

Genetic Architecture, studies to identify the Selection Criteria for Yield in Long Duration Rice Lines (*Oryza sativa* L.)

Abstract

The current study aimed to explore the genetic variability, narrow sense heritability, genetic advance, Intra and Inter character associations, path coefficient analysis and principal factor - component analysis of yield component traits in long duration varieties of rice. The goal was to identify keynote factor for grain yield promoting, in event on exposure to long duration vegetative phase and engaged in long photosynthetic duration. High heritability and genetic advance, along with strong correlations with yield, were observed for filled grains per panicle and total grains per panicle, suggesting their suitability for direct phenotypic selection to improve these traits. Test weight showed a genuine relationship with grain yield, indicating its effectiveness for direct selection. Principal component analysis noted four components, with eigenvalues higher than 1, explaining 86.5 percent of the total variability. Among these components, the highest variability was attributed to filled grains per panicle and total grains per panicle. Filled grains per panicle is identified with positive direct effect and noted positive significant correlation for the grain yield per plant, making it an effective selection criterion for improving grain yield in long-duration rice crops.

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

Introduction

Rice is the key component of food for over 100 nations worldwide over the generations in companion over many cultural and geological arenas, sustaining nearly 70% of the global population and playing a vital factor in cultural, nutritional and the

food security, in many Asian countries [1]. India, heads a second position worldwide for rice culture following China, contributes 22% to the total world rice output [2]. But, the direct evaluation for grain yield, a multifaceted trait influenced by numerous characters and often polygenic in nature, faces challenges due to its susceptibility to environmental factors [3]. Therefore, there is a pressing need to identify traits governed by additive gene action to enhance grain yield [4].

In this context, studies on the narrow sense heritability and the genetic advance of mean for yield factors are important for effectively selecting breeding materials based on their genotypic inheritance of yield attributes [5]. Analysing the associations among yield component traits and their mutual relationships is also essential for devising effective breeding strategies to boost grain yield [6]. Additionally, path analysis, commonly employed, aids in identifying traits with significant influences on grain yield by delineating their relative direct and indirect contributions toward yield, thereby assisting breeders in formulating effective selection criteria [7].

“The Principal Factor-Component Analysis (PCA), a method for reducing multivariate factors, is largely utilized to assess the importance and proportion of each factor to total variability. It also offers insights into the impact of specific attributes on total variance, providing valuable information for decision-making” [8]. Given this background, the research commenced by employing advanced breeding lines of rice selected for favourable traits, aiming to develop a high yielding variety, addressing the requirements of farmers in Deccan states. This investigation documents the degree of genetic variability, associations among traits, path analysis and principal factor-component analysis concerning grain yield and its contributing factors in these advanced breeding generations of rice at early stages.

Material and Methods

The Agricultural Research Station in Ragolu, located in Andhra Pradesh's North-Coastal districts, hosted the recent study. Twenty genetically pure seeds from improved breeding lines, developed by ANGRAU, Andhra Pradesh, were used. These lines were initially grown in nursery beds and then transplanted into the main field during the Kharif season of 2022. Twelve traits were meticulously recorded and subjected to statistical analysis. Genetic variability parameters [9], heritability [10], genetic advance [11], correlation coefficients [12], and path coefficient analysis [13] were conducted. Principal Component Analysis [14] was also performed. R software version 4.3.1 and SPSS16.0 [15] were utilized for statistical analysis and data visualization.

Results and Discussion

The study's findings regarding the variability and genetic parameters of grain yield and its component traits are presented in Table 1 and visualized in Figure 1. The duration to 50 percent flowering ranged from 72.00 to 140.00 days, while plant height varied between 101.40 and 160.00 cm. Productive tillers per square meter spanned from 164.00 to 336.60, and panicle length ranged from 22.50 to 33.50 cm. Filled grains per panicle exhibited a range of 148.50 to 345.08, while total grains per panicle ranged from 165.22 to 402.03. Spikelet fertility showed variations from 75.78 to 92.87, and test weight ranged from 12.76 to 30.86 grams. Furthermore, grain yield per square meter ranged from 2495.00 grams to 7437.00 kilograms, with a mean of 5014.12 kilograms per square meter. These findings are largely consistent with the results reported by Manojkumar *et al.* [16] in their investigations on rice segregating populations.

The genotypic (GCV) and phenotypic (PCV) coefficients of variation are summarized in Table 1 and Figure 1. Examination of these coefficients revealed higher PCV values compared to GCV values for all studied traits, indicating the influence of environmental factors. Notably, test weight showed a substantial disparity between phenotypic and genotypic coefficients of variation, indicating a significant environmental impact on this trait and resulting in low heritability values. This observation aligns with the findings of Satyanarayana *et al.* [8]. Conversely, minimal variation between GCV and PCV values was observed for plant height and duration to 50 percent flowering, indicating lesser environmental influence and high heritability values (≥ 90 percent), consistent with the findings of Duppala *et al.* [5].

The results also revealed moderate genotypic and phenotypic coefficients of variation for duration to 50 percent flowering, plant height, productive tillers per square meter, filled grains per panicle, total grains per panicle, test weight, and grain yield per hectare. These observations corroborate the findings of Kishore *et al.* [17] for duration to 50 percent flowering and filled grains per panicle, Sudeepthi *et al.* [18] for plant height, total grains per panicle, test weight, and grain yield per hectare, and Singh *et al.* [19] for productive tillers per square meter. In contrast, low genotypic and phenotypic coefficients of variation were noted for panicle length and spikelet fertility in the current study, consistent with previous reports by Kishore *et al.* [17] for panicle length and Sudeepthi *et al.* [18] for spikelet fertility.

Table 1. Variability characteristics in long-duration rice varieties

| 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 per cent flowering | 112.58 | 72.00 | 140.00 | 14.83 | 15.46 | 95.930 | 31.80 |
| 2 | Plant height (cm) | 126.12 | 101.40 | 160.00 | 10.44 | 10.70 | 95.22 | 20.98 |
| 3 | Productive tillers per sqmt | 256.07 | 165.00 | 336.60 | 13.83 | 14.90 | 86.19 | 26.45 |
| 4 | Panicle length (cm) | 27.46 | 22.50 | 33.50 | 8.56 | 9.66 | 78.55 | 15.64 |
| 5 | Filled grains per panicle | 230.67 | 148.50 | 345.08 | 16.05 | 19.60 | 67.10 | 27.09 |
| 6 | Total grains per panicle | 269.61 | 165.22 | 402.03 | 15.57 | 19.21 | 65.65 | 25.98 |
| 7 | Spikelet fertility (%) | 85.57 | 75.78 | 92.87 | 4.05 | 4.61 | 87.95 | 9.49 |
| 8 | Test weight (g) | 19.06 | 12.76 | 30.86 | 12.98 | 17.05 | 57.87 | 20.36 |
| 9 | Grain yield per ha (Kg) | 5014.12 | 2495.00 | 7437.00 | 18.00 | 19.67 | 83.77 | 33.94 |

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

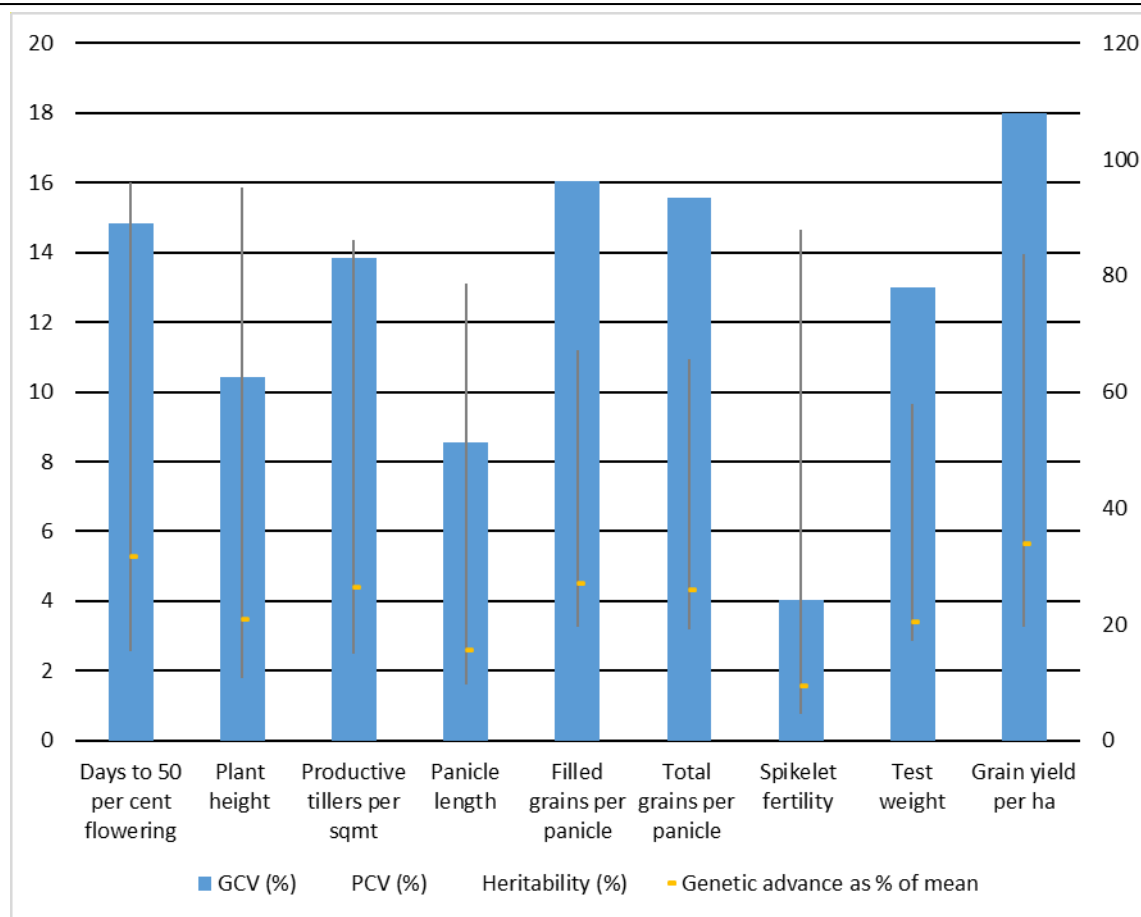


Fig. 1. Assessment of genetic parameters in long-duration rice varieties.

Findings unveiled high heritability levels exceeding 60% and significant genetic advances, surpassing 20% of the mean, for characteristics such as duration to 50 percent flowering, plant height, productive tillers per square meter, filled grains per panicle, total grains per panicle, and grain yield per hectare (see Table 1 and Fig. 1). These results align with findings by Lakshmi *et al.* [20] for duration to 50 percent flowering, plant height, productive tillers per square meter, and filled grains per panicle; Singh *et al.* [19] for total grains per panicle; and Sameera *et al.* [21] for grain yield per hectare. The high heritability and substantial genetic advance for these traits indicate a predominant additive genetic effect, suggesting the effectiveness of direct phenotypic selection in early breeding stages, as noted by Manojkumar *et al.* [16]. Conversely, for panicle length, high heritability (>60%) coupled with moderate genetic advance as a percentage of the mean (10-20%) was observed, while high heritability coupled with low genetic advance as a percentage of the mean was noted for spikelet fertility, consistent with findings by Sudeepthi *et al.* [18]. In contrast, moderate heritability (>60%) coupled with high genetic advance as a percentage of the mean (10-20%) was observed for test weight.

In Table 2, the relationships between yield and yield component traits are depicted. It is noteworthy that grain yield showed positive and noteworthy correlations with panicle length, filled grains per panicle, and total grains per panicle, indicating the possibility of enhancing them concurrently with grain yield per plant. These findings align with reports by Duppala *et al.* [22] for filled grains per panicle and total grains per panicle and by Muthuvijayaragavan and Jebaraj [23] for panicle length. Furthermore, positive and significant associations were observed between plant height and panicle length, productive tillers per square meter and spikelet fertility, and filled grains per panicle and total grains per panicle indicating

Table 2. Correlation coefficients among grain yield and yield components in long-duration rice varieties

| Traits | Plant height | Productive tillers per sqmt | Panicle length | Filled grains per panicle | Total grains per panicle | Spikelet fertilities | Test weight | Grain yield per ha |
|-------------------------------|--------------|-----------------------------|------------------|---------------------------|--------------------------|----------------------|-----------------|--------------------|
| Days to 50 per cent flowering | 0.039 | -0.222 | -0.044 | 0.268 | 0.219 | 0.200 | -0.267 | 0.288 |
| Plant height | | 0.138 | 0.8269 ** | -0.044 | -0.164 | 0.388 | 0.391 | 0.341 |
| Productive tillers per sqmt | | | 0.329 | 0.223 | 0.112 | 0.4465 * | -0.403 | 0.444 |
| Panicle length | | | | 0.165 | 0.094 | 0.205 | 0.362 | 0.5617 ** |
| Filled grains per panicle | | | | | 0.9666 ** | 0.233 | -0.470 * | 0.6905 ** |
| Total grains per panicle | | | | | | -0.023 | -0.432 | 0.5914 ** |
| Spikelet fertilities | | | | | | | -0.249 | 0.418 |
| Test weight | | | | | | | | -0.346 |

* - indicates significance with $P < 0.05$, ** - indicates significance with $P < 0.01$

opportunities for concurrent enhancement of these traits. These observations are in line with the findings of Duppala *et al.* [22]. However, it is noteworthy that filled grains per panicle exhibited a significant negative association with test weight, suggesting indirect selection for lower test weights of finer quality with an increased number of filled grains per panicle.

Table 3 presents the findings of the path analysis investigating the influence of yield component traits on grain yield per plant. Upon examination, it was observed that the residual effect of 0.192 suggested that the variables under study in this research elucidated about 80.80% of the variability in grain yield per plant. However, this implies that there are other unexplored factors that also play a role in determining grain yield per plant. Noteworthy is the significantly positive direct impact of panicle length and filled grains per panicle on grain yield per plant. These identifications are consistent with those reported by Tejaswani *et al.* [24] for panicle length and Manojkumar *et al.* [16] for filled grains per panicle. Additionally, moderate positive effects were observed for spikelet fertility, while days to 50 percent flowering exhibited negligible effect. Conversely, test weight and plant height demonstrated very high direct effects in the negative direction, followed by low-value negative direct effects exhibited by productive tillers per square meter and total grains per panicle. These results align with the findings of Panja *et al.* [26] for test weight, Vengatesh and Govindarasu [27] for plant height, and Singh *et al.* [28] for productive tillers per square meter. Despite the positive correlation coefficient for total grains per panicle, the negative direct effect suggests that indirect effects may be influencing this correlation. Similar findings were reported by Sowjanya *et al.* [29].

Table 3. Direct and indirect impacts of yield component traits in long-duration rice varieties

| 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 | 0.092 | -0.014 | 0.024 | -0.040 | 0.093 | -0.011 | 0.044 | 0.098 | 0.288 |
| Plant height | 0.004 | -0.347 | -0.015 | 0.764 | -0.015 | 0.008 | 0.086 | -0.144 | 0.341 |
| Productive tillers per sqmt | -0.021 | -0.048 | -0.110 | 0.304 | 0.078 | -0.006 | 0.098 | 0.148 | 0.444 |
| Panicle length | -0.004 | -0.287 | -0.036 | 0.923 | 0.057 | -0.005 | 0.045 | -0.133 | 0.5617 ** |
| Filled grains per panicle | 0.025 | 0.015 | -0.025 | 0.152 | 0.349 | -0.050 | 0.051 | 0.172 | 0.6905 ** |
| Total grains per panicle | 0.020 | 0.057 | -0.012 | 0.087 | 0.337 | -0.051 | -0.005 | 0.159 | 0.5914 ** |
| Spikelet fertility | 0.019 | -0.135 | -0.049 | 0.189 | 0.081 | 0.001 | 0.221 | 0.092 | 0.418 |
| Test weight | -0.025 | -0.136 | 0.044 | 0.334 | -0.164 | 0.022 | -0.055 | -0.367 | -0.346 |

Residual effect = 0.192; Diagonal with bold values infers the direct effects

The Principal Component Analysis (PCA) results indicated that the first four principal components, each with Eigenvalues exceeding 1, collectively explained 86.93% of the total variability (see Table 4), indicating that these components encapsulate the main characteristics of the dataset. This observation aligns with previous findings reported by Sudeepthi *et al.* [30]. Components with Eigenvalues less than one were deemed insignificant. PC 1, contributing 34.19% to the total variability, was primarily influenced by grain yield per hectare and filled grains per panicle, consistent with studies by Sar and Kole [31] and Bhargavi *et al.* [32]. PC 2, explaining 24.23% of the total variance, was predominantly influenced by total grains per panicle and filled grains per panicle, in accordance with research by Kashyap and Yadav [33] and Prakash *et al.* [34]. PC 3, which accounted for 16.03% of the total variability, was largely influenced by productive tillers per square meter and spikelet fertility, as observed in studies by Upadhyay *et al.* [35] and Behera *et al.* [36]. PC 4, contributing 12.49% to the total variability, showed significant variance in days to productive tillers per square meter and total grains per panicle, consistent with findings by Krishna *et al.* [37]. Filled grains per panicle and productive tillers per square meter emerged as crucial traits driving variability in the study, **Quantitative trait selection criteria relies predominantly on genetic architecture of the crop [38].** Figure 2 illustrates that all nine variables exhibited high loadings on different principal factors, with none left after varimax-rotation of the principal component axes. “Furthermore, it effectively grouped similar variables together on common principal factors. Additionally, Figure 3 depicts genotypes positioned towards the positive end of both factors, suggesting their superiority collectively for filled grains per panicle, total grains per panicle, and grain yield”. [8]

Table 4. Component loading of various characteristics related to yield and yield components in long-duration rice varieties

| S.No. | Components | Principal component analysis | | | |
|-------|-------------------------------|------------------------------|-------|-------|-------|
| | | PC 1 | PC 2 | PC 3 | PC 4 |
| 1. | Eigen Value | 3.08 | 2.18 | 1.44 | 1.12 |
| 2. | Explained % of variance | 34.19 | 24.23 | 16.03 | 12.49 |
| 3. | Cumulative % of variance | 34.19 | 58.41 | 74.44 | 86.93 |
| | | | | | |
| S.No. | Characters contribution | PC 1 | PC 2 | PC 3 | PC 4 |
| 1. | Days to 50 per cent flowering | 0.18 | 0.18 | -0.12 | -0.80 |
| 2. | Plant height | 0.20 | -0.57 | -0.13 | -0.17 |
| 3. | Productive tillers per sqmt | 0.30 | -0.12 | 0.53* | 0.38* |
| 4. | Panicle length | 0.30 | -0.50 | -0.21 | 0.11 |
| 5. | Filled grains per panicle | 0.45* | 0.30* | -0.27 | 0.15 |
| 6. | Total grains per panicle | 0.38 | 0.36* | -0.37 | 0.23* |
| 7. | Spikelet fertility | 0.31 | -0.18 | 0.39* | -0.31 |
| 8. | Test weight | -0.19 | -0.36 | -0.53 | 0.10 |
| 9. | Grain yield per ha | 0.52* | -0.04 | -0.02 | -0.01 |

Table 5. Contribution of individual entries to different principal components in long-duration rice varieties

| Genotype | Genotypes Contribution for PCA | | | |
|-----------------|---------------------------------------|------------|------------|------------|
| | PC1 | PC2 | PC3 | PC4 |
| L 678 | 0.00 | 3.07 | 1.46 | 10.56 |
| L 679 | 35.63* | 0.68 | 26.41* | 2.07 |
| L 680 | 0.67 | 0.19 | 0.06 | 1.56 |
| L 681 | 0.55 | 10.98 | 5.79 | 3.31 |
| L 682 | 6.55 | 0.50 | 0.00 | 0.05 |
| L 683 | 7.34 | 0.64 | 1.26 | 8.87 |
| L 684 | 7.28 | 15.33* | 0.70 | 6.21 |
| L 685 | 0.15 | 0.01 | 1.06 | 0.31 |
| L 686 | 1.76 | 0.17 | 6.77 | 0.43 |
| L 687 | 0.11 | 15.25 | 2.08 | 7.96 |
| L 688 | 0.10 | 15.49* | 0.56 | 0.60 |
| L 689 | 0.96 | 6.31 | 0.81 | 1.98 |
| L 690 | 2.87 | 0.25 | 0.26 | 0.00 |
| L 691 | 7.87 | 0.26 | 26.04* | 0.13 |
| L 692 | 0.15 | 13.46 | 3.00 | 14.62* |
| L 693 | 13.27* | 1.13 | 10.28 | 0.38 |
| L 694 | 5.88 | 9.13 | 2.83 | 4.74 |
| L 695 | 0.05 | 0.02 | 4.85 | 1.56 |
| L 696 | 1.41 | 0.02 | 0.37 | 0.82 |
| L 697 | 2.42 | 2.12 | 0.41 | 28.84* |

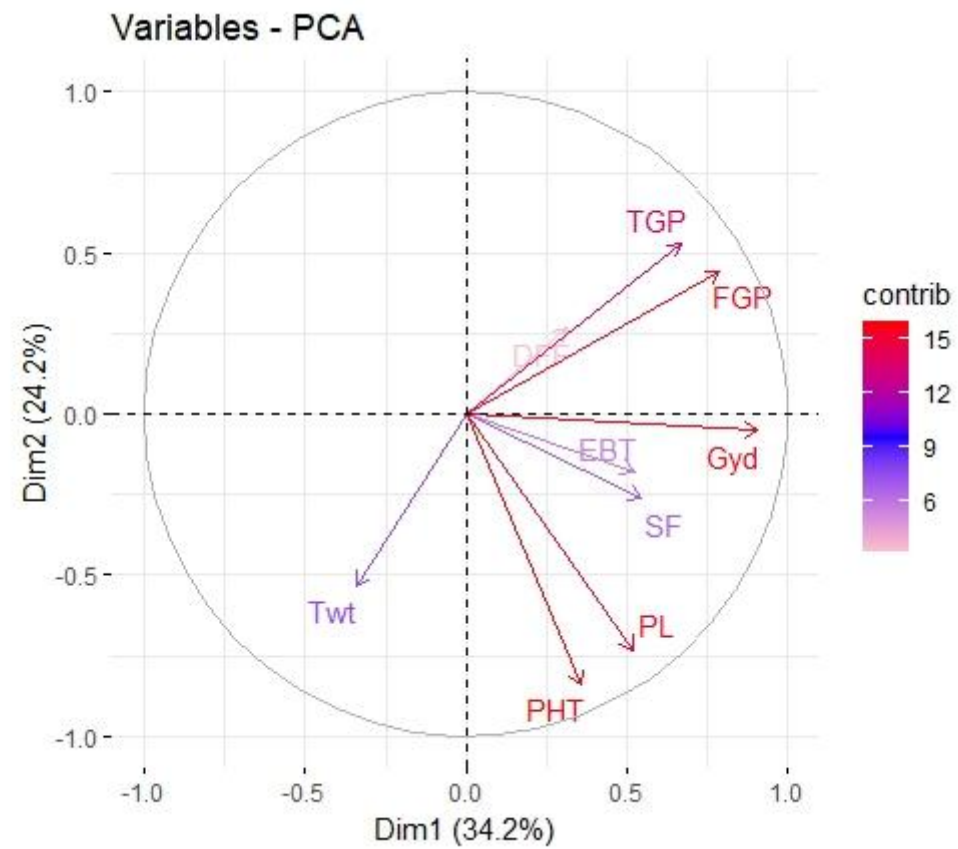


Fig.2. Dispersion of variables across the primary principal components.

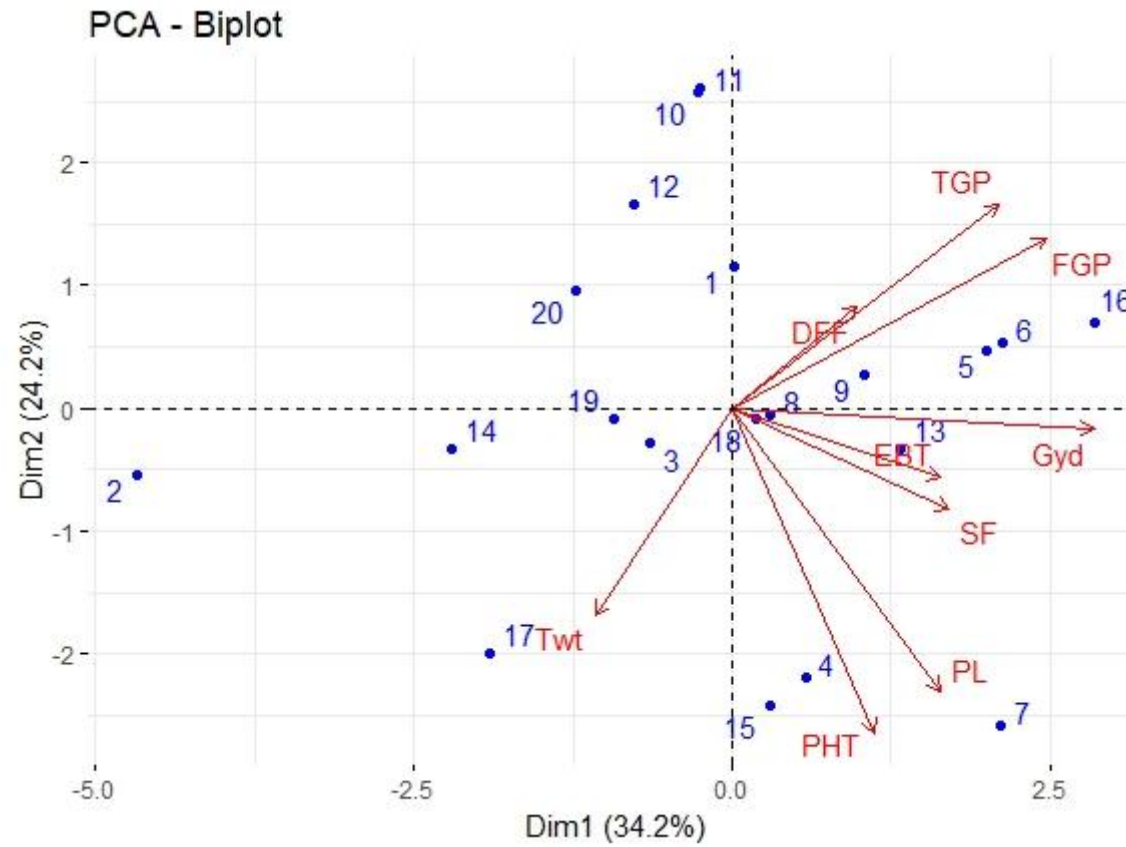


Fig.3. Projection of genotypes across the primary principal components.

Based on the present investigation, entry 16 has been identified as superior for filled grains per panicle and grain yield, corresponding to principal component 1, while entry 11 appears superior for filled grains per panicle and total grains per panicle. Since entries 16 and 11 are located on different components at the positive ends, they can be utilized in further breeding programs to capitalize on the diversity present among them for further crop improvement, **genomic selection of the elite cultivars largely reflected by their genetic constitution and is highly reliable in crop improvement [39].**

Conclusion:

Significant heritability and substantial genetic advance percentages were noted for productive tillers per plant, filled grains per panicle, total grains per panicle, and grain yield per plant. This suggests that increasing these qualities through direct phenotypic selection may be beneficial. The significant association and favorable direct influence between the number of filled grains per panicle and the total grain yield per plant are particularly notable. Therefore, one of the most important selection criteria for increasing rice crop output is the number of filled grains per panicle. Furthermore, filled grains per panicle stand out as the most important characteristic for selection, as supported by principal component analysis.

Acknowledgement

The financial support provided in the form of planned budget for technical program of plant breeding from Acharya N G Ranga Agricultural University, Lam, Guntur, at Agricultural College, Bapatla, Andhra Pradesh, is acknowledged.

References

1. Manojkumar D, Srinivas T, Rao LS, Suneetha Y, Sundaram RM, Kumari VP, Bhuvaneshwari V, Ganesh B. Screening of recombinant inbred lines for resistance to bacterial leaf blight pathotypes in rice (*Oryza sativa* L.). *Plant Science Today*. 2023;10(3): 343–353.
2. Vasudev R, Suneetha Y, Ravikumar BNVS, Ramesh D, Manojkumar D, Srinivas T. Studies on Promising Restorer Lines for Yield and Yield Components in Rice (*Oryza sativa* L.). *Journal of Rice Research*. 2023;16(2): 31-42.
3. Duppala MK, Srinivas T, Suneetha Y, Suresh G. Generation Mean Analysis for quantitative traits in the population of AKDRMS 21-54 x YH3 cross of rice (*Oryza sativa* L.). *Journal of Environmental Biology*. 2023;44(1): 826-832.
4. Manojkumar D, Srinivas T, Rao LS, Suneetha Y, Sundaram RM, Kumari VP and Ratnam TV. Generation Mean Analysis for Yield and Yield Component Traits in Inter-specific Cross of Rice (*Oryza sativa* L.). *Agricultural Science Digest*. 2023;7(1):1-7.
5. Duppala MK, Nair B, Srinivas T, Suneetha Y, Kumar KM, Reddy DV. Elucidation of genetic variability and inter-relationship studies for seed yield and quality traits in advanced lines of *mustard spp.* *International Journal of Advanced Biochemistry Research*. 2024;8(3): 25-30.
6. Manojkumar D, Nair B, Srinivas T, Suneetha Y, Reddy DV, Kumar KM. Genetic studies of genetic variability and trait associations in *mustard spp.* (*Brassica juncea* L. & *Brassica carinata* A.). *International Journal of Research in Agronomy*. 2024;7(2): 435-440.
7. Reddy DV, Suneetha Y, Ravikumar BNVS, Ramesh D, Manojkumar D, Srinivas T. Combining Ability Studies of Promising Restorer Lines for Yield and Yield Components in Rice (*Oryza sativa* L.). *Agricultural Science Digest*. 2024;1(1):1-7.
8. Satyanarayana PV, Madhukumar K, Udayababu P, Srinivas T, Manojkumar D. Association Studies for Identifying the Selection Criteria Among Early varieties of Rice in North Coastal Zone of Andhra Pradesh. *Biological Forum – An International Journal*. 2023;15(11): 329-335.
9. Burton GW, Devane. Estimating heritability in tall tissue (*Festularia undnacea* L.) from replicated clonal material. *Agronomy Journal*. 1953;45: 478 -481.
10. Allard RW. *Principles of Plant Breeding*. 2nd ed. John Wiley and Sons. Inc. 1960;485.

11. Johnson HW, Robinson HF, Comstock RW. Estimates of genetic and environment variability in Soybean. *Agronomy Journal*.1955;47: 314–318
12. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis, Kalyani Publishers, New Delhi. 1977;57-58.
13. Dewey DI, Lu KH. A Correlation and Path-Coefficient Analysis of Components of Crested Wheatgrass Seed Production. *Agronomy Journal*. 1959; 51: 515-518.
14. Banfield, CF. Multivariate analysis in genstat. *Journal of Statistical Computation and Simulation*. 1978; 6(4): 211-222.
15. R Core Team R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria. 2023; <http://www.R-project.org/>.
16. Manojkumar D, Srinivas T, Subba Rao LV, Suneetha Y, Sundaram RM, Prasannakumari V. Genetic Variability and Trait Association Analysis in F₃ Population of YH3 x AKDRMS 21-54 Cross. *The Andhra Agricultural Journal*. 2022;69 (1): 46-57.
17. Kishore NS, Srinivas T, Nagabhushanam U, Pallavi M, Sameera SK. Genetic variability, correlation and path analysis for yield and yield components in promising rice (*Oryza sativa* L.) genotypes. *SAARC Journal of Agriculture*. 2015;13 (1): 99-108.
18. Sudeepthi K, Srinivas TV, Kumar BR, Jyothula DP, Umar SN. Assessment of genetic variability, character association and path analysis for yield and yield component traits in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*. 2020; 11(01):144-8.
19. Singh KS, Suneetha Y, Kumar GV, Rao VS, Raja DS, Srinivas T. Variability, correlation and path studies in coloured rice. *International Journal Chemical Studies*. 2020; 8(4), 2138-2144.
20. Lakshmi MS, Suneetha Y, Srinivas T. Genetic variability, correlation and path analysis for grain yield and yield components in rice genotypes. *Journal of Pharmacognosy and Phytochemistry*. 2021; 10(1):1369-1372.
21. Sameera, S.K., Prasanna, R.A., Jayalakshmi, P., Nirmala, J. and Srinivas, T. Genetic variability studies for yield and yield components in rice. *Electronic Journal of Plant Breeding*. 2015; 6(1): 269-273.

22. Duppala MK, Srinivas T, Rao LS, Suneetha Y, Sundaram RM, Kumari VP. Study of genetic variability and trait associations in F₂ Population of YH3 x AKDRMS 21-54 intra-specific cross of rice. *The Pharma Innovation Journal*. 2022; 11(9): 1735-1742.
23. Muthuvijayaragavan R, Jebaraj S. Correlation and path coefficient analysis in F₂ families of rice (*Oryza sativa* L.) under direct seeded condition. *Journal of Genetics, Genomics and Plant Breeding*. 2022;6(2): 44-53.
24. Tejaswini KL, Kumar BR, Mohammad LA, Raju SK, Srinivas M, Rao PR. Study of genetic parameters in F₅ families of rice (*Oryza sativa* L.). *International Journal of Environment, Agriculture and Biotechnology*. 2016; 1(4): 238-592.
25. Abhilash R, Thirumurugan T, Sassikumar D, Chitra S. Genetic studies in F₂ for biometrical traits in Rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*. 2018; 9(3): 1067-1076.
26. Panja S, Garga HS, Debnath K, Sarkar KK, Mukherjee S, Bhattacharya C. Effect of water stress on different morphological traits of rice (*Oryza sativa* L.) genotypes in red and laterite zone of West Bengal. *International Journal of Advanced Biological Research*. 2017;7 (3): 419-425.
27. Vengatesh M, Govindarasu R. Studies on correlation and path analysis in rice (*Oryza sativa* L.) genotypes. *Electronic Journal of Plant Breeding*. 2018; 9(4):1570-1576.
28. Singh AK, Mall AK, Singh PK, Singh S, Verma OP. Genetic architecture, heterosis and inbreeding depression for yield and yield associated physiological traits in rice (*Oryza sativa* L.) under drought condition. *SAARC Journal of Agriculture*. 2015;13(1):50-62.
29. Sowjanya PR, Hittalmani, S. Trait association studies to determine selection indices in two F₃ segregating populations of rice (*Oryza sativa* L.) under aerobic condition. *Oryza-An International Journal on Rice*. 2017; 54(3):276-81.
30. Sudeepthi K, Srinivas T, Ravi Kumar BNVS, Jyothula DPB, Umar SN. Genetic Diversity Studies for Yield and Yield Component Traits using Principal Component Analysis in Rice (*Oryza sativa* L.). *International Journal of Pure Applied Biosciences*. 2020; 8(3): 228-235.
31. Sar P, Kole PC. Principal component and cluster analyses for assessing agro-morphological diversity in rice. *Oryza*. 2023; 60(1): 117-124.
32. Bhargavi B, Yadla S, Jukanti AK, Thati S. Genetic divergence studies for yield and quality traits in high protein landraces of rice (*Oryza sativa* L.). *Plant Science Today*. 2023; 10(2):195-204.

33. Kashyap A, Yadav VK. Principal component analysis and character association for yield components in rice (*Oryza sativa* L.) genotypes of salt tolerance under alkaline condition. *International Journal of Current Microbiology and Applied Sciences*. 2020; 9: 481-495.
34. Prakash S, Reddy SS, Chaudhary S, Vimal SC, Kumar A. Multivariate analysis in rice (*Oryza sativa* L.) germplasms for yield attributing traits. *Plant Science Today*. 2024; 11(1): 64-75.
35. Upadhyay S, Rathi S, Choudhary M, Snehi S, Singh V, Singh PK, Singh RK. Principal component analysis of yield and its attributing traits in advanced inbred lines of rice under sodicity condition (*Oryza sativa* L.). In *Biological Forum—An International Journal*. 2022;14(2):1273-1276.
36. Behera P, Singh SK, Sivasankarreddy K, Majhi PK, Reddy B J, Singh DK. Yield attributing traits of high zinc rice (*Oryza sativa* L.) genotypes with special reference to principal component analysis. *Environment Conservation Journal*. 2022;23(3):458-470.
37. Krishna K, Chandra MY, Krishna L, Parimala G, Jagadeeshwar R. Multivariate analysis-based prediction of phenotypic diversity associated with yield and yield component traits in germplasm lines of rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*. 2022; 13(3):764-771.
38. Oladosu Y, Rafii MY, Abdullah N, Abdul Malek M, Rahim HA, Hussin G, Abdul Latif M, Kareem I. Genetic variability and selection criteria in rice mutant lines as revealed by quantitative traits. *The Scientific World Journal*. 2014; 11(1):1-12.
39. Spindel J, Begum H, Akdemir D, Virk P, Collard B, Redona E, Atlin G, Jannink JL, McCouch SR. Genomic selection and association mapping in rice (*Oryza sativa*): effect of trait genetic architecture, training population composition, marker number and statistical model on accuracy of rice genomic selection in elite, tropical rice breeding lines. 2015. *PLoS Genetics*, 11(2):1-25.