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Delineating the Association of Component Traits and their Effects on Yield in Elite Rice (*Oryza sativa* L.) Genotypes of Telangana and Andhra Pradesh

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Abstract

The current study was conducted at Seed Research and Technology Center (SRTC), Professor Jayashankar Telangana State Agricultural University, Hyderabad, Telangana state, India to understand traits association with yield components and their direct and indirect influence on seed/grain yield during the *khari* season (July to November) 2018–19. Eighteen elite rice genotypes were evaluated for eight yield attributing traits in randomized complete block design (RCBD) with three replications. Correlation study among the genotypes reveals that, genotypic correlation coefficients were slightly higher than phenotypic correlation coefficients for most traits showed the influence of genetic composition on the lines' expression. Highly significant and positive strong correlation observed for days to maturity and days to 50% flowering (0.8955 and 0.8230), while moderate positive correlation observed for productive tillers plant⁻¹ and panicle length (0.5744 and 0.3571) at genotypic and phenotypic level respectively. However, Seed yield plant⁻¹ depicted a strong and positive correlation with thousand seed weight (0.4048 and 0.3895), while very low with number of productive tillers plant⁻¹ (0.0579 and 0.0524) at the phenotypic and genotypic levels. The results of path analysis revealed that the thousand seed weight has a high and significant genotypic (0.3286*) and phenotypic path coefficient value (0.3198) indicates high positive direct effects on the seed yield and days to 50% flowering (0.2252) shows strong and positive direct impact on the seed yield. These traits could be used as selection criteria to improve the grain yield and grain quality in the rice breeding programs.

Keywords: Character association, path analysis, rice, yield component traits

1. Introduction

Rice (*oryza sativa* L.) is one of the most important leading cereal grain produced, consumed and traded in the world after wheat, as a source for food and nourishment (Fukagawa *et al.*, 2019). Being staple food for more than half of the world, it producing globally (on a milled basis) around 520.5 mt (Anonymous, 2022). India has shown a tremendous increase in its rice production over the past few decades and this trend has continued in recent years. In India, it is grown on around 45.5 m.ha area with estimated production of 124.0 MT during 2022-23 crop seasons (Anonymous, USDA, 2022-23). A number of complex variables, including polygenes, the environment, and genetic variability, have an impact on yield (Iqbal *et al.*, 2015, Devi *et al.*, 2017, Usman *et al.*, 2017, Zeng *et al.*, 2017, Abhilash *et al.*, 2018). Given the intricacy of yield and the interactions it has with

other yield-enhancing traits, selection for increased grain yield should not be just based on yield. As a result, several component traits that increase yield should be taken into account (Gour *et al.*, 2017, Zhou *et al.*, 2018, Tome *et al.*, 2019). In rice, both direct features like panicle number per unit area and/or per plant, filled grains per panicle, and 1000-grain weight, as well as indirect traits like plant height, growth time, tillering ability, panicle length, seed length, seed setting rate, and grains per panicle, determine yield (Huang *et al.*, 2013, Islam *et al.*, 2021). In order to formulate suitable criteria for direct and indirect selection through components when breeding for high yielding crop varieties, information on the extent of association between various plant characters and seed yield is required (Fischer and Rebetzke, 2018). Rice breeding strategy is influenced by the degree of associated characters, as well as the size



and nature of variation (Akhtar et al., 2011). The majority of breeder-relevant traits are complex, the result of multiple factors interacting (Singh et al., 2015, Zhou et al., 2018, Sanghamitra et al., 2021). Understanding the relationship between yield and its constituents is critical to making the most of these relationships in selection. Correlation and path analysis determine the degree of link between the qualities of interest and their attributes, as well as the relative relevance of direct and indirect effects, allowing for a clear understanding of their relationship with the traits of interest. The mutual relationship between variables is described as correlation, and it aids in determining the most effective strategies for picking superior genotypes. Breeding strategies would be quite effective if there was a positive correlation between main yield components, but selection would be very challenging. Due to mutual cancellation of component features, estimates of correlation coefficients alone might be misleading (Aye and Htwe, 2019). The virtue of path analysis developed by wright (1921) is that it enables the partition of the correlation coefficient into its components. According to Dewey and Lu (1959), first element in the path coefficient represents the direct impact of a predictor variable on its response variable (Pearl, 2022). The second element is the indirect impact (s) of a predictor variable via the predictor variables on the response variable. The most effective method for determining the relationships between crucial yield components is correlation in conjunction with path coefficient analysis (Sofiya et al., 2020). In light of the foregoing, the current research was conducted to investigate the inter-relationship between yield and yield attributing traits in order to reveal the associated characters that can assist breeders in developing appropriate breeding plans for genotype selection and to assess the direct and indirect effects of various components on grain yield.

2. Materials and Methods

The current study includes a total of eighteen rice genotypes that were commercially farmed in the Indian states of Telangana and Andhra Pradesh, India have a high market demand, and are in the regular seed chain. Table 1 provides information on the genotypes as well as the names of the centers where they were developed and released. The Nucleus seeds of selected genotypes obtained from the respective research stations were raised at Seed Research and Technology Center (SRTC), Professor Jayashankar Telangana State Agricultural University, Hyderabad, Telangana State, India (17.3226° N, 78.4172° E and 559 meter above MSL) during *kharif* (July to November 2018–19).

In a randomized complete block design (RCBD) with three replications, 25–30 day old seedlings of each genotype were transplanted in 4 rows of 4 meters length with a spacing of 30 cm between rows and 20 cm between plants were followed. All the necessary precautions and management practices were adopted to maintain uniform plant population. Days to 50%

flowering, productive tillers plant⁻¹, thousand seed weight (g), plant height (cm), grains panicle⁻¹, panicle length (cm), days to maturity, and seed yield plant⁻¹ (g) were among the yield and yield contributing variables are recorded. For each entry in each replication, 10 randomly selected plants were observed for plant height, panicle length, productive tillers plant⁻¹, and number of filled grains panicle⁻¹. However, days to 50% flowering, Days to maturity and seed yield were recorded on plot basis. In contrast, observations for thousand seed weight were obtained from a random grain sample drawn from each plot in each entry and replication. The standard statistical procedures of Singh and Chaudhary (1979) and Dewey and Lu (1959) were used to estimate correlation coefficients and path analysis respectively.

Table 1: List of rice genotypes and research centers where they developed and released

Genotypes	Name of the research center
JGL 1798, JGL 3855, JGL 11470, JGL 18047, JGL 11118, JGL 17004 and JGL 24423	Regional Agricultural Research Station, Polasa, Jagtial
KNM 118	Agricultural Research Station, Kunaram, Karimnagar District
RNR 15048, Tellahamsa, RNR 2458 and RNR 2465	Rice Research Unit, Rajendranagar, Hyderabad
WGL 44, Ramappa and WGL 32100	Regional Agricultural Research Station, Warangal
BPT 5204 and MTU 1010	Acharya N. G. Ranga Agriculture University, Bapatla and Maruteru
KPS 2874	Agricultural Research Station, Kamapasagar, Nalgonda District

3. Results and Discussion

3.1. Correlation analysis

The interrelationship of several traits with yield and among themselves makes it easier to evaluate high yielding and higher performing genotypes in a selection procedure. For most traits analysed in this study, genotypic correlation coefficients were higher than phenotypic correlation coefficients, with the exception of a few cases where they were similar or the difference was insignificant (Table 2). This shows the influence of genetic composition on majority of the lines' expression.

Days to 50% flowering exhibit positive and significant correlation with days to maturity (0.8955^{***}) at both phenotypic and genotypic level (0.8230^{***}) respectively. Some previous studies reveal that significant and positive association of days to 50% flowering with plant height, the number of ear bearing tillers plant⁻¹ (Tejaswini et al., 2018). Tillers plant⁻¹ exhibited positive and significant correlation with panicle length (0.5744^{**}). Accompanying panicle



Table 2: Phenotypic and genotypic correlation for eight yield attributing traits in rice

Traits	G/P	Days to 50% flowering	Tillers plant ⁻¹	Thousand seed weight (g)	Plant height (cm)	Grains panicle ⁻¹	Panicle length (cm)	Days to Maturity	Seed yield plant ⁻¹ (g)
Days to 50% Flowering	P	1	0.1849	-0.2582	0.2017	0.1036	0.0860	0.8230***	-0.4092
	G	1	0.1982	-0.2754	0.2202	0.1785	0.1136	0.8955***	-0.4519
Tillers plant ⁻¹	P		1	-0.0428	0.1863	0.1101	0.3571**	0.0744	0.0524
	G		1	-0.0433	0.2229	0.1963	0.5744**	0.0733	0.0579
Thousand seed weight (g)	P			1	0.1520	0.0415	-0.0728	-0.2983*	0.3895
	G			1	0.1526	0.0487	-0.0892	-0.3254*	0.4048
Plant height (cm)	P				1	-0.0301	0.1401	0.0287	-0.1361
	G				1	-0.0519	0.1876	0.0534	-0.1404
Grains panicle ⁻¹	P					1	0.0363	-0.0439	-0.0276
	G					1	-0.0235	-0.1039	0.0031
Panicle length (cm)	P						1	0.1386	-0.0813
	G						1	0.1916	-0.0406
Days to maturity	P							1	-0.4455
	G							1	-0.4812

* $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$; If correlation $r \Rightarrow$ 0.26808 0.34763 0.37662 0.43539

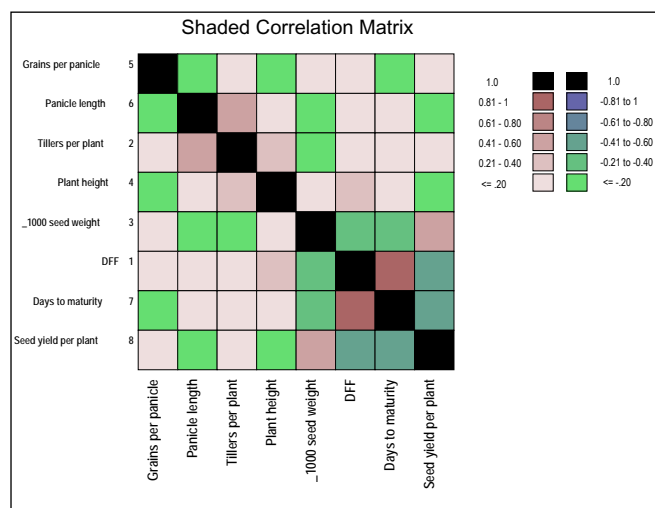
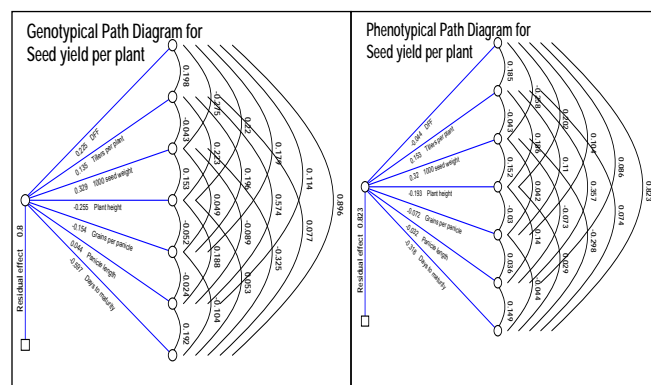


Figure 1: Correlogram visualizing the correlation in yield and yield attributing traits

length, it also correlated with plant height, grains panicle⁻¹ days to maturity and grain yield plant⁻¹ positively and non-significantly. This implies that these traits are interdependent, more productive tillers plant⁻¹ bears more grains and have greater yield advantage. Similar results are delineated by Padmaja et al. (2011). Thousand seed weight exhibited highly significant negative correlation with days to maturity (-0.3254*) both at phenotypic and genotypic level. This indicates the genotypes having longer duration, gives less thousand seed weight compared shorter/medium duration

genotypes. Hence selecting genotype with high thousand seed weight with shorter/medium duration is ideal for yield improvement. These results have close agreement with Saleh et al. (2020). Plant height showed negative correlation with seed yield plant⁻¹ and grains panicle⁻¹. This implies that plants with reduced height give more grains panicle⁻¹ and gives yield advantage. Grains panicle⁻¹ is correlated positively with days to 50% flowering, tillers plant⁻¹ thousand seed weight. This shows that increase in productive tillers plant⁻¹, leads to increase in the seed yield plant⁻¹ and ultimately yield of plants increased. These results have close agreement with Sameera et al. (2016). But it correlated negatively with traits like plant height, days to maturity, seed yield plant⁻¹ and panicle length. Correlogram (Figure 2) depicted seed yield plant⁻¹ having strong and positive correlation with thousand seed weight

Figure 2: Genotypic and phenotypic path diagram for seed (Grain) yield plant⁻¹ in rice genotypes

and numbers of productive tillers plant⁻¹ at both phenotypic and genotypic level. Whereas, seed yield plant⁻¹ exhibited negative correlation with days to 50% flowering, plant height, panicle length and days to maturity both at phenotypic and genotypic level (Figure 1). Saleh et al. (2020) and Naik et al. (2021) observed that the seed yield plant⁻¹ exhibited highly significant and positive correlation with thousand seed weight and numbers of productive tillers plant⁻¹.

3.2. Path coefficient analysis

Figure 2 shows the path analysis results, which show the cause-and-effect Relationship between per se yield and yield components attributing and the values are presented in Table 3. The results of path analysis revealed that the thousand seed weight has a high and significant genotypic (0.3286*) and phenotypic path coefficient value (0.3198) indicates high positive direct effects on the seed yield. Except for the days

Table 3: Genotypic (G) and phenotypic (P) path coefficient analysis of yield and yield attributing traits in rice genotypes

Traits	G/P	Days to 50% flowering	Tillers plant ⁻¹	Thousand seed weight (g)	Plant height (cm)	Grains panicle ⁻¹	Days to maturity	Seed yield plant ⁻¹ (g)
Days to 50% flowering	G	0.2252*	0.0446	-0.0620	0.0496	0.0402	0.0256	0.2017
	P	-0.0440	-0.0081	0.0114	-0.0089	-0.0046	-0.0038	-0.0362
Tillers plant ⁻¹	G	0.0268	0.1354	-0.0059	0.0302	0.0778	0.0778	0.0105
	P	0.0283	0.1532	-0.0066	0.0285	0.0169	0.0547	0.0114
Thousand seed weight (g)	G	-0.0905	-0.0142	0.3286*	0.0501	-0.0293	-0.0293	-0.1069
	P	-0.0826	-0.0137	0.3198	0.0486	0.0133	-0.0233	-0.0954
Plant height (cm)	G	-0.0561	-0.0568	-0.0389	-0.2547	-0.0478	-0.0478	-0.0136
	P	-0.0389	-0.0359	-0.0293	-0.1930	0.0058	-0.0270	-0.0055
Grains panicle ⁻¹	G	-0.0275	-0.0302	-0.0075	0.0080	0.0036	0.0036	0.0160
	P	-0.0074	-0.0079	-0.0030	0.0022	-0.0718	-0.0026	0.0032
Panicle length (cm)	G	0.0050	0.0253	-0.0039	0.0083	0.0440	0.0440	0.0084
	P	-0.0028	-0.0114	0.0023	-0.0045	-0.0012	-0.0320	-0.0048
Days to maturity	G	-0.5348	-0.0462	0.1943	-0.0319	-0.1144	-0.1144	-0.5972
	P	-0.2618	-0.0237	0.0949	-0.0091	-0.0140	-0.0473	-0.3181
Seed yield panicle ⁻¹ (g)	G	-0.4519	0.0579	0.4048*	-0.1404	-0.0406	-0.0406	-0.4812
	P	-0.4092	0.0524	0.3895	-0.1361	-0.0276	-0.0813	-0.4455

Genotypic Path: R square=0.3599 Residual effect=0.800; Phenotypic Path: R square=0.3232 Residual effect=0.823

to maturity (DM), TSW has minor indirect effect on grain yield through other component characteristics (0.1943). The magnitude of direct effects of days to 50% flowering (DFF) is high and positively significant (0.2252), therefore it can be another crucial yield component to consider for selection, in addition to TSW. Although there is a strong positive correlation between days to maturity (DM) and DFF, the indirect influence of DM on seed yield via DFF is largely negative. The results are in conformity with the findings of Zahid et al. (2006) and Akhtar et al. (2011). In terms of genotypic (0.1354) and phenotypic (0.1532) path coefficient values, the trait tillers plant⁻¹ (TPP) had a positive but minor direct effect on seed yield.

Further, panicle length and grains panicle⁻¹ had recorded low to moderate positive direct effects on seed yield plant⁻¹. These findings are in agreement with Tejaswini et al. (2018) for panicle length. However, association of these traits was noticed to be positive and significant with seed yield plant⁻¹

indicating indirect effects to be the cause of correlation and hence, the need for consideration of indirect causal factors during selections for yield improvement through these traits. The remaining traits under consideration like plant height and days to maturity reported to have moderate to high but negative influence on seed yield. This points towards the selection of short heighted and early maturing genotypes to improve main target i.e., seed/grain yield.

The indirect influence of plant height on seed yield was positive but minor via all yield parameters except days to maturity, according to genotypic path coefficient values (-0.0319). The total correlation (-0.0406) was negative and insignificant in case of panicle length mainly due to the indirect negative effects on seed yield via plant height (-0.0478), days to maturity (-0.1144) and thousand seed weight (-0.0293). This implies that the indirect association of panicle length via these traits does not influence yield. The direct effect of days to maturity versus seed yield was negative and high (-0.5972).

However, there was moderate and negative (-0.4812) total correlation for this trait with seed yield. This is due to the significant indirect effects of days to maturity to thousand seed weight and plant height.

The estimated residual effect for the genotypic and phenotypic path coefficients in this study was 0.800 and 0.823, respectively, indicating that the characters included in the study contributed about 20% of the variability in seed yield. The explanation for this appears to be that more traits must be incorporated in order to explain the complete variation in seed yield. As a result, this study recommends the future research to include more component traits to record the variation in yield.

4. Conclusion

Genetic correlation coefficient was shown relatively higher in magnitude than its phenotypic correlation coefficient, which amply demonstrated that the variables under consideration were inherently linked. The traits, thousand seed weight, days to 50% flowering and productive tillers per plant, showed that positive and significant correlation and direct/indirect effect on grain yield. Therefore, it would be advisable to lay more attention on these critical attributes/traits in the selection process to increase rice grain yield.

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