



Analysis of genetic parameters and characters association for yield components and quality attributes in rice cultivars

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Abstract: Genetic analysis was carried out for 55 diverse rice genotypes (10 parents and 45 F₁s) through half-diallel mating design during *kharif* season 2011-2012 and 2012-2013. The analysis of variance showed highly significant differences among the treatments for all the 19 traits under study. High heritability (broad sense) coupled with high genetic advance was observed for number of grains per panicle, harvest index, grain yield per plant, productive tillers per plant, plant height, biological yield per plant, kernel length after cooking indicating selection will be 100 percent effective based on these traits because they were under the influence of additive and additive x additive type of gene action. Highest coefficient of variation (GCV & PCV) was recorded for plant height (13.85 % & 13.87 %), productive tillers per plant (14.58 % & 15.13%), number of grains per panicle (17.93 % & 18.07 %), biological yield per plant (12.67 % & 12.71 %), grain yield per plant (15.88 % & 15.97 %), harvest index (16.80 % & 16.90 %) and kernel length after cooking (10.09 % & 10.19 %), indicating that these traits are under the major influence of genetic control. The traits, panicle length ($gr=0.31^{**}$ & $pr=0.30^{**}$), number of grain per panicle ($gr=0.80^{**}$ & $pr=0.79^{**}$), biological yield per plant ($gr=0.31^{**}$ & $pr=0.30^{**}$) and harvest index ($gr=0.67^{**}$ & $pr=0.67^{**}$) had positive and significant correlation with grain yield per plant and these traits also had highest positive direct effects on grain yield therefore the above mentioned traits contributed maximum to higher grain yield compared to other traits indicating that we can improve grain yield by improving these traits as well as emphasis should be given based on these traits for the selection of elite genotypes from the segregating generation.

Key words: Rice, Diallel analysis, Genetic parameters, Yield components and Quality attributes

Introduction

Rice is one of the most important cereal crops in the world after wheat in term of the annual production and India is the second largest producer and consumer of rice in the world after China. Rice is equal to wheat in importance as a staple food for human being. Rice has been one of the world's most important food crops, feeding more than half of the world's population (Khush, 1997). Worldwide, rice occupies an area of 166 million hectares with the production of 745 million tons of rough rice at an average productivity of 4.48 tons per hectare (FAOSTAT, 2013). In India rice is cultivated in 44 million hectares, the largest area in the world with the production of 106 million tons, whereas China produces 144 million tons from 30.6 million hectares itself (RICESTAT, 2014). With the ever increasing population, rice production must be increased by about 40% by 2025 to satisfy the growing demand without adversely affecting the resource base (Khush, 2004). *Oryza sativa* is widely cultivated due to its better adaptation to a wide range of environmental conditions and better economic yield with good quality. The yield of transplanted paddy is reached as its plateau; further improvement can be done only by heterosis breeding. Grain yield is a complex polygenic character control by many genes interacting with the environment and is the product of many factors called yield components. However, direct selection for yield alone is usually not very effective thus selection should be done based on its contributing traits. At present time, there is urgent need to evolve short duration, disease resistance, fertilizer responsive, high yielding with good quality traits genotypes of the rice crop best suited to different cultivated region of the country and to

exploit the various genetically aspects such as genetic variability, desirable associations among different characters and heritability of important characters and using effective breeding programme to achieve maximum improvement in the yield potential as well as quality of rice crop. The task of developing new varieties with high yield potential and quality attributes becomes more effective if the plant breeder has knowledge about these important genetically aspects. Because improvement in rice productivity and quality remains constant, crop improvement programs should aim to broaden the genetic base of breeding materials (Vanaja and Babu, 2004). Continued improvement for yield and quality traits remains the top priority in any breeding programme. The foremost requirement for developing new varieties is that genetic variation must be present in a crop. The study of correlation between plant characters is of great importance to a plant breeder as it provides measures of the degree of association between yield and other component traits. The choice of plant breeding methodology for upgrading the yield potential with preference quality traits largely depends on the availability of reliable information on the nature and magnitude of genetic variability present in the population. The main objective of the present investigation was to analysis of genetic parameters and characters association for yield components and quality attributes in rice cultivars through half diallel mating design.

Materials and Methods

The experimental material used in the present investigation, consisted of ten diverse genotypes namely Vallabh Basmati 21, Vallabh Basmati 22, MAUB 57, Pusa 1121, CSR 30, Pusa Basmati 1, Basmati 370, Pusa 1401, CSR 13, and CSR 10 and their 45 F₁s cross

combinations. Ten diverse rice genotypes were grown during *kharif* 2011-2012 for attempting all possible single crosses by adopting (10 x 10) diallel mating design (excluding reciprocals). In next year, all the experimental material (10 parents and 45 F₁s) were evaluated in a Randomized Block Design with three replications during *kharif* season 2012-2013. Observations were recorded on five randomly selected plants from each genotype (Parents and F₁s) in each replication and the mean value was used for statistical analysis. The data were recorded on 19 quantitative characters namely, days to 50 % flowering, days to maturity, plant height (cm), panicle length (cm), number of productive tillers per plant, number of branches per panicle, number of grains per panicle, flag leaf area (cm²), 1000 grain weight (g), biological yield per plant (g), grain yield per plant (g), harvest index (%), kernel length (mm), kernel breadth (mm), L/B ratio, kernel length after cooking (mm), elongation ratio, amylose content and hulling per cent. Analysis of variance was carried out by method suggested by Panse and Sukhatme (1967) for all the traits among the treatments. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated following method suggested by Burton and De Vane (1953). Heritability in narrow sense was calculated according to the formula suggested by Crumpacker and Allard (1962). The correlation at genotypic and

phenotypic level between yield and its contributing traits and among themselves as well as among quality traits were worked out as per the method suggested by Searle *et al.* (1961). The expected genetic advance was calculated by the formula suggested by Hanson *et al.* (1956) and Path analysis was carried out following the method suggested by Wright (1921). The significance of variance for treatments was tested by "F" at 5% and 1% level of probability.

Results and Discussion

The analysis of variance was highly significant among the treatments for the traits namely days to 50% flowering, days to maturity, plant height, panicle length, number of productive tillers per plant, number of branches per panicle, number of grains per panicle, flag leaf area, 1000 grain weight, biological yield per plant, grain yield per plant, harvest index, kernel length, kernel breadth, L/B ratio, kernel length after cooking, elongation ratio, amylose content and hulling per cent. This indicated that considerable amount of variability is present among the parents and their F₁s derived by all possible single cross combination. Significant variability for various yield contributing traits and quality attributes in rice genotypes were also reported by Dhurai *et al.* (2014), Patel *et al.* (2014), Chouhan *et al.* (2014), Allam *et al.* (2015) and Kumar *et al.* (2015). The understanding of variability and genetic architecture of population is essential for the

Table-1: The pedigree and origin of the parental lines are as follows :-

Name of Varieties	Parentage	Source/Origin
Vallabh Basmati-21	Khalasa-7/Type-3	SVPUA&T, MEERUT
MAUB-162 (Vallabh Basmati-22)	Pusa-1121×Type-3	SVPUA&T, MEERUT
MAUB-57 (Vallabh Basmati-23)	Pusa-1121×Type-3	SVPUA&T, MEERUT
Pusa-1121	Traditional Basmati	IARI New Delhi
CSR-30	BR4-10/Basmati 370	CSSRI- Karnal, Haryana
Pusa Basmati-1	Pusa-150/Karnal Local	IARI, New Delhi
Basmati-370	Traditional Basmati	Rice Research Station Kaul, Haryana
PUSA-1401	Pusa Basmati-1/Pusa 1121-92-8-2-7-1	IARI New Delhi
CSR-13	CSR-1/Basmati-370/CSR-5	CSSRI-Karnal, Haryana
CSR-10	M40-431-24-114/jaya	CSSRI-Karnal, Haryana

Table-2: Analysis of variance for yield components and quality attribute in rice

Character	Replication (d f=2)	Treatments (d f=54)	Parents (d f=9)	Hybrids (d f=44)	Parents Vs Hybrids (d f=1)	Error (d f=108)	Total (d f=164)
Days to 50% Flowering	0.079	48.136**	86.741**	39.757**	69.399**	0.437	16.138
Days to Maturity	0.509	10.562**	17.441**	9.47**	2.101*	0.342	3.709
Plant Height	0.127	668.236**	1323.837**	548.797**	23.112**	0.887	220.614
Panicle Length	0.083	8.917**	17.219**	7.182**	10.553**	0.054	2.973
Productive tillers per plant	0.073	14.429**	26.700**	11.685**	24.728**	0.363	4.991
Branches per Panicle	1.655	2.857**	3.293**	1.858**	42.912**	0.476	1.274
Grains per Panicle	19.242	2009.758**	3577.319**	1723.482**	497.864**	10.317	668.778
Flag Leaf Area	4.149	17.650**	10.779**	18.476**	43.112**	1.515	6.860
1000 Grain Weight	0.036	4.034**	3.622**	4.154**	2.461*	0.483	1.647
Biological Yield	1.436	443.673**	918.700**	355.312**	56.324**	0.714	146.575
Grain Yield per plant	0.045	64.453**	118.646**	54.784**	2.115**	0.248	21.386
Harvest Index	0.423	80.149**	150.614**	67.387**	7.464**	0.336	26.617
Kernel Length	0.014	0.671**	1.356**	0.546**	0.007	0.006	0.221
Kernel Breadth	0.009	0.006**	0.011**	0.005**	0.003	0.002	0.002
L/B Ratio	0.011	0.360**	0.728**	0.293**	0.006	0.004	0.119
Kernel Length After Cooking	0.018	3.653**	6.259**	3.199**	0.149**	0.021	1.217
Elongation Ratio	0.022	0.028**	0.041**	0.025**	0.005**	0.001	0.009
Amylose Content	0.261	3.073**	5.811**	2.398**	8.089**	0.359	1.252
Hulling %	0.041	4.774**	8.554**	4.086**	1.052**	0.061	1.613

implementation of suitable breeding method. The general mean of F_{1s} crosses were greater than their corresponding parents for all the characters except harvest index, L/B ratio and hulling percent. The range of variability among material gives high chance of selection for desirable types for different characters under study.

Genetic parameters: The estimates of GCV and PCV for 19 characters were worked out and results showed that the estimates of PCV were slightly greater than GCV for all the characters under study which suggested the little effects of environment in the expression of the traits. The differences between the value of PCV and GCV were small. Similar findings were also reported by Chouhan *et al.* (2014), Kumar *et al.* (2015) and Kumar *et al.* (2015). The estimates of GCV ranged from 1.23% in days to maturity to 17.93% in number of grains per panicle, whereas for PCV, it was 1.29% in days to maturity to 18.07% in number of grains per panicle. The highest percentage of GCV and PCV was found for plant height, productive tillers per plant, number of grains per panicle, biological yield, grain yield, harvest index and kernel length after cooking, which comes under the category of moderate type of GCV and PCV (10 - 25%) indicating these traits are under the major influence of genetic control therefore simple selection can be practiced for further improvement. In this regard, Kumar *et al.* (2015) reported moderate type of PCV and GCV for plant height and kernel length after cooking, Kumar *et al.* (2015) for grain yield, harvest index and productive tillers per plant; Dhanwani *et al.* (2013) for productive tillers per plant, biological yield per plant and harvest index; and Ketan and Sarkar (2014) for number of grains per panicle and grain yield per plant. Low PCV and GCV for days to 50% flowering, days to maturity, grain length, grain breath were also reported by Patel *et al.* (2014) whereas Kumar *et al.* (2015) for days to flowering, panicle length, test weight. Low PCV and GCV for hulling percentage and days to flowering were also reported by Dhanwani *et al.* (2013). The results indicated that useful variability in progenies developed through hybridization can be utilized

and selection of suitable genotypes on the basis of different genetic parameters can be done to get high yield in rice crop.

The GCV provides a measure of comparison of variability and gives some indication of validity of trait for selection. Heritability and genetic advance both are important direct selection parameters but high heritability with high genetic advance of a character are more effective for selection. In the present investigation, high heritability (narrow sense) was observed for the kernel length (99.80) followed by L/B ratio (99.62), plant height (99.60), biological yield (99.10), grain yield (98.60), kernel breadth (97.60), harvest index (96.50), days to 50% flowering (95.90), days to maturity (94.91), kernel length after cooking (93.09), panicle length (93.00), hulling% (93.90), number of productive tiller per plant (90.70), number of grain per panicle (90.40), amylose content (85.30), elongation ratio (80.40), 1000-grain weight (75.00). The similar finding were earlier reported by Bornare *et al.* (2014) and Kumar *et al.* (2015) for plant height, days to 50% flowering, days to maturity, panicle length, number of productive tiller per plant, number of grain per panicle, 1000-grain weight, kernel breadth, and grain yield per plant and Kumar *et al.* (2015) also reported high heritability for kernel length, L/B ratio, elongation ratio and kernel length after cooking. High heritability also observed by Chouhan *et al.* (2014) for kernel breadth, test weight and filled grains per panicle. High heritability indicates the scope of genetic improvement of these traits through selection.

High genetic advance as percent of mean were observed for number of grains per panicle (36.66), harvest index (34.39), grain yield per plant (32.52), number of productive tillers per plant (28.93), plant height (28.46), biological yield per plant (26.04), kernel length after cooking (20.62). These findings are similar to the results earlier reported by Chouhan *et al.* (2014) and Kumar *et al.* (2015) for grain yield per plant, number of grains per panicle, number of productive tillers per plant, plant height; Pandey *et al.* (2012) for biological yield per plant. Genetic advance as percent of

Table-3: Mean, Range, PCV, GCV, Heritability and Genetic advance for yield components and quality attributes in rice

Genetic parameters Character	Range		Mean		Coefficient of variation		h ² (Narrow Sense)	G A as % of Mean
	Parents	F _{1s}	parents	F _{1s}	GCV	PCV		
Days to 50% flowering	99.00-116.00	103.33-116.33	106.67	108.35	3.69	3.74	95.90	7.50
Days to maturity	146.33-154.33	146.67-153.67	149.63	149.93	1.23	1.29	94.91	2.41
Plant height	75.00-158.00	86.33-138.33	106.93	107.90	13.85	13.87	99.60	28.46
Panicle length	21.82-30.73	23.69-29.81	26.11	26.76	6.45	6.51	93.00	13.17
Productive tillers per plant	11.33-19.67	12.33-20.67	14.03	15.04	14.58	15.13	90.70	28.93
Branch per panicle	9.67-12.67	11.00-14.00	11.30	12.62	7.19	9.09	41.40	11.72
Grains per panicle	98.67-197.00	104.00-195.00	140.27	144.77	17.93	18.07	90.40	36.66
Flag leaf area	25.92-31.54	26.34-38.32	29.04	30.36	7.69	8.71	67.80	14.00
1000 grain weight	24.81-28.24	23.77-27.96	26.25	25.93	4.18	4.96	75.00	7.26
Biological yield	62.33-117.67	70.67-114.33	94.63	96.15	12.67	12.70	99.10	26.04
Grain yield	21.98-38.95	21.96-37.96	28.89	29.18	15.88	15.97	98.60	32.52
Harvest index	20.68-40.86	21.93-40.28	31.15	30.60	16.80	16.90	96.50	34.39
Kernel Length	5.98-7.98	6.19-7.95	7.19	7.20	6.56	6.57	99.80	13.50
Kernel Breadth	1.64-1.82	1.65-1.81	1.73	1.74	2.48	2.50	97.90	5.06
L/B Ratio	3.28-4.85	3.45-4.79	4.15	4.15	8.34	8.35	99.60	17.16
Kernel Length After Cooking	8.37-12.33	8.61-12.86	10.83	10.91	10.09	10.18	93.00	20.62
Elongation Ratio	1.33-1.57	1.29-1.72	1.50	1.51	6.28	6.47	80.40	12.56
Amylose Content	18.33-22.67	19.33-22.67	20.70	21.27	4.49	5.31	85.30	7.82
Hulling%	75.74-80.37	75.61-80.11	78.21	78.00	1.60	1.63	93.90	3.24

Table-4: Estimates of phenotypic and genotypic correlation coefficient for yield components and quality attributes in rice

Character	Days to Maturity	Plant Height	Panicle Length	Tillers per plant	Branches per panicle	Grains per panicle	Flag Leaf Area	1000 Grain Weight	Biological Yield/plant	Harvest Index	Kernel Length	Kernel Breadth	L/B Ratio	Kernel Length After Cooking	Elongation Ratio	Amylose Content	Hulling %	Grain yield/plant
Days to 50% flowering	P	0.823**	0.227**	0.691**	0.150	-0.456**	-0.171*	0.049	0.437**	-0.584**	0.226**	-0.164*	0.218**	0.145	0.001	0.144	0.111	-0.285**
	G	0.870	0.229	0.722	0.216	-0.465	-0.202	0.045	0.443	-0.596	0.230	-0.174	0.222	0.148	-0.004	0.176	0.113	-0.290**
Days to maturity	P	1.000	-0.021	0.387**	0.076	-0.275**	-0.126	0.170*	0.277**	-0.396**	0.445**	-0.121	0.377**	0.395**	0.182*	0.227**	-0.210**	-0.185**
	G	1.000	-0.021	0.433	0.104	-0.288	-0.160	0.232	0.291	-0.418	0.469	-0.130	0.398	0.416	0.189	0.274	-0.218	-0.196**
Plant Height	P	1.000	0.449**	0.536**	0.079	-0.084	0.324**	-0.214**	0.674**	-0.426**	0.263**	-0.479**	0.339**	0.032	-0.217**	0.210**	-0.043	0.077
	G	1.000	0.454	0.554	0.101	-0.084	0.367	-0.264	0.676	-0.430	0.262	-0.486	0.339	0.033	-0.220	0.246	-0.042	0.077
Panicle Lengths	P		1.000	-0.099	-0.030	0.444**	0.307**	-0.282**	0.511**	-0.143	0.432**	-0.301**	0.420**	0.350**	0.113	0.274**	-0.377**	0.300**
	G		1.000	-0.104	-0.028	0.452	0.344	-0.335	0.517	-0.144	0.437	-0.308	0.424	0.353	0.114	0.325	-0.390	0.306**
Tillers per plant	P			1.000	0.101	-0.422**	-0.193*	-0.128	0.494**	-0.675**	-0.038	-0.197*	0.021	-0.172*	-0.241**	0.032	0.326**	-0.362**
	G			1.000	0.115	-0.440	-0.253	-0.177	0.513	-0.707	-0.043	-0.213	0.021	-0.172	-0.231	0.038	0.359	-0.384**
Branches per panicle	P				1.000	0.212**	0.210**	0.231**	0.101	0.112	0.048	0.239**	-0.046	0.081	0.077	0.181*	0.032	0.231**
	G				1.000	0.287	0.321	0.343	0.118	0.147	0.059	0.312	-0.058	0.115	0.122	0.207	0.053	0.286**
Grains per panicle	P					1.000	0.333**	0.001	0.146	0.596**	-0.077	0.454**	-0.205**	0.005	0.074	-0.134	-0.057	0.789**
	G					1.000	0.386	0.017	0.148	0.604	-0.077	0.461	-0.206	0.005	0.072	-0.153	-0.063	0.801**
Flag leaf area	P						1.000	0.190*	0.129	0.292**	0.252**	-0.119	0.235**	0.069	-0.149	0.075	-0.302**	0.459**
	G						1.000	0.202	0.144	0.340	0.283	-0.152	0.260	0.080	-0.173	0.056	-0.346	0.520**
1000 grain weight	P							1.000	-0.182*	0.210**	0.074	0.350**	-0.040	0.044	-0.013	-0.103	-0.079	0.094
	G							1.000	-0.236	0.254	0.069	0.393	-0.065	0.057	0.019	-0.145	-0.068	0.097
Biological yield/plant	P								1.000	-0.484**	0.145	-0.137	0.136	-0.024	-0.209**	-0.041	0.194*	0.304**
	G								1.000	-0.486	0.143	-0.140	0.135	-0.025	-0.213	-0.051	0.200	0.306**
Harvest index	P									1.000	-0.327**	0.576**	-0.428**	-0.080	0.200**	-0.139	-0.102	0.677**
	G									1.000	-0.328	0.586	-0.431	-0.082	0.209	-0.157	-0.102	0.677**
Kernel Length	P										1.000	-0.616**	0.969**	0.806**	0.582**	-0.779**	-0.189*	
	G										1.000	-0.625	0.970	0.815	0.304	0.690	-0.794	-0.191*
Kernel Breadth	P											1.000	-0.302**	0.123	-0.369**	0.420**	0.490**	
	G											1.000	-0.305	0.135	-0.432	0.436	0.496**	
L/B Ratio	P												1.000	0.183*	0.559**	-0.740**	-0.309**	
	G												1.000	0.192	0.662	-0.754	-0.312**	
Kernel Length After Cooking	P													0.792**	0.749**	-0.793**	-0.084	
	G													0.800	0.894	-0.817	-0.084	
Elongation Ratio	P														1.000	0.617**	-0.496**	0.036
	G														1.000	0.756	-0.534	0.044
Amylose Content	P															1.000	-0.637**	-0.176*
	G															1.000	-0.783	-0.198**
Hulling %	P																1.000	0.009
	G																1.000	0.017

*, ** Significance level at 5% and 1% respectively

Table-5: Estimates of phenotypic and genotypic correlation coefficient for yield components and quality attributes in rice

Character	Days to 50% flowering	Days to maturity	Plant Height	Panicle Length plant	Tillers per panicle	Branches per panicle	Grains per Panicle	Flag Leaf Area	1000 Grain Weight	Biological Yield / plant	Harvest Index	Kernel Length	Kernel Breadth	L/B Ratio	Kernel Length After Cooking	Elongation Ratio	Amylose Content	Hulling %	Grain yield / plant
Days to 50% flowering	P -0.029	-0.023	-0.006	0.008	-0.020	-0.004	0.013	0.005	-0.001	-0.012	0.017	-0.006	0.005	-0.006	-0.004	0.003	-0.004	-0.003	-0.285**
G	2.545	2.215	0.582	-0.698	1.837	0.549	-1.183	-0.515	0.114	1.128	-1.516	0.585	-0.443	0.584	0.376	-0.009	0.449	0.286	-0.290**
Days to maturity	P	0.029	0.036	-0.001	-0.005	0.014	0.003	-0.004	0.006	0.010	-0.014	0.016	-0.004	0.013	0.014	0.006	0.008	-0.007	-0.185*
G	2.266	2.605	0.054	0.402	-1.126	-0.270	0.749	0.416	-0.605	-0.757	1.089	-1.220	0.339	-1.036	-1.083	-0.493	-0.714	0.567	-0.196**
Plant Height	P	-0.010	0.001	-0.043	-0.019	-0.023	0.004	-0.014	0.009	-0.029	0.018	-0.011	0.021	-0.015	-0.001	0.009	-0.009	0.002	0.077
G	-0.252	0.023	-1.102	-0.500	-0.611	-0.111	0.093	-0.404	0.291	-0.745	0.474	-0.289	0.535	-0.374	-0.037	0.242	-0.271	0.046	0.077
Panicle Lengths	P	0.003	0.002	-0.005	-0.011	0.001	-0.005	-0.003	0.003	-0.006	0.002	-0.005	0.003	-0.005	-0.004	-0.001	-0.003	0.004	0.300**
G	-0.138	-0.078	0.228	0.303	-0.052	-0.014	0.227	0.173	-0.169	0.260	-0.072	0.220	-0.155	0.213	0.177	0.057	0.163	-0.196	0.316**
Tillers per plant	P	-0.046	-0.026	-0.036	0.007	-0.007	0.028	0.013	0.009	-0.033	0.045	0.003	0.013	-0.001	0.012	0.016	-0.002	-0.022	-0.362**
G	0.376	0.225	0.289	-0.054	0.621	0.060	-0.229	-0.132	-0.092	0.267	-0.368	-0.022	-0.111	0.011	-0.089	-0.120	0.020	0.187	-0.384**
Branches per panicle	P	0.006	0.003	0.003	-0.001	0.004	0.009	0.009	0.010	0.004	0.005	0.002	0.010	-0.002	0.003	0.003	0.007	0.001	0.231**
G	-0.104	-0.050	-0.049	0.014	-0.056	-0.483	-0.139	-0.155	-0.166	-0.057	-0.071	-0.028	-0.150	0.028	-0.055	-0.059	-0.100	-0.026	0.286**
Grains per panicle	P	-0.020	-0.012	-0.004	0.019	-0.018	0.009	0.015	0.004	0.006	0.026	-0.003	0.020	-0.009	0.006	0.003	-0.006	-0.002	0.789**
G	-0.101	-0.062	-0.018	0.098	-0.095	0.062	0.217	0.084	0.004	0.032	0.131	-0.017	0.100	-0.045	0.001	0.016	-0.033	-0.014	0.811**
Flag leaf area	P	-0.006	-0.005	0.012	0.011	-0.007	0.008	0.012	0.007	0.005	0.011	0.009	-0.004	0.009	0.003	-0.005	0.003	-0.011	0.459**
G	0.042	0.033	-0.076	-0.072	0.053	-0.067	-0.080	-0.208	-0.042	-0.030	-0.071	-0.059	0.032	-0.054	-0.017	0.036	-0.012	0.072	0.520**
1000 grain weight	P	0.002	0.001	-0.002	-0.002	0.002	0.001	0.001	0.008	-0.001	0.002	0.001	0.003	0.002	0.001	0.002	-0.001	-0.001	0.894
G	0.025	0.131	-0.149	-0.189	-0.100	0.193	0.009	0.113	0.582	-0.133	0.143	0.039	0.221	-0.036	0.032	0.011	-0.081	-0.038	0.897
Biological yield / plant	P	0.365	0.232	0.564	0.427	0.413	0.422	0.108	-0.152	0.837	-0.405	0.121	-0.114	0.114	-0.020	-0.175	-0.034	0.162	0.304**
G	5.003	3.330	0.767	0.587	0.583	0.134	0.168	0.163	-0.268	1.135	-0.552	0.163	-0.158	0.154	-0.028	-0.241	-0.058	0.227	0.316**
Harvest index	P	-0.562	-0.381	-0.411	-0.137	-0.650	0.108	0.282	0.202	-0.466	0.963	-0.315	0.555	-0.412	-0.077	0.193	-0.134	-0.098	0.677**
G	-1.068	-0.750	-0.770	-0.257	-1.267	0.264	1.083	0.609	0.456	-0.872	1.793	-0.588	1.050	-0.772	-0.147	0.374	-0.281	-0.183	0.677**
Kernel Length	P	0.022	0.043	0.026	0.042	-0.004	0.005	0.024	0.007	0.014	-0.032	0.097	-0.060	0.094	0.078	0.028	0.056	-0.076	-0.188*
G	0.721	1.469	0.823	1.370	-0.134	0.184	-0.242	0.886	0.215	0.449	-1.029	3.134	-1.958	3.041	2.555	0.952	2.162	-2.489	-0.181*
Kernel Breadth	P	0.011	0.008	0.033	0.021	0.013	-0.016	0.008	-0.024	0.009	-0.039	0.042	-0.068	0.054	0.021	-0.008	0.025	-0.029	0.490**
G	0.101	0.075	0.281	0.178	0.123	-0.180	-0.267	0.088	-0.227	0.081	-0.338	0.361	-0.578	0.459	0.176	-0.078	0.250	-0.252	0.496**
L/B Ratio	P	-0.035	-0.061	-0.055	-0.068	-0.003	0.007	-0.038	0.006	-0.022	0.069	-0.156	0.127	-0.161	-0.116	-0.030	-0.090	0.119	-0.309**
G	-0.334	-0.599	-0.511	-0.639	-0.031	0.087	0.310	-0.391	0.097	-0.204	0.649	-1.461	1.197	-1.506	-1.092	-0.289	-0.996	1.136	-0.312**
Kernel Length After Cooking	P	-0.006	-0.016	-0.001	-0.014	0.007	0.004	-0.003	-0.002	0.001	0.003	-0.032	0.012	-0.029	-0.040	-0.032	-0.030	0.032	-0.084
G	-0.298	-0.840	-0.067	-0.713	0.347	-0.232	-0.010	-0.161	-0.116	0.050	0.165	-1.647	0.616	-1.466	-2.021	-1.617	-1.806	1.651	-0.084
Elongation Ratio	P	0.001	-0.001	0.001	0.002	0.001	0.002	0.001	0.002	0.001	-0.001	-0.001	0.002	-0.001	-0.002	-0.003	-0.002	0.001	0.036
G	-0.004	0.196	-0.227	0.118	-0.239	0.126	0.075	-0.179	0.020	-0.220	0.216	0.315	0.140	0.198	0.828	1.035	0.783	-0.553	0.044
Amylose Content	P	0.002	-0.001	-0.001	-0.001	0.001	0.002	0.001	0.002	0.001	0.001	-0.002	0.001	-0.002	-0.002	-0.002	-0.003	0.002	-0.176*
G	0.005	0.008	0.007	0.009	0.001	0.006	-0.004	0.002	-0.004	-0.001	-0.004	0.019	-0.012	0.019	0.025	0.021	0.028	-0.022	-0.198*
Hulling %	P	-0.007	0.014	0.003	0.025	-0.022	0.004	0.020	0.005	-0.013	0.007	0.052	-0.028	0.049	0.053	0.033	0.042	-0.067	0.009
G	-0.043	0.084	0.016	0.150	-0.034	-0.020	0.024	0.133	0.026	-0.077	0.039	0.306	-0.168	0.290	0.315	0.206	0.301	-0.385	0.017

Residual effect = 0.1092 (Phenotypic path); Residual Effect = 0.1778 (genotypic path)

mean was medium for L/B ratio (17.16), flag leaf area (14.00), kernel length (13.50), panicle length (13.17), elongation ratio (12.56) and number of branches per plant (11.72). These results are similar to the finding of Kumar *et al.* (2015) for kernel length and L/B ratio.

High heritability does not always indicate high genetic gain; high heritability coupled with high genetic advance should be used in predicting the ultimate effects for selecting the superior varieties. High heritability coupled with high genetic advance as percent of mean was observed for the number of grains per panicle, harvest index, grain yield per plant, number of productive tillers per plant, plant height, biological yield per plant, kernel length after cooking showing the less effects of environment on these traits. Similar results were also observed by Singh *et al.* (2014) and Kumar *et al.* (2015) for plant height and number of productive tillers per plant, Chouhan *et al.* (2014) for number of grains per panicle and grain yield per plant; Sandhya *et al.* (2014) for biological yield, Patel *et al.* (2014) for grain yield per plant and harvest index and Kumar *et al.* (2015) for number of grains per panicle, harvest index, grain yield per plant, number of productive tillers per plant, plant height and biological yield per plant. High heritability coupled with high genetic advance for these traits indicating additive gene action controlling these traits. These traits could be improved by mass selection or progeny or family selection or any selection scheme, aimed at exploiting additive genetic variance, a widely adapted genotype could be developed possessing good productivity. Johnson *et al.* (1955) have also suggested that characters with high heritability coupled with high genetic advance would response better to selection than those with high heritability with low genetic advance. High heritability coupled with low genetic advance was recorded for days to maturity, kernel breadth, hulling percent, 1000 grain weight, days to 50% flowering and amylose content. High heritability with low genetic advance was also reported by Chouhan *et al.* (2014) for days to maturity and Days to flowering. It suggested non additive gene action for the expression of these traits. The characters which showed high heritability coupled with moderate to low genetic advance can improve by intermating of superior genotypes of segregating population developed by combination breeding Samadhia (2005). The high heritability is being exhibited due to favorable influence of environment rather than genotype therefore, direct selection for such traits might not be rewarding.

Correlation coefficient: The main objective of correlation studies is primarily to know about the suitability of various attributes for indirect selection. The results on correlation coefficient revealed that both genotypic and phenotypic correlations follow the same trend but the genotypic correlation was slightly higher than phenotypic correlations except someone. It indirectly revealed that significant genotypic association between attributes was primarily due to genetic cause, which may be due to pleiotropic effects and linkage, indicating low environmental effects on the degree of association with grain yield and among themselves. The understanding of the association of plant characters among themselves and with yield is essential for successful crop improvement programme. It enables the breeders to manipulate the expression of these traits in crop improvement.

In the present investigation, it was observed that grain yield had positive and significant correlation with panicle length ($rg = 0.306$ and $rp = 0.300$), number of branches per panicle ($rg = 0.286$ and $rp = 0.231$), number of grain per panicle ($rg = 0.801$ and $rp = 0.789$),

flag leaf area ($rg = 0.520$ and $rp = 0.459$), biological yield per plant ($rg = 0.306$ and $rp = 0.304$), harvest index ($rg = 0.677$ and $rp = 0.677$), and kernel breadth ($rg = 0.496$ and $rp = 0.490$), at genotypic as well as phenotypic level. Other characters such as plant height, 1000 grain weight, elongation ratio and hulling % contributed positive correlation with yield in respective order of magnitude. The negative significant but desirable correlation of grain yield were also found with days to 50% flowering ($rg = -0.290$ and $rp = -0.285$), and days to maturity ($rg = -0.196$ and $rp = -0.185$) at both genotypic and phenotypic level. Some other traits such as productive tillers per plant, kernel length, L/B ratio and amylase content showed significant but negative association towards grain yield. The strong positive correlation of panicle length, number of branches per panicle, number of grain per panicle, flag leaf area, biological yield per plant, harvest index, and kernel breadth with grain yield per plant indicated that these characters might be utilized as selection criteria for improving grain yield in rice. The observed positive correlation of grain yield with various traits was supported by earlier workers viz., Sravan *et al.* (2012), Patel *et al.* (2014) for panicle length; Bhadru *et al.* (2011) and Patel *et al.* (2014) for number of grains per panicle; Neelima *et al.* (2007) for number of branches per panicle; Pandey *et al.* (2012) for biological yield per plant and flag leaf area; Sravan *et al.* (2012) and Patel *et al.* (2014) for harvest index. Negative significant association of grain yield has been observed with days to 50% flowering and days to maturity as similar to the earlier finding of Pandey *et al.* (2012) and Bornare *et al.* (2014) and it has been demonstrated by many other researchers that some time negative correlation may also observed. In present investigation, number of productive tiller per plant has negative correlation with grain yield, that could be happened due to induced relationship between pleiotropic effects and linkage, this induced linkage can be break in the next generation by adopting the triple test cross and bi-parental mating. In any breeding programme, a positive correlation would be desired when the characters were improved simultaneously. Correlation analysis provides information on the nature and magnitude of the association of different component characters with grain yield, which is regarded as a complex trait and also help us to understand the nature of association among the component traits among themselves. Therefore this kind of analysis could be helpful to the breeder to design selection strategies to improve the grain yield. From the above discussion it is evident that grain yield can be increased whenever there is an increase in characters that showed positive and significant association with grain yield. These associations can be well utilized as an indicator of grain yield in designing selection strategy to improve grain yield with good quality for nutritional security.

Path coefficient analysis: The correlation coefficient alone is inadequate to interpret the cause and effects relationship among the traits and ultimately with grain yield. Yield is the most economic trait which is the result of overall contribution of several traits from the beginning of germination to the final development of the crop. A close inspection of (Table 5) showing that at genotypic level kernel length had highest direct effects on grain yield per plant followed by days to 50% flowering, harvest index, biological yield per plant, kernel elongation ratio, 1000 grain weight, number of productive tiller per

plant, panicle length, number of grains per panicle and amylose contain. This may indicate that direct selection of these characters is likely to be effective in increasing grain yield. Days to maturity, plant height, branches per panicle, flag leaf area, kernel length, L/B ratio, kernel length after cooking and hulling percent exhibited higher negative direct effects on grain yield. The observed positive direct effects of various traits on grain yield was also supported by earlier workers viz., Sravan *et al.* (2012) for days to 50% flowering; Bornare *et al.* (2014) and Ratna *et al.* (2015) for productive tillers per plant; Allam *et al.* (2015) for panicle length, kernel length and 1000 grain weight; Patel *et al.* (2014) for number of grains per panicle, kernel length and harvest index. Negative direct effect of plant height on grain yield was also reported by Patel *et al.* (2014) and Ratna *et al.* (2015) and negative direct effects of kernel length and L/B ratio on grain yield. Patel *et al.* (2014) and Allam *et al.* (2015) reported negative direct effects of kernel length after cooking on grain yield. From the present findings, it may be expected that most of the quality attributes affect the grain yield directly in negative direction genotypic level. Only some quality traits like kernel length, kernel elongation ratio and amylose contain have positive direct effects on grain yield. All the characters have direct and indirect effects on grain yield through other characters except someone. Therefore the characters which were showing positive direct and indirect effects on grain yield except days to flowering, plant height and days to maturity (where negative effects are desired) should also be used for the improvement of grain yield. It means these are the best characters by which we improved the grain yield per plant with good quality by improving these characters, because these traits have positive direct and indirect effect on grain yield with positive and significant correlation coefficient. In plant breeding, it is very difficult to have complete knowledge of all component traits of yield. The phenotypic and genotypic residual effects were recorded 0.1092 and 0.1778 respectively.

In the present investigation, it may be concluded that highest coefficient of variation (GCV & PCV) with high heritability along with high genetic advance for number of grains per panicle, harvest index and biological yield per plant, and their positive significant association with positive direct effects on grain yield, indicating that these traits can be used as a selection criteria for the improvement of grain yield and these traits can be manipulated through mass selection or progeny or family selection or any selection scheme, aimed at exploiting additive genetic variance, a widely adapted genotype could be developed possessing good productivity because they were under the influence of additive and additive x additive type of gene action. It is evident that genotypes studies may provide good source of material, contains desirable genes can be evaluated for further breeding programme. Therefore information on genetic parameters (coefficient of variation, heritability, genetic advance) and characters association (correlation and path coefficient) can help the breeders to develop suitable cultivars within a short time, which can be help to enhance the production and productivity of rice at national level as well as global level.

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