA 1121	6.60	11.73	19.43	20.65	88.50	3.62	54.84
IR-64 x Vasumati	6.25	10.61	17.28	19.91	75.30	2.70	43.20
IR-64 x Tarori Basmati	6.74	11.62	18.09	18.74	93.20	3.24	48.07
MTU1010 x PUSA 1121	9.38	11.73	7.50	10.42	51.80	1.14	12.15
MTU1010 x Vasumati	6.86	12.00	15.24	15.88	92.10	2.77	26.28
MTU1010 x Tarori Basmati	6.52	10.12	17.21	19.77	75.80	2.73	41.87
Crosses	Min.	Max.	GCV (%)	PCV (%)	h ²	Genetic advance	Genetic advance as % over F ₂ mean
Number of panicles/plant							
PKVHMT x PUSA 1121	6.34	10.61	18.31	20.33	81.10	2.95	46.45
PKVHMT x Vasumati	6.24	10.20	19.36	20.00	93.70	3.15	50.48
PKVHMT x Tarori Basmati	6.40	10.26	16.29	17.63	85.40	2.69	42.03
IR-64 x PUSA 1121	5.90	9.53	16.44	16.74	96.40	2.69	45.59
IR-64 x Vasumati	6.08	9.54	16.21	19.60	68.40	2.15	35.36
IR-64 x Tarori Basmati	5.95	9.53	19.58	19.77	98.10	3.23	54.28
MTU1010 x PUSA 1121	7.87	9.35	5.57	8.33	44.80	0.66	8.38
MTU1010 x Vasumati	5.80	10.62	17.93	17.99	99.30	2.88	33.41
MTU1010 x Tarori Basmati	5.45	9.46	20.10	20.98	91.80	3.10	36.68
Crosses	Min.	Max.	GCV (%)	PCV (%)	h ²	Genetic advance	Genetic advance as % over F ₂ mean
Number of grains/panicles							
PKVHMT x PUSA 1121	106.00	226.46	30.90	31.87	94.00	92.79	60.29
PKVHMT x Vasumati	118.06	228.47	27.96	29.44	90.20	83.46	54.27
PKVHMT x Tarori Basmati	79.20	226.46	34.67	35.83	93.70	103.26	67.21
IR-64 x PUSA 1121	73.86	136.60	21.69	21.85	98.50	47.27	46.82
IR-64 x Vasumati	72.85	164.43	28.15	28.99	94.30	69.52	42.27
IR-64 x Tarori Basmati	73.86	143.66	30.12	31.21	93.20	68.70	49.38
MTU1010 x PUSA 1121	117.13	134.00	5.32	6.86	60.30	10.35	8.81
MTU1010 x Vasumati	101.53	138.21	9.66	10.78	80.30	21.44	17.67
MTU1010 x Tarori Basmati	79.20	134.00	18.21	19.58	86.40	37.14	33.73
Crosses	Min.	Max.	GCV (%)	PCV (%)	h ²	Genetic advance	Genetic advance as % over F ₂ mean
Spikelet fertility (%)							
PKVHMT x PUSA 1121	57.98	92.90	19.02	21.34	79.40	26.49	39.51
PKVHMT x Vasumati	63.45	93.92	16.63	17.83	87.10	24.04	37.88
PKVHMT x Tarori Basmati	55.39	93.90	19.82	21.42	85.60	27.52	43.19
IR-64 x PUSA 1121	62.98	88.64	14.61	15.38	90.30	20.07	30.13
IR-64 x Vasumati	62.88	82.88	10.63	12.48	72.50	12.95	18.79
IR-64 x Tarori Basmati	67.44	79.68	7.22	8.46	72.70	8.90	13.10
MTU1010 x PUSA 1121	66.42	88.64	15.12	15.67	93.00	22.69	33.27
MTU1010 x Vasumati	67.05	88.69	12.32	13.69	81.00	17.12	25.05
MTU1010 x Tarori Basmati	66.12	87.68	10.93	13.86	62.30	13.26	18.76
Crosses	Min.	Max.	GCV (%)	PCV (%)	h ²	Genetic advance	Genetic advance as % over F ₂ mean
Harvest Index (%)							
PKVHMT x PUSA 1121	37.28	52.50	12.16	15.25	63.60	8.87	23.79
PKVHMT x Vasumati	34.99	51.59	15.40	16.68	85.30	12.24	34.98
PKVHMT x Tarori Basmati	28.14	47.42	21.14	22.34	89.50	16.35	58.10
IR-64 x PUSA 1121	33.95	47.20	13.87	15.97	75.40	9.50	24.09
IR-64 x Vasumati	33.14	51.59	17.76	18.10	96.30	15.19	33.08
IR-64 x Tarori Basmati	35.07	45.86	11.09	15.02	54.50	6.75	18.06
MTU1010 x PUSA 1121	40.82	57.77	13.55	14.19	91.20	12.64	21.87
MTU1010 x Vasumati	42.77	56.53	9.28	11.93	60.50	7.36	13.01
MTU1010 x Tarori Basmati	38.77	53.61	11.32	13.60	69.20	8.88	16.56
Crosses	Min.	Max.	GCV (%)	PCV (%)	h ²	Genetic advance	Genetic advance as % over F ₂ mean
100-grain weight (g)							
PKVHMT x PUSA 1121	1.66	2.14	9.36	12.23	58.50	0.29	14.42
PKVHMT x Vasumati	1.64	2.53	15.41	16.80	84.20	0.61	31.93
PKVHMT x Tarori Basmati	1.63	2.64	20.42	21.00	94.60	0.81	46.28
IR-64 x PUSA 1121	2.04	2.79	11.17	11.84	89.00	0.55	21.65

IR-64 x Vasumati	2.13	2.78	8.63	12.61	46.80	0.31	12.40
IR-64 x Tarori Basmati	2.12	4.71	35.31	35.79	97.30	2.40	93.02
MTU1010 x PUSA 1121	2.04	2.94	15.88	16.25	95.50	0.79	29.81
MTU1010 x Vasumati	2.08	2.62	10.07	13.65	54.40	0.37	14.39
MTU1010 x Tarori Basmati	2.06	4.58	41.12	42.60	93.20	2.56	56.63
Crosses	Min.	Max.	GCV (%)	PCV (%)	h²	Genetic advance	Genetic advance as % over F₂ mean
Yield/plant (g)							
PKVHMT x PUSA 1121	9.90	21.03	27.55	28.03	96.60	7.73	78.08
PKVHMT x Vasumati	7.36	20.05	40.03	40.26	98.90	10.37	114.96
PKVHMT x Tarori Basmati	6.87	19.03	51.01	52.46	94.60	12.22	112.41
IR-64 x PUSA 1121	7.07	12.62	19.46	20.83	87.30	3.86	36.86
IR-64 x Vasumati	8.07	18.73	38.49	39.08	97.00	9.55	84.43
IR-64 x Tarori Basmati	5.97	10.95	26.22	26.48	98.00	4.44	40.54
MTU1010 x PUSA 1121	12.62	18.53	13.28	15.30	75.30	3.92	22.32
MTU1010 x Vasumati	10.47	18.46	19.32	20.22	91.30	5.95	33.42
MTU1010 x Tarori Basmati	7.19	17.45	34.33	34.96	96.40	7.68	72.93

Min. = Minimum, Max. = Maximum, GCV= Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, h² bs = Broad sense heritability, Genetic advance, Genetic advance as % over F₂ mean

Conclusion

The present study showed significant amount of variation among the genotypes for all the yield related traits. Since crop improvement is depends on magnitude of genetic variation so in the current study high heritability coupled with high genetic advance as percentage of mean governed by additive gene action and these types of characters indicates that direct selection could be effectively be made for yield improvement.

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References

1. Abebe T, Alamerew S, Tulu L. Genetic variability, heritability and genetic advance for yield and its related traits in rainfed lowland rice (*Oryza sativa* L.) genotypes at Fogera and Pawe, Ethiopia. *Advances in crop Science and Technology*. 2017;5(2):272.
2. Allam CR, Jaiswal HK, Qamar A. Character association and path analysis studies of yield and quality parameters in basmati rice (*Oryza sativa* L.). *Journal of Progressive Agriculture*. 2015;6(1):117-121.
3. Ansari MU, Shaheen T, Bukhari S, Husnain T. Genetic improvement of rice for biotic and abiotic stress tolerance. *Turkish Journal of Botany*. 2015;39(6):911-919.
4. Bioversity International. Descriptors for wild and cultivated rice (*Oryza sativa* L.). International Rice Research Institute Los Banos, Cotonou, Benin; c2007. p. 63.
5. Burton GW, Devane DE. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material 1. *Agronomy journal*. 1953 Oct;45(10):478-81.
6. Chakravarthi BK, Naravaneni R. SSR marker based DNA fingerprinting and diversity study in rice (*Oryza sativa* L.). *African Journal of Biotechnology*. 2006;5(9):24.
7. Chauhan JS, Chauhan VS. Genetic analysis of grain dimensions and weight and their association with grain yield in rainfed rice (*Oryza sativa*). *Indian Journal of Agricultural Sciences*. 1994;64(9):613-8.
8. Cochran WG, Cox GM. *Experimental designs*. Asia Publication House, Bombay. *Indian J Pl. Sci*. 1957;14(6):69-72.
9. Das SH, Sarma DE, Kalita PR. Morpho-physiological variability in boro rice (*Oryza sativa* L.). *Bioscan*. 2015;9(1/2):611-619.
10. Dejen B. Improvement of Rice Breeding for Salinity Tolerance. *Journal of Environment and Earth Science*. 2020;10(5):14.
11. Dutta P, Borua PK. Morphological traits as selection indices in rice: A statistical view. *Universal Journal of Agricultural Research*. 2013;1(3):85-96.
12. FAO. International Year of Rice 2015, Statistical database of the food and agriculture of the United Nations; c2015.
13. FAO. Food and Agriculture Organization of the United Nations; c2017. (<http://faostat.fao.org>.)
14. Gross BL, Zhao Z. Archaeological and genetic insights into the origins of domesticated rice. *Proceedings of the National Academy of Sciences*. 2014 Apr 29;111(17):6190-6197.
15. Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating populations of Korean lespedeza 1. *Agronomy journal*. 1956 Jun;48(6):268-272.
16. IRRI International rice research institute. *Rice Almanac*, source book for the most important economic activity on earth. Third edition; c2002.
17. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans 1. *Agronomy journal*. 1955 Jul;47(7):314-318.
18. Kamboj G, Kumar P, Kumar R, Kumar S, Singh D. Analysis of genetic parameters and characters association for yield components and quality attributes in rice cultivars. *Research in Environment and Life Sciences*. 2016;9(11):1416-1422.
19. Khare R, Singh AK, Eram S, Singh PK. Genetic variability, association and diversity analysis in upland Rice (*Oryza sativa* L.). *SAARC Journal of Agriculture*. 2014;12(2):40-51.
20. Konate AK, Zongo A, Kam H, Sanni A, Audebert A. Genetic variability and correlation analysis of rice (*Oryza sativa* L.) inbred lines based on agro-morphological traits; c2016.
21. Kumar A, Lal GM, Kumar S. Assessment of genetic variability for yield and quality traits in rice (*Oryza sativa*

- L.) genotypes. *Research in Environment and Life Sciences*. 2016;9(11):1310-1312.
22. Kumar SU, Babu SG, Chandra RA, Kumar AR. Estimation of genetic variation for quantitative and qualitative characters in elite rice (*Oryza sativa* L.) genotypes. *The Bioscan*. 2015;9(3):893-896.
 23. Kumar S, Van Rheenen HA, Singh O. Genetic analysis of different components of crop duration in chicken pea. *Journal of Genetic and Breeding*. 1999;53:189-200.
 24. Luz VKD, Silveira SFDS, Fonseca GMD, Grolí EL, Figueiredo RG, Baretta D, *et al.* Identification of variability for agronomically important traits in rice mutant families. *Bragantia*. 2016;75(1):41-50.
 25. Maclean JL, Dawe DC, Hardy B, Hettel GP. (Eds.) *International Rice Research Institute*, Manila, Philippines, 1-253.
 26. Messeguer J, Fogher C, Guiderdoni E, Marfa V, Catala MM, Baldi G, Melé E. Field assessments of gene flow from transgenic to cultivated rice (*Oryza sativa* L.) using a herbicide resistance gene as tracer marker. *Theoretical and Applied Genetics*. 2001;103(8):1151-1159.
 27. Mickel A, Donini B, Maluszynski M. Induced mutations for crop improvement. *Mutation Breeding Review*, No.7. IAEA, Vienna; c1990. p. 1-16.
 28. Mulugeta S, Sentayehu A, Bantte K. Genetic Variability, Heritability, Correlation Coefficient and Path Analysis for Yield and Yield Related Traits in Upland Rice (*Oryza sativa* L.). *Journal of Plant Sciences*. 2012;7:13-12.
 29. Nandeshwar BC, Pal S, Senapati BK, De DK. Genetic variability and character association among biometrical traits in F₂ generation of some Rice crosses. *Electron J Plant Breed*. 2010;1(4):758-763.
 30. Oka HI. *Weedy forms of rice. Origin of cultivated rice.* Elsevier, Amsterdam; c1988. p. 107-114.
 31. Pandey P, PR. Estimation of genetic parameters in indigenous rice. *Journal of Bioflux Society*. 2010;2:79-84.
 32. Paul AKMA, Islam MJ, Hasan MMH, Chowdhury AZMKA. Genetic variation of some morpho-physiological characters in *Triticum durum* wheat. *Int. J Sustain. Agric. Tech*. 2006;2(8):11-14.
 33. Prasad RS, Babu GS, Ram BJ, Rai PK. Evaluation of early mature elite rice (*Oryza sativa* L.) hybrids for yield and quality traits. *Journal of Pharmacognosy and Phytochemistry*. 2017;6(4):18-21.
 34. Rahman MA, Hossain MS, Chowdhury IF, Matin MA, Mehraj H. Variability study of advanced fine rice with correlation, path co-efficient analysis of yield and yield contributing characters. *International Journal of Applied Sciences and Biotechnology*. 2014;2(3):364-370.
 35. Rahman MM, Syed MA, Adil M, Ahmad H, Rashid MM. Genetic variability, correlation and path coefficient analysis of some physiological traits of transplanted Aman rice (*Oryza sativa* L.). *Middle East Journal of Scientific Research*. 2012;11(5):563-566.
 36. Raiz R, Chowdhry MA. Estimation of variation and heritability of some physio-morphic traits of wheat under drought condition. *Asian Journal of Plant Science*. 2003;2(10):748-755.
 37. Rashid MM, Nuruzzaman M, Hassan L, Begum SN. Genetic variability analysis for various yield attributing traits in rice genotypes, Department of Genetics and Plant Breeding, Bangladesh Agricultural University (BAU), Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh-2202, Bangladesh. *J Bangladesh Agri. Univ*. 2017;15(1):15-19.
 38. Sala M. Rice breeding for biofortification with high iron and zinc content in segregating population [M.Sc. (Ag.) Thesis]. Madurai: TNAU (Unpublished); c2012.
 39. Sangeetha LNE. Genetic variability studies for grain yield and grain quality traits in F₂ and F₃ populations of rice (*Oryza sativa* L.) [M.Sc. (Ag.) Thesis]. Madurai: TNAU (Unpublished); c2013.
 40. Singh AK, Sharma P, Singh PK. Studies on genetic characteristic of upland rice (*Oryza sativa* L.). *International Journal of Agriculture, Environment and Biotechnology*. 2013;6(4):515-520.
 41. Singh G, Singh A, Shrivastav SP. Genetic Variability, Heritability and Genetic Advance for Yield and its Contributing Traits in Garlic (*Allium sativum* L.). *Int. J Curr. Microbiol. App. Sci*. 2018;7(2):1362-1372.
 42. Singh SK, Bhati PK, Sharma A, Sahu V. Super hybrid rice in China and India: current status and future prospects. *Int. J Agric. Biol*. 2015;(17):221-232.
 43. Sivasubramanian S, Madhavamenon P. Genotypic and phenotypic variability in rice. *Madras Agric J* 1973;60:1093-1096
 44. Welsh JR. *Fundamentals of plant genetics and breeding.* John Willey and Sons. Inc., New York, 1981, 290.
 45. Zibae A. Rice: importance and future. *J. Rice Res*. 2013;1:e102.