

## Original Research Article

# ANALYSIS OF CORRELATION AND PATH CO-EFFICIENT BETWEEN YIELD AND QUALITY TRAITS IN LOWLAND RICE OF NAGALAND

### ABSTRACT

Yield and quality are among the most important traits of rice and its improvement has become the main focus of rice breeder across the country. Considering the influence of good quality rice on marketing and the need of high yielding rice variety to meet global demand of rice this research was taken up in ICAR-RC, NEH, Medziphema, Nagaland during *Kharif* 2020-2021 to evaluate the inter-relationship and association of quality and yield traits in 81 rice genotypes collected from various parts of Nagaland. Each genotype was evaluated for important yield and quality parameters. After careful analysis, the general phenotypic correlation coefficient was slightly higher than the corresponding genotypic coefficient of correlation. A significant positive correlation with grain yield was observed in no. of filled grains per panicle, days to 50% flowering, no. of panicles per plant and days to maturity. A positive association between yield traits and quality parameters were also observed. No. of filled grains per panicle, no. of panicles per plant and 1000 grains weight were detected to have high direct effect on grains yield per plant. The results of this investigation could be used for estimating direct of selection for improvement of yield and quality traits in rice breeding program.

**Keywords:** Correlation, Direct effect, Quality, Yield

### INTRODUCTION

Rice (*Oryza sativa* L.) is one of the major food crops that is consumed by more than half of the world population. It is globally grown in an area of around 154 million hectares annually with a total production of 509.2 million tons (World Food Situation, 2020). India stands as the second largest producer of rice in the world next to China, around 44.5-million-hectare area is under rice cultivation with production of 116.42 million tonnes (Agricultural Statistics, 2019). The constant growth in global population and conversion to rice as a staple food from native foods such as roots and tubers at some countries has led to an urgent need of boosting rice production at the rate of approximately 30% to meet the increasing global demands (Seck *et al.* 2019; Mohanty *et al.* 2010; Ray *et al.* 2013). The standard of living is also improving simultaneously with increase in population and this has led to the demand of superior quality of rice as the consumers are willing to purchase at higher price. This opens a gateway in global market and become a priority issue in most of the rice producing countries across the world and thus challenges plant breeders in developing a variety having a desirable grain

quality for the consumers as well as high yielding for the farmers. However, simultaneous improvement of grain yield and grain quality is difficult since there is conflict between these two important traits as much emphasis on either of them causes into poor results of the other trait (Khan *et al.*, 2015). These agriculturally important traits are controlled by polygenes and multifactorial factors that greatly depends on genetic x environmental (G x E) interactions, this made them a complex trait which are depending on additive effect of component traits. Grain yield alone is the ultimate contribution of other components such as plant height, panicle length, no. of filled grains per panicle and 1000 grains weight, the identification of these component traits and simultaneous improvement of their genotype is an important strategy in yield improvement program. Direct selection of genotypes based on their performance on grain yield alone is not an ideal strategy in crop breeding programme since grain yield is a complex character. The study of the association of yield with yield components is important for fixing up the character, which plays an ultimate role in influencing the yield (Rajeswari and Nadarajan, 2004). Therefore, measurement of relationship and association between yield and its component characters will determine the direct of selection and no. of component traits to be considered in improving grain yield. This association between them can be measured using correlation coefficients which present the degree of relationship between grain yield and its component traits as well as relationship among the component traits. Furthermore, selection based on correlation component characters is not enough as they may sometimes be misleading due to over and under-estimation. Splitting of correlation coefficient into direct and indirect effects would provide a more meaningful interpretation of such association. Therefore, estimation of path coefficient that splits the genotypic correlation coefficient into the measure of direct and indirect effects is necessary.

## **MATERIALS AND METHOD**

This present investigation was conducted in research farm and central laboratory of ICAR-RC, NEH region, Medziphema. A total of 81 germplasm collected from different region of Nagaland were laid down in Randomize Block Design at a spacing of 3 x 3 m<sup>2</sup> with three replications. A recommended management practices were followed for successful growth of plants throughout the field experiment, important yield attributing traits such as days to 50% flowering, days to maturity, plant height, panicle length, no. of panicles per plant, no. of filled grains per panicle, no. of unfilled grains per panicle, 1000 grains weight, grain yield per plant were collected from five randomly selected plants. Grain length, grain width, decorticated grain length and decorticated grain width were measured from ten grains from the sampled plant using DUS guidelines (Rani *et al.*, 2006), amylose content in each genotype were estimated using a method described by Juliano (1971), gelatinization temperature was estimated against each genotype using Little *et al.* (1958) method while, gel consistency was estimated by a method described by Cagampang *et al.* (1973). Analysis of correlation coefficient and path co-efficient was done in RStudio software.

## **RESULTS AND DISCUSSION**

The analysis of variance (Table 1) revealed significant variation among the genotypes for all the quality and yield traits indicating presence of variation among the genotypes. The coefficient of correlation at genotypic and phenotypic level is presented in Table 2. A significant positive correlation

with grain yield was observed in component traits such as no. of filled grains per panicle (0.64\*\*,0.60\*\*), days to 50% flowering (0.41\*\*, 0.40\*\*), no. of panicles per plant (0.37\*\*, 0.35\*\*) and days to maturity (0.37\*\*, 0.36\*\*). Whereas, plant height, 1000 grains weight and no. of unfilled grains per panicle show negative correlation with grain yield per plant.

Among the component traits, days to 50% flowering was recorded to exhibit a significant positive correlation with days to maturity (0.69\*\*,0.69\*\*) and no. of filled grains per panicle (0.42\*\*,0.41\*\*). Days to maturity was also recorded to have significant positive association with no. of filled grains per panicle (0.41\*\*,0.41\*\*).

No significant positive correlation was observed between grain yield per plant and quality parameters. However, among the grain quality traits, grain length shows significant positive correlation with decorticated grain length (0.83\*\*,0.82\*\*) and gelatinization temperature (0.99\*\*, 0.97\*\*), association between decorticated grain length and gelatinization temperature was also positively significant (0.83\*\*, 0.84\*\*) at both genotypic and phenotypic level. While decorticated grain width also shows significant positive correlation with grain width (0.25\*,0.25\*) and decorticated grain length (0.25\*,0.25\*).

Important yield attributes were also observed to have a significant positive correlation with grain quality traits. Association between days to maturity with grain width (0.26\*,0.26\*) and decorticated grain length (0.20\*) were observed to be significant. A significant positive correlation was also observed between 1000 grains weight with grain length (0.26\*,0.26\*) and grain width (0.34\*,0.34\*).

The pattern of the above relationship was also reported by Dhurai *et al.* (2014), Ratna *et al.* (2015) and Sadhana *et al.* (2022). However, negative relationship between days to 50% flowering and grain yield per plant was also observed by other researchers such as Mustafa *et al.* (2007), Seyoum *et al.* (2012), Faysal *et al.* (2022). Therefore, selection of those traits that have significant positive association with grain yield could be beneficial for varietal improvement for increasing grain yield.

### **Path coefficient analysis**

Even though the studies of correlation coefficient reflect association between important traits and their impact on grain yield, selection based on correlation component characters may sometimes be misleading due to over and under-estimation. Splitting of correlation coefficient into direct and indirect effects would provide a more meaningful interpretation of such association. Path analysis splits the genotypic correlation coefficient into the measure of direct and indirect effects. Therefore, correlation in combination with path coefficient analysis will be an important tool to find out the association and quantify the direct and indirect influence of one character upon another (Dewey and Lu, 1959). Path coefficient analysis provides an exact picture of the relative importance of direct and indirect effects of each of the component character towards yield.

In the present study high direct effects (Table 3) of component traits on grain yield were recorded in no. of filled grains per panicle (0.73,0.62), no. of panicles per plant (0.53,0.50) and 1000 grains weight (0.35,0.28) indicating that these traits have high contribution on increasing yield. A positive direct effect of days to 50% flowering (0.06,0.10), days to maturity (0.04,0.05), panicle length (0.08,0.06), no. of unfilled grains per panicle (0.12,0.09), grain width (0.04,0.05), decorticated grain

width (0.05, 0.03) and gel consistency (0.00,0.01) were negligible. Direct effect of plant height (-0.04, -0.06), grain length (-0.41,0.01), decorticated grain length (-0.05, -0.07), grain elongation ratio (-0.04, -0.01) and amylose content (-0.09, -0.12) were recorded to be negative at negligible level.

Days to 50% flowering (0.31, 0.25) and days to maturity (0.30, 0.24) were observed to have moderate positive effect on grain yield through no. of filled grain per panicle. Amylose content (0.11, 0.11) shows low indirect effect through no. of panicles per plant. The indirect effect of plant height (-0.20, -0.16) and panicle length (-0.13, -0.10) through no. of filled grains per panicle were recorded to be negative at low to moderate level. In the overall path analysis highest direct effect was observed in no. of filled grains per panicle (0.73, 0.62) while indirect effect of days to 50% flowering (0.31, 0.25) through no. of filled grains per panicle was highest, which suggest that improving these traits will have high positive effect on increasing grain yield. Highest negative direct effect and indirect effect was observed in grain length (-0.41, 0.01) and plant height (-0.20, -0.16) through no. of filled grain per panicle. The above findings are in conformity with the report given by Mustafa *et al.* (2007), Faysal *et al.* (2022) and Sadhana *et al.* (2022).

**CONCLUSION:** The study of correlation and path analysis can provide direction of selection. In the present study for improvement of yield, selection of yield traits such as no. of filled grains per panicle, days to 50% flowering, no. of panicles per plant and days to maturity can be effective as they have high significant positive correlation with grain yield per plant. Improvement of these characters not only ensure improvement of the yield but also simultaneous improvement on each other as they are having significant positive correlation with each other. Since no significant positive correlation between grain yield and quality traits was observed improvement of either of traits may not have positive effect on the other trait. But selection based on grain length may be effective for quality enhancement as it has a high significant positive association with decorticated grain length and gelatinization temperature. Since, correlation study can either under or overestimate the relationship between variables, the study of path co-efficient analysis is helpful in estimating direct of selection. Therefore, enhancement of yield can be expected based on selection of no. of filled grain per panicle, no. of panicles per plant and 1000 grains weight as they exhibited high direct effects on grain yield per plant.

Table 1 Analysis of variance for grain quality and yield traits

Source of Variation	Treatments	Replication	Error
<b>Df</b>	80	2	160
<b>DF</b>	386.21**	165.60	15.64
<b>DM</b>	325.24**	56.11	2.32
<b>PH (cm)</b>	2313.53**	453.60	153.06
<b>PL (cm)</b>	66.70**	14.71	1.38
<b>NPPP</b>	42.73**	0.38	0.40
<b>NFGPP</b>	5511.82**	1707.68	328.68
<b>NUFGPP</b>	2090.67**	271.59	83.58
<b>1000 GW (g)</b>	103.51**	21.25	3.15
<b>GL (mm)</b>	2.09**	0.05	0.02
<b>GW (mm)</b>	0.65**	0.01	0.01
<b>DGL (mm)</b>	1.4**	0.36	0.02
<b>DGW (mm)</b>	4.76 **	0.07	0.01
<b>GEL</b>	19.51 **	0.01	0.00
<b>AC (%)</b>	84.96 **	0.05	0.08
<b>GC (mm)</b>	2159.88**	2.74	3.58
<b>GT</b>	162.29**	1.37	6.83
<b>GY (g)</b>	671.59 **	118.08	7.37

**Df**; Degree of freedom, **DF**; Days to 50% flowering, **DM**; Days to Maturity, **PH**; Plant height, **PL**; Panicle length, **NPPP**; Panicles per plant, **NFGPP**; Filled grains per panicle, **NUFGPP**; Unfilled grains per panicle, **GW**; Grains weight, **GL**; Grain length, **GW**; Grain width, **DGL**; Decorticated grain length, **DGW**; Decorticated grain width, **GEL**; Grain elongation ratio, **AC**; Amylose content, **GC**; Gel consistency, **GT**; Gelatinization temperature, **Gy**; Grain yield per plant.

**Table 2 Genotypic (G) and Phenotypic (P) correlation coefficient of grain quality and yield traits**

Characters	DF	DM	PH	PL	NPP	NFGPP	NUFGPP	TW	GL	GW	DGL	DGW	GER	AC	GC	GT	YPP	
DF	G	1	0.69**	-0.08	-0.47	-0.05	0.42**	-0.14	0.14	0.09	0.12	0.09	0.04	-0.16	-0.28	0.04	0.09	0.41**
	P	1	0.69**	-0.08	-0.46	-0.05	0.41**	-0.14	0.15	0.09	0.10	0.10	0.05	-0.16	-0.27	0.04	0.10	0.40**
DM	G		1	-0.15	-0.49	-0.07	0.41**	-0.11	0.10	0.18	0.26*	0.19	0.05	-0.06	-0.26	-0.12	0.17	0.37**
	P		1	-0.14	-0.47	-0.07	0.41**	-0.11	0.11	0.19	0.26*	0.20*	0.05	-0.06	-0.26	-0.12	0.18	0.36**
PH	G			1	0.19	0.05	-0.28	-0.14	0.18	-0.09	0.18	-0.10	-0.12	0.12	-0.49	-0.02	-0.09	-0.15
	P			1	0.18	0.05	-0.26	-0.01	0.17	-0.12	0.18	-0.10	-0.11	0.12	-0.05	-0.02	-0.08	-0.14
PL	G				1	-0.04	-0.18	0.13	-0.10	-0.14	-0.13	-0.17	-0.18	0.16	0.20	0.18	-0.14	-0.19
	P				1	-0.04	-0.17	0.12	-0.09	-0.12	-0.12	-0.15	-0.17	0.16	0.19	0.18	-0.11	-0.18
NPP	G					1	-0.06	-0.14	-0.22	-0.18	-0.23	-0.15	-0.10	-0.10	0.21*	0.13	-0.16	0.37**
	P					1	-0.06	-0.14	-0.21	-0.17	-0.22	-0.15	-0.10	-0.09	0.20*	0.12	-0.15	0.35**
NFGPP	G						1	-0.22	-0.28	0.13	-0.02	0.10	0.05	0.03	-0.34	-0.01	0.12	0.64**
	P						1	-0.21	-0.25	0.12	-0.01	0.10	0.05	0.03	-0.32	-0.01	0.12	0.60**
NUFGPP	G							1	-0.12	0.10	0.03	0.17	0.05	0.00	-0.02	-0.08	0.10	-0.16
	P							1	-0.11	0.10	0.03	0.16	0.05	0.00	-0.02	-0.07	0.10	-0.15
TW	G								1	0.26*	0.34*	0.11	-0.11	0.14	0.14	0.15	0.24*	0.00
	P								1	0.26*	0.34*	0.12	-0.11	0.14	0.14	0.15	0.25*	0.00
GL	G									1	0.00	0.83**	0.18	-0.02	-0.30	-0.19	0.99**	0.10
	P									1	0.01	0.82**	0.19	-0.02	-0.29	-0.18	0.97**	0.09
GW	G										1	-0.03	0.25*	-0.02	-0.46	0.10	0.00	0.10
	P										1	0.00	0.25*	-0.02	-0.45	0.10	0.03	0.10
DGL	G											1	0.25*	-0.01	-0.33	-0.13	0.83**	0.04
	P											1	0.25*	-0.01	-0.32	-0.29	0.84**	0.04
DGW	G												1	-0.05	-0.32	-0.09	0.19	0.03
	P												1	-0.05	-0.32	-0.13	0.19	0.03
GER	G													1	0.07	-0.09	-0.02	-0.03
	P													1	0.07	-0.09	-0.02	-0.03
AC	G														1	0.04	-0.32	-0.22
	P														1	0.04	-0.31	-0.22
GC	G															1	-0.16	0.13
	P															1	-0.15	0.13*
GT	G																1	0.10
	P																1	0.10
YPP	G																	1
	P																	1

\*, \*\* significant at 5% and 1% level, respectively

Table 3 Genotypic (G) and Phenotypic (P) path coefficient analysis of grain quality and yield traits

Characters		DF	DM	PH	PL	NPP	NFGPP	NUFGPP	TW	GL	GW	DGL	DGW	GER	AC	GC	GT	YPP
DF	G	<b>0.06</b>	0.03	0.00	-0.03	-0.03	0.31	-0.02	0.05	-0.04	0.01	0.00	0.00	0.01	0.03	0.00	0.00	0.41**
	P	<b>0.10</b>	0.03	0.00	-0.03	-0.03	0.25	-0.01	0.04	0.00	0.01	-0.01	0.00	0.00	0.03	0.00	0.01	0.40**
DM	G	0.04	<b>0.04</b>	0.01	-0.04	-0.04	0.30	-0.01	0.04	-0.08	0.01	-0.01	0.00	0.00	0.02	0.00	0.00	0.37**
	P	0.07	<b>0.05</b>	0.01	-0.03	-0.03	0.24	-0.01	0.03	0.00	0.01	-0.01	0.00	0.00	0.03	0.00	0.00	0.36**
PH	G	0.00	-0.01	<b>-0.04</b>	0.01	0.03	-0.20	0.00	0.06	0.04	0.01	0.01	-0.01	0.00	0.00	0.00	0.00	-0.15
	P	-0.01	-0.01	<b>-0.06</b>	0.01	0.02	-0.16	0.00	0.05	0.00	0.01	0.01	0.00	0.00	0.01	0.00	0.00	-0.14
PL	G	-0.03	-0.02	0.00	<b>0.08</b>	-0.02	-0.13	0.02	-0.03	0.06	-0.01	0.01	-0.01	-0.01	-0.02	0.00	0.01	-0.19
	P	-0.05	-0.02	-0.01	<b>0.06</b>	-0.02	-0.10	0.01	-0.02	0.00	-0.01	0.01	-0.01	0.00	-0.02	0.00	0.00	-0.18
NPP	G	0.00	0.00	0.00	0.00	<b>0.53</b>	-0.05	-0.02	-0.08	0.07	-0.01	0.01	-0.01	0.00	-0.02	0.00	-0.08	0.37**
	P	-0.01	0.00	0.00	0.00	<b>0.50</b>	-0.04	-0.01	-0.06	0.00	-0.01	0.01	0.00	0.00	-0.03	0.00	-0.07	0.35**
NFGPP	G	0.03	0.02	0.01	-0.01	-0.03	<b>0.73</b>	-0.03	-0.10	-0.05	0.00	-0.01	0.00	0.00	0.03	0.00	0.09	0.64**
	P	0.04	0.02	0.02	-0.01	-0.03	<b>0.62</b>	-0.02	-0.07	0.00	0.00	-0.01	0.00	0.00	0.04	0.00	0.07	0.60**
NUFGPP	G	-0.01	0.00	0.00	0.01	-0.07	-0.16	<b>0.12</b>	-0.04	-0.04	0.00	-0.01	0.00	0.00	0.00	0.00	0.01	-0.16
	P	-0.01	0.00	0.00	0.01	-0.07	-0.13	<b>0.09</b>	-0.03	0.00	0.00	-0.01	0.00	0.00	0.00	0.00	0.00	-0.15
TW	G	0.01	-0.01	-0.01	-0.01	-0.11	-0.20	-0.01	<b>0.35</b>	-0.11	0.02	-0.01	-0.01	-0.01	-0.01	0.00	0.08	0.00
	P	0.01	0.00	-0.01	-0.01	-0.10	-0.16	-0.01	<b>0.28</b>	0.00	0.02	-0.01	0.00	0.00	-0.02	0.00	0.07	0.00
GL	G	0.01	0.01	0.00	-0.01	-0.09	0.09	0.01	0.09	<b>-0.41</b>	0.00	-0.04	0.01	0.00	0.03	0.00	-0.41	0.10
	P	0.01	0.01	0.01	-0.01	-0.09	0.08	0.01	0.07	<b>0.01</b>	0.00	-0.06	0.01	0.00	0.04	0.00	0.00	0.09
GW	G	0.01	0.01	-0.01	-0.01	-0.12	-0.01	0.00	0.12	0.00	<b>0.04</b>	0.00	0.01	0.00	0.04	0.00	0.00	0.10
	P	0.01	0.01	-0.01	-0.01	-0.11	-0.01	0.00	0.09	0.00	<b>0.05</b>	0.00	0.01	0.00	0.06	0.00	0.00	0.10
DGL	G	0.01	0.01	0.00	-0.01	-0.08	0.07	0.02	0.04	-0.34	0.00	<b>-0.05</b>	0.01	0.00	0.03	0.00	-0.04	0.04
	P	0.01	0.01	0.01	-0.01	-0.07	0.06	0.01	0.03	0.01	0.00	<b>-0.07</b>	0.01	0.00	0.04	0.00	-0.05	0.04
DGW	G	0.00	0.00	0.01	-0.01	-0.05	0.04	0.01	-0.04	-0.08	0.01	-0.01	<b>0.05</b>	0.00	0.03	0.00	0.00	0.03
	P	0.00	0.00	0.01	-0.01	-0.05	0.03	0.00	-0.03	0.00	0.01	-0.02	<b>0.03</b>	0.00	0.04	0.00	0.00	0.03
GER	G	-0.01	0.00	-0.01	0.01	-0.05	0.02	0.00	0.05	0.01	0.00	0.00	0.00	<b>-0.04</b>	-0.01	0.00	0.00	-0.03
	P	-0.02	0.00	-0.01	0.01	-0.05	0.02	0.00	0.04	0.00	0.00	0.00	0.00	<b>-0.01</b>	-0.01	0.00	0.00	-0.03
AC	G	-0.02	-0.01	0.00	0.02	0.11	-0.25	0.00	0.05	0.12	-0.02	0.02	-0.02	0.00	<b>-0.09</b>	0.00	0.03	-0.22
	P	-0.03	-0.01	0.00	0.01	0.11	-0.20	0.00	0.04	0.00	-0.02	0.02	-0.01	0.00	<b>-0.12</b>	0.00	0.03	-0.22
GC	G	0.00	-0.01	0.00	0.01	0.07	-0.01	-0.01	0.05	0.08	0.00	0.02	-0.01	0.00	0.00	<b>0.00</b>	0.00	0.13
	P	0.00	-0.01	0.00	0.01	0.06	-0.01	-0.01	0.04	0.00	0.00	0.02	0.00	0.00	0.00	<b>0.01</b>	0.00	0.13*
GT	G	0.00	0.00	0.00	0.01	-0.08	0.09	0.01	0.08	-0.41	0.00	-0.04	0.00	0.00	0.03	0.00	<b>0.40</b>	0.10
	P	0.01	0.00	0.00	0.00	-0.07	0.07	0.00	0.07	0.00	0.00	-0.05	0.00	0.00	0.03	-0.00	<b>0.01</b>	0.10

Residual effect = 0.30 (Genotypic), 0.37 (Phenotypic), Bold; Direct effects, Normal; Indirect effects, \*, \*\* significant at 5% and 1% level respectively

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