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Association Studies for Identifying the Selection Criteria Among Early varieties of Rice in North Coastal Zone of Andhra Pradesh

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ABSTRACT: Rice yields were affected by various heritable and non-heritable components, the present investigation was undertaken to study the variability, heritability, genetic advance, character associations, path coefficients, principal component analysis of yield component traits along with principal component analysis study in early duration varieties of rice for identification of effective selection criteria for grain yield improvement. A notable observation was made regarding the high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), accompanied by elevated heritability and genetic advance as a percentage of the mean for traits such as filled grains per panicle, total grains per panicle, test weight, and grain yield per plant. This suggests the viability of direct phenotypic selection for enhancing these characteristics. Principal component analysis revealed that four principal components with eigenvalues exceeding 1 accounted for 86.5% of the variability in PC1. Filled grains per panicle and total grains per panicle contributed significantly to this variability, with filled grains per panicle showing a positive direct effect and a noteworthy positive correlation with grain yield per plant. Consequently, filled grains per panicle is identified as a promising selection criterion for improving grain yield in the early stages of rice crop cultivation.

Keywords: Rice, Correlation Analysis, Genetic Advance, Heritability, Path Analysis, Principal component analysis.

INTRODUCTION

Rice serves as the fundamental food source for over 100 countries globally and plays a vital role in nourishing nearly 70% of the world's population. It holds significant dietary and food security importance, particularly in numerous Asian nations. India, ranking second globally in rice production, contributes 22% to the total global rice output (Duppala *et al.*, 2023), following China. However, the direct phenotypic selection for grain yield poses challenges due to its complex nature, relying on multiple traits, often being polygenic, and heavily influenced by environmental factors. As a result, such direct selection methods are frequently ineffective. Therefore, the identification of effective criteria for enhancing grain yield becomes a top priority. In this context, the exploration of heritability and genetic advance of yield component traits emerges as a crucial area of study. An analysis of the association of yield component traits with grain yield and their inter-associations is also important for formulation of effective breeding strategy to improve grain yield (Awad *et al.*, 2022; Bakya *et al.*, 2020; Priyanka *et al.*, 2019; Rao *et al.*, 2021). Further, to detect the traits, having high influence on grain yield, path analysis is commonly applied to elucidate information on the relative direct and indirect contribution of each component character towards yield and help the breeders in formulation of effective selection criteria for grain yield improvement. Principal Component Analysis (PCA), a reduction approach for multivariate data, is increasingly utilized to evaluate the relevance and contribution of each factor to the overall variance as well as to provide information on the impact of a particular attribute on the total variance was employed (Bhargavi *et al.*, 2023; Prasanth *et al.*, 2023; Ratnam *et al.*, 2022 and Sharma *et al.*, 2021).

In this context, the study was initiated using advanced breeding lines of rice having desirable characters to have a variety which is high yielding combined with early duration to cater the farmer needs from the states of Andhra Pradesh and Telangana. The present study, reports the extent of genetic variability, inter-relationships and path coefficients, principal component analysis for grain yield and yield contributing traits in the advanced breeding lines of rice.

MATERIAL AND METHODS

The current study was conducted at the Agricultural Research Station, Ragolu, situated in the North-Coastal districts of Andhra Pradesh. Sixteen genetically pure seeds from improved breeding lines, developed by Acharya NG Ranga Agricultural University

(ANGRAU), Andhra Pradesh, India, were utilized. These 16 advanced breeding lines were initially sown in a raised nursery bed and later transplanted into the main field 20 days after sowing, following a spacing of 20 × 15 cm in a replicated trial during the Kharif season of 2022 at Agricultural Research Station, Ragolu.

To ensure a good crop stand, all recommended agronomic practices and crop protection measures were adhered to throughout the crop growth period. The study involved the recording of twelve traits, including days to 50 percent flowering (days), plant height (cm), productive tillers per sqmt, panicle length (cm), filled grains per panicle, total grains per panicle, spikelet fertility (%), test weight (g), and grain yield per hectare (g). These traits were documented for five random plants within each entry, replicated three times. The collected data underwent thorough statistical analysis.

Genetic variability parameters, specifically Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV), were computed following the formula outlined by Burton and Dewane (1953). Heritability was determined using the formula provided by Allard (1960), and the genetic advance as a percentage of the mean was calculated by employing the formula from Johnson *et al*. (1955). Correlation coefficients were computed utilizing the formula presented by Singh and Choudhary (1977). To assess the direct and indirect effects of various components on grain yield, path coefficient analysis was conducted as recommended by Dewey and Lu (1959). Principal Component Analysis was carried out following the procedure described by Banfield (1978). For statistical analysis, R software version 4.3.1 was employed to create association plots. Additionally, SPSS16.0 software was utilized to represent the frequency distribution through histograms for the studied traits.

RESULTS AND DISCUSSION

The findings related to variability and other genetic parameters for the studied grain yield and yield component traits are outlined in Table 1 and depicted in Fig. 1. The duration for 50 percent flowering varied between 78.00 and 111.00 days, while plant height exhibited a range of 96.20 to 130.60 cm. Productive tillers per square meter ranged from 224.40 to 356.40, panicle length varied from 17.60 to 31.50 cm, filled grains per panicle showed a range of 111.38 to 329.18, and total grains per panicle spanned from 126.61 to 422.16. Additionally, spikelet fertility ranged from 74.15 to 93.15, and test weight fluctuated between 13.04 and 31.75. Moreover, the present study reported a test weight range of 18.81 g to 32.26 g, and grain yield per square meter exhibited a variation from 2115.00 g to 6442.00 g, with a mean of 4533.52 g per square meter. These results align closely with the findings of Savitha and Kumari (2015) in their investigations on rice segregating populations.

The outcomes regarding genotypic (GCV) and phenotypic (PCV) coefficients of variation are detailed in Table 1 and illustrated in Fig. 1. An examination of these findings unveiled a consistent pattern wherein the PCV values surpassed the GCV values for all the studied traits, underscoring the impact of the environment. Notably, Days to 50 percent flowering exhibited a substantial disparity between phenotypic and genotypic coefficients of variation in comparison to the other traits, signifying a heightened influence of the environment on this particular trait and resulting in comparatively low heritability values. This trend aligns with the findings of Yuvaraja *et al.* (2019). Conversely, both plant height and spikelet fertility displayed minimal variation between GCV and PCV values, indicating a diminished influence of the environment and consequently yielding high heritability values, exceeding 90 percent. These observations resonate with the conclusions drawn by Priyanka *et al.* (2019).

The findings also unveiled substantial genotypic and phenotypic coefficients of variation for filled grains per panicle, total grains per panicle, test weight, and grain yield per plant. Specifically in relation to filled grains per panicle, total grains per panicle, test weight, and with the findings of Kumar *et al.* (2022) for grain yield per plant. In contrast, the present study reported moderate genotypic and phenotypic coefficients of variation for panicle length and spikelet fertility. These observations correspond with the outcomes documented by Cholan *et al.* (2017) for panicle length. Furthermore, low genotypic and phenotypic coefficients of variation were noted for days to 50 percent flowering, plant height, and productive tillers per square meter. This pattern aligns with the research findings of Sameera *et al.* (2015) for days to 50 percent flowering and Kishore *et al.* (2015) for plant height and productive tillers per square meter.

The analysis revealed high heritability (>60%) and substantial genetic advance as a percentage of the mean (>20%) for traits such as days to 50 percent flowering, panicle length, filled grains per panicle, total grains per panicle, test weight, and grain yield per plant (refer to Table 1 and Fig. 1) concerning filled grains per panicle, total grains per panicle, and test weight, as well as with Madhavilatha *et al.* (2005) regarding days to 50 percent flowering and panicle length.

However, for plant height and spikelet fertility, there was a combination of high heritability (>60%) with a moderate genetic advance as a percentage of the mean (10-20%). These results are consistent with the reports of Santhipriya *et al.* (2017) for plant height and Kumar *et al.* (2022) for spikelet fertility. Additionally, traits like productive tillers per square meter exhibited low heritability along with a low genetic advance as a percentage of the mean, resembling the outcomes reported by Krishna *et al.* (2020).

Filled grains per panicle, total grains per panicle, test weight, and grain yield per hectare exhibited high Genetic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) values (>20%), along with elevated heritability (>60%) and substantial genetic advance as a percentage of the mean (>20%). These results suggest the prevalence of an additive type of gene action for these traits. Consequently, direct phenotypic selection is likely to be effective in enhancing these traits in the early generations. Total grains per panicle, and test weight, as well as by Gupta *et al.* (2020) for grain yield per hectare.

Table 2 presents the associations between yield and its components. A careful examination of these outcomes reveals a positive and significant correlation between grain yield and the traits associated with yield components, specifically filled grains per panicle and total grains per panicle. This implies the potential for their simultaneous improvement alongwith grain yield per plant. These findings concur with the reports of Lakshmi *et al*. (2021) for filled grains per panicle and Sudeepthi *et al.* (2020) for total grains per panicle. Moreover, positive and significant associations were also identified, such as days to fifty percent flowering with filled grains per panicle and total grains per panicle, plant height with test weight, and filled grains per panicle with total grains per panicle. These associations suggest the possibility of simultaneously enhancing these traits. These results align with the findings of Nath and Kole (2021) for days to fifty percent flowering with filled grains per panicle and total grains per panicle, Prasannakumari *et al.* (2020) for test weight with plant height, and Priyanka *et al.* (2019) for filled grains per panicle with total grains per panicle.

Table 3 presents the results of the path analysis of yield component traits on grain yield per plant. Upon examination, the findings reveal a residual effect of 0.369, suggesting that the variables under study in this investigation explain approximately 63.10% of the variability in grain yield per plant. Consequently, other unexamined attributes contribute to the overall grain yield per plant. Notably, a high positive direct effect of plant height on grain yield per plant was observed in the present study, aligning with the findings of Sudeepthi *et al.* (2019). Regarding total grains per panicle, the positive correlation coefficient alongside a negative direct effect indicates that indirect effects likely contribute to the observed correlation. In such instances, it is essential to consider indirect causal factors simultaneously for selection. In the negative direction, test weight exhibited very high direct effects, followed by productive tillers per square meter, spikelet fertility, panicle length, and total grains per panicle.

Conversely, there were positive but low direct effects observed for days to 50 percent flowering and filled grains per panicle. These outcomes align with the findings reported by Katiyar *et al.* (2019) for filled grains per panicle. Moreover, a high negative direct effect, coupled with a significant positive correlation, was noted for total grains per panicle, in agreement with the results reported by Kohnaki *et al.* (2013). Additionally, substantial negative direct effects were recorded for test weight, productive tillers per square meter, spikelet fertility, and panicle length. These results coincide with the findings of Katiyar *et al.* (2019) for test weight, Muthuvijayaragavan and Jebraj (2022) for productive tillers per square meter, Sowjanya and Hittalmani (2017) for spikelet fertility, and Vengatesh and Govindarasu (2018) for panicle length.

The Principal Component Analysis (PCA) also indicated a significant contribution of 86.50% from the first four principal components, each having an Eigen value greater than 1, to the overall variability (refer to Table 4). This suggests that the essential features of the dataset are effectively represented in the first three principal components, consistent with the findings reported by Salunkhe *et al.* (2023). Principal components with Eigen values less than one were deemed non-significant. The first principal component (PC 1) accounted for 33.10% of the total variability, where total grains per panicle (loading of 0.554) and filled grains per panicle (loading of 0.552) demonstrated the highest variance. These outcomes mirror similar findings reported by Pavithra and Vengadessan (2020), highlighting the usefulness of selecting lines and traits from this component. The second principal component (PC 2) contributed 22.40% to the total variance, with test weight (loading of 0.105) and filled grains per panicle (loading of 0.063) recording the highest loadings in this component, in agreement with the results reported by Rahangdale *et al.* (2021). The third principal component (PC 3) contributed 16.10% to the total variability. Within the third principal component (PC 3), the characteristics panicle length (loading of 0.441) and test weight (loading of 0.174) exhibited the highest variance. These results are consistent with the findings reported by Upadhyay *et al.* (2022). Moving on to the fourth principal component (PC 4), it contributed 15.00% to the total variability. In this component, the traits days to productive tillers per plant (loading of 0.613) and days to 50 percent flowering (loading of 0.204) demonstrated the maximum variance. Similar results were reported by Shanmugam *et al.* (2023).

As depicted in Fig. 2, each of the nine variables exhibited substantial loadings on distinct principal factors, and none remained unaccounted for following the varimax rotation of the principal component axes. Additionally, the figure effectively grouped similar types of variables by consolidating them onto common principal factors. Furthermore, Fig. 3 illustrates that genotypes positioned towards the positive end of both factors are presumed to be collectively superior for filled grains per panicle, total grains per panicle, and spikelet fertility, consequently contributing to overall grain yield. Based on the current study, entry 11 has been identified as superior across all characters collectively.

Table 1: Variability parameters in Early varieties of Rice.

Sr. No.	Character	Mean	Range		Coefficient of variation		Heritability (%)	Genetic advance as % of mean
			Minimum	Maximum	GCV (%)	PCV (%)		
1	Days to 50 per cent flowering	91.13	78.00	111.00	1.29	9.82	98.30	20.06
2	Plant height (cm)	116.41	96.20	130.60	7.57	7.91	91.48	14.91
3	Productive tillers per sqmt	311.42	224.40	356.40	4.45	9.46	22.08	4.31
4	Panicle length (cm)	25.63	17.60	31.50	11.73	13.35	77.20	21.23
5	Filled grains per panicle	201.54	111.38	329.18	25.28	27.90	82.05	47.16
6	Total grains per panicle	238.04	126.61	422.16	25.58	28.17	82.47	47.85
7	Spikelet fertility (%)	84.87	74.15	93.15	6.06	6.88	88.08	14.17
8	Test weight (g)	21.04	13.04	31.75	20.29	23.18	76.59	36.57
9	Grain yield per ha (g)	4533.52	2115.00	6442.00	21.21	22.46	89.25	41.28

Table 2: Correlation coefficients for grain yield and yield components in Early varieties of Rice.

Traits	Plant height	Productive tillers per sqmt	Panicle length	Filled grains per panicle	Total grains per panicle	Spikelet fertility	Test weight	Grain yield per ha
Days to 50 per cent flowering	**0.020**	0.047	0.254	0.670**	0.733 **	-0.203	-0.247	0.307
Plant height		**0.411**	0.403	0.028	0.026	0.092	0.642 **	0.426
Productive tillers per sqmt			**-0.142**	-0.335	-0.212	-0.456	-0.183	0.481
Panicle length				**0.223**	0.254	-0.094	0.488	-0.164
Filled grains per panicle					**0.962 ****	0.124	-0.373	0.560*
Total grains per panicle						**-0.146**	-0.314	0.505 *
Spikelet fertility							**-0.151**	0.260

Table 3: Direct and indirect effects for yield component traits in Early varieties of Rice.

Traits	Days to 50 per cent flowering	Plant height	Productive tillers per sqmt	Panicle length	Filled grains per panicle	Total grains per panicle	Spikelet fertility	Test weight	Grain yield per ha
Days to 50 per cent flowering	**0.137**	0.035	-0.039	-0.109	0.112	-0.256	0.114	0.313	0.307
Plant height	0.003	**1.807**	-0.343	-0.173	0.005	-0.009	-0.052	-0.812	0.426
Productive tillers per sqmt	0.006	0.742	**-0.834**	0.061	-0.056	0.074	0.256	0.231	0.481
Panicle length	0.035	0.729	0.118	**-0.430**	0.037	-0.089	0.053	-0.617	-0.164
Filled grains per panicle	0.092	0.051	0.280	-0.096	**0.166**	-0.336	-0.069	0.472	0.560*
Total grains per panicle	0.100	0.047	0.176	-0.109	0.160	**-0.350**	0.082	0.397	0.505 *
Spikelet fertility	-0.028	0.166	0.381	0.040	0.021	0.051	**-0.562**	0.191	0.260
Test weight	-0.034	1.160	0.153	-0.210	-0.062	0.110	0.085	**-1.265**	-0.063

Residual effect = 0.369; Diagonal and bold values indicate the direct effects

Table 4: Component loading of different characters in rice for yield and yield components in Early varieties of Rice.

Sr. No.	Components	Principal component analysis			
		PC 1	PC 2	PC 3	PC 4
1.	**Eigen Value**	2.9815	2.0138	1.4446	1.347
2.	**Explained % of variance**	33.10	22.40	16.10	15.00
3.	**Cumulative % of variance**	33.10	55.50	71.60	86.50
Sr. No.	**Characters contribution**	**PC 1**	**PC 2**	**PC 3**	**PC 4**
1.	Days to 50 per cent flowering	0.466	0.015	0.17	0.204*
2.	Plant height	0.067	-0.611	-0.271	-0.108
3.	Productive tillers per sqmt	-0.011	-0.212	-0.437	0.613*
4.	Panicle length	0.135	-0.455	0.441*	-0.093
5.	Filled grains per panicle	0.552*	0.063*	0.057	-0.155
6.	Total grains per panicle	0.554*	0.023	0.138	0.029
7.	Spikelet fertility	0.001	0.105*	-0.338	-0.713
8.	Test weight	-0.15	-0.587	0.174*	-0.162
9.	Grain yield per ha	0.353	-0.12	-0.587	-0.063

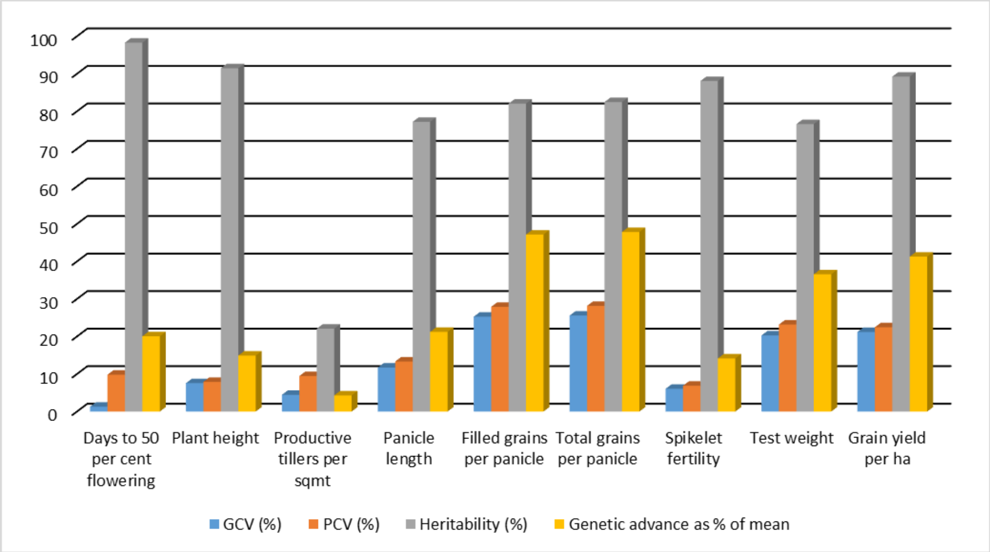

Fig. 1. Estimation of genetic parameters in early duration varieties of rice.

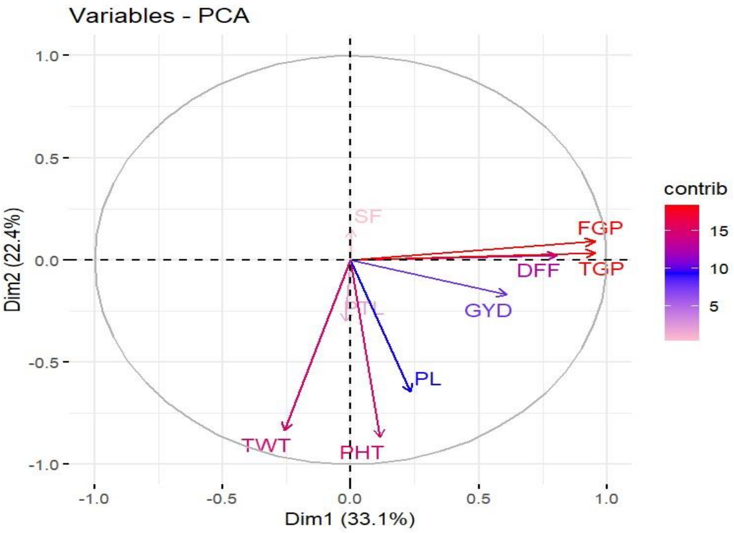

Fig. 2. Distribution of variables on the major principal components.

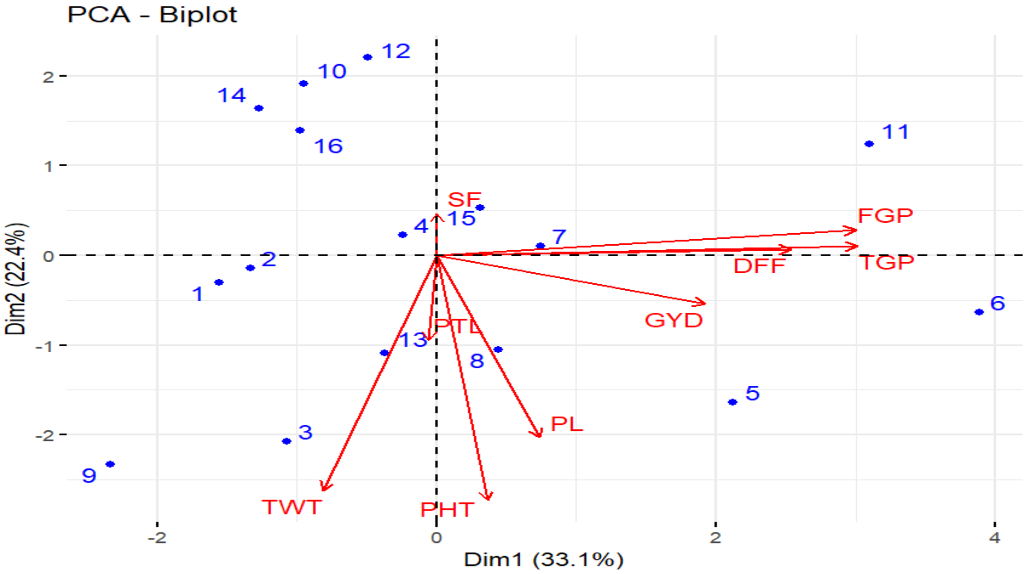

Fig. 3. Distribution of genotypes on the major principal components.

CONCLUSIONS

Substantial Genetic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability, and genetic advance as a percentage were observed for productive tillers per plant, filled grains per panicle, total grains per panicle, and grain yield per plant. This observation indicates the viability of employing direct phenotypic selection to enhance these traits. Notably, productive tillers per plant and filled grains per panicle demonstrated a positive direct effect, along with a significant and positive correlation with grain yield per plant. Consequently, these traits, particularly productive tillers per plant and filled grains per panicle, are identified as effective selection criteria for enhancing grain yield in the early stages of rice crop cultivation. Principal component analysis further underscores the significance of filled grains per panicle as the key selection trait.

FUTURE SCOPE

The promising genotypes identified in the present study, need to be evaluated across seasons and locations prior to their potential commercial exploitation as high yielding genotype with early duration. Filled grains per panicle, with high GCV, PCV, heritability, genetic advance as per cent mean along with positive and significant correlation coupled with high positive direct effects were identified as effective selection criteria for improvement of grain yield per plant.

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Conflict of Interest. None.

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