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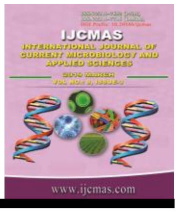

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Genetic Studies of Yield Variation and Association Analysis in Rice (*O. sativa* L.) Genotype

Laxmi Singh* and Prabha R. Chaudhari

Department of Genetics and Plant Breeding, College of Agriculture,
IGKV, Raipur (C.G.)-492012, India

**Corresponding author*

ABSTRACT

The present investigation consists of 80 rice genotypes with seven checks and the experiment was conducted during *Kharif*-2017 in Randomized Block Design with two replications. The data were recorded for twelve quantitative characters to estimate the variability, heritability, genetic advance and genetic advance as percentage and association analysis. The high PCV and GCV values was obtained for grain yield per plant, effective tillers per plant, total tillers per plant, filled grains per plant, total grains per plant, flag leaf area, biological yield per plant and low PCV and GCV was observed for spikelet fertility per panicle. The traits filled grains per panicle, days to 50% flowering, test weight, plant height, flag leaf area and grain yield per plant had high heritability along with high genetic advance as per cent of mean indicate that these characters attributable to additive gene effects which are fixable and possibilities of effective selection for the improvement of these characters. The harvest index, biological yield per plant, effective tillers per plant, filled grains per panicle, total tillers per plant, total grains per panicle and spikelet fertility% showed positive and highly significant or significant association with grain yield per plant. The highest positive direct contribution on grain yield per plant at genotypic level was expressed by effective tillers per plant and spikelet fertility%, while high positive direct contribution on test weight and total grains per panicle.

Keywords

PCV, GCV,
heritability,
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Introduction

Rice is a cereal grain and the most widely consumed staple food for a large part of the world's human population, especially in Asia. Rice provides 21% energy and 15% of per capita protein of global human (Maclean *et al.*, 2002). In a rice improvement programme, it is the Germplasm, which virtually determine the success and nature of end product. The development of superior rice population involved the intelligent use of available genetic variability both indigenous as well as exotic to cater the need of various farming situations of rice. The grain yield is the primary trait targeted for improvement of rice productivity in both favourable and unfavourable environments from its present level. Germplasm lines have a high level of genetic heterogeneity that comprise of the unique source for gene of high adaptability. The success of breeding programme regarding crop improvement for trait of interest is possible through proper evaluation of genetic divergence genotype for development of superior genotype.

Knowledge on the genetic architecture of genotypes is necessary to formulate efficient breeding methodology. It is essential to find out the relative magnitude of additive and non additive genetic variances, heritability and genetic gain with regard to the characters of concern to the breeder. The presence and magnitude of genetic variability in a gene pool is the pre-requisite of a breeding programme. Correlation and path analysis establish the extent of association between yield and its components and also bring out relative importance of their direct and indirect effects, thus giving idea about their association with grain yield. Therefore, the present study has been undertaken to determine the estimates of variability, heritability genetic advance as per cent of mean and association analysis for grain yield and its component traits in 80 rice genotype.

Materials and Methods

The present investigation was carried out during *kharif*- 2017 at Research cum Instructional farm of IGKV, Raipur. The experiment material consisted 80 rice genotypes with seven checks and trials were laid out in a Randomized Block Design with two replications with the spacing of 20 x 15 cm and the recommended cultural practices were followed days to 50% flowering, Plant height, total tillers per plant, effective tillers per plant, flag leaf area, panicle length, number of filled grains per panicle, total number of grains per panicle, spikelet fertility%, test weight, biological yield per plant, grain yield per plant and harvest index were recorded.

The variability was estimated as per procedure for analysis of variance suggested by Panse and Sukhatme (1967) PCV and GCV were calculated by the formula given by Burton (1952), heritability in broad sense (h2) by Burton and De Vane (1953) and genetic advance i.e. the expected genetic gain were calculated by using the procedure given by Johnson *et al.*, (1955). Correlation coefficient was computed as per the procedure outlined by Karl Pearson (1932) and path coefficient analysis was carried out as suggested by Dewey and Lu (1959).

Results and Discussion

Genetic variability

Analysis of variance revealed highly significant differences among the genotypes for all the characters, indicating presence of high variability among the rice genotype (Table 1). Thus, there is ample scope for selection of different quantitative and qualitative characters for rice improvement.

For all the traits studied, high estimates of PCV were observed than GCV indicating the role of environmental forces in the inheritance of these traits. Similar findings were earlier reported by Vanisree *et al.*, (2013), Ketan and Sarkar (2014).

The Genotypic Coefficient of Variation (GCV) provides a measure to compare genetic variability present in various quantitative characters. In this study, the highest values of GCV were recorded in grain yield per plant (36.39%), filled grains per panicle (30.51%), effective tillers per plant (30.47%), total tillers per plant (29.54%), total grains per panicle (26.59%), biological yield per plant (24.16%) and flag leaf area (22.21%) whereas the moderate values were found in test weight (18.89%), plant height (17.15), panicle length (11.56%) and days to

50% flowering (10.49%) and low GCV was found in spikelet fertility % (6.53%). Similar results were reported by Das (2015) and Chandramohan *et al.*, (2016). The phenotypic (Vp) and genotypic (Vg) variation were obtained for different characters are presented in Table 2.

Heritability is a measure of extent of phenotypic variation caused by the action of genes. The major function of heritability estimates is to provide information on transmission of characters from the parents to the progeny. In the present study high heritability was observed for all the twelve traits. The highest heritability value (97.32%) was found in filled grains per plant followed by days to 50% flowering (196.34%) test weight (95.13%), plant height (94.41%) flag leaf area (93.37%) and grain yield per plant (91.87%). Similar results were reported by Ketan and Sarkar (2014).

The genetic advance as percent of mean was recorded highest in grain yield per plant (71.83%) followed by filled grains per panicle (61.69%), effective tillers per plant (58.38%) and total tillers per plant (57.04), whereas low value was recorded in spikelet fertility% (12.25%).

The estimate of heritability alone is not very much useful on predicting resultant effect for selecting the best individual because it includes the effect of both additive gene as well as non additive gene. High genetic advance only occurs due to additive gene action (Panse, 1967). So heritability coupled with genetic advance would be more useful than heritability alone. In this study, both heritability and genetic advance are considered, it is observed that total grain per panicle, filled grain per panicle, plant height and harvest index showed high heritability coupled with high genetic advance. Similar result was reported by Sharma *et al.*, (2014). The characters showing high heritability along with moderate or low genetic advance can be improved by intermating superior genotypes of segregating population developed from combination breeding.

Genotypic and phenotypic correlation coefficient

Correlation studies help the plant breeder during selection and provide the understanding of yield components. Genotypic correlations were higher than phenotypic ones in magnitude for all the characters. The estimates of phenotypic and genotypic correlation coefficients are presented in Table 3.

At both genotypic and phenotypic level days to 50% flowering showed positive and highly significant relationship with biological yield per plant and panicle length. Similar results were earlier reported by Patel *et al.*, (2014) for biological yield, Aditya and Anuradha (2013) for panicle length.

Plant height exhibited positive and significant relationship with test weight and panicle length. Similar findings were earlier reported by Dhurai *et al.*, (2016) and Harsha *et al.*, (2017) for panicle length, Babu *et al.*, (2012) and Ramya *et al.*, (2017) for test weight. Negative and highly significant relationship of plant height was observed with total grains per panicle, effective tillers per plant, total tillers per plant and filled grains per panicle.

Total tillers per plant exhibited positive and highly significant relationship with effective tillers per plant, grain yield per plant, harvest index, biological yield per plant, filled grains per panicle and total grains per panicle. But negative and highly significant relationship with plant height. Effective tillers per plant exhibited positive and highly significant or significant relationship with total tillers per plant, grain yield per plant, harvest index, biological yield per plant, filled grain per panicle and total grains per panicle and spikelet fertility %. But negative and highly significant relationship with plant height. Similar findings were earlier reported by Yogameenakshi *et al.,* (2004) by harvest index, Kalyan *et al.,* (2017) for effective tillers per plant and grain yield per plant.

Flag leaf area exhibited positive and highly significant relationship with panicle length. Panicle length exhibited positive and highly significant or significant relationship with flag leaf area, days to 50% flowering, plant height and test weight. Filled grains per panicle exhibited positive and highly significant relationship with total grains per panicle, grain yield per plant, harvest index, biological yield per plant, and effective tillers per plant, total tillers per plant and spikelet fertility%. But negative and highly significant relationship with plant height. Total grains per panicle exhibited positive and highly significant relationship with filled grains per panicle, grain yield per plant, harvest index, biological yield per plant, and effective tillers per plant and total tillers per plant. But negative and highly significant relationship with plant height. Spikelet fertility% exhibited positive and highly significant or significant relationship with filled grains per panicle, harvest index, grain yield per plant and effective tillers per plant. Test weight exhibited positive and significant genotypic correlation with plant height and panicle length and positive and significant phenotypic correlation with plant height.

Biological yield per plant exhibited positive and highly significant relationship with grain yield per plant, total grains per panicle, effective tillers per plant, filled grains per panicle, total tillers per plant, days to 50% flowering, harvest index. Harvest index exhibited positive and highly significant relationship with grain yield per plant, filled grains per panicle, effective tillers per plant, total grains per panicle, total tillers per plant, biological yield per plan and spikelet fertility%.

Table.1 Analysis of Variance (ANOVA) for yield and yield attributing traits in rice

S. No.	Character	Replication	Treatment	Error
1	Days to 50% flowering	7.87	167.06**	3.11
2	Plant height(cm)	30.29	902.05**	25.96
3	Total tillers per plant	1.66	18.94**	1.02
4	Effective tillers per plant	3.68	17.30**	1.10
5	Flag leaf area(cm)	0.02	66.13**	2.27
6	Panicle length(cm)	0.02	15.22**	1.01
7	Filled grains per panicle	73.32	3129.73**	42.59
8	Total grains per panicle	258.32	3159.74**	242.74
9	Spikelet fertility%	12.70	75.35**	6.96
10	Test Weight(g)	0.34	0.01**	0.01
11	Grain yield per plant(g)	16.40	107.18**	4.54
12	Biological yield per plant(g)	25.44	125.46**	7.46
13	Harvest index (%)	46.17	320.73**	36.36

* & ** represent significant levels at 5% and 1% respectively.

Table.2 Genotypic and phenotypic variance, genotypic coefficient and phenotypic coefficient of variance, broad sense heritability, genetic advance and genetic advance as per cent of mean for all the traits

S. No.	Character	Mean	Range	Vg	Vp	Ve	PCV(%)	GCV(%)	h2 (bs) (%)	GA	GA as % of mean
1	Days to 50% flowering	86.28	63-108	81.97	85.08	3.11	10.69	10.49	96.34	18.31	21.21
2	Plant height (cm)	122.03	79-172.4	438.05	464.00	25.96	17.65	17.15	94.41	41.89	34.50
3	Total tillers per plant	10.13	5.33-17.67	8.96	9.98	1.02	31.18	29.54	89.75	5.84	57.04
4	Effective tillers per plant	9.34	5-17	8.10	9.20	1.10	32.47	30.47	88.07	5.50	58.38
5	Flag leaf area (cm)	25.44	45.46-13.57	31.93	34.20	2.27	22.98	22.21	93.37	11.25	44.24
6	Panicle length (cm)	23.07	16.6-37.5	7.11	8.12	1.01	12.35	11.56	87.58	5.14	22.25
7	Filled grains per panicle	128.79	31.33-265	1543.57	1586.16	42.59	30.92	30.51	97.32	79.84	61.69
8	Total grains per panicle	143.63	34.66-273.33	1458.50	1701.24	242.74	28.72	26.59	85.73	72.84	50.53
9	Spikelet fertility%	89.51	67.88-99.58	34.20	41.16	6.96	7.17	6.53	83.09	10.98	12.25
9	Test weight (g)	2.15	1.11-3.28	0.17	0.17	0.01	19.37	18.89	95.13	0.82	37.83
10	Grain yield per plant (g)	19.69	6.33-40.4	51.32	55.86	4.54	37.96	36.39	91.87	14.15	71.83
11	Biological yield per plant(g)	31.79	12-55.2	59.00	66.46	7.46	25.64	24.16	88.77	14.91	46.86
12	Harvest index (%)	61.43	28.12-87.94	142.19	178.55	36.36	21.75	19.41	79.63	21.92	35.58

Vp-Genotypic variance, Vp- Phenotypic variance, GCV- Genotypic coefficient of variance, PCV-Phenotypic coefficient of variance, h2 (bs)-Broad sense heritability, GA- Genetic advance

Table.3 Estimation of genotypic and phenotypic correlation coefficient among 13 characters in rice genotype

		PH	TTP	ETP	FLA	PL	FGP	TGP	SF	TW	BYP	HI	GYP
DFF	g	0.060	0.004	0.040	0.073	0.303**	0.153	0.173	-0.082	-0.151	0.364**	-0.086	0.139
	p	0.058	-0.016	0.023	0.062	0.279**	0.148	0.166	-0.073	-0.139	0.358**	-0.082	0.141
PH	g		-0.417**	-0.419**	0.011	0.257*	-0.293**	-0.307**	0.033	0.230*	-0.077	-0.173	-0.146
	p		-0.372**	-0.365**	0.011	0.224*	-0.283**	-0.300**	0.040	0.215*	-0.061	-0.143	-0.132
TTP	g			0.998**	-0.048	-0.099	0.374**	0.342**	0.209	-0.161	0.502**	0.513**	0.637**
	p			0.980**	-0.051	-0.115	0.347**	0.321**	0.166	-0.164	0.429**	0.446**	0.574**
ETP	g				-0.048	-0.101	0.411**	0.38**	0.217*	-0.183	0.527**	0.539**	0.667**
	p				-0.055	-0.118	0.376**	0.348**	0.179	-0.176	0.46**	0.456**	0.601**
FLA	g					0.396**	0.132	0.147	-0.046	0.041	0.043	-0.061	-0.014
	p					0.35**	0.124	0.139	-0.029	0.040	0.037	-0.059	-0.019
PL	g						0.012	-0.001	0.039	0.217*	0.129	-0.188	-0.054
	p						0.006	-0.011	0.051	0.207	0.112	-0.145	-0.046
FGP	g							0.972**	0.336**	-0.080	0.517**	0.552**	0.641**
	p							0.969**	0.315**	-0.080	0.478**	0.474**	0.598**
TGP	g								0.105	-0.093	0.529**	0.533**	0.634**
	p								0.085	-0.095	0.487**	0.462**	0.591**
SF	g									0.116	0.100	0.288**	0.239*
	p									0.109	0.077	0.192	0.183
TW	g										0.041	0.158	0.113
	p										0.056	0.140	0.121
BYP	g											0.346**	0.814**
	p											0.243*	0.782**
HI	g												0.82**
	p												0.778**

* & ** represent significant levels at 5% and 1% respectively.

DFF-Days to 50% flowering, PH-Plant height, TTP-Total tillers per plant, ETP-Effective tillers per plant, FLA-Flag leaf area, PL-Panicle length, FGP-Filled grains per panicle, TGP- Total grains per panicle, TW-Test weight, BYP-Biological yield per plant, HI-Harvest index, GYP-Grain yield per plant

The grain yield per plant exhibited positive and highly significant or significant correlation with harvest index, biological yield per plant, effective tillers per plant, filled grains per panicle, total tillers per plant, total grains per panicle and spikelet fertility%. This indicated that simultaneous selection of all these characters was important for yield improvement. But negative and non significant relationship with plant height, panicle length and flag leaf area. Similar findings were reported by Rangare *et al.,* (2012) for harvest index and biological yield per plant; Sarawgi *et al.,* (2014), Mustafa and Elsheikh (2007) for panicle length; Dhurai *et al.,* (2016) for plant height, flag leaf area and panicle length. Basavaraja *et al.,* (2011) reported that productive tillers per plant showed significant positive correlation with grain yield.

Path coefficient analysis

Correlation gives only the relation between two variables, whereas path coefficient analysis allows separation of the direct effect and their indirect effects through other attributes by partitioning the correlations. Path-coefficient computed on the basis of genotypic correlation is given in Table 3. The highest positive direct contribution on grain yield per plant at genotypic level was expressed by effective tillers per plant and spikelet fertility%, while high positive direct contribution on test weight and total grains per panicle. The residual effect at genotypic level was -0.068. Similar findings were reported by Chouhan *et al.,* (2014) and Rashmi *et al.,* (2017) for effective tillers per plant; Dhurai *et al.,* (2016) and Rashmi *et al.,* (2017) for test weigh and total grains per panicle.

Studies on correlation and path co-efficient analysis revealed the importance of productive tillers per plant, spikelet fertility% and total grains per panicle which showed highly significant positive correlation and positive direct effect with grain yield per plant, these characters can be used as selection criteria for effective yield improvement.

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