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Correlation study of yield and yield related traits of doubled haploid rice lines (*Oryza sativa* L.)

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Abstract

In the experiment was done to investigate the correlation analysis of 10 traits, namely the number of days 50% flowering, plant height, total production tiller per hill, ear length, grain length, grain width, grain ratio 1000 seeds weight, also known as test weight, days to first harvest, and yield of a single plant among 64 rice DH lines and 2 parents. The genotype correlation coefficient is larger than the phenotypic correlation coefficient, indicating the masking or altering effect of the environment. Genetic correlations showed that single plant yields had a strong positive and significant association with total productive tiller at the genotype level. From this it can be concluded that the total grain yield and total productive tiller can be used as a selection criterion for improving grain yield per plant. Therefore, traits should be considered in breeding programs to develop maximum threshold yields for new rice varieties or hybrids.

Keywords: Correlation, doubled haploid, rice, variability, genotypic correlation coefficient, phenotypic correlation coefficient

Introduction

Rice (*Oryza sativa*) is one of the most important cereal crop in the world with increased consumption mainly due to population growth, urbanization and economic growth [1]. The global rice productivity is rising at a rate of 1% per year instead of the needed 2.4% per year in order to double production by 2050. It is the second most widely consumed food grain after wheat [2] and provides 20% caloric intake worldwide [3].

It is an important cereal crop, grown under diverse agro ecological conditions. It is also a major food crop, as it ranks second to wheat among the most cultivated cereals in the world. To feed the ever-growing population, the targeted rice production of World, China and India for the year 2030 were envisaged as 771.02, 168.90 and 130.02 million tonnes respectively.

The development of Anther culture techniques for production of rice was a major advance in the field of rice breeding in the last few decades and Anther culture is one of the most intensively investigated areas of *in vitro* culture methods of rice, as doubled haploid approach can effectively reduce the time required for varietal improvement [4].

A successful breeding program depends on the genetic diversity of a crop for achieving the goal so improving the crop and producing high yielding varieties [5]. Grain yield is a complex polygenic quantitative trait, greatly affected by environment and determined by the magnitude and nature of their genetic variability [6].

Correlation coefficient measures the relationship between two variables [7]. It simply measures mutual association without regard to causation [8]. Phenotypic and genetic correlations are commonly used in plant breeding. Phenotypic correlations involve both genetic and environmental effects [9]. Correlation analysis is a handy technique, which provides information that selection for one-character results in progress for other positively correlated characters [10]. The importance of correlation studies in selection programs is appreciable when highly heritable characters are associated with the important characters like yield.

Correlation coefficients, although very useful in quantifying the size and direction of trait associations, can be misleading if the high correlation between two traits is a consequence of the indirect effect of other traits [11]. The estimates of correlation coefficients reveal only the relationship between yield and yield associated traits, but could not explain the direct and indirect effects of different traits on yield. This is because the attributes that are in association do not exist by themselves, but are linked to other components traits.

Materials and Methods

A field experiment was conducted using 64 doubled haploids rice lines developed from the cross of Mahulata x IR20 with the two parent Mahulata and IR20, at ICAR- National Rice Research Institute, Cuttack during 2021 *kharif* cropping season. Randomized complete block design (RCBD) was used for the assessment. The two parents were taken as the check. The experimental material was planted in two blocks. Each block consisted of 66 rice lines randomized and replicated within each block. Twenty-seven days old seedlings were transplanted 20cm apart between rows and 15cm within the row. All necessary precautions were taken to maintain uniform plant population in each treatment per replication. All the recommended package of practices was followed along with necessary prophylactic plant protection measures to raise a good crop.

Data Collection and Analysis

Data was collected on days to 50% flowering, plant height, total productive tiller per hill, panicle length, grain length, grain width, ratio of grain 1000 seed weight which is also known as test weight, days to first harvest and single plant yield.

All the data were collected, Analysis of variance (ANOVA) was carried out on the data to assess the genotypic effects and their interaction using general linear model (GLM) procedure for randomized complete blocks design (RCBD) using R-studio software with variability package. Mean comparisons among treatment means were conducted by the least significant difference (LSD) test at 5% levels of significance. The RCBD design analysis of variance was used to derive variance components as structured in Table 1^[12].

Estimation of Phenotypic and genotypic correlation coefficient (r)

The phenotypic and genotypic correlation coefficients between two variables including genotype were estimated as described by^[13]. Correlation coefficients at genotypic level (rgxy) were calculated as;

$$rgxy = \frac{GCOV_{xy}}{\sigma^2_{gx} \times \sigma^2_{gy}}$$

Where

rgxy = genotypic correlation coefficient between traits x and y

GCOV_{xy} = genotypic covariance between traits x and y

σ^2_{gx} = genotypic variance of trait x

σ^2_{gy} = genotypic variance of trait y

Correlation coefficients at phenotypic level (rpxy) were calculated as;

$$rpxy = \frac{PCOV_{xy}}{\sigma^2_{px} \times \sigma^2_{py}}$$

Where

rpxy = phenotypic correlation coefficient between traits x and y

PCOV_{xy} = phenotypic covariance between traits x and y.

σ^2_{px} = phenotypic variance of trait x

σ^2_{py} = phenotypic variance of trait y

The calculated phenotypic correlation value was tested for its significance using t-test:

$$t = r_{ph}/SE (r_{ph})$$

Where, r_{ph} = Phenotypic correlation; SE (r_{ph}) = Standard error of phenotypic correlation was obtained using the following formula^[14].

$$SE (r_{ph}) = \sqrt{(1-r^2_{ph})/(n-2)}$$

Result and Discussion

Analysis of variance (ANOVA)

The results of RCBD analysis were presented in table 1. The analysis of variance suggested that there was a significant variation among the DH lines for all the traits under study. The significant differences observed among the lines imply that there is diversity within these lines and that is vital in crop breeding, as superior ones are there to be advanced and/or be used as parents during hybridization.

Direct selection for yield is not effective as yield is a complex and quantitatively inherited character with low heritability. Therefore, indirect selection could be made for the component characters contributing to yield through character association as it provides information about the characters that are correlated with each other in improving yield. Estimates of correlation between yield and yield component characters in rice genotypes are presented in table 2.

Table 1: Analysis of variance for different traits under study

Traits	RMSS (1)	TMSS (65)	EMSS (65)
DFE	0.03	80.55**	3.34
PH (cm)	222.56	473.44**	10.77
TPT	0.924	60.1**	0.205
PL (cm)	133.0	8.82**	6.11
GL (mm)	0.02	0.66**	0.1
GW (mm)	0.02	0.19**	0.01
L/B	0.01	0.26**	0.004
TW (mg)	2.01	7.98**	0.001
DFH	0.27	143.11**	2.56
SPY (g)	40.41	98.15**	6.04

Estimates of correlation coefficients at phenotypic and genotypic levels

In present study the correlation analyses revealed that, the genotypic correlation coefficients were higher than the phenotypic correlation coefficients demonstrating that, the observed relationships among the various traits were due to genetic causes indicating the phenotypic expression of correlations is reduced under the influence of the environment. This is also in agreement with the findings of the previous findings^[15, 16].

A positive value of correlation shows that the changes of two variables are in the same direction, i.e., high value of one variable are associated with high values of the other and *vice versa*. The breeder is always concerned for the selection of superior genotypes on the basis of phenotypic expression. However, for the quantitative characters, genotypes are influenced by environment, thereby affecting the phenotypic expression. Information regarding the nature and extent of association of morphological characters would be helpful in developing suitable plant type, in addition to the improvement of yield a complex character for which direct selection is not effective. In general, the genotypic and the 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 [17]. In our investigation days to 50 percent flowering was registered positive and significant correlation with days to first harvest at both genotypic and phenotypic level suggesting if 50 percent flowering is earlier then the harvesting will be earlier and *vice versa*. Same type of results was reported by Venkata [18]. Again, 50 percent flowering was phenotypically positively correlated with plant height and grain length.

Also, plant height was genotypically and phenotypically directly correlated with panicle length, grain length and days to first harvest significantly. Similar reports were reported [19] for significance and positive correlation in panicle length at phenotypic level, Thippeswamy [20] for positive significant correlation in panicle length. The results clearly indicated that long duration genotypes would be tall yet contribute less grain yield. Similar result were reported for days to first flower had positive significant correlation with plant height at both levels

[21, 20].

Grain length was genotypically directly related to L/B ratio whereas grain width was directly correlated with L/B ratio both at genotypic and phenotypic level significantly.

Total number of productive tillers was found to be positively correlated significantly with grain length at phenotypic level only and with single plant yield genotypically while negative and non-significant association with 1000 grain weight. The results were in unison with the previous findings [22, 23, 24]. It indicated that grain yield can be increased whenever there is an increase in characters that showed positive and significant association with grain yield. Hence, these characters can be considered as criteria for selection for higher yield as these were mutually and directly associated with yield.

Panicle length had highest direct correlation with grain length and days to first harvest both at genotypic and phenotypic level, whereas only genotypically directly related with grain width and test weight. Therefore, this trait can be used in selection for yield improvement in rice.

Table 2: Estimation of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients between yield and yield related traits in 64 DH lines rice lines and 2 parents

	DFF	PH(cm)	TPT	PL (cm)	GL (mm)	GW (mm)	L/B	TW (mg)	DFH	SPY(g)
DFF	1	0.200	-0.166	0.153	0.227	-0.051	0.166	0.049	0.315**	-0.022
PH(cm)	0.179*	1	0.121	0.764**	0.354**	0.061	0.175	0.176	0.254 *	-0.082
TPT	-0.165	0.119	1	0.102	0.178	0.055	0.075	-0.094	-0.151	0.109*
PL (cm)	0.079	0.330**	0.044	1	0.922**	0.437**	0.146	0.254*	0.436**	0.073
GL (mm)	0.209 *	0.33 **	0.1724 *	0.342**	1	0.105	0.51 **	0.072	0.147	-0.137
GW (mm)	-0.055	0.05	0.0485	0.094	0.152	1	-0.791**	-0.064	0.052	0.014
L/B	0.161	0.171	0.0774	0.111	0.467**	-0.79 **	1	0.098	0.005	-0.087
TW (mg)	0.048	0.171*	-0.094	0.111	0.07	-0.063	0.098	1	-0.009	0.006
DFH	0.294**	0.24**	-0.151	0.179 *	0.151	0.065	-0.008	-0.007	1	0.039
SPY(g)	-0.014	-0.081	0.102	0.009	-0.126	0.014	-0.084	0.006	0.051	1

*,** Indicate significance at 0.1 and 0.05 probability levels, respectively.

Where: DFF=Days to 50% flowering, PH= Plant height, TPT= total productive tillers, PL=Panicle length, GL= Grain length, GW= Grain width, L/B= ratio of grain length and width, TW= Test weight, DFH= Days to first harvest, SPY= Single plant yield

cm= Centimeter, mm= millimeter, mg= milligram, g= gram

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