



Variability and correlation among yield and yield component traits in rice (*Oryza sativa* L.)

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ABSTRACT

Investigation was carried out to study the genetic variability and correlation among yield and yield component traits with forty-eight rice genotypes at Regional Agricultural Research Station, Maruteru, West Godavari. A high phenotypic coefficient of variation compared to the genotypic coefficient of variation was observed for all the traits studied which indicates the influence of environment in the expression of the trait. High heritability coupled with high genetic advance as per cent of the mean was recorded for traits like test weight, grain yield/plant and number of filled grains/panicle indicating the predominance of additive gene action. Hence, direct phenotypic selection may be fruitful for the improvement of these traits. Correlation studies revealed grain yield/plant positively correlated with number of ear bearing tillers/m², number of filled grains/panicle, panicle length and test weight. Positive direct effect was exhibited by the trait's days to maturity, number of filled grains/panicle, number of ear bearing tillers/m² and test weight. Hence, direct selection for these traits would simultaneously improve the grain yield/plant.

Keywords: Correlation, Genetic advance, Heritability, Path Analysis, Rice and Variability

Rice (*Oryza sativa* L., 2n=24) is a self-pollinated, short day, monocotyledonous angiosperm belonging to the genus *Oryza* of the family Poaceae. In India it is occupying a significant portion of cultivated land and supporting millions of farmers (Gupta, 2024). Globally rice production reached 495.78 million tons in recent years, with the projections of 525 million tons by 2050 (Salihi *et al.*, 2024). In India, rice production reached 149.07 million tonnes and average yield of rice was 2899 kg/ha according to 2024-25 crop season.

The success of any crop improvement program relies on the genetic variability present in the material. Relying solely on phenotypic selection based on performance might not always be effective, as these genotypes could underperform in future generations. Therefore, selecting genotypes based on their genetic potential, which includes factors like heritability and genetic advance, is crucial. Genetic variability combined with heritability estimates helps in predicting the expected genetic gains from selection. Understanding variability and heritability is essential for developing effective selection criteria to enhance seed yield and its related traits. Heritability estimates, when paired with genetic advance, are typically more

useful for predicting gains from selection than heritability estimates alone.

Correlation refers to the relationship between two variables and measures the strength and direction of this relationship. In plant studies, this analysis helps to identify important traits linked to yield, guiding selection for genetic improvement. However, relying solely on correlation might not yield accurate results. To better understand how traits influence yield, both directly and indirectly, path coefficient analysis is used. This method clarifies the cause-and-effect relationships between traits and yield. Therefore, combining correlation and path analysis provides deeper insight and can lead to more effective selection for yield improvement. Thus, the present study was undertaken with the objective to study the variability, correlation and direct and indirect effects of yield component traits on yield in rice genotypes.

MATERIALS AND METHODS

The experiment was conducted at Regional Agricultural Research Station Maruteru. The experimental material for this investigation included 48 rice genotypes including two yield checks (MTU 1156 and MTU 1121). Twenty-five-days-old

Table 1. List of genotypes used in the present study

S. No	Genotype	S. No	Genotype	S. No	Genotype
1	MTU 3002-15-2-1-2	17	MTU 3006-1	33	MTU 3006-11
2	MTU 2994-26-2-2-1	18	MTU 3004-1	34	MTU 3006-3
3	MTU 2993-26-1-1-1	19	MTU 3003-2	35	MTU 3004-7
4	MTU 2992-11-1-1-1	20	MTU 3004-8	36	MTU 3007-12
5	MTU 2992-6-1-2-1	21	MTU 2995-3-2-1-1	37	MTU 2994-28-2-1-1
6	MTU 2993-9-1-1-1	22	MTU 3003-5	38	MTU 3005-5
7	MTU 2995-3-2-1-2	23	MTU 3003-19	39	MTU 3006-4
8	MTU 2994-19-1-1-1	24	MTU 3006-8	40	MTU 3054-1-17
9	MTU 2993-25-2-1-1	25	MTU 3005-4	41	MTU 3055-1
10	MTU 2995-30-1-1-1	26	MTU 3006-7	42	MTU 3056-1
11	MTU 2943-16-1-1-2	27	MTU 3004-15	43	MTU 1156
12	MTU 3000-21-1-1-1	28	MTU 3004-27	44	MTU 1293
13	MTU 3000-7-1-2-1	29	MTU 3007-3	45	MTU 1121
14	MTU 2940-40-1-2-1	30	MTU 3004-10	46	TN-1
15	MTU 3004-17	31	MTU 3006-15	47	PTB-33
16	MTU 3004-26	32	MTU 3007-6	48	BM-71

seedlings of the genotypes were transplanted in Alpha Lattice Design in two replications by adopting a spacing of 20×15 cm between and within the rows. All the recommended packages of practices and need-based plant protection measures were followed to raise a healthy crop. At various stages of plant growth, data was recorded on days to 50% flowering, days to maturity, plant height, number of ear bearing tillers/m², panicle length, number of filled grains/panicle, test weight and grain yield/plant. The analysis of genetic parameters was performed on the mean data using established statistical methods. Correlation coefficients were estimated according to Johnson *et al.* (1955), while path coefficient analysis was conducted using the Wright (1921) and Dewey and Lu (1959), to quantify the direct and indirect influences of individual characters on yield.

RESULTS AND DISCUSSION

Analysis of variance for yield and yield component traits indicated significant differences among the genotypes for all the eight traits. The genotypic and phenotypic coefficients of variation (GCV and PCV), heritability and genetic advance as per cent of mean values were obtained for various yield components and were presented in Table 2. In the present study high heritability coupled with high genetic advance as per cent of the mean was recorded

for traits like test weight, grain yield/plant and number of filled grains/panicle indicate the predominance of additive gene action. Hence, direct phenotypic selection may be fruitful for the improvement of these traits. High heritability coupled with moderate genetic advance as per cent of mean was exhibited by plant height, ear-bearing tillers/m² and panicle length indicate that these characters were governed by both additive and non additive gene action and further improvement of these characters would be effective through hybridization followed by selection.

High heritability coupled with low genetic advance was exhibited by days to 50% flowering and days to maturity indicate that these characters were governed by non-additive gene action. The high heritability may be due to the influence of the environment rather than the genotype hence, simple selection for the above traits may not be rewarding.

The results obtained from statistical analysis under the correlation studies among yield and yield-component traits Table 3 revealed that a positive non significant association was observed for test weight. Days to 50 % flowering exhibited positive significant association with days to maturity ($r_g=0.8868^{**}$) ($r_p=0.8825^{**}$) at both genotypic and phenotypic level. It indicated that increase in days to 50% flowering would lead to increase in days to maturity as well as plant height where as in return increase in days to

Table 4. Direct and Indirect effects of yield and yield attributing traits on grain yield/plant in rice genotypes at genotypic level

TRAITS	DFE	DM	PH	No-EBT	PL	NFGP	TW	GYP
DFE	-0.5475	0.3997	-0.0415	0.08910	0.0550	-0.0163	-0.1255	-0.1871
DM	-0.4856	0.4508	-0.0457	0.06470	-0.0352	0.0691	-0.1823	-0.1642
PH	-0.1104	0.1000	-0.2060	0.03350	-0.1447	0.0351	-0.0585	-0.3510 *
No EBT	0.3000	-0.0600	0.1116	0.21300	0.1961	0.0971	-0.0110	0.7468 *
PL	0.1244	0.0271	-0.0120	0.02430	-0.2050	0.1120	0.3663	0.4371
NFGP	0.1060	0.2757	-0.0150	-0.09500	-0.1200	0.4114	-0.2970	0.2661
TW	0.1014	-0.1212	0.0177	0.00900	-0.3169	-0.1770	0.6779	0.1909

Residual effect : 0.34

DFE-Days to 50% flowering, **DM**-Days to maturity, **PH**-Plant height, **NoEBT**-Number of ear bearing tillers/m², **PL**-Panicle length **NFGP**-Number of filled grains/panicle, **TW**- Test weight, **GYP**- Grain yield/plant, * significant at 5% level and Diagonal bold values indicate direct effect.

Table 5. Direct and Indirect effects of yield and yield attributing traits on grain yield/plant in rice genotypes at phenotypic level

TRAITS	DFE	DM	PH	NoEBT	PL	NFGP	TW	GYP
DFE	-0.2813	0.1320	-0.0460	0.0482	0.0116	-0.0060	-0.0389	-0.1804
DM	-0.2482	0.1495	-0.0508	0.0358	-0.0036	0.0209	-0.0579	-0.1543
PH	-0.0477	0.0280	-0.2713	0.0177	-0.0275	0.0100	-0.0216	-0.3124 **
No EBT	0.0416	-0.0164	0.0147	0.3259	0.1052	0.1351	-0.0065	0.6996 *
PL	0.0229	0.1237	-0.0101	0.1124	-0.1430	0.0363	0.1200	0.4622
NFGP	0.2101	0.0187	-0.0115	-0.0589	-0.1101	0.1672	-0.0824	0.2331
TW	0.0450	-0.0355	0.0241	0.0088	-0.0589	-0.0565	0.2437	0.1707

Residual effect : 0.39

DFE-Days to 50% flowering, **DM**-Days to maturity, **PH**-Plant height, **NoEBT**-Number of ear bearing tillers/m², **PL**-Panicle length, **NFGP**-Number of filled grains/panicle, **TW**- Test weight, **GYP**- Grain yield/plant, * significant at 5% level and Diagonal bold values indicate direct effect

with it. Similar results were reported by Priyanka *et al.* (2019).

Panicle length recorded positive non-significant with days to maturity ($r_g=0.0602$) ($r_p=0.0253$) and plant height ($r_g=0.2467$) ($r_p=0.1923$) at both genotypic and phenotypic level. Number of filled grains/panicle exhibited positive non-significant association with days to maturity ($r_g=0.168$) ($r_p=0.1251$), plant height ($r_g=0.0854$) ($r_p=0.0599$). It showed positive non-significant association ($r_g=0.2357$) genotypically, but it showed significant positive association ($r_p=0.2100^*$) phenotypically with number of ear bearing tillers/m², positive non-significant association ($r_g=0.2286$) at genotypically and positive significant association ($r_p=0.2171$) at phenotypically with panicle length. Similar results were reported by Sameera *et al.* (2016) for plant height.

Path analysis revealed that days to maturity (0.4508) (0.1495), number of filled grains/plant (0.4114) (0.1672), number of ear bearing tillers/m² (0.2130) (0.3259) and test weight (0.1910) (0.2437) exhibited positive direct effect on grain yield/plant at both genotypically and phenotypically. Similar results were reported by Archana *et al.* (2018), Heera *et al.* (2023) and Thuy *et al.* (2023).

Negative direct effect was exhibited by days to 50% flowering, plant height and panicle length on grain yield/plant at both genotypically and phenotypically. However, number of ear bearing tillers/m² (0.7468*), panicle length (0.4371), number of filled grains/panicle (0.2661) and test weight (0.1909) had positive association with grain yield/plant.

Since correlation coefficient and direct effect are positive for number of ear bearing tillers/m²,

number of filled grains/panicle and test weight, selection process on these traits will give desirable outcome.

The residual effect at the genotypic level is 0.34 indicating that the characters included in the present investigation are contributing around 66% of variability pertaining to the dependent variable *i.e.*, yield. Remaining 34% of the contribution is from the few other characters which are not included in the present study.

The residual effect at the phenotypic level is 0.39 indicating that the characters included in the present investigation are contributing around 61% of variability pertaining to the dependent variable. 39% of the contribution is from a few other characters which are not included in the present study.

CONCLUSION

The analysis of genetic variability in this experiment revealed that high phenotypic coefficient of variation compared to the genotypic coefficient of variation was observed for all traits. High heritability coupled with high genetic advance as per cent of mean was observed for variables such as test weight, grain yield/plant and number of filled grains/panicles in the current study. Therefore, the enhancement of these qualities may benefit from direct phenotypic selection. High heritability coupled with moderate genetic advance as per cent of mean was exhibited by plant height, ear-bearing tillers/m² and panicle length indicate that these characters were governed by both additive and non additive gene action and further improvement of these characters would be effective through hybridization followed by selection. High heritability coupled with low genetic advance as per cent of mean was observed for days to 50% flowering and days to maturity. The heritability was exhibited due to favourable influence of environment rather than genotype and indicating the possibility of improvement of these traits through heterosis breeding as simple selection would be ineffective.

Correlation among traits revealed grain yield/plant was positively correlated with the number of ear bearing tillers/m², panicle length, number of filled grains/panicle and test weight indicating that enhancing traits would lead to improvement of grain yield/plant.

The results of path analysis revealed a positive direct effect exhibited by days to maturity, number of ear bearing tillers/m², number of filled grains/panicle and test weight on grain yield/plant at both

genotypical and phenotypical level. Number of ear bearing tillers/m² recorded positive significant association on grain yield/plant at genotypic level. Hence direct selection for the traits would be recommended for yield improvement in rice improvement programmes. High direct effects of the traits therefore appear to be the main factor for their association with grain yield/plant. Hence, these traits should be considered as an important selection criterion and direct selection for the traits is recommended for yield improvement in rice improvement programmes.

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Received on 06.08.2025 and Accepted on 15.09.2025