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Correlation Studies on Yield and Yield Contributing Traits in Rice (*Oryza sativa* L.)

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ABSTRACT

*The rice genotype panel comprised of 30 varieties which includes indica group, landraces, improved varieties, interspecific derivatives (Oryza glaberrima× Oryza sativa), aromatic and japonica rice etc. were evaluated for yield and yield contributing traits, during kharif 2019. ANOVA test showed highly significant variation for the twelve traits under study. The correlation analysis showed a total of 28 significant associations between 12 yield and yield- related traits measured under study. Very high significant positive correlation in the present study was detected between number of filled grains per panicle (FG) and total grain number per panicle (GN) (r^2=0.948**) followed by grain length (GL) and grain length to width ratio (GLW) (r^2=0.799**) while, very high significant negative correlation was detected between grain width (GW) and grain length to width ratio (GLW) (r^2= -0.847**) followed by number of chaffy grains per panicle (CG) and spikelet fertility (SF) (r^2= -0.832**). This indicates the effect of selections for strongly associated traits are dependent and worked in directional manner either in positive direction or in negative direction. Therefore, a breeder should be well understood the effect of a trait on other prior handling with a trait improvement breeding programme.*

Keywords: *Rice (Oryza sativa L.), Yield components, Correlation coefficients, Quantitative traits*

INTRODUCTION

Rice (*Oryza sativa* L.) is a major staple food in the world, especially in the developing countries of Asia. In Africa, it is the most rapidly growing food source and, according to a conservative estimate, about 30 million tons more rice will be needed by 2035 (Kim et al., 2016). Rice occupies pivotal place in Indian Agriculture. In order to meet the domestic demand of the increasing population the present day production of 107.40 million tons (Thorat et al., 2019) of milled rice has to be increased to 125 million tons by the year 2030. Within existing agricultural lands, the genetic improvement of yield potential in rice could be the ideal way to increase yield.

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The improvement of yield of food crops in general and rice in particular, is a permanent concern due to the consistent demand projection in lieu of rapid increase of global human population and also due to the decrease of arable land and water resources. Grain yield in rice can be improved by targeting diverse yield contributing traits viz., plant height, number of tillers, number of productive tillers per plant, number of grains per panicle, and grain weight. Among these, the most reliable traits are number of panicles, grains per panicle and grain weight (Anh *et al.*, 2015). Grain Weight is measured as the 1000-grain weight (TGW). Grain size of rice is determined by grain length (GL), grain width (GW), grain thickness (GT) and grain length to width ratio (GL/GW). GL/GW is the major determinant of grain appearance quality and grain weight of rice (Xing and Zhang, 2010).

Economic product of rice is the grain yield, which exhibits complex genetics as it is influenced by various yield contributing characters and the environment. In general, increased number of fertile panicles is the single most important yield component associated with rice yield, number of spikelets/panicle; percent filled grains/panicle are also of secondary and tertiary importance (Ratna *et al*., 2015). Another trait directly related to panicle is panicle density which chiefly affects the yield potential. These yield contributing components are interrelated with each other showing a complex chain of relationship and also highly influenced by the environmental conditions (Prasad *et al*., 2001). Breeding strategy in rice mainly depends upon the degree of associated characters as well as its magnitude and nature of variation (Anis *et al*., 2016 and Prasad *et al*., 2001).Therefore, information about the yield contributing traits is of immense importance to the plant breeders for the development of improved varieties/ lines of rice with increased yield potential.

Furthermore, the grain yield is a complex character dependent on many component characters and it responds poorly to the direct selection (Thorat *et al.*, 2019). For the improvement of grain yield, the knowledge on the association between grain yield and its component characters will be helpful. The present study was, therefore, undertaken to understand the association among grain yield and its component characters in rice.

MATERIALS AND METHODS

In the present study, a core set of 30 rice genotypes were chosen based on their yield component trait diversity under different subgroups (japonica, indica and aromatic) from around 250 genotypes available at the Department of Genetics and Pant Breeding, S.V. Agricultural College, Tirupati. The panel comprises of landraces, improved varieties, interspecific derivatives (*Oryza glaberrima*× *Oryza sativa*), aromatic and japonica rice etc were used for correlation analysis of yield contributing traits (Supplementary Table 1).

The experiment was carried out at Wetland Farm, S.V. Agricultural College, Tirupati, ANGRAU during *Kharif*, 2019. The experiment was laid out in three replications in Randomized Block Design (RBD) with spacing of 20 cm × 15 cm and 2 rows of 4 m length for each genotype. The agronomic management was done as per the standard recommendations. The phenotypic data was recorded for the twelve yield contributing traits from 5 plants per replication per genotype. The productive tillers(PT), plant height(PH),panicle length(PL), filled grains (FG), chaffy grains(CG), number of total grains(GN), percentage of spikelet fertility (SF), grain length (GL), grain width (GW), ratio of grain length-to-grain width (GR),1000-grain weight (TGW) and grain yield per plant (GY), were evaluated. For each trait, means of the replicates were used in the data analyses.

Statistical analysis: The data with respect to yield and yield-related traits were subjected to analysis of variance to determine the significant differences among genotypes for all the characters evaluated by the OPSTAT program. Pearson's Correlation analysis between character pairs was computed at probability levels of $P<0.05$ and $P<0.01$ in Microsoft Excel using trait average for the trait pairs among genotypes. Significance of correlation coefficients (r) at p = 0.05 or 0.01 is indicated by * or **, respectively.

RESULTS AND DISCUSSION

Mean performance of individual genotype for each trait and its analysis of variance was given in Table 1.Grain yield per plant the genotype's mean observed was of 18.66 g with a range of 7.90 g to 32.71 g. Similar results reported by Anh *et al*.(2018) and Anh *et al*.(2015). The analysis of variance of all traits of 30 rice genotypes showed highly significant difference among the genotypes (Table 2). This is in agreement with work of Shahriar *et al*., 2014.

Correlation between different character pairs occur because of either linkage or pleiotropy. Correlation studies provide information on the nature and extent of association between any two characters. From this it would be possible to bring about genetic up-gradation in one trait by the selection of the other trait of a pair. Pearson's Correlation analysis between character pairs was conducted for all traits using diverse genotypes (Table 3).

The correlation analysis showed 28 significant associations between all traits measured under study. Significant positive correlations were observed between trait pairs, panicle length (PL) and plant height (PH) (r^2= 0.589**); panicle length and grain length (GL) (r^2=0.643**), panicle length and grain length to width ratio (GR) (r^2= 0.527**). Ratna *et al*. (2015) and Anis *et al*. (2016) also reported that plant height was significantly and positively correlated with panicle length.

Plant height (PH) had significant positive associations with number of filled grains per panicle (FG) (r^2= 0.546**), total grain number per panicle (GN) (r^2= 0.391*), spikelet fertility (SF) (r^2= 0.519**) and with grain yield per plant (YP) (r^2= 0.485**).

Number of filled grains per panicle (FG) has significant association with total grains number per panicle (GN) (r^2=0.948**)and grain yield per plant (GY)(r^2=0.948**), whereas number of chaffy grains per panicle(CG) had positive association with total grains number per panicle(GN) (r^2= 0.578**), grain length to width ratio(GR) (r^2= 0.378*). Eidikohnaki *et al.* (2013), Haider *et al.* (2012), Kiani and Nematzadeh (2012), Seyoum *et al*. (2012), Akinwale *et al*. (2011), Akhtar *et al*. (2011) and Shanthi *et al.* (2011) also reported the positive association of grain yield with filled grains/panicle.

Further, positively significant associations were found between the trait pairs, total grains number per panicle(GN) and grain yield per plant (YP) (r^2= 0.578**), spikelet fertility (SF) and grain width(GW) (r^2= 0.455**), spikelet fertility and grain yield per plant (r^2= 0.316*), grain length (GL) and grain length to width ratio(GR) (r^2=0.799**),grain width and 1000-grain weight (TGW) (r^2=0.670**)(Table 4.3).Similar positive correlation observed between grains number (GN) and grain yield (YP) reported by Thorat *et al*. (2019) and Swamy *et al*. (2014).

Significant negative correlations were found between trait pairs, number of productive tillers per plant (PT) and FG (r^2= -0.331*), number of productive tillers per plant and total grains number per panicle (GN) (r^2= -0.356*). Number of filled grains per panicle with 1000-grain weight (TGW) (r^2= -0.325*), number of chaffy grains per panicle (CG) with spikelet fertility (SF) (r^2= -0.832**), with grain width (r^2= -0.481**), and with 1000-grain weight (r^2= -0.461**) had significant negative correlations.

As assumed, negative associations also found between the total grains number per panicle(GN) and 1000-grain weight(TGW) (r^2= -0.430**), spikelet fertility(SF) and grain length(GL) (r^2= -0.382*),spikelet fertility (SF) and grain length to width ratio (GR) (r^2= -0.407*),grain length (GL) and grain width(GW) (r^2= -0.423**),grain width(GW) and grain length to width ratio(GR) (r^2= -0.847**),and lastly grain length to width ratio(GR) and 1000-grain weight (TGW) (r^2= -0.424**).

Very high significant positive correlation in the present study was detected between number of filled grains per panicle(FN) and total grains number per panicle(GN) (r^2=0.948**) followed by grain length(GL) and grain length to width ratio(GR) (r^2=0.799**) while, very high significant negative correlation was detected between grain width(GW) and grain length to width ratio(GR) (r^2= -0.847**) followed by number of chaffy grains per panicle(CG) and spikelet fertility(SF) (r^2= -0.832**) (Table 3).

Li *et al*. (2019) reported that plant height, filled grain number/panicle, 1000-grain weight, plant height, panicle length, grains per panicle, seed setting rate and low seed length/width ratio have positive association on high grain yield.

Thorat *et al*. (2019) evaluated the nature and extent of correlations among yield and yield attributing characters in rice, the results revealed that grain yield per plant to be positively and significantly associated with productive tillers per plant (r^2= 0.849**), panicle length (r^2= 0.978**), total spikelets per panicle (r^2= 0.806**) and fertile spikelets per panicle (r^2= 0.979**).

Similar analyses of two rice populations by Swamy *et al*. (2014), were estimated the correlations between the trait pairs. Eighteen correlations in population 1 and 22 correlations in population 2 were found to be significant, and these were observed between plant height and number of spikelets per plant (r^2= -0.173**) in population 2, plant height and number of filled grains(r^2= 0.394**) in population 1, plant height and yield per plant(r^2= 0.405**) in population 1, number of spikelets per plant (r^2= 0.998** and r^2= 0.960**) in population 1 and 2, respectively, number of spikelets per plant and yield per plant (r^2= 0.869** and r^2= 0.554**) in population 1and 2, respectively and number of filled grains and yield per plant (r^2= 0.855** and r^2= 0.551**) in population 1and 2, respectively.

The present study, as many of earlier reports, proved that almost all the traits are interdependent and associated with multitude of traits. Hence, selections for a trait either affect gain or loss of the other. Being rice is marketed mostly based on region preference/consumer preference, it is quite obvious to keep always in mind of a breeder that the effect of selected trait on the grain quality traits.

Table 1: *Per se* Performance of the 30 rice genotypes for grain yield and its related traits and their ANOVA (*P*-value)

S.No.	Genotype	PT	PL(cm)	PH(cm)	FG	CG	GN	SF(%)	GL(mm)	GW(mm)	GR	TGW(g)	YP(g)
1	Abhaya	10.60	25.27	120.80	123.43	16.38	139.82	89.00	8.71	2.41	3.61	22.58	22.18
2	Aditya	10.60	21.93	81.20	58.58	11.60	70.18	84.00	8.81	2.77	3.18	24.69	7.90
3	AMO	11.58	24.07	101.60	158.73	34.00	192.73	83.00	8.16	2.55	3.21	21.40	25.49
4	Anjali	6.80	26.33	113.60	78.53	12.67	91.20	86.00	8.03	3.02	2.66	24.34	8.48
5	Azucena	15.00	26.13	98.42	125.58	23.92	149.50	84.00	10.41	2.91	3.57	27.71	29.47
6	Badshabhog	10.33	28.73	118.87	147.27	29.87	177.13	83.00	10.03	2.41	4.16	21.74	21.42
7	Burma Black	7.02	28.33	175.33	190.47	18.33	208.80	91.00	9.57	3.49	2.74	28.71	28.14
8	Daddiga	7.20	23.60	128.73	180.17	21.67	201.83	89.00	7.36	3.31	2.22	24.65	19.03
9	Disang	11.47	23.93	95.80	86.85	15.88	102.73	85.00	8.09	2.58	3.14	24.43	10.22
10	Haryana Basmati	8.93	22.07	87.87	137.60	29.87	167.47	82.00	8.48	2.17	3.91	15.00	16.64
11	HIM799	15.00	25.87	106.60	103.00	41.00	144.00	72.00	9.00	2.55	3.54	30.03	19.68
12	Kesari	15.53	21.13	97.60	148.80	16.67	165.47	90.00	8.14	2.53	3.22	18.54	29.93
13	Krishna	8.13	24.20	101.40	175.27	51.07	226.33	78.00	8.57	2.16	3.98	15.94	20.08
14	Luit	7.67	23.13	95.13	106.87	25.87	132.73	80.00	9.14	2.59	3.53	22.27	11.03
15	Mrunalini	10.87	28.73	130.47	189.49	49.89	239.37	79.00	9.44	2.39	3.95	22.57	32.71
16	NL1	10.67	22.87	82.47	78.87	34.87	113.73	69.00	9.80	2.45	3.99	22.78	13.59
17	NL16	9.87	25.67	109.20	101.55	28.80	130.35	78.00	9.75	2.52	3.87	26.21	19.91
18	NL3	10.53	26.13	92.67	89.25	29.50	118.75	76.00	10.36	2.68	3.87	25.35	10.74
19	NL9	11.00	26.07	82.33	75.00	27.00	102.20	74.00	10.11	2.52	4.01	26.15	14.27
20	Numali	7.00	24.33	129.60	221.63	30.58	252.22	88.00	8.14	2.81	2.90	21.23	22.39

21	Pant Sugandh 15	11.58	29.20	99.93	95.82	48.97	144.78	66.00	10.46	2.27	4.61	21.01	16.88
22	Pathariya	21.60	24.07	126.00	75.22	7.11	82.33	92.00	8.41	3.18	2.65	24.45	17.32
23	RPBio/248	12.11	27.53	117.27	128.27	23.93	152.20	84.00	8.29	2.79	2.97	26.77	25.01
24	SannaJajula	9.53	32.33	157.73	170.77	38.30	209.07	81.00	11.49	1.77	6.51	17.86	22.82
25	Savitri	7.13	22.93	93.73	140.17	42.28	182.44	77.00	9.16	2.66	3.45	23.22	21.63
26	Sharbati	13.16	25.60	109.27	126.10	25.75	151.85	83.00	9.69	2.11	4.72	20.40	18.78
27	Solumpiket	9.84	26.00	102.20	84.25	25.30	109.55	80.00	9.30	2.50	3.78	23.99	16.01
28	Taramati	9.53	22.00	100.87	170.27	59.67	229.93	74.00	7.71	2.29	3.37	16.08	13.11
29	TKM6	10.13	25.07	82.40	114.87	76.13	191.00	60.00	9.93	2.22	4.47	17.95	12.86
30	WAB-450	9.00	25.20	101.00	104.80	56.60	161.40	66.00	8.97	2.64	3.39	20.43	12.11
	Mean	**10.65**	**25.28**	**108.00**	**126.25**	**31.78**	**158.04**	**80.00**	**9.12**	**2.57**	**3.64**	**22.62**	**18.66**
	Range	**14.80**	**11.20**	**94.12**	**163.05**	**69.02**	**182.04**	**31.00**	**4.13**	**1.72**	**4.28**	**15.03**	**15.03**
	C.D.	**4.64**	**2.40**	**11.21**	**32.60**	**19.77**	**40.36**	**0.11**	**0.53**	**0.14**	**0.47**	**5.26**	**8.57**
	S.D.	**3.18**	**2.54**	**21.67**	**42.03**	**16.36**	**49.31**	**0.08**	**0.99**	**0.37**	**0.85**	**3.80**	**6.70**
	S.E.	**0.97**	**0.51**	**2.08**	**3.75**	**2.93**	**3.94**	**0.09**	**0.33**	**0.23**	**0.23**	**0.80**	**1.56**
	C.V.	**26.57**	**5.79**	**6.34**	**15.76**	**37.95**	**15.58**	**7.99**	**3.54**	**3.38**	**7.95**	**14.18**	**28.02**
	ANOVA *P*-value	**0.00****	**0.00****	**0.00****	**0.00****	**0.00****	**0.00****	**0.00****	**0.00****	**0.00****	**0.00****	**0.00****	**0.00****

PT, Number of productive per plant; PL, Panicle length; PH, Plant height; FG, Number of filled grains per panicle; CG, Number of chaffy grains per panicle; GN, Total grains number per panicle; GL, Grain length(mm); GW, Grain width(mm); GL/GW, Grain length to width ratio; TGW,1000-grain weight; YP, Yield per plant; CD, Critical difference; SD, Standard Deviation;SE, Standard error; Coefficient of variation.

Trait means, range,critical difference, standard deviation,standard error,coefficient of variation and ANOVA (*P*-Value), were done with ANOVA and Microsoft Excel Programme.

Table 2: Analysis of Variance (ANOVA) for yield and yield contributing traits

S.No	Trait	Replication Df=2	Treatment Df=29	Error Df=58	F ratio	P value
1	PT	39.39632	29.29591	8.00406	3.6601	0.000**
2	PL(cm)	3.612	18.81945	2.143035	8.7817	0.000**
3	PH(cm)	0.728007	1392.645	46.8082	29.7522	0.000**
4	FG	201.3338	5260.321	395.7462	13.2922	0.000**
5	CG	73.17824	752.1923	145.615	5.1656	0.000**
6	GN	56.29593	7037.815	606.5634	11.6028	0.000**
7	SF(%)	0.7054	1.8652	0.4094	4.5565	0.000**
8	GL(mm)	0.036743	2.791779	0.104347	26.7548	0.000**
9	GW(mm)	0.000724	0.39802	0.007573	52.5597	0.000**
10	GR	0.00772	1.940174	0.083727	23.1727	0.000**
11	TGW(g)	20.0928	42.55748	10.28684	4.1371	0.000**
12	YP(g)	25.9534	130.6254	27.34488	4.777	0.000**

PT, Number of productive per plant; PL, Panicle length; PH, Plant height; FG, Number of filled grains per panicle; CG, Number of chaffy grains per panicle; GN,Total grains number per panicle; GL, Grain length (mm); GW, Grain width (mm); GL/GW, Grain length to width ratio; TGW,1000-grain weight; YP, Yield per plant

Table 3: Correlation coefficients for yield and its related traits observed between trait pairs

Trait	PT	PL(cm)	PH(cm)	FG	CG	GN	SF(%)	GL(mm)	GW(mm)	GR	TGW(g)	YP(g)
PT	1.000											
PL(cm)	-0.028	1.000										
PH(cm)	-0.129	0.589**	1.000									
FG	-0.331*	0.121	0.546**	1.000								
CG	-0.224	0.076	-0.223	0.288	1.000							
GN	-0.356*	0.128	0.391*	0.948**	0.578**	1.000						
SF(%)	0.103	-0.044	0.519**	0.236	-0.832**	-0.075	1.000					
GL(mm)	0.099	0.643**	0.039	-0.164	0.216	-0.068	-0.382*	1.000				
GW(mm)	-0.011	-0.183	0.298	-0.027	-0.481**	-0.182	0.455**	-0.423**	1.000			
GL/GW	0.047	0.527**	-0.031	0.001	0.378*	0.126	-0.407**	0.799**	-0.847**	1.000		
TGW(g)	0.170	0.197	0.192	-0.325*	-0.461**	-0.430**	0.213	0.060	0.670**	-0.424**	1.000	
YP(g)	0.204	0.273	0.485**	0.671**	0.020	0.578**	0.316*	0.086	0.058	0.031	0.080	1.000

PT, Number of productive per plant; PL, Panicle length; PH, Plant height; FG, Number of filled grains per panicle; CG, Number of chaffy grains per panicle; GN, Total grains number per panicle, GL, Grain length; GW, Grain width; GL/GW, Grain length to width ratio; TGW,1000-grain weight and YP, Yield per plant.

Significance levels: *Significant at P <0.05, 0.317; ** Highly significant at P <0.01, 0.479

Supplementary Table 1: List of rice genotypes used in the study

S.No.	Genotype	Subspecies/Group
1	Abhaya	Indica
2	Aditya	Indica
3	AMO	Indica
4	Anjali	Indica
5	Azucena	Aromatic, Japonica
6	Badshabhog	Indica
7	Burma Black	Indica/Landrace
8	Daddiga	Indica
9	Disang	Indica
10	Haryana Basmati	Aromatic, Indica
11	HIM 799	Indica
12	Kesari	Indica
13	Krishna	Indica
14	Luit	Indica
15	Mrunalini	Indica
16	NL 1 (Nerica line 1)	*Og/os*
17	NL 16 (Nerica line 16)	*Og/os*
18	NL 3 (Nerica line 3)	*Og/os*
19	NL 9 (Nerica line 9)	*Og/os*
20	Numali	Indica
21	Pant Sugandh Dhan 15	Aromatic, Indica
22	Pathariya	Indica
23	RPBio 248	Indica/Indica wild
24	SannaJajula	Indica
25	Savithri	Indica
26	Sharbati	Indica
27	Solumpiket	Indica
28	Taramati	Aromatic, Indica
29	TKM 6	Indica
30	WAB450-24-32-P18-HB	*Og/os*

Og/Os: Oryza glaberrima/Oryza sativa

CONCLUSION

From results on character associations for grain yield and yield components, it can be concluded that selection of genotypes based on correlation analysis enhances simultaneous improvement of several yield and grain quality contributing traits in rice. This can be attributed further to the pleiotropic effect of a gene and/or involvement of common regulator factors (positive/negative gene regulation) at associated yield contributing traits, which might result in either positive or negative relationships. Thus, it is worthy to notice effect of selected/desired yield contributing trait(s) on grain quality, as ultimately the marketing of developed rice is highly influenced by the grain quality alone in rice.

Conflicts of Interest

The authors declare no conflicts of interest

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