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Analysis of variability, correlation and path coefficient studies for yield and quality traits in rice (*Oryza Sativa* L.)

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ABSTRACT

Variability, correlation and path analysis for yield and quality traits were studied on 27 rice genotypes. The higher estimates of PCV and GCV were observed for yield per plant (42.04) and filled seeds per panicle (33.9) indicate possibility of genetic improvement through direct selection. High heritability in broad sense coupled with high genetic advance as percent of mean exhibited by effective tillers, plant height, flag leaf length, filled grains per panicle, test weight, yield per plant, head rice recovery and length/breadth ratio indicating preponderance of additive gene action which provide good scope for further improvement by selection. Grain yield per plant had highest significant positive association with filled seeds per panicle, plant height, flag leaf length, effective tillers, flag leaf width and panicle length indicating importance of these characters for yield improvement, while head rice recovery was found to be significantly and positively correlated with milling percent and hulling percent. Path analysis reveals that test weight (3.48), effective tillers (1.57), and filled grains per panicle (1.41) had positive direct effect on grain yield per plant. Among the quality traits kernel length followed by milling percent and kernel elongation ratio had direct effect on head rice recovery.

Key words: Correlation, Grain quality, Path analysis, Rice, Variability, Yield.

INTRODUCTION

Rice is one of the most important food grain crops in the world. It is considered as staple diet of more than 2.7 billion people all over the world. To fulfil the requirement of ever increasing population, enhancing crop yield is one of the top most priorities in crop breeding programmes. Quality traits are yet another important consideration of rice breeding in India. The most important criteria in any crop improvement programme are the selection of genotypes with all possible desirable quality and yield contributing traits. Variability in genotypes for yield and its component traits forms the basic factor to be considered while making selection. Any successful hybridization programme for varietal improvement mainly depends on the selection of parents having high variability, so that desired character combination may be selected to improve grain quality and higher grain yield. Moreover, knowledge of heritability is essential for selection based improvement as it indicates the transmissibility of a character into future generations. Johnson *et.al* (1955) suggested that heritability estimates along with genetic advance would be more useful in predicting grain yield under phenotypic selection than heritability estimates alone.

Yield is a complex quantitative character controlled by many gene interactions with environment and is product of many factors called yield components. Selection of parents based on yield alone is often misleading. Hence, knowledge about relationship between yield and its contributing characters is needed for an efficient selection strategy for the plant breeders to evolve an economic variety. Path coefficient analysis furnishes information of influence of each contributing trait to yield directly as well as indirectly and also enables breeders to rank the genetic attributes according to their contribution. The present investigation was undertaken to gather some useful information on genetic variability character association and path coefficient analysis in a set of 27 rice genotypes.

MATERIALS AND METHODS

The experimental material used in the study consisted of 9 parents and 18 F_1 hybrid combinations of rice, grown in a completely randomized block design with three replications at Regional Agricultural Research Station, Warangal during *Kharif* 2014. Twenty five days old seedlings of each genotype were transplanted in three rows of 2.0 m length by adopting a spacing of 20 cm between rows and 15 cm between the plants at the rate of 20 plants per row. The crop was grown with the application of fertilizers N, P and K at the rate of 120:60:40 Kg /ha respectively. Standard agronomic practices were followed to raise a good crop.

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A composite sample of 10 plants from the middle row was used to record observation on these plants for plant height (cm), effective tillers per m^2, panicle length (cm), flag leaf length (cm), flag leaf width (cm), filled seeds per panicle, test weight, yield per plant, except days to 50% flowering which was computed on plot basis. Data were recorded on physical, chemical and cooking quality characters *viz,* hulling recovery %, milling percent, head rice recovery, kernel length (mm), kernel width, length / breadth ratio, kernel length after cooking (mm), kernel breadth after cooking (mm), kernel elongation ratio, alkali spreading value, volume expansion ratio and water uptake. The seed was dehusked in a satake laboratory huller (Type THU 35A) and polished in a satake rice polisher (Type TM05) and data on head rice recovery was recorded. Observations on hulling and milling were taken. The polished kernel were utilized for the analysis of above 14 seed quality traits. Kernel length and kernel width of 20 whole milled rice were measured by means of dial caliper and length / breadth ratio was computed as per Murthy and Govinda Swamy (1967). Kernel elongation was determined by soaking 5 g of whole milled rice in 12 ml distilled water for 10 minutes and later cooked for 15 minutes in water bath. Observations on length and breadth of cooked kernels and elongation ratio were recorded with the help of graph sheet to quantify cooking traits. Water uptake,volume expansion ratio and alkali spreading value were estimated by following the standard procedures. The treatment means for all the characters were subjected to compute the analysis of variance on the basis of model proposed by Panse and Sukhtme (1961). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation were calculated by the formula given by Burton and Devane (1953). Heritability in broad sense h^2_b and genetic advance as percent of mean were estimated by the formula as suggested by Hanson *et al* (1956) and Jonnson *et al* (1955). The path and correlation coefficient analysis was done following the method of Dewey and Lu (1959).

RESULTS AND DISCUSSION

Genetic variability: The analysis of variance indicated the existence of significant differences among all genotypes for all the characters expect hulling percent, volume expansion ratio and water uptake (Table 1) indicating the existence of sufficient amount of variability. The magnitude of variation between genotypes was reflected by high values of mean and range for genotypic traits studied (Table 2). High genetic variability for different quantitative traits in rice was also reported by Khan *et al.* (2009). The magnitude of phenotypic coefficient of variation (PCV) in general was found to be higher than genotypic coefficient of variation (GCV) for all the characters studied indicated the influence of environment on the manifestation of these characters. Among the characters the higher estimates of PCV and GCV were observed for yield per plant (42.04) and filled seeds per panicle (33.9). This indicates the existence of wide genetic base among the genotypes taken for study and possibility of genetic improvement through direct selection for these traits. These results are in conformity with the findings of Bhadru *et al.* (2012) and Dhanwan *et al.* (2013). The PCV and GCV

Table 1: Analysis of variance (mean squares) for grain yield and quality traits in rice (*Oryza sativa*.L)

Characters	Replication(d.f=1)	Treatments(d.f=26)	Error(d.f=26)
Days to 50% flowering	21.42	116.53**	5.33
Effective tillers	275.6	5411.0**	315.4
Plant height(cm)	5.35	844.6**	15.27
Panicle length (cm)	8.08	12.62**	1.71
Flag leaf length(cm)	4.68	79.8**	7.0
Flag leaf width(cm)	0.40	0.09**	0.03
Filled seeds /Panicle)	93.35	11068.0**	217.77
Test weight(g)	0.58	27.85**	0.585
Yield/Plant (g)	64.4	385.1**	3.42
Hulling recovery(%)	3.28	3.07	2.54
Milling recovery(%)	14.9	65.4**	9.25
Head rice recovery	30.98	148.6**	4.44
Kernel length(mm)	0.005	0.444**	0.033
Kernel width (mm)	0.019	0.059**	0.004
L/B ratio	0.035	0.178**	0.006
Kernel length after cooking(mm)	0.520	0.817**	0.049
Kernel breadth after cooking (mm)	0.66	0.122**	0.022
Kernel elongation ratio	0.003	0.009**	0.003
Alkali spreading value	0.074	1.514**	0.420
Volume expansion ratio	0.015	0.11	0.08
Water uptake	4125.6	1649.3	1056.7

*Significant at 5% level ** Significant at 1 % level

Table 2: Components of genetic parameters for yield and quality traits in rice (*Oryza sativa*.L)

Character	Mean	Range	PV	GV	PCV	GCV	Heritability in broad sense(%)	Genetic advance over mean (%)
Days to 50% flowering	100	89 - 119	60.93	55.59	7.80	7.45	91.25	14.7
Effective tillers	327	231 - 433	2863.22	2547.78	6.38	15.45	88.98	30.2
Plant height(cm)	117	83 - 152	429.95	414.68	17.75	17.44	96.0	35.3
Panicle length (cm)	24.7	20.9-29.6	7.168	5.455	10.82	9.44	76.0	16.9
Flag leaf length(cm)	34.8	23.0-48.9	43.42	36.42	18.96	17.36	84.0	32.8
Flag leaf width(cm)	1.8	1.6 - 2.3	0.06	0.03	13.63	9.66	50.0	14.11
Filled seeds /Panicle)	217	107 - 352	5642.89	5425.12	34.67	33.99	96.0	68.7
Test weight(g)	19.0	13.7-26.2	14.22	13.63	19.81	19.39	96.0	39.1
Yield/Plant (g)	32.9	13.8-58.9	194.28	190.86	42.42	42.04	98.0	85.8
Hulling recovery(%)	81.1	76.9-83.2	2.80	0.26	2.06	0.63	9.00	0.39
Milling recovery(%)	68.7	47.1-75.9	37.31	28.06	8.89	7.71	75.0	13.8
Head rice recovery	61.3	36.9-71.5	76.55	72.11	14.27	13.85	94.0	27.7
Kernel length(mm)	5.2	4.5 - 6.2	0.24	0.21	9.45	8.77	86.0	16.8
Kernel width (mm)	1.8	1.5 - 2.3	0.031	0.027	9.75	9.07	87.0	17.4
L/B ratio	2.9	2.3 - 3.6	0.09	0.08	10.64	10.27	93.0	20.4
Kernel length after cooking(mm)	6.5	5.6 - 7.7	0.43	0.38	10.19	9.59	89.0	18.6
Kernel breadth after cooking (mm)	2.2	1.9 - 2.7	0.07	0.049	12.06	9.99	69.0	17.0
Kernel elongation ratio	**1.3**	**1.1 - 1.39**	**0.0061**	**0.0036**	**6.24**	**4.78**	59.0	7.5
Alkali spreading value	4.7	2.0 - 6.0	0.97	0.55	20.75	15.60	57.0	24.2
Volume expansion ratio	1.8	1.6 - 2.2	0.09	0.0153	17.58	7.05	16.0	5.8
Water uptake	161.8	122 - 242	1353.01	296.30	22.73	10.64	22.0	10.3

recorded moderate values for the traits *viz.,* test weight, flag leaf length, plant height, alkali spreading value, effective tillers and head rice recovery. The selection for these traits may be ambiguous if adopted for improvement. Similar kinds of findings were also observed by Venkata subbaiah *et.al* (2011) for effective tillers and test weight, Kumar *et al.* (2014) for plant height.

The estimates of PCV and GCV were low (< 10%) for the characters hulling percent, milling percent, kernel length, kernel width, panicle length and length/breadth ratio. The selection for these traits offers very little scope for genetic improvement of the genotypes under study. Similar results were also obtained by Singh *et al.* (2005) for kernel length, kernel width, kernel length / breadth ratio while Mamata *et al.* (2007) registered for days to 50% flowering and Nirmala Devi *et al.* (2015) reported for hulling percent.

High estimates of heritability were obtained by most of the characters except hulling percent, volume expansion ratio and water uptake indicating the major role of additive gene action in inheritance of these traits. According to Panse (1957) if a character is governed by non additive gene action, it may give heritability but low genetic advance whereas if it is governed by additive gene action, high heritability (above 60%) along with high genetic advance (above 20%) provide good scope for further improvement. The traits effective tillers per m^2, plant height, flag leaf length, filled seeds per panicle, test weight, yield per plant, head rice recovery and length/breath ratio expressed high heritability values with high genetic advance as percent of mean. These results were in accordance with the findings of Singh *et al.* (2005) for effective tillers, Dhurai *et al.* (2014) for test weight, effective tillers, plant height, filled grains per panicle and yield per plant, Krishnaveni *et al.* (2013) for grain yield per plant and effective tillers.

Correlation coefficient: The estimates of correlation coefficients revealed that in general genotypic and phenotypic correlation coefficients showed similar trend but genotypic correlation coefficients were of higher in magnitude than the corresponding phenotypic correlation coefficients which might be due to masking or modifying effect of environment (Singh, 1980). Very close values of genotypic and phenotypic correlation were also observed between the traits (Table 3). In this study genotypic correlation coefficients were in general higher than corresponding phenotypic ones demonstrating that the observed relationships among various characters were due to genetic causes. Grain yield per plant had highest significant positive association with filled seeds per panicle, plant height, flag leaf length, flag leaf width, effective tillers and panicle length at phenotypic and genotypic level indicating the importance of the characters for yield improvement. This was in agreement with the earlier reports of Chakravarty and Ghosh (2014) for filled seeds, Nandan *et al.* (2010) for plant height and Krishnaveni *et al.* (2013) for effective tillers and panicle length. Grain yield had significant negative association with days to 50% flowering. Similar result for days to 50% flowering was reported by Kole *et al.* (2008) and Mulugela Seyoum *et al.* (2012). Wide differences between genotypic and phenotypic correlation between two characters is due to dual nature of phenotypic correlation which is determined by genotypic and environmental correlations and heritability of the characters (Falconer, 1981). Significant negative association of days to 50% flowering with effective tillers, plant height, panicle length, flag leaf length and test weight at phenotypic level and negative association at genotypic level. Significant positive correlation was observed for effective tillers with filled seeds per panicle and plant height, plant height with panicle length, filled seeds per panicle, flag leaf width, panicle length with test weight and filled seeds. Previous studies have mentioned similar findings (Ghaffar Kalani *et.al* 2012) for panicle length with filled grains, Kole *et al.* (2008) for plant height with filled seeds and panicle length. Effective tillers, plant height and panicle length had significant positive association with filled seeds. Similar results were previously reported by Krishna *et al.* (2013).

Correlation coefficient analysis among grain quality characters between head rice recovery and quality traits were computed (Table 4). Correlation estimates showed the possibility of improvement of a character through selection for other characters. Head rice recovery had significant positive association with milling percent at phenotypic and genotypic level and hulling percent at genotypic level indicated that hulling percent, milling percent and HRR are important quality attributes for rice that enhances commercial success of a variety. Simultaneous improvement of these three quality traits namely hulling percent, milling percent and head rice recovery can be made with the selection of a single trait is either hulling percent, milling percent or head rice recovery. HRR showed negative significant association with kernel length after cooking, kernel breadth after cooking, kernel elongation ratio, alkali spreading value and water uptake while, negative non significant association with kernel length, kernel breadth, length/breadth ratio and volume expansion ratio. Hulling and milling percent had significant negative association with kernel breadth after cooking. Kernel length is one of the important character and it had showed significant positive association with kernel length after cooking, length/breadth ratio, volume expansion ratio and kernel breadth after cooking. Kernel width exhibited significant negative association with length/breadth ratio and kernel elongation ratio. While significant positive association with kernel breadth after cooking at phenotypic level and genotypic level and volume expansion ratio at phenotypic level. Length/breadth ratio had significant positive association with kernel length after cooking, similar

Table 3: Phenotypic and genotypic correlation coefficient for yield traits in rice (*Oryza sativa.L*)

Characters		Days to 50% flowering	Effective tillers	Plant height (cm)	Panicle length (cm)	Flag leaf length(cm)	Flag leaf width(cm)	Filled seeds / Panicle)	Test weight(g)
Days to 50 % flowering	P	1.0000	-0.0892	-0.4141 **	-0.4780 **	-0.5424 **	-0.3202 *	-0.2333	-0.2845 *
	G	1.0000	-0.1328	-0.4412**	-0.6127**	-0.6064**	-0.5018*	-0.2261	-0.3001*
Effective tillers	P		1.0000	0.4753 **	0.2577	0.1485	0.2038	0.4758 **	-0.2244
	G		1.0000	0.4902**	0.2772	0.1325	0.2532	0.5177	-0.2767
Plant height (cm)	P			1.0000	0.6772 **	0.6171 **	0.1178	0.6772 **	0.2168
	G			1.0000	0.7504**	0.6455**	0.0778	0.6936**	0.2119
Flag leaf length(cm)	P				1.0000	0.5295 **	0.2415	0.3190 *	0.6525 **
	G				1.0000	0.5738**	0.0969	0.3513*	0.7385**
Flag leaf width(cm)	P					1.0000	0.4167 **	0.5768 **	0.1985
	G					1.0000	0.4423**	0.6129**	0.2073
Panicle length(cm)	P						1.0000	0.3769 **	0.0305
	G						1.0000	0.5023**	0.0319
No. of grains / panicle	P						1.0000	1.0000	-0.1212
	G							1.0000	-0.1255
Test weight(g)	P								1.0000
	G								1.0000
Yield(g/pl)	P	-0.3653**	0.2731*	0.6332**	0.5227**	0.5652**	0.4125**	0.6543**	0.1969
	G	-0.3891**	0.2925*	0.6596**	0.6034**	0.6320**	0.5943**	0.6770**	0.1953

& ** Significant at 5 % and 1 % level respectively

P -phenotypic correlation coefficient G- genotypic correlation coefficient

Table 4: Phenotypic and genotypic correlation coefficient for quality traits in rice (*Oryza sativa. L*)

Characters		Hulling recovery (%)	Milling recovery (%)	Kernel length (mm)	Kernel width (mm)	L/ B ratio	Kernel length after cooking (mm)	Kernel breadth after cooking (mm)	Kernel elongation ratio	Alkali spreading value	Volume expansion ratio	Water uptake
Hulling recovery (%)	P	1.0000	0.1616	0.01941	-0.1578	0.2048	0.0220	-0.3652**	-0.0576	-0.0350	0.2136	-0.0945
	G	1.0000	0.1645	-0.1061	-0.6375	0.4886	-0.1320	-1.1829**	0.1151	-0.2546	0.9042	0.1932
Milling recovery (%)	P		1.000	-0.1094	-0.2050	0.1040	-0.1795	-0.4521**	-0.1125	-0.1673	-0.0494	-0.2340
	G		1.0000	-0.1821	-0.3411	0.1379	-0.2420	-0.5846**	-0.1193	-0.3145	-0.5695	-0.7008
Kernel length(mm)	P			1.0000	0.3534	0.5138**	0.8051**	0.3290**	-0.2107	-0.2250	0.3970**	0.2452
	G			1.0000	0.3476	0.5409**	0.8728**	0.4688**	-0.0806	-0.3647	1.2081**	0.6227
Kernel width (mm)	P				1.0000	-0.5838**	0.2081	0.6029**	-0.2874*	-0.0272	0.3532**	0.1352
	G				1.0000	-0.5998**	0.2106	0.7706**	-0.3734*	-0.1289	0.7386	0.1108
L/B ratio	P					1.0000	0.4614**	-0.2269	0.0663	-0.2072	0.1041	0.1164
	G					1.0000	0.5114**	-0.2560	0.1769	-0.2720	0.3283	0.3339
Kernel length after cooking(mm)	P						1.0000	0.2679	0.3569**	0.0386	0.3826**	0.2850*
	G						1.0000	0.3689	0.4088**	0.1136	0.8756**	0.7024*
Kernel breadth after cooking (mm)	P							1.0000	-0.0991	0.0332	0.3903**	0.2662
	G							1.0000	-0.2112	0.0377	0.3479	0.9755
Kernel elongation ratio	P								1.0000	0.4672**	-0.0528	0.1850
	G								1.0000	0.9536**	-0.4866	0.2681
Alkali spreading value	P									1.0000	-0.1586	0.1998
	G									1.0000	-0.7560	0.4152
Volume expansion ratio	P										1.0000	0.0916
	G										1.0000	0.3430
Water uptake	P											1.0000
	G											1.0000
Head rice recovery	P	0.1898	0.5427**	-0.1874	-0.0484	-0.0557	-0.4056**	-0.3310*	-0.3351*	-0.3118*	0.0100	-0.3318**
	G	0.3371*	0.5873**	-0.2408	-0.0692	-0.0582	-0.4789**	-0.3733*	-0.4592*	-0.4484**	0.0643	-0.6722**

*Significant at 5 % level

**Significant at 1 % level

P represents phenotypic correlation coefficient

G represents genotypic correlation coefficient results of kernel breadth with length/breadth ratio was reported by Nirmala Devi *et al.* (2015). Alkali spreading value recorded negative association with volume expansion ratio but possess positive association with water uptake indicating with high water uptake had low gelatinization temperature which is parallel with the results reported by Shivani *et al.* (2007).

Kernel length after cooking is one of the important quality attribute. Length wise expansion after cooking is considered as a highly desirable trait in high quality rice. Grain shape and visual appearance of rice before and after cooking are important to determine the quality of a rice variety. In this study, kernel length after cooking and kernel elongation ratio are inter dependent as evidenced by the positive significant association between them (r = 0.41). Selection of either of the traits will ultimately enhance the mean performance of the inter dependent trait. From the findings of present study that selection of traits with high positive significant association and high positive direct effect on grain yield can help in improving yield.

Path coefficient analysis: Considering grain yield as effect and other quantitative characters as causes, genotypic correlation coefficient were partitioned by using method of path analysis to find out direct and indirect effect of yield contributing characters towards grain yield (Table 5). From the path analysis, it was revealed that test weight (3.48) followed by effective tillers per m^2(1.57), filled grains per panicle(1.41), plant height (0.50) and flag leaf length (0.75) had positive direct effect on grain yield per plant, however indirect effect of test weight through plant height, panicle length, flag leaf length, flag leaf width have been observed, whereas negative effective with filled seeds per panicle. Filled grains per panicle had high positive indirect effect on grain yield through effective tillers, plant height, panicle length, flag leaf length, flag leaf width. Similar results were reported by Vanisree *et al.* (2013) for effective tillers, plant height, panicle length and Vinodini *et al.* (2005) for test weight.

Considering head rice recovery as effect and other quality characters as causes path analysis revealed that kernel length followed by milling percent and kernel elongation ratio had direct effect on head rice recovery. Thus development of genotypes with higher kernel length, milling percent and kernel elongation ratio might help in obtaining high HRR (Table 6). Grain size and shape are among the first criteria of rice quality that breeders may consider these traits in development of new varieties for commercial production.

Kernel length had highest positive direct effect on HRR and indirect positive effect through kernel length after cooking, length/breadth ratio and volume expansion ratio

Table 5: Phenotypic and genotypic path coefficient analysis of yield traits in rice(*Oryza sativa.L*)

Characters		Days to 50% flowering	Effective tillers	Plant height (cm)	Panicle length (cm)	Flag leaf length(cm)	Flag leaf width(cm)	Filled seeds / Panicle)	Test weight (g)
Days to 50 % flowering	P	-0.0171	0.0015	0.0071	0.0082	0.0093	0.0055	0.0040	0.0049
	G	**-1.6253**	0.2159	0.7171	0.9958	0.9856	0.8155	0.3675	0.4877
Effective tillers	P	0.0108	-0.1214	-0.0577	-0.0313	-0.0180	-0.0247	-0.0578	0.0272
	G	-0.2090	**1.5732**	0.7712	0.4361	0.2085	0.3983	0.8145	-0.4353
Plant height (cm)	P	-0.1172	0.1346	0.2831	0.1917	0.1747	0.0334	0.1917	0.0614
	G	-0.2220	0.2466	**0.5032**	0.3776	0.3248	0.0392	0.3490	0.1066
Panicle length(cm)	P	-0.0690	0.0372	0.0977	0.1443	0.0764	0.0349	0.0460	0.0941
	G	2.7992	-1.2663	-3.4281	**-4.5686**	-2.6213	-0.4429	-1.6048	-3.3741
Flag leaf length(cm)	P	0.0043	-0.0012	-0.0049	-0.0042	-0.0079	-0.0033	-0.0046	-0.0016
	G	-0.4571	0.0999	0.4866	0.4325	**0.7538**	0.3334	0.4620	0.1563
Flag leaf width(cm)	P	-0.0686	0.0437	0.0253	0.0518	0.0893	0.2143	0.0808	0.0065
	G	0.6872	-0.3468	-0.1066	-0.1328	-0.6057	**-1.3696**	-0.6880	-0.0437
Filled grains / panicle	P	-0.0934	0.1905	0.2712	0.1277	0.2309	0.1509	0.4004	-0.0485
	G	-0.3195	0.7315	0.9799	0.4963	0.8659	0.7097	**1.4129**	-0.1773
Test weight(g)	P	-0.0150	-0.0118	0.0114	0.0344	0.0105	0.0016	-0.0064	0.0528
	G	-1.0427	-0.9616	0.7364	2.5665	0.7204	0.1108	-0.4361	**3.4751**
Yield(g/pl)	P	-0.3653	0.2731	0.6332	0.5227	0.5652	0.4125	0.6543	0.1969
	G	-0.3891	0.2925	0.6596	0.6034	0.6320	0.5943	0.6770	0.1953

Phenotypic residual effect = 0.6449Genotypic residual effect = 1.0169

Table 6: Phenotypic and genotypic path coefficient analysis for quality traits in rice (*Oryza sativa.L*)

Characters		Hulling recovery (%)	Milling recovery (%)	Kernel length (mm)	Kernel width (mm)	L/ B ratio	Kernel length after cooking (mm)	Kernel breadth after cooking (mm)	Kernel elongation ratio	Alkali spreading value	Volume expansion ratio	Water uptake
Hulling recovery (%)	P	**0.0315**	0.0051	0.0030	-0.0050	0.0065	0.0007	-0.0115	-0.0018	-0.0011	0.0067	-0.0030
	G	0.4140	-0.0681	0.0439	0.2639	-0.2023	0.0546	0.4897	-0.0476	0.1054	-0.3743	-0.0800
Milling recovery(%)	P	0.0579	**0.3583**	-0.0392	-0.0737	0.0373	-0.0643	-0.1620	-0.0403	-0.0599	-0.0177	-0.0838
	G	-0.0039	-0.0235	0.0043	0.0080	-0.0032	0.0057	0.0137	0.0028	0.0074	0.0134	0.0165
Kernel length(mm)	P	0.0099	-0.0116	**0.1056**	0.0373	0.0543	0.0850	0.0347	-0.0223	-0.0238	0.04193	0.0259
	G	-1.0442	-1.7918	9.8372	3.4194	5.3212	8.5857	4.6116	-0.7933	-3.5873	11.8845	6.1252
Kernel width (mm)	P	-0.1048	-0.1366	0.2346	**0.6639**	-0.03876	0.1382	0.4003	-0.1908	-0.0181	0.2385	0.0898
	G	1.6284	0.8713	-0.8879	-2.5543	1.5321	-0.5380	1.9684	0.9538	0.3292	-1.8867	-0.2831
L/B ratio	P	0.1092	0.0555	0.2739	-0.3112	**0.5331**	0.2459	-0.1210	0.0353	-0.1104	0.0555	0.0620
	G	-1.5202	-0.4291	-1.6830	1.8663	-3.1113	-1.5911	0.7965	-0.5505	0.8462	-1.0216	-1.0389
Kernel length after cooking(mm)	P	-0.0184	0.1495	-0.6704	-0.1733	-0.3842	**-0.8327**	-0.2230	-0.2972	-0.0322	-0.3186	-0.2373
	G	0.9706	1.7791	-6.4175	-1.5487	-3.7602	-7.3530	-2.7127	-3.0060	-0.8350	-6.4383	-5.1648
Kernel breadth after cooking (mm)	P	0.0785	0.0972	-0.0707	-0.1296	0.0488	-0.0576	**-0.2150**	0.0213	-0.0071	-0.0839	-0.0572
	G	0.8010	0.3959	0.3174	0.5218	0.1734	-0.2498	-0.6772	0.1430	-0.0255	-0.2356	-0.6606
Kernel elongation ratio	P	-0.0148	-0.0289	-0.0541	-0.0738	0.0170	0.0917	-0.0254	**0.2568**	0.1200	-0.0135	0.0475
	G	0.2518	-0.2610	-0.1765	-0.8171	0.3871	0.8945	-0.4622	2.1881	2.0866	-1.0648	0.5866
Alkali spreading value	P	0.0046	0.0221	0.0297	0.0036	0.0273	-0.0051	-0.0044	-0.0616	**-0.1319**	0.0209	-0.0264
	G	-0.2043	-0.2524	-0.2926	-0.1034	-0.2182	0.0911	0.0302	0.7653	0.8025	-0.6067	0.3332
Volume expansion ratio	P	0.0211	-0.0049	-0.0392	0.0348	0.0103	0.0377	0.0385	-0.0052	-0.0156	**0.0987**	0.0090
	G	-0.0327	0.0206	-0.0437	-0.0267	-0.0119	-0.0317	-0.0126	0.0176	0.0274	-0.0362	-0.0124
Water uptake	P	0.0150	0.0370	-0.0388	-0.0214	-0.0184	-0.0451	-0.0421	-0.0293	-0.0316	-0.0145	**-0.1583**
	G	-0.0954	0.3462	-0.3076	-0.0548	-0.1650	-0.3471	-0.4820	-0.1325	-0.2052	-0.1695	-0.4941
Head rice recovery	P	-0.1898	0.5427	-0.1874	-0.0484	-0.0557	-0.4056	-0.3310	-0.3351	-0.3118	0.0100	-0.3318
	G	0.3371	0.5873	-0.2408	-0.0692	-0.0582	-0.4789	-0.3733	-0.4592	-0.4484	0.0643	-0.6722

Phenotypic residual effect = 0.6810 Genotypic residual effect = 0.6521 P-phenotypic path coefficient G- genotypic path coefficient and negative effect through hulling percentage (genotypic level), milling percent, kernel elongation ratio and alkali spreading value.

Kernel length after cooking had negative direct effect on HRR but indirect effect through milling recovery was positive. Kernel elongation ratio had direct positive effect on length/breadth ratio, kernel length after cooking, alkali spreading value but negative with kernel breadth after cooking.

Elongation ratio had negative direct effect on HRR but its indirect effect through length/breadth ratio, kernel length after cooking, alkali spreading value and water uptake were positive and showed negative effect through kernel breadth after cooking and volume expansion ratio.

The genetic architecture of grain yield is based on the balance or overall net effect produced by various yield components interacting with one another. Based on the studies on genetic variability, correlation and path analysis, it may be concluded that the yield components number of filled seeds per panicle, test weight, effective tillers, plant height and among quality traits length/breadth ratio, milling percent, head rice recovery, kernel length, kernel width and kernel length after cooking were important contributing traits for selection to achieve high grain yield with good quality traits.

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