



## Research Article

# GENETIC PARAMETERS AND ASSOCIATION STUDIES FOR YIELD AND YIELD CONTRIBUTING TRAITS AMONG PARENTS AND ITS HYBRID IN RICE (*Oryza sativa* L)

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**Abstract-** In existing experiment, eighteen crosses along with nine parents were evaluated for genetic parameter and association study for identification yield contributing traits. The analysis of variance was showed that the huge amount of variability is present between parents and their hybrids for all traits. The PCV is greater than GCV revealing the little influence the environment on character expression (ECV) for most of the traits except hundred grain weight (1.11) and grain yield (1.23). The high magnitudes of phenotypic and genotypic coefficient of variation were recorded for the traits viz., grain yield per plant (69.94% and 71.52%), effective tillers (68.15% and 68.36%), total tillers (58.08% and 58.86%) and flag leaf width (29.30% and 29.42%). The high value of heritability along with high genetic advance were recorded for days to 50% flowering, flag leaf length, plant height, effective tillers, grain yield, panicle length and flag leaf width. Generally, phenotypic correlations are found higher than corresponding phenotypic and environmental correlation owing to modified cause of environment traits by which associated at genetic level. Grain yield per plant exhibited highly significant and positively associated with tiller per plant at genotypic (0.599), phenotypic (0.606) and environmental (0.646) level, effective tiller per plant at genotypic (0.730), phenotypic (0.734) and environmental (0.824) level. Decorticated grain breadth was found positive and significant correlation at environmental (0.620) level at 1% level of probability. This indicates that the relative utility of these traits for selection with respect to grain yield.

**Key words-** Genetic variability, Correlation, Heritability, Hybrid rice and grain yield

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## Introduction

Rice (*Oryza sativa* L.) is a staple food for more than half of the world's population and plays pivotal role in Indian economy. India is the second largest producer of rice after china and rice crop covered in most of the state with more than 30 percent of total cultivated area [1&2]. Despite the fact that, massive progress has been made in current past to improve the yield levels by use of high yielding rice varieties, still there is a necessity to enhance the production for rising population. The hybrid rice is the counter to feed of world hunger population by the approach of its elevated yield potential and agronomic performance. The degree of genetic variability in a gene pool is the pre requisite for breeding programme. For that reason, it is necessary to employ the steps like creating variability, vigorous selection and exploitation of elected genotypes to develop elevated rice varieties. Estimation of heritability gives the information regarding amount of variation that is contagious to the progenies. Genetic advance gives the information regarding genetic gain resultant selection can be made of superior individuals. The grain yield is associated with several traits and it is quantitative in nature and integrated function with number of essential traits [3]. Knowledge of association study between yield and its contributing traits are essential and play significant role to find out the more attempt of plant selection at genotypic and phenotypic level [4]. Keeping in view the above facts, the present study was carried out to identify the level of variability and traits association study among parent and their hybrids for further utilization in rice improvement programme.

## Materials and Methods

### Experimental location and design

The investigation was conducted at Research cum Instructional farm Indira Gandhi Krishi Vishwavidyalaya Raipur (C.G.). In existing experiment, nine parents were used for development of hybrids. Among them three high yielding rice varieties viz., Karma Mahsuri, MTU 1010 and Swarna were used as recipient while, Chapti Gurmatiya, Moroberekan, IR 42342, IR 42253, IC 336354 and IC115875 were used as donor. Crossing was carried out by following in Line x Tester Mating Design [5] during Kharif-2014. For crossing, wet cloth method suggested by [6] was followed and maximum numbers of crosses were made to develop sufficient F1 seeds, resultant 18 crosses along with their parent were evaluated in Randomized Complete Block Design (RCBD) with spacing of 20x15 cm during Rabi-2015. Five representative plants were randomly selected from each parent along with their hybrids in each replication to record the quantitative observations.

### Estimation of degree of variation

A total of fifteen yield and yield related traits were considered for data recording viz., flag leaf length (cm), flag leaf width (cm), days to 50% flowering(days), plant height (cm), panicle length (cm), total tiller per plant, effective tillers, 100 grain weight, grain length, grain breadth, grain length breadth ratio, decorticated grain length (mm), decorticated grain breadth (mm), decorticated grain length breadth ratio and grain yield per plant (g).

Table-1 ANOVA for different quantitative traits

Source	d.f.	FLL	FLW	DTF	PHT	PL	TT	EFT	100 GW	GL	GB	GLBR	DGL	DGB	DGLBR	GYP
Replication	1	5.65	0.02	1.75	36.05	0.20	1.25	1.61	0.00	0.30	0.00	0.00	0.04	0.05	0.05	1.64
Treatment	26	48.62**	0.26**	57.29**	563.34**	13.29**	151.97**	37.63**	0.23**	1.18**	0.0812**	0.34**	0.50**	0.037**	0.16**	73.83**
Error	26	4.142	0.005	1.781	7.610	1.721	14.016	7.044	0.006	0.169	0.001	0.253	0.047	0.070	0.032	5.631

Table-2 GCV, PCV and Genetic Advance for variability

SN	Traits	GCV	PCV	ECV	Heritability % (bs)	Genetic Advance	Genetic Advance % Mean
1	FLL	13.91	13.97	0.32	99.11	19.67	28.52
2	FLW	29.30	29.42	0.11	91.37	8.09	25.38
3	DTF	4.35	4.55	0.29	99.56	10.83	27.94
4	PHT	14.91	15.98	0.39	97.93	14.33	30.70
5	PL	11.27	11.37	0.89	93.17	13.24	24.13
6	TT	58.08	58.86	0.47	87.53	16.74	19.23
7	EFT	68.15	68.36	0.86	95.97	12.27	44.83
8	100 GW	15.83	16.29	1.11	58.98	9.88	10.12
9	GL	12.34	12.95	0.18	72.89	15.25	13.15
10	GB	11.23	11.31	0.76	80.19	13.02	19.78
11	GLBR	8.50	8.87	0.59	29.04	11.01	1.22
12	DGL	10.19	10.66	0.12	18.38	6.14	2.23
13	DGB	5.88	6.13	0.77	26.43	8.03	1.45
14	DGLBR	8.70	9.79	0.53	17.38	10.03	1.11
15	GYP	69.94	71.52	1.23	94.83	18.14	38.06

The mean value of the recorded data was subjected to analysis of variance (ANOVA) and phenotypic coefficient of variation (PCV), genotypic coefficient (GCV), heritability (bs) and genetic advance was estimated as indicated by Burton G.W. (1952) [7] while, data were analyzed for association study by using the 'Statistical Package for Agricultural Research (SPAR2.0)' software.

## Results and Discussion

### Estimates of magnitude of variance components (ANOVA) among parents and its hybrids

The analysis of variance was showed that the huge amount of variability is present between parents and their hybrids for all traits ( $P < 0.01$ ) [Table-1]. This gives an opportunity to breeder for improvement and pick up the desirable traits through hybridization and selection. Goswami, (2018) [8] were also reported parallel work in twenty-four F1 and eleven parents for quantitative traits in his study.

### Estimates of phenotypic and genotypic coefficients of variation among parents and its hybrids

The selection depends on the existence of the genetic variability available in source material for initiating the breeding programme. The study revealed with significant variability is available breeding lines to assure the production of suitable recombinants for crop improvement. Phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) ranged from 4.35 (GCV) and 4.55 (PCV) for days to 50 flowering to 69.94 (GCV) and 71.52 (PCV) for grain yield per plant are existing in [Table-2]. The scale of phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were categorized as high ( $> 20\%$ ), moderate (10-20%) and low (0-10%) as indicated by Sivasubramanian S. and Madhavamenon P. (1973) [9]. Hence, according to the classification, the high magnitudes of phenotypic and genotypic coefficient of variation were recorded for the traits viz., grain yield per plant (69.94 and 71.52), effective tillers (68.15 and 68.36), total tillers (58.08 and 58.86) and flag leaf width (29.30 and 29.42). Consequently, moderate GCV and PCV were recorded for the traits i.e., hundred grain weight (15.83 and 16.29), plant height (14.91 and 15.98) and flag leaf length (13.91 and 13.97). The results showed that the high degree of GCV reveals the high genetic variability among the traits. The PCV was recorded higher than GCV with the harmony of [10, 11 & 12]. On the other hand low amount of GCV and PCV were recorded for the traits such as panicle length (11.27 and 11.37),

grain length, decorticated grain length breadth ratio (8.70 and 9.79), grain breadth (11.23 and 11.31), decorticated grain length (10.19 and 10.66), decorticated grain breadth (5.88 and 6.13), grain length breadth ratio (8.50 and 8.87) and days to 50% flowering (4.35 and 4.55). In common, a high coefficient of variability indicates that there is a scope of selection and improvement of these traits while, low value require for creation of variability moreover via hybridization or mutation followed by selection [13].

### Estimation of heritability in broad sense and genetic advance

A perusal of data on heritability in broad sense, genetic advances, and genetic advances as percent mean are showed in [Table-2]. Heritability in broad sense estimated of the 15 quantitative traits ranged from 64.35% for thousand grain weight to 99.93% for plant height across traits. In addition, genetic advance varied from 1.22% for grain length breadth ratio and 38.06% for grain yield per plant. Heritability was classified as low (below 30%), medium (30-60%) and high (above 60%) as suggested by Johnson et al. 1955 [14]. Bearing in minds of this description, high heritability values were recorded for the traits i.e., days to 50% flowering (99.56), flag leaf length (99.11), plant height (97.93), effective tillers (95.97), grain yield per plant (94.83), panicle length (93.17) and flag leaf width (91.37). The finding of Rukmini, et al., 2016 [15] is also concluded that the traits viz., days to 50% flowering, plant height, flag leaf length, effective tillers, panicle length, grain yield were found high heritability except flag leaf width, which showed moderate heritability. These indicate that the traits under study are less inclined by environment in their appearance. Due this reason, the breeders may make superior genotypes selection based on phenotypic performance for these traits. The traits viz., total tillers (87.53), grain breadth (80.19), grain length (72.89) and hundred grain weight (58.98) showed moderate heritability. This indicates that improvement can be done through simple selection. The results were mostly supported by the reports made earlier in rice by Anyaoha et al., 2018 [16 & 17]. In contrast with the traits such as grain length breadth ratio (29.04), decorticated grain breadth (26.43), decorticated grain length (18.38) and decorticated grain length breadth ratio (17.38) had found low heritability which indicates significant role of environment on the expression of the traits. Therefore, direct selection for these traits will be ineffective. So, methods of selection based on families and progeny testing are more effective and competent. Parallel findings were also coded by several researchers [18].

Table-3 Genotypic, Phenotypic and Environmental Correlation among the crosses and parents

Traits		FLL	FLW	DTF	PHT	PL	TT	EFT	100 GW	G L	G B	GLBR	DGL	DGB	DGLBR	GYPP
FLL	G	1														
	P	1														
	E	1														
FLW	G	0.378**	1													
	P	0.353**	1													
	E	0.16	1													
DTF	G	-0.093	0.043	1												
	P	-0.083	0.043	1												
	E	0.063	0.132	1												
PHT	G	0.146	0.324*	0.694**	1											
	P	0.128	0.323*	0.688**	1											
	E	-0.116	0.331*	0.009	1											
PL	G	-0.014	0.236	0.497**	0.838**	1										
	P	0.005	0.218	0.455**	0.769**	1										
	E	0.101	0.093	0.173	0.280*	1										
TT	G	0.105	0.148	0.187	0.061	-0.179	1									
	P	0.064	0.142	0.175	0.048	-0.163	1									
	E	-0.163	0.122	0.117	-0.169	-0.08	1									
EFT	G	0.15	0.136	-0.203	-0.079	-0.283*	0.799**	1								
	P	0.089	0.139	-0.17	-0.068	-0.235	0.762**	1								
	E	-0.112	0.267	-0.064	-0.045	-0.098	0.699**	1								
100GW	G	-0.065	0.116	0.176	0.487**	0.431**	0.086	0.093	1							
	P	-0.064	0.133	0.171	0.482**	0.403**	0.083	0.095	1							
	E	-0.07	0.519**	-0.04	0.383**	0.233	0.074	0.158	1							

Cont.....

Traits		FLL	FLW	DF	PH	PL	TPLT	ETPL	100 G	G LTH	G WTH	L/B	DL	DW	D L/B	GY
G L	G	-0.177	0.014	0.437**	0.654**	0.659**	0.043	-0.035	0.804**	1						
	P	-0.077	0.02	0.377**	0.568**	0.508**	0.021	-0.033	0.683**	1						
	E	0.319*	0.086	-0.01	0.108	-0.049	-0.07	-0.026	0.037	1						
G B	G	0.038	0.379**	0.368**	0.513**	0.562**	-0.014	-0.139	0.514**	0.350**	1					
	P	0.02	0.369**	0.361**	0.502**	0.504**	0.001	-0.101	0.501**	0.290*	1					
	E	-0.231	0.058	-0.166	-0.101	0.001	0.216	0.14	0.17	-0.106	1					
GLBR	G	-0.159	-0.285*	-0.259	-0.107	-0.062	-0.031	0.129	0.211	0.538**	-0.603**	1				
	P	-0.133	-0.278*	-0.258	-0.105	-0.063	-0.039	0.085	0.202	0.473**	-0.602**	1				
	E	0.23	-0.003	-0.095	0.086	-0.132	-0.218	-0.303*	-0.057	0.183	-0.542**	1				
DGL	G	-0.206	0.076	0.098	0.418**	0.458**	-0.138	-0.04	0.505**	0.861**	0.026	0.667**	1			
	P	-0.219	0.083	0.088	0.394**	0.442**	-0.138	-0.005	0.450**	0.690**	0.046	0.586**	1			
	E	-0.288*	0.19	-0.043	0.331*	0.366**	-0.135	0.108	0.007	0.052	0.346*	-0.345*	1			
DGB	G	0.029	0.440**	0.032	0.429**	0.497**	-0.056	-0.05	0.741**	0.392**	0.785**	-0.268	0.189	1		
	P	0.019	0.338*	0.027	0.350**	0.390**	0.023	0.096	0.594**	0.289*	0.645**	-0.224	0.114	1		
	E	-0.014	-0.173	0.018	-0.044	0.068	0.298*	0.413**	-0.04	0.029	0.035	-0.058	-0.126	1		
DGLBR	G	-0.192	-0.218	0.077	0.096	0.073	-0.118	-0.042	-0.033	0.509**	-0.495**	0.769**	0.753**	-0.502**	1	
	P	-0.194	-0.149	0.062	0.095	0.094	-0.154	-0.097	-0.018	0.362**	-0.377**	0.607**	0.735**	-0.582**	1	
	E	-0.219	0.23	-0.03	0.269*	0.165	-0.286*	-0.212	0.064	0.009	0.246	-0.22	0.737**	-0.749**	1	
GYPP	G	0.178	0.16	0.026	0.071	-0.152	0.599**	0.730**	-0.099	-0.053	0.128	-0.176	-0.034	-0.156	0.061	1
	P	0.133	0.151	0.02	0.066	-0.125	0.606**	0.734**	-0.071	-0.024	0.127	-0.169	-0.02	0.011	-0.035	1
	E	-0.125	0.069	-0.176	0.029	0.016	0.646**	0.824**	0.222	0.098	0.168	-0.154	0.053	0.620**	-0.373**	1

**Genetic Advance (GA) and GA percent mean**

After the examination of data on genetic advance as percent of mean [Table-2] for all the quantitative traits under study ranged from 6.14 (decorticated grain length) to 19.67 (flag leaf length). The genetic advance as percent of mean was categorized as high (>20%), moderate (10-20%) and low (<10%). The high

estimate of genetic advance were exhibited as per cent of mean by the characters for effective tillers (44.83), grain yield per plant (38.06), plant height (30.70), flag leaf length (28.52), days to 50% flowering (27.94), flag leaf width (25.38) and panicle length (24.13). The similar finding was reported by Roy et. al., 2015 [19] for the traits viz., productive tillers, grain yield per plant and panicle length.

At the same time as, moderate genetic advance as percent of mean were recorded for the traits such as grain breadth (19.78), total tillers (19.23), grain length (13.15) and hundred grain weight (10.12). However, low mean percent were noted for the character decorticated grain length (2.23), decorticated grain breadth (1.45), grain length breadth ratio (1.22) and decorticated grain length breadth ratio (1.11). The high heritability as well as genetic advance was recorded as percent of mean for the character effective tillers grain yield per plant, plant height, flag leaf length, days to 50% flowering, flag leaf width and panicle length.

Therefore, these traits can be improving by selection which is the significant way to achieve the genetic gain generation by generation. High heritability coupled with high genetic advance indicates prevalence of additive gene action and such traits could be improved through selection. Idris et. al., 2013 [20] were also reported the high heritability coupled with high genetic advance. In present investigation low heritability and low genetic advance shows non-additive gene action. Similar work has been done for genetic advance in two crosses of F<sub>2</sub> populations in rice by Mamata, et al., (2018) [21] whereas, in hybrid rice [22].

### Association analysis among parents and its hybrids

Association analysis is an important approach and extensively applied in breeding programme which gives an idea about the existing relationship among various characters. The correlation coefficient measures the degree and direction of linear relationship between two variables and determines the component characters on which relation can be based for genetic improvement for the yield and its contributing traits. Most of the characters are associated with one another through one or more paths. The degrees of association also affect the effectiveness of selection process. In this study, correlation coefficient was estimated for all fifteen quantitative traits in all possible combinations at phenotypic (P), genotypic (G) and environmental (E) levels [Table-3]. Many economically important traits of plants are usually related to one another in one or several ways.

Grain yield per plant exhibited highly significant and positive correlation with tiller per plant at genotypic (0.599\*\*), phenotypic (0.606\*\*) and environmental (0.646\*\*) level, effective tiller per plant at genotypic (0.730\*\*), phenotypic (0.734\*\*) and environmental (0.824\*\*) level. The phenotypic and genotypic correlation has been done by Harsha et. al., 2017 [23] for various quantitative traits while phenotypic, genotypic and environmental level of correlation has already been reported [24]. Decorticated grain breadth was found positive and significant correlation at environmental (0.620\*\*) level. This indicates that the relative utility of these traits for selection with respect to grain yield. Whereas, negative significant correlation with decorticated length breadth ratio at environmental (-0.373\*\*) level which revealed that negative correlation due to environmental effect. In existing analysis, flag leaf length exhibited positive and highly significant correlation with flag leaf width (0.378\*\*) at genotypic and (0.353\*\*) phenotypic level, flag leaf width exhibits positive significant correlation with plant height (0.324\*\*) at genotypic, (0.323\*) at phenotypic and (0.331\*) at environmental levels and decorticated grain breadth (0.440\*\*) at genotypic and (0.338\*) at phenotypic levels while with grain breadth (0.379\*\*) at genotypic (0.369\*\*) at phenotypic. The similar results were presented by several researchers [25 & 26]. Days to 50% flowering positive and significant correlation with plant height (0.694\*\*) at genotypic and (0.688\*\*) at phenotypic level and with panicle length (0.497\*\*) at genotypic (0.455\*\*) at phenotypic level and also positive significant with grain length and grain breadth at genotypic and phenotypic level. Plant height showed positive and significant association with panicle length, hundred grain weight, grain length, grain breadth, decorticated grain length and decorticated grain breadth at genotypic and phenotypic level. The finding of [25] supported with current findings for the trait panicle length. Panicle length exhibits positive significant correlation with hundred grain weight, grain length, grain breadth, decorticated grain length and decorticated grain breadth at both levels. Hundred grain weight positive significant correlation with grain length (0.804\*\*) (0.683\*\*), grain breadth (0.350\*\*) (0.290\*), decorticated grain length (0.505\*\*) (0.450\*\*) and decorticated grain breadth at genotypic (0.741\*\*) and phenotypic (0.594\*\*) levels. The similar study is also reported by [27&28] for hundred grain weight and grain breadth at both genotypic and phenotypic level. Total tillers per plant highly positive and significant correlation with effective tiller per plant and grain yield per plant at genotypic and phenotypic level. It means that

total tillers per plant and effective tiller per plant correlated with grain yield per plant due to its genotype. The result is confirmed with the finding of various researchers viz., [24, 29 &30] also revealed the same result.

### Conclusion

The current finding concluded that the enormous variability is present among parents and their hybrids for all traits. The PCV is greater than GCV revealing the little influence the environment in character expression (ECV). The genotypic correlation in general was higher than corresponding phenotypic and environmental correlation. This is due to modified effect of environment character association at genetic level. This study indicates that the relative utility of selection with respective of useful traits.

**Application of research:** This article is helps to identification of genetically distant parents for development of high yielding rice varieties.

**Research Category:** Genetic variability for Crop improvement

### Abbreviations:

cm: centimetre, df: degree of freedom, mm: milli meter, g: gram, et al.: et al., viz., = videlicet, bs: broad sense, %: percentage, P= Phenotypic G= Genotypic and E= Environmental, \* = Significant at 0.05 %, \*\* = Significant at 0.01, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation and ECV= Environmental coefficient of variation, FLL= Flag leaf length (cm), FLW=Flag leaf width (cm), DTF=Days to 50% flowering (days), PHT=Plant height (cm), PL=Panicle length(cm), TT=Total tillers, EFT=Effective tillers, 100 GW= 100 grain weight (gm), GL=Grain length (mm), GB=Grain breadth (mm), GLBR=Grain length breadth ratio, DGL=Decorticated grain length (mm), DGB=Decorticated grain breadth (mm), DGLBR= Decorticated grain length breadth ratio and GYPP=Grain yield per plant (g).

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