

Original Research Article

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Studies on Variability, Heritability and Genetic Advance for Yield and its Related Traits in Rice (*Oryza sativa* L) Genotypes

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ABSTRACT

Keywords

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The panel comprises of landraces, improved varieties, interspecific derivatives (*Oryza glaberrima* × *Oryza sativa*), aromatic and japonica rice etc. were evaluated during Kharif 2019 used for studying genetic variability, heritability and genetic advance for yield and its related traits in rice. The analysis of variance of 12 different characters of 30 rice genotypes showed differences among the genotypes which revealed that there was genetic variation among the genotypes studied. Phenotypic coefficient of variance was found higher than genotypic coefficient of variance for all studied traits indicate the environmental influence on the expression of these traits. Among the studied traits broad sense heritability ranged from 47.00% (productive tillers) to 94.50% (grain width). The characters plant height, filled grains, total grains, grain length, grain width and grain ratio have high genetic advance as per cent of mean along with high heritability. High heritability with high genetic advance as per cent of mean indicates that these characters are largely controlled by additive gene action would be effective for selecting superior varieties.

Introduction

Rice (*Oryza sativa* L.) is an important crop, which supplies staple food for more than fifty percent of the global population. Among the most cultivated cereals in the world, rice ranks as second to wheat (*i.e.* 161.62 million hectares) (USDA, 2020). Over 90 percent of the world's rice is produced and consumed in the Asian Region by six countries (China, India, Indonesia, Bangladesh, Vietnam and Japan) comprising 80% of the world's

production and consumption (USDA, 2020). The genus, *Oryza* consists of mainly two cultivated species and 22 wild species. The cultivated species, *Oryza sativa* (2n=24 AA) is grown worldwide while *Oryza glaberrima* (2n=24 AA) is planted on a limited scale in West Africa.

The primary consideration to bring about genetic improvement of crop is the study of genetic variability. Assessment of genetic variability of any trait is pre-requisite for a

plant breeder to planning effective breeding programmes. Heritability is an index of the transmission of characters from parents to their offspring and it plays an important role in plant breeding. Genetic advance provides information on expected gain resulting from selection of superior individuals (Lingaiah, 2015). Heritability estimates along with genetic advance is more precise in predicting the genetic gain under selection than heritability alone (Adhikari *et al.*, 2018). The present study was undertaken to determine the extent variability, heritability and genetic advance for yield and its contributing traits in rice genotypes.

Materials and Methods

In the present study, a core set of 30 rice genotypes were chosen based on their yield component trait diversity under different subgroups (japonica, indica and aromatic) from around 250 genotypes available at the Department of Genetics and Plant Breeding, S.V. Agricultural College, Tirupati. The panel comprises of landraces, improved varieties, interspecific derivatives (*Oryza glaberrima* × *Oryza sativa*), aromatic and japonica rice etc were used for correlation analysis of yield contributing traits (Table 1).

The experiment was carried out at Wetland Farm, S.V. Agricultural College, Tirupati, ANGRAU during *Kharif*, 2019. The experiment was laid out in three replications in Randomized Block Design (RBD) with spacing of 20 cm × 15 cm and 2 rows of 4 m length. The agronomic management was done as per the standard recommendations. The phenotypic data was recorded for the twelve yield contributing traits from 5 plants per replication per genotype. The productive tillers (PT), plant height (PH), panicle length (PL), filled grains (FG), chaffy grains (CG), number of total grains (GN), percentage of spikelet fertility (SF), grain length (GL), grain

width (GW), grain ratio (GR), 1000-grain weight (TGW) and grain yield per plant (GY), were evaluated. For each trait, means of the replicates were used in the data analyses (Table 2). The data was subjected to INDOSTAST 9.2 software to estimate genetic co-efficient of variation (%) (GCV), phenotypic co-efficient of variation (%) (PCV), heritability (%) (broad sense), genetic advance and genetic advance as per cent of mean. The estimates for variability treated as per the categorization proposed by Sivasubramanian and Madhavamenon (1973) *i.e.*, low: less than 10 per cent, moderate: 10-20 per cent and high: more than 20 per cent. Heritability (Low: less than 30%, moderate: 30-60% and high: more than 60%) and genetic advance as mean per cent of mean estimates (Low: less than 10%, moderate: 10-20% and high: more than 20% according to criteria proposed by Johnson *et al.*, (1955).

Results and Discussion

The analysis of variance of 12 different characters of 30 rice genotypes showed differences among the genotypes which revealed that there was genetic variation among the genotypes studied (Table 3). This is in agreement with works of (Shahriar *et al.*, 2014; Singh *et al.*, 2014). This suggested the selection of superior and diverse genotypes for use in escalating the genetic yield potential of rice. Mean, along with the variability estimates such as the phenotypic coefficient of variation (PCV), the genotypic coefficient of variation (GCV), broad sense heritability, and genetic advance as percent of means are presented in Table 4. Phenotypic coefficient of variance was found higher than genotypic coefficient of variance for all studied traits indicate the environmental influence on the expression of these traits (Table 4). Similar results were presented by Rashid *et al.*, 2017; Gyawali *et al.*, 2018. The extent of the influence of growing

environment on observed traits is explained by the magnitude of the differences between GCV and PCV. Large difference between PCV and GCV indicate high environmental influence on the expression of particular traits. In the present study, phenotypic coefficient of variation in general were higher than genotypic coefficient of variation for all the traits indicating high environmental effect

on the expression of these traits except grain length (PCV 10.97%, GCV 10.38%) and grain width(PCV 14.41%, GCV 14.01%) which were less affected by environment for expression (Table 4). Thus, selection based on phenotypic performance for grain length and grain width would be effective to bring about considerable genetic improvement.

Table.1 List of rice genotypes used in the present study

S.No.	Genotype	Subspecies/Group
1	Abhaya	Indica
2	Aditya	Indica
3	AMO	Indica
4	Anjali	Indica
5	Azucena	Aromatic, Japonica
6	Badshabhog	Indica
7	Burma Black	Indica/Landrace
8	Daddiga	Indica
9	Disang	Indica
10	Haryana Basmati	Aromatic, Indica
11	HIM 799	Indica
12	Kesari	Indica
13	Krishna	Indica
14	Luit	Indica
15	Mrunalini	Indica
16	NL 1 (Nerica line 1)	<i>Og/os</i>
17	NL 16 (Nerica line 16)	<i>Og/os</i>
18	NL 3 (Nerica line 3)	<i>Og/os</i>
19	NL 9 (Nerica line 9)	<i>Og/os</i>
20	Numali	Indica
21	Pant Sugandh Dhan 15	Aromatic, Indica
22	Pathariya	Indica
23	RPBio 248	Indica/Indica wild
24	SannaJajula	Indica
25	Savithri	Indica
26	Sharbati	Indica
27	Solumpiket	Indica
28	Taramati	Aromatic, Indica
29	TKM 6	Indica
30	WAB450-24-32-P18-HB	<i>Og/os</i>

Og/Os: Oryza glaberrima/Oryza sativa

Table.2 Agronomic performance of rice genotypes

S.No.	Genotype	PT	PL(cm)	PH(cm)	FG	CG	GN	SF(%)	GL	GW	GR	TGW(g)	YP(g)
1	Abhaya	10.60	25.27	120.80	123.43	16.38	139.82	89.00	8.71	2.41	3.61	22.58	22.18
2	Aditya	10.60	21.93	81.20	58.58	11.60	70.18	84.00	8.81	2.77	3.18	24.69	7.90
3	AMO	11.58	24.07	101.60	158.73	34.00	192.73	83.00	8.16	2.55	3.21	21.40	25.49
4	Anjali	6.80	26.33	113.60	78.53	12.67	91.20	86.00	8.03	3.02	2.66	24.34	8.48
5	Azucena	15.00	26.13	98.42	125.58	23.92	149.50	84.00	10.41	2.91	3.57	27.71	29.47
6	Badshabhog	10.33	28.73	118.87	147.27	29.87	177.13	83.00	10.03	2.41	4.16	21.74	21.42
7	Burma Black	7.02	28.33	175.33	190.47	18.33	208.80	91.00	9.57	3.49	2.74	28.71	28.14
8	Daddiga	7.20	23.60	128.73	180.17	21.67	201.83	89.00	7.36	3.31	2.22	24.65	19.03
9	Disang	11.47	23.93	95.80	86.85	15.88	102.73	85.00	8.09	2.58	3.14	24.43	10.22
10	Haryana Basmati	8.93	22.07	87.87	137.60	29.87	167.47	82.00	8.48	2.17	3.91	15.00	16.64
11	HIM799	15.00	25.87	106.60	103.00	41.00	144.00	72.00	9.00	2.55	3.54	30.03	19.68
12	Kesari	15.53	21.13	97.60	148.80	16.67	165.47	90.00	8.14	2.53	3.22	18.54	29.93
13	Krishna	8.13	24.20	101.40	175.27	51.07	226.33	78.00	8.57	2.16	3.98	15.94	20.08
14	Luit	7.67	23.13	95.13	106.87	25.87	132.73	80.00	9.14	2.59	3.53	22.27	11.03
15	Mrunalini	10.87	28.73	130.47	189.49	49.89	239.37	79.00	9.44	2.39	3.95	22.57	32.71
16	NL1	10.67	22.87	82.47	78.87	34.87	113.73	69.00	9.80	2.45	3.99	22.78	13.59
17	NL16	9.87	25.67	109.20	101.55	28.80	130.35	78.00	9.75	2.52	3.87	26.21	19.91
18	NL3	10.53	26.13	92.67	89.25	29.50	118.75	76.00	10.36	2.68	3.87	25.35	10.74
19	NL9	11.00	26.07	82.33	75.00	27.00	102.20	74.00	10.11	2.52	4.01	26.15	14.27
20	Numali	7.00	24.33	129.60	221.63	30.58	252.22	88.00	8.14	2.81	2.90	21.23	22.39
21	Pant Sugandh 15	11.58	29.20	99.93	95.82	48.97	144.78	66.00	10.46	2.27	4.61	21.01	16.88
22	Pathariya	21.60	24.07	126.00	75.22	7.11	82.33	92.00	8.41	3.18	2.65	24.45	17.32
23	RPBio/248	12.11	27.53	117.27	128.27	23.93	152.20	84.00	8.29	2.79	2.97	26.77	25.01
24	Sanna Jajula	9.53	32.33	157.73	170.77	38.30	209.07	81.00	11.49	1.77	6.51	17.86	22.82
25	Savitri	7.13	22.93	93.73	140.17	42.28	182.44	77.00	9.16	2.66	3.45	23.22	21.63
26	Sharbati	13.16	25.60	109.27	126.10	25.75	151.85	83.00	9.69	2.11	4.72	20.40	18.78
27	Solumpiket	9.84	26.00	102.20	84.25	25.30	109.55	80.00	9.30	2.50	3.78	23.99	16.01
28	Taramati	9.53	22.00	100.87	170.27	59.67	229.93	74.00	7.71	2.29	3.37	16.08	13.11
29	TKM6	10.13	25.07	82.40	114.87	76.13	191.00	60.00	9.93	2.22	4.47	17.95	12.86
30	WAB-450	9.00	25.20	101.00	104.80	56.60	161.40	66.00	8.97	2.64	3.39	20.43	12.11
	Mean	10.65	25.28	108.00	126.25	31.78	158.04	80.00	9.12	2.57	3.64	22.62	18.66
	Lowest range	21.60	32.33	175.33	221.63	76.13	252.22	91.00	11.49	3.49	6.50	30.03	32.72
	Highest range	6.80	21.13	81.20	58.58	7.11	70.18	60.00	7.36	1.77	2.22	15.00	7.90
	C.V.	26.57	5.79	6.34	15.76	37.95	15.58	7.99	3.54	3.38	7.95	14.18	28.02
	ANOVA P-value	0.00**	0.00**	0.00**	0.00**	0.00**	0.00**	0.00**	0.00**	0.00**	0.00**	0.00**	0.00**

PT, Number of productive per plant; PL, Panicle length; PH, Plant height; FG, Number of filled grains per panicle; CG, Number of chaffy grains per panicle; GN, Total grains number per panicle; GL, Grain length(mm); GW, Grain width(mm); GL/GW, Grain length to width ratio; TGW,1000-grain weight; YP, Yield per plant and CV, Coefficient of variation

Table.3 Analysis of Variance (ANOVA) for yield and contributing traits

S.No	Trait	Replication	Treatment	Error	F ratio	P value
1	PT	39.39632	29.29591	8.00406	3.6601	0.000**
2	PL(cm)	3.612	18.81945	2.143035	8.7817	0.000**
3	PH(cm)	0.728007	1392.645	46.8082	29.7522	0.000**
4	FG	201.3338	5260.321	395.7462	13.2922	0.000**
5	CG	73.17824	752.1923	145.615	5.1656	0.000**
6	GN	56.29593	7037.815	606.5634	11.6028	0.000**
7	SF(%)	0.7054	1.8652	0.4094	4.5565	0.000**
8	GL(mm)	0.036743	2.791779	0.104347	26.7548	0.000**
9	GW(mm)	0.000724	0.39802	0.007573	52.5597	0.000**
10	GR	0.00772	1.940174	0.083727	23.1727	0.000**
11	TGW(g)	20.0928	42.55748	10.28684	4.1371	0.000**
12	YP(g)	25.9534	130.6254	27.34488	4.777	0.000**

PT, Number of productive per plant; PL, Panicle length; PH, Plant height; FG, Number of filled grains per panicle; CG, Number of chaffy grains per panicle; GN, Total grains number per panicle; GL, Grain length (mm); GW, Grain width (mm); GL/GW, Grain length to width ratio; TGW, 1000-grain weight; YP, Yield per plant

Table.4 Mean, phenotypic (V_p) and genotypic variance (V_g), phenotypic coefficient (PCV) and genotypic coefficient of variance (GCV), heritability (broad sense), genetic advance (GA) and genetic advance as percent of mean (GAM) for observed traits

S.No	Trait	Mean	V_g	V_p	Hbs(%)	GCV(%)	PCV(%)	GA	GAM(%)
1	PT	10.65	7.10	15.10	47.00	25.02	36.50	3.76	35.34
2	PL(cm)	25.28	5.56	7.70	72.20	9.32	10.98	4.13	16.32
3	PH(cm)	108.00	448.61	495.42	90.60	19.61	20.61	41.52	38.44
4	FG	126.25	1621.53	2017.27	80.40	31.90	35.58	74.37	58.91
5	CG	31.78	202.19	347.81	58.10	44.73	58.67	22.33	70.26
6	GN	158.04	2143.75	2750.31	77.90	29.30	33.18	84.21	53.28
7	SF(%)	80.00	0.50	0.90	54.20	8.70	11.81	10.60	13.20
8	GL(mm)	9.12	0.90	1.00	89.60	10.38	10.97	1.85	20.24
9	GW(mm)	2.57	0.13	0.14	94.50	14.01	14.41	0.72	28.06
10	GR	3.64	0.62	0.70	88.10	21.62	23.04	1.52	41.80
11	TGW(g)	22.62	10.76	21.04	51.10	14.50	20.28	4.83	21.36
12	YP(g)	18.66	34.43	61.77	55.70	31.44	42.12	9.02	48.35

PT, Number of productive per plant; PL, Panicle length; PH, Plant height; FG, Number of filled grains per panicle; CG, Number of chaffy grains per panicle; GN, Total grains number per panicle; GL, Grain length(mm); GW, Grain width(mm); GL/GW, Grain length to width ratio; TGW, 1000-grain weight; YP, Yield per plant

Higher phenotypic variation (PCV) was observed for productive tillers (36.50%), plant height (20.61%), filled grains (35.58%), chaffy grains (58.67%), total grains (33.18%), grain ratio (23.04), 1000-grain weight (20.28%) and grain yield (42.12%) where as panicle length (10.98%), spikelet fertility per cent (11.81%), grain length (10.97%) and grain width (14.41) showed medium phenotypic coefficient of variation (Table 4). Higher genotypic variation (GCV) was observed for productive tillers (25.02%), filled grains (31.90%), chaffy grains (44.73%), total grains (29.30%), grain ratio (21.62%) and grain yield (31.44%) while plant height (19.61%), grain length (10.38%), grain width (14.01%) and 1000-grain weight (14.50%) showed medium genotypic coefficient variation and plant length (9.32%) and spikelet fertility per cent (8.70%) showed low genotypic coefficient of variation (Table 4). High PCV on grain yield was also reported by Abebe *et al.*, (2017) which is in agreement with this present study. In general, high coefficient of variability shows scope of selection in favour of traits of interest and low coefficient of variability indicates the need for creation of variability and selection.

Among the studied traits broad sense heritability ranged from 47.00% (productive tillers to 94.50% grain width). Panicle length (72.20%), plant height (90.60%), field grains (80.40%), total grains (77.90%), grain length (89.60%), grain width (94.50%) and grain ratio (88.10%) were observed highly heritable traits. Productive tillers (47.00%) and chaffy grains (58.10%), spikelet fertility per cent (54.20%), 1000-grain weight (51.10%) and grain yield (55.70%) showed moderately heritable traits (Table 4). Similar report was reported by Gyawali *et al.*, (2018) for grain yield. High to medium level heritability for grain yield was reported by Gyawali *et al.*, (2018), Bandhi *et al.*, (2018), Abebe *et al.*, (2017) may be due to the influence of the environment on the yield as it is polygenic trait. Low heritability estimates might be due to the variation of environmental component involved for those traits and vice versa. High heritability estimated traits

indicated a high response to selection for particular traits. Estimated heritability itself alone is not very much useful because it includes the effect of both additive and non additive gene. The genetic advance is therefore a useful indicator to achieve expected result on the trait of interest of a population after selection. Genetic advance in percentage of mean give more precise result in comparison to only genetic advance. In the present study moderate genetic advance as percent of mean was estimated for panicle length (16.32%) and spikelet fertility per cent (13.20%) and other traits showed high genetic advances (>20%) in Table 4. This indicates most of observed characters among tested genotypes governed by additive gene action. The characters plant height, filled grains, total grains, grain length, grain width and grain ratio have high genetic advance as per cent of mean along with high heritability (Table 4). Similar reports were reported by (Dhurai *et al.*, 2018 and Anjaneyulu *et al.*, 2010) for plant height and total grains. High heritability with high genetic advance as per cent of mean indicates that these characters are largely controlled by additive gene action would be effective for selecting superior varieties.

In conclusion this study generally indicated that there were differences among the genotypes which revealed that there was genetic variation among the genotypes studied. In the present study, phenotypic coefficient of variation in general were higher than genotypic coefficient of variation for all the traits indicating high environmental effect on the expression of these traits except grain length (PCV 10.97%, GCV 10.38%) and grain width (PCV 14.41%, GCV 14.01%) which were less affected by environment for expression. Thus, selection based on phenotypic performance for grain length and grain width would be effective to bring about considerable genetic improvement. High heritability with high genetic advance as per cent of mean indicates that these characters are largely controlled by additive gene action would be effective for selecting superior varieties.

Conflicts of Interest

The authors declare no conflicts of interest

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