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Genetic insights into yield potential in advanced rice cultures: A multivariate analysis of yield components

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Abstract

The goal of the current study was to unravel the extent of genetic variability, genetic advance, broad sense heritability, intra- and inter-character relationships and principal component analysis of yield and yield component traits in 62 advanced rice cultures. The Phenotypic coefficient of variation was higher than Genotypic Coefficient of variation for all the traits implying that these characters are influenced by environment effects. High PCV and GCV were observed for number of grains per panicle, test weight and grain yield per hectare. High heritability coupled with high genetic advance as *percent* of mean were observed for number of grains per panicle and test weight indicating that these traits were mainly governed by additive gene effects and response to selection could be affected for further yield improvement through simple selection. Correlation analysis displayed that grain yield (Kg/hectare) exhibited highly significant positive association with test weight (0.72**) and panicle length (0.50**). Principal component analysis found that first four principal components with eigen value more than one contributed to total variation of 83.1%. The varieties *viz.*, M 962, M 682, M 696, M 699, E 663, E 647 and E 666 were identified as promising divergent varieties which can be exploited for developing rice varieties in future or in further breeding programme.

Keywords: Rice, genetic variability, genetic advance, heritability, correlation and principal component analysis

Introduction

For more than 100 countries worldwide, rice has been a staple food throughout the ages in conjunction with numerous cultural and geological areas, supporting almost 70% of the world's population and being essential to many Asian nations' food, nutrition, and cultural security (Manoj Kumar *et al.* 2023) [15]. India, which ranks second in the world after China in terms of rice production, produces 22% of the world's rice (Vasudev *et al.* 2023) [25]. However, due to its vulnerability to environmental factors, the direct evaluation of grain yield, a multifaceted trait influenced by numerous characteristics and frequently polygenic in nature faces difficulties. To increase grain yield, it is imperative to find the traits controlled by additive gene action (Kumar *et al.* 2023) [11]. To select breeding materials effectively based on their genotypic inheritance of yield attributes, research on the heritability and the genetic advance of mean for yield factors is crucial (Duppala *et al.* 2024) [7]. Correlation analysis reveals the direction and extent of the genetic relationships between any given pair of traits without regards to cause/effect relationship is also essential for devising effective breeding strategy to increase grain yield (Kumar *et al.* 2024) [12]. The Principal Component Analysis (PCA) is a widely used technique in multivariate factor reduction that evaluates the contribution of each factor to overall variability as well as its significance. Additionally, it provides insights into how particular attributes affect total variance, which is important information for making decisions in selection of elite parents (Ravi Kumar *et al.* 2015) [20]. The present investigation documents the degree of variability, associations among traits and principal component analysis related to grain yield and its component traits in these breeding lines of rice at early generations.

Materials and Methods

The experimental material comprised of 62 advanced rice cultures which were evaluated at Regional Agricultural Research Station (RARS), Nandyal, Andhra Pradesh, India during *kharif*, 2023. All the varieties were evaluated in Randomized Block Design, replicated twice with plot size of 10 m² per variety with a spacing of 20 cm x 15 cm. All the agronomic practices recommended by Acharya N.G. Ranga Agricultural University were followed to raise a healthy crop. Data was collected from five competitive and randomly selected plants for recording yield and yield component traits *viz.*, Days to 50% flowering (DFF), Days to maturity (DM), Plant height (PH), Effective bearing tillers/m² (EBT/m²), Panicle length (PL), Number of Grains per panicle (NGP), Test weight (TW) and grain yield GY (Kg/ha). The data collected is subjected to assess Genetic variability, heritability, genetic advance, correlation and principal component analysis using statistical software - General R based Analysis Platform 2020 empowered by statistics (GRAPES) software version 1.0.0.

Results and Discussions

The findings regarding the variability and genetic parameters for yield and yield component traits are presented in Table 1. The trait DFF ranged from 92.00 to 117.00 days while days to maturity ranged from 115.00 to 144.00 days with general mean of 102 and 130 days respectively. Plant height varied between 82.40 and 130.50 cm with mean plant height of 105.70 cm. Ear bearing tillers per square meter spanned from 475.00 to 657.00 with mean ear bearing tillers of 555. Similarly, panicle length ranged from 17.90 to 28.30 cm with general mean of 23.68 cm. The traits *viz.*, Number of grains per panicle and test weight exhibited a range of 104.00 to 608.00 and 9.18 to 27.71 g with mean number of grains per panicle of 287 and mean test weight of 18.84 g. Furthermore, grain yield (Kg/ha) ranged from 3148.00 grams to 7552.00 kilograms, with a mean of 5237.25 kilograms per hectare. These findings are largely consistent with the result reported by Satyanarayana *et al.* 2024 [21] in their investigations on rice.

The estimates of range, variance, phenotypic and genotypic coefficient of variation (GCV, PCV), heritability in broad sense and genetic advance as percent of mean for eight characters of 62 advanced rice cultures are furnished in Table 1. The PCV showed high magnitude than the GCV for all the characters indicating the influence of environment in the expression of these traits. High magnitude of PCV and GCV were registered by number of grains per panicle and test weight indicated that these characters had sufficient variability to effect selection for improvement of these characters. This was inconformity with the results of Adjah *et al.* (2020) [1] and Debsharma *et al.* (2022) [4]. Further, moderate values of PCV and GCV were registered for grain yield (Kg/ha).

In the present study, high heritability was recorded for all the traits ranging from 64.10% for grain yield (Kg/ha) to 98.20% for plant height indicating least influence of environment on the genetic expression of the characters under study. The estimates of heritability alone will not be of much value for selection and genetic gain should be considered in conjunction with heritability estimates (Johnson *et al.*, 1955) [9] to estimate realized genetic improvement possible in the character through simple selection methods. High heritability and high genetic advance estimates were registered for test weight ($h^2(b) = 97.0\%$, GAM = 48.75%), number of grains per panicle (95.8%, 60.30%) and grain yield (Kg/ha) (64.1%, 30.20%) indicating additive gene effects in inheritance of these characters and

simple selection would be effective to augment further genetic improvement of these traits. These were inconformity with results of Ravikumar *et al.* (2015) [20], Satyanarayana *et al.* (2024) [21]. High heritability coupled with moderate genetic advance as percent of mean was observed for the traits plant height (98.2%, 19.40%), days to maturity (97.4%, 11.79%) and days to 50% flowering (91.1%, 12.57%) indicating the role of both additive and non-additive gene effects in their genetic control and simple selection methods may not be rewarding to effect further genetic gain in these traits. Hybridization of selects followed by selection in later generations of segregating populations would be effective to capitalize both additive and non-additive gene effects observed in these traits and inconsistent with the results of Barhate *et al.* (2021) [2]. From the foregoing discussion, it can be concluded that high GCV, heritability and genetic advance as percent of mean were observed for number of grains per panicle, test weight and grain yield per hectare indicating that variation in above traits was most-likely due to additive gene effects, hence simple selection may be effective to improve these traits in the present material under study.

Phenotypic correlation coefficients of grain yield (Kg/ha) with its component traits are presented in the Table 2. In the present investigation, grain yield (Kg/ha) showed highly significant positive association with test weight (0.72**) and panicle length (0.50**). This association indicates that these yield related parameters can be used as preliminary screening tools for selecting the high yielding rice cultures in the present material. These observations are in line with the findings of Kashyap *et al.* (2020) [10]. Positive and significant associations were observed between days to 50% flowering and days to maturity, plant height and panicle length, plant height and number of grains per panicle, panicle length and test weight, indicating opportunities for concurrent enhancement of these traits. However, it is noteworthy that number of grains per panicle exhibited a significant negative association with test weight, suggesting indirect selection for lower test weights of finer quality will increase number of grains per panicle and inconsistent with the findings of Satyanarayana *et al.* (2024) [21]. Principal component analysis (PCA) was used to calculate the effective contribution of various traits based on the corresponding variance in order to comprehend variable independence and balanced loading of traits. The eigen values and total cumulative percentage of variances explained by PCs is furnished in Table 3. It provides the eigen values, percent variability, and cumulative percent variability of various characters. As a potential source of diversity, principal components (PCs) with eigen values greater than 1 should be considered for study (Kumari *et al.* 2021) [13]. The first four principal components (PC1 to PC4) in the current investigation, with eigen values more than one 2.29, 1.95, 1.35, 1.52 and 1.04, respectively, explained 83.10% of the total variance for all the analyzed features and this observation is in congruence with previous findings reported by Sudeepthi *et al.* (2020) [23] and Satyanarayan *et al.* (2024) [21]. The first PC displayed high positive weight to DM (0.574), DFF (0.556) and NGP (0.277). While, the third PC gave positive loading to GP (0.36), DFF (0.35), PH (0.33) followed by DM (0.32). Similarly, fourth PC noticed highest positive weight to EBT/m² (0.888), PH (0.21) followed by TW (0.028) Table 4. In contrast, PC 1, contributing 28.70% to the total variability, was primarily influenced by days to 50% flowering, days to maturity and number of grains per panicle. PC 2, explaining 24.40% of the total variance, was predominantly influenced by panicle length and plant height. PC

3, which accounted for 16.98% of the total variability, was largely influenced by test weight and grain yield (Kg/ha). PC 4, contributing 13.05% to the total variability was influenced by ear bearing tillers per square meter and panicle length. Similar kind of results are in agreement with findings of Sudeepthi *et al.*, (2020) [23], Christina *et al.*, (2021) [3], Dhanuja *et al.*, (2021) [5], Venkata Ratnam *et al.*, (2022), Lakshmi *et al.*, (2022), Mushtaq and Kumar (2023) [11], Nayak *et al.*, (2023) [17] in rice.

The interaction between the traits and the genotypes that perform better for the traits are depicted in the biplot diagram. The length of the vector for each trait represents its offering to total divergence, longer the vector length, more is the contribution of concerned traits. The biplot depicted the relationship of 62 advanced rice cultures for eight yield and yield component traits (Figure 1). The trait GP displayed greater

vector length implying its contribution to the total divergence followed by DM and FF. These results are in congruence with the research findings of Lakshmi *et al.* (2022) [14], Tiwari *et al.* (2022) [24] and Gayathridevi *et al.* (2023) [8] and Satyanarayan *et al.* (2024) [21].

The study revealed that the varieties viz., M 962, M 682, M 696, M 699, E 663, E 647 and E 666 were identified as promising divergent varieties which can be exploited in hybrid breeding programme were located at extreme ends of distinct quadrants of the plot. Hence, these varieties were recognized as highly divergent and could be utilized as potential parents in yield improvement programmes. These results aligns with findings of Rahimi *et al.* (2013) [19], Pandit *et al.*, (2016) [18], Sharafi *et al.*, (2018) [22], Divya *et al.*, (2022) [6] in rice.

Table 1: Mean, Range, Coefficient of variation, Heritability, Genetic Advance as percent of mean in 62 advanced rice cultures

S. No.	Character	Mean	Range		Coefficient of variation		Heritability (%) h ² (bs)	Genetic advance as% of mean (GAM)
			Minimum	Maximum	GCV (%)	PCV (%)		
1	Days to 50 percent flowering	102.435	92.000	117.000	6.393	6.696	91.1	12.573
2	Days to maturity	130.065	115.000	144.000	5.803	5.879	97.4	11.799
3	Plant height (cm)	105.697	82.400	130.500	9.502	9.588	98.2	19.400
4	Ear bearing tillers/ m ²	554.613	475.000	657.000	4.797	8.321	33.2	5.697
5	Panicle length (cm)	23.676	17.900	28.300	8.900	9.562	86.6	17.065
6	Number of grains per panicle	287.355	104.000	608.000	32.884	33.596	95.8	66.303
7	Test weight (g)	15.843	9.180	27.710	24.032	24.404	97.0	48.750
8	Grain yield (Kg/ha)	5237.258	3148.00	7552.000	18.313	22.874	64.1	30.202

PCV and GCV: Phenotypic and genotypic coefficients of variation, h²(bs): Broad-sense heritability, GAM: Genetic advance as a percentage of the mean

Table 2: Correlation coefficients among grain yield and yield components in 62 advanced rice cultures

	DFF	DM	PH (Cm)	EBT/m ²	PL (Cm)	NGP	TW (G)	Yield (Kg/ha)
DFF	1	0.859**	0.168	0.079	-0.041	0.023	-0.093	-0.034
DM	0.859**	1	0.133	0.056	-0.088	0.127	-0.189*	-0.059
PH (Cm)	0.168	0.133	1	0.067	0.497**	0.353*	0.075	0.153
EBT/m ²	0.079	0.056	0.067	1	-0.118	-0.077	0.002	-0.17
PL (Cm)	-0.041	-0.088	0.497**	-0.118	1	0.489**	0.362**	0.503**
NGP	0.023	0.127	0.353*	-0.077	0.489**	1	-0.404**	0.026
TW (G)	-0.093	-0.189*	0.075	0.002	0.362**	-0.404**	1	0.721**
Grain Yield (Kg/ha)	-0.034	-0.059	0.153	-0.17	0.503**	0.026	0.721**	1

Note: DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; EBT/m²: Ear bearing tillers per sq mt; PL: panicle length; NGP: Number of grains per panicle; TW: Test weight; GY: Grain yield

Table 3: Total variances explained by different principal components in advanced rice cultures

S. No		Principal component analysis							
		PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8
1.	Eigen Value	2.295	1.952	1.359	1.044	0.605	0.478	0.223	0.043
2.	Explained% of variance	28.69	24.403	16.988	13.051	7.561	5.978	2.786	0.543
3.	Cumulative% of variance	28.7	53.1	70.1	83.1	90.7	96.7	99.5	100.0

Table 4: Factor loading of different characters with respect to different principal factor in rice hybrids

Principal components	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
DFF	0.556	-0.211	0.352	-0.067	0.068	0.1	-0.031	0.709
DM	0.574	-0.158	0.326	-0.101	0.118	0.128	-0.072	-0.702
PH (cm)	-0.146	-0.487	0.337	0.211	-0.29	-0.702	-0.061	-0.054
EBT/m ²	-0.022	-0.225	-0.008	0.888	0.14	0.358	0.106	-0.02
PL (cm)	-0.188	-0.559	-0.037	-0.323	-0.308	0.395	0.543	-0.034
NGP	-0.476	-0.23	0.36	-0.165	0.184	0.36	-0.632	0.015
TW(g)	0.277	-0.28	-0.597	0.028	-0.444	0.088	-0.532	0.005
GY (Kg/ha)	0.01	-0.445	-0.411	-0.139	0.743	-0.244	0.034	0.015

Note: DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height; EBT/m²: Ear bearing tillers per sq mt; PL: panicle length; NGP: Number of grains per panicle; TW: Test weight; GY: Grain yield

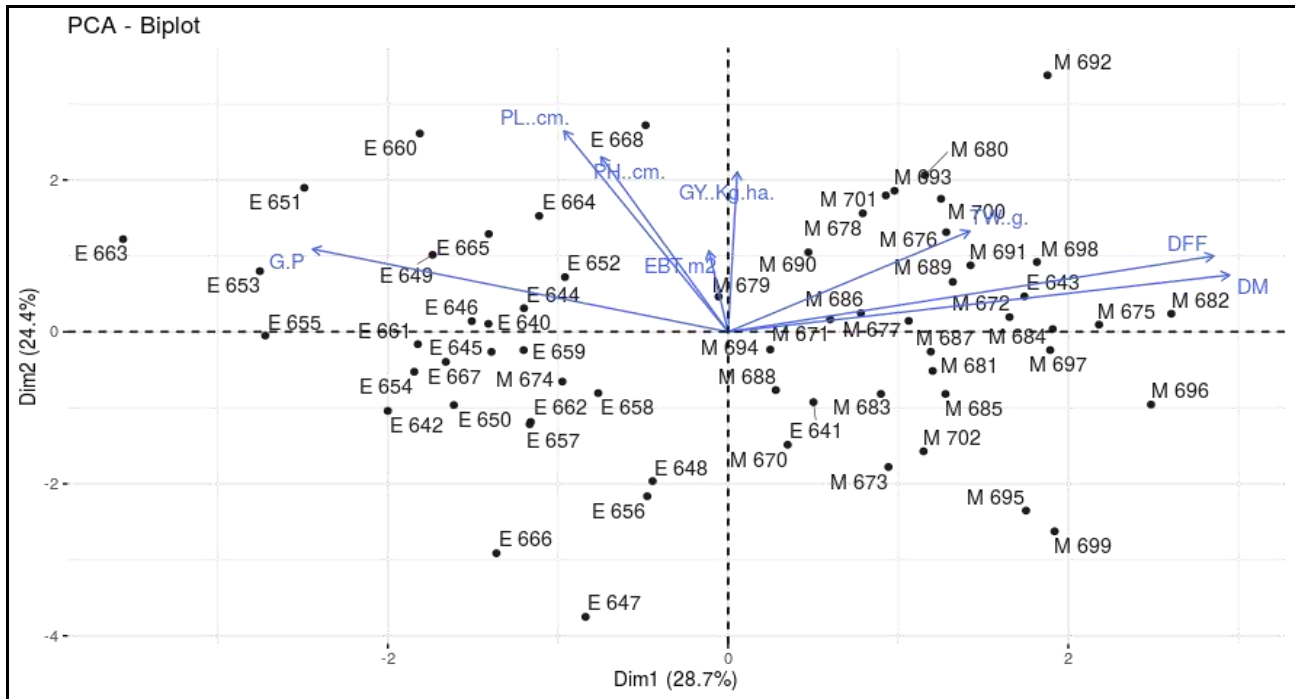


Fig 1: Biplot depicting 62 advanced rice cultures for eight yield and yield component traits

Conclusion

Ample amount of PCV, GCV, heritability and substantial genetic advance percentages were displayed by number of grains per panicle and test weight implying that direct phenotypic selection of these traits would be rewarding. The significant positive association of grain yield with test weight and panicle length suggests that these traits are predominantly governed by additive gene action and hence direct selection for these traits will lead to simultaneous improvement in grain yield. PCA concluded that the first four PCs with eigen values more than one describing 28.69%, 24.40%, 16.98% and 13.05% respectively attributed 83.10% of total variation. The varieties *viz.*, M 962, M 682, M 696, M 699, E 663, E 647 and E 666 were recognized as superior and genetically divergent which can be utilized for further crop improvement programme.

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