Genetic Variability Studies in Rice Genotypes

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Abstract

Seventy-four rice genotypes were evaluated to assess their genetic variability, heritability and genetic advance as per cent of mean. The analysis of variance revealed significant differences for all the characters under the study except number of productive tillers per plant, indicating the presence of high genetic variability among the genotypes. The genotypes per se performance revealed BPT 3130, BPT 3164, BPT 3264, BPT 3092, BPT 3275, BPT 2824, BPT 2954, BPT 3276, BPT 3095 and BPT 3178 exhibiting significant superiority over the check Samba Mahsuri for the characters *viz.*, grain yield per plant, test weight and panicle length. The high estimates of GCV and PCV were observed for grain yield per plant. High heritability coupled with high expected genetic advance as per cent of mean was observed for test weight and grain yield per plant suggesting that selection for the improvement of these traits may be rewarding.

Introduction

Rice (*Oryza sativa*, 2n=2x=24) occupies a notable position among food grains by directly feeding the majority of people more than any other crop. The demand for rice production is increasing day by day because of the increase in the number of rice consumers. To meet this demand, it is necessary to enhance the production and productivity of rice cultivars. The success of any breeding programme depends on the degree of variability present in the germplasm. Before initiating any breeding programme, knowledge on the nature and magnitude of genetic variation governing the inheritance of characters and as well as adopting appropriate selection techniques is essential for genetic improvement. Genetic parameters such as Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) are useful in detecting the amount of variability present in the population (Idris *et al.,* 2012). It is very difficult to judge whether detected variability is heritable or not. Heritability indicates the extent of transmissibility of a character into future generations. Heritability can be either broad sense or narrow sense. Broad sense heritability is the relative magnitude of genotypic and phenotypic variances for the traits and has a predictive role in selection procedures (Allard, 1960). This gives an idea of total variation ascribed to genotypic effects, which are the exploitable portion of variation (Mba and Dixon, 1995). The magnitude of variation due to the heritable component is very important because it would be a guide for the selection of parents for crop improvement (Dutta *et al.,* 2013) and also plays a vital role to plan an efficient breeding program for the genetic improvement of quantitative traits (Seyoum *et al.,* 2012). The estimate of heritability alone is

not very much useful because it includes the effect of both additive and non-additive genes. The genetic advance is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population (Vanniarajan *et al.,*1996).

Identification of effective selection criteria is very important in any breeding programme for effective yield improvement. The present investigation was undertaken in this context to elucidate information on variability, heritability and genetic advance in rice genotypes for utilization in the further breeding programme.

Materials and Methods

The material for the present study consists of 74 rice genotypes including yield check Samba Mahsuri. These genotypes were evaluated in an augmented randomized complete block design during *kharif,* 2021 at Agricultural College Farm, Bapatla and Andhra Pradesh. Observations were recorded for the characters, plant height (cm), number of productive tillers per plant, panicle length (cm), spikelet fertility (%), test weight (g), grain yield per plant (g) and days to 50 per cent flowering.

Statistical analysis

The mean data of all the characters were subjected to analysis of variance (ANOVA) based on the model proposed by Federer (1956) using Windostat Version 9.3. Different genetic parameters such as genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as per cent of mean were estimated by using the following formula.

Estimation of genotypic and phenotypic variances

The genotypic and phenotype variances were calculated as per the formulae proposed by Burton and Devane (1953).

Phenotypic standard deviation (σp) =	$\sqrt{\sigma^2 p} = \sqrt{\sigma^2 g} + \sqrt{\sigma^2 e}$

$$GCV = \frac{\text{Genotypic standard deviation } (\sigma g)}{\text{General mean } (\bar{x})} \times 100$$

$$PCV = \frac{\text{Phenotypic standard deviation } (\sigma p)}{\text{General mean } (\bar{x})} \times 100$$

GCV and PCV values were categorized as low (<10%), moderate (10-20%) and high (>20%) (Subramaniam and Menon, 1973).

Estimation of heritability (broad sense)

Heritability in broad sense (h^2) was computed and categorized as per the suggestions of Hanson *et al.,* (1956) and Johnson *et al.,* (1955) respectively.

$$GCV = \frac{\text{Genotypic variance } (\sigma^2 g)}{\text{Phenotypic variance } (\sigma^2 p)} \times 100$$

Heritability was classified as low (below 30%), medium (30-60%) and high (above 60%) as suggested by Johnson *et al.,* (1955).

Estimation of genetic advance

From the heritability estimates, the genetic advance (GA) was calculated by the following formula given by Lush (1940) and Johnson *et al.,* (1955).

Genetic Advance (GA) = K x σ_p x $h^2_{(b)}$

Where,

K=Selection differential at 5% selection intensity which accounts to a constant value of 2.06

$h^2_{(b)}$ = Heritability in broad sense.

σ_p = Phenotypic standard deviation.

Estimation of Genetic advance as per cent of mean (GAM)

Genetic advance as per cent of mean was calculated as per the formula

$$GAM = \frac{\text{Genetic advance}}{\text{General mean } (\bar{x})} \times 100$$

The degree of genetic advance as per cent of mean was classified as suggested by Johnson *et al.,* (1955) as low (<10%), moderate (10-20%) and high (>20%).

Results and Discussions

Analysis of variance

The ANOVA results indicated significant variability among the genotypes for all the characters studied except for the trait number of productive tillers per plant. Similar results were reported by Chandramohan *et al.,* (2016). Analysis of variance for the yield and yield component traits was furnished in **Table 1**.

Table 1: Analysis of variance for yield and yield component traits

Sources of variation	d. f	DFF	PH	NPT	PL	SF	TW	GYP
		Mean sum of squares						
Blocks	4	3.576	20.401	1.175	0.376	4.09	0.066	1.591
Entries	73	94.345 **	143.158 **	4.296	4.262 **	26.372 **	9.456 **	45.571 **
Genotypes	69	49.023 **	82.952 **	3.962	3.952 **	24.139 **	5.014 **	45.524 **
Checks	3	797.333 **	1138.847 **	6.467	3.729 *	47.576 **	110.531 **	53.010 **
Checks vs Genotypes	1	1112.584 **	1310.292 **	20.829 *	27.280 **	116.870 **	12.714 **	26.518 *
Error	12	3.375	8.573	2.342	1.05	4.944	0.089	3.421

*Significant at 5% level; **Significant at 1% level; DFF: Days to 50% flowering; PH: Plant hieght; NPT No. of productive tillers; PL: Panicle length; SF: Spikelet fertility %; TW: Test weight; GYP: Grain yield for plot.

Mean performance

Mean values of the seventy-four genotypes along with the standard yield check Samba Mahsuri for the studied seven quantitative characters were presented in **Table 2**. Genotype TN1 was found earliest in flowering (85 days) suggesting that this genotype can be used as a donor in the hybridization programme for evolving short-duration rice variety. Genotype Samba Mahsuri and BPT 3068 were recorded as the shortest and tallest, respectively. The highest mean performance for productive tillers per plant was observed in BPT 2808 (15 tillers) followed by BPT 2824 (13 tillers). Genotype BPT 3137 (29.80 cm) exhibited the highest mean performance for panicle length. The maximum grain yield per plant was observed 41.71 g by BPT 2854 indicating that these genotypes can be used in a hybridization programme to achieve a desirable increment in yield. A critical analysis on the mean performance of the genotypes studied revealed that BPT 3130, BPT 3164, BPT 3264, BPT 3092, BPT 3275, BPT 2824, BPT 2954, BPT 3276, BPT 3095, BPT 3178 exhibited significant superiority over the check Samba Mahsuri for the characters grain yield per plant, test weight, panicle length and were also on par for spikelet fertility and productive tillers per plant.

Table 2: Mean performance of rice genotypes for yield and yield components

Sl. No	Genotypes	DFF	PH	NPT	PL	SF	TW	GYP
1	BPT 1235	90	101.90	7	24.04	88.47	18.83	24.30
2	BPT 2231	116	98.40	10	25.30	93.21	19.39	26.81
3	BPT 2295	122	109.80	12	22.26	88.54	15.13	30.55
4	BPT 2411	113	116.00	8	25.25	79.69	19.56	23.01
5	BPT 2595	121	102.20	8	22.88	92.42	14.81	18.25
6	BPT 2620	102	108.40	7	23.10	90.07	16.01	20.88
7	BPT 2677	98	103.00	8	24.90	85.97	21.44	25.62
8	BPT 2764	121	105.80	8	23.50	88.72	16.48	15.54

Sl. No	Genotypes	DFF	PH	NPT	PL	SF	TW	GYP
9	BPT 2766	110	104.40	8	22.10	89.75	14.93	19.61
10	BPT 2776	116	107.80	10	22.90	94.39	16.03	27.05
11	BPT 2782	114	95.80	8	20.88	96.23	15.14	20.75
12	BPT 2808	112	101.00	15	21.80	87.82	15.81	30.52
13	BPT 2824	110	109.80	13	23.88	86.76	16.17	34.82
14	BPT 2846	111	101.40	6	22.30	84.45	15.28	32.12
15	BPT 2848	109	117.80	8	20.04	87.79	14.38	24.65
16	BPT 2849	111	111.00	8	24.28	79.60	19.38	16.12
17	BPT 2854	112	111.20	12	21.00	92.61	20.28	41.71
18	BPT 2863	114	105.00	9	23.40	91.82	16.35	29.08
19	BPT 2950	110	115.60	5	22.00	86.63	19.80	13.65
20	BPT 2954	96	130.80	9	22.90	93.65	18.68	34.48
21	BPT 2958	108	105.60	7	20.90	82.92	19.53	23.50
22	BPT 3032	101	104.40	8	22.20	91.08	22.19	22.61
23	BPT 3033	115	106.00	10	20.50	86.10	15.00	20.14
24	BPT 3061	110	117.60	8	24.20	94.60	15.57	19.34
25	BPT 3068	110	137.20	9	26.30	93.02	16.93	19.72
26	BPT 3074	95	114.80	9	21.90	92.94	16.94	30.51
27	BPT 3081	106	103.00	6	20.50	90.09	16.26	18.33
28	BPT 3086	110	122.20	5	28.70	86.29	16.57	16.86
29	BPT 3092	90	125.40	10	24.70	93.14	22.28	36.89
30	BPT 3095	114	118.80	8	24.80	96.32	21.19	34.04
31	BPT 3111	106	110.00	8	24.80	88.21	19.08	27.29
32	BPT 3113	107	104.20	9	26.50	84.07	18.13	32.16
33	BPT 3114	110	117.80	9	23.90	93.59	15.84	20.92
34	BPT 3115	110	97.60	12	21.70	94.67	14.58	30.71
35	BPT 3118	111	98.20	11	21.80	79.31	14.61	30.28
36	BPT 3120	110	93.60	9	21.40	86.53	20.02	23.50
37	BPT 3121	106	101.00	11	22.25	88.29	15.61	28.62
38	BPT 3129	110	109.40	7	22.38	81.92	16.55	24.04
39	BPT 3130	110	111.60	11	23.70	91.74	17.04	41.02
40	BPT 3133	109	115.40	10	22.80	94.07	15.78	27.01
41	BPT 3135	102	128.00	8	24.30	91.68	16.96	27.94
42	BPT 3136	107	116.20	7	24.10	87.02	17.85	26.95
43	BPT 3137	114	132.40	6	29.80	79.31	14.59	22.32
44	BPT 3145	119	107.60	7	25.10	91.73	23.61	20.33
45	BPT 3147	114	116.60	9	22.20	85.71	14.60	24.97
46	BPT 3148	110	109.60	6	21.90	85.40	19.60	28.08
47	BPT 3150	110	102.80	7	25.40	89.78	18.02	23.06
48	BPT 3151	101	106.80	9	22.30	76.74	16.06	32.93

Sl. No	Genotypes	DFF	PH	NPT	PL	SF	TW	GYP
49	BPT 3159	114	112.80	10	25.10	91.97	18.53	29.28
50	BPT 3164	105	105.20	12	22.75	87.87	20.40	40.86
51	BPT 3168	110	116.40	7	22.63	85.29	16.92	18.54
52	BPT 3170	106	114.20	7	22.60	85.54	19.32	23.61
53	BPT 3172	96	104.20	7	21.30	88.86	14.34	20.33
54	BPT 3178	106	100.60	11	24.20	91.53	18.90	33.56
55	BPT 3208	108	107.40	8	21.60	93.59	17.29	21.48
56	BPT 3244	105	108.60	10	22.60	90.76	15.54	27.54
57	BPT 3260	111	112.40	11	25.00	76.82	16.99	31.80
58	BPT 3261	113	111.40	6	26.83	85.70	19.30	15.91
59	BPT 3262	98	122.60	6	26.50	89.62	21.03	18.20
60	BPT 3263	112	126.00	9	25.70	90.80	17.68	23.03
61	BPT 3264	96	115.00	11	23.60	91.85	17.03	37.25
62	BPT 3269	98	109.40	8	21.70	95.64	14.69	20.36
63	BPT 3270	118	118.20	8	28.60	87.02	17.85	22.92
64	BPT 3274	118	116.00	6	25.30	88.73	18.89	27.61
65	BPT 3275	119	114.40	8	22.20	76.85	15.63	36.32
66	BPT 3276	113	116.40	7	23.60	94.13	19.19	34.25
67	BPT 3277	108	100.60	7	21.20	82.35	17.79	20.09
68	BPT 3279	106	108.20	10	24.20	93.41	16.42	25.33
69	BPT 3291	110	101.00	7	22.90	89.78	16.35	21.21
70	BPT 4358	117	93.50	7	23.00	82.38	13.64	12.87
71	Improved Samba Mahsuri	96	92.06	9	21.84	87.42	13.99	19.87
72	Krishnaveni	108	97.56	8	22.82	90.14	19.29	24.83
73	TN 1	85	123.46	10	22.86	92.60	24.43	25.87
74	Samba Mahsuri (Yield Check)	113	91.66	11	21.06	94.23	15.45	27.40
	Min	85	91.66	5	20.04	76.74	13.64	12.87
	Max	122	137.20	15	29.80	96.32	24.43	41.71
	Mean	**108**	**109.87**	**9**	**23.40**	**88.65**	**17.46**	**25.73**
	CV %	6.99	8.62	13.60	8.70	5.61	13.64	15.68
	C.D. (0.05)	2.53	4.03	2.11	1.41	3.06	0.41	2.55

Variability, Heritability and Genetic advance as per cent of mean

The estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) and genetic advance as per cent of mean (GAM) are presented in **Table 3** and **Figures 1 and 2**. The results are discussed here under. GCV and PCV are high for grain yield per plant (22.66% and 23.77%) indicating the existence of sufficient variation among the genotypes for potential yield improvement through selection. High GCV,

PCV for grain yield per plant were also observed in the findings of Nithya *et al.,* (2020), Bhargava *et al.,* (2021), Chamar *et al.,* (2021), Gupta *et al.,* (2021) and Priyanka *et al.,* (2023). The traits like days to 50% flowering (5.84% and 5.59%), plant height (7.52% and 7.04%), panicle length (7.86% and 6.54%), spikelet fertility (5.12% and 4.46%) exhibited low phenotypic and genotypic coefficient of variation indicating the presence of less genetic variability as a result of which there is less scope for selection. Similar results were observed by Mohan *et al.,* (2016), Jan *et al.,* (2017), Adhikari *et al.,* (2018), Nithya *et al.,* (2020), Bhargava *et al.,* (2021) and Teja *et al.,* (2023).

High estimates of heritability combined with high genetic advance was observed for test weight (97.83%, 23.40) and grain yield per plant (90.90%, 44.51) provides evidence that this was under the control of additive gene effects and selection may be effective. Similar results were also reported earlier by Anyaoha *et al.,* (2018), Nithya *et al.,* (2020), Chamar *et al.,* (2021), Bhargava *et al.,* (2021), Gupta *et al.,* (2021) and Priyanka *et al.,* (2023). Similarly high heritability coupled with moderate genetic advance was observed for days to 50% flowering (91.65%, 11.03), plant height (87.57%, 13.57), panicle length (69.17%, 11.20) indicating the preponderance of additive and non-additive gene actions in the expression of this trait. The results were in conformity with Gampala *et al.,* (2015), Mohan *et al.,* (2016), Adhikari *et al.,* (2018) and Bhargava *et al.,* (2021) whereas spikelet fertility (75.91%, 8.01) had exhibited high heritability combined with low genetic advance as per cent of mean due to the favourable influence of environment rather than the genotype, indicating the possibility of improvement of the trait through heterosis breeding rather than simple selection. High heritability coupled with low genetic advance as per cent of mean for spikelet fertility was reported by Parimala *et al.,* (2021).

Conclusion

In a nutshell, based on the results obtained, the studied rice genotypes showed adequate variability. High PCV and GCV were recorded for grain yield per plant indicating the existence of large variation among the genotypes for potential yield improvement through selection. High heritability coupled with high genetic advance as per cent of mean was observed for the traits test weight and grain yield per plant revealing that these traits are governed by additive gene action and therefore selection can be practiced based on phenotypic performance.

Table 3: Variability, heritability and genetic advance as per cent of mean for yield and yield component traits

| S. No.	Character	Coefficient of variation		Heritability (%)	Genetic advance as Per cent of mean
		PCV (%)	GCV (%)		
1	Days to 50 per cent flowering	5.84	5.59	91.65	11.03
2	Plant height	7.52	7.04	87.57	13.57
3	Number of productive tillers	22.39	13.43	35.97	16.58
4	Panicle length	7.86	6.54	69.17	11.20
5	Spikelet fertility	5.12	4.46	75.91	8.01
6	Test weight	11.61	11.49	97.83	23.40
7	Grain yield per plant	23.77	22.66	90.90	44.51
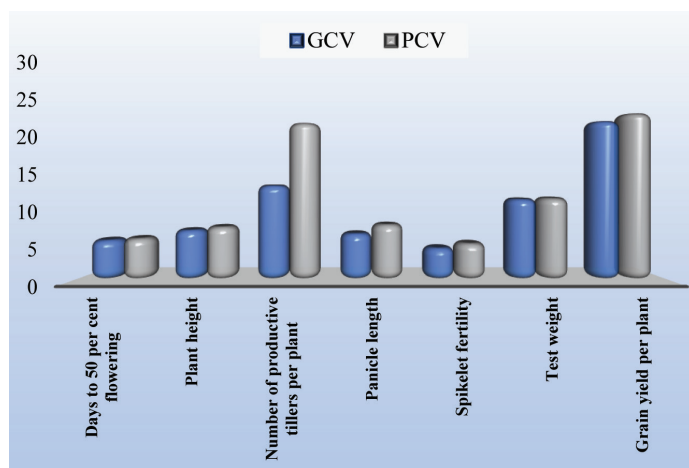
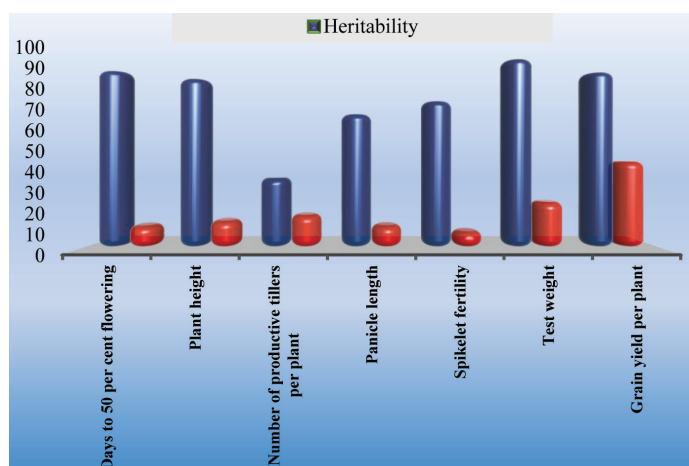**Figure 1: Variability parameters for yield and yield component traits**

Figure 2: Heritability and Genetic advance as per cent mean for yield and yield component traits

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