



E-ISSN: 2618-0618
P-ISSN: 2618-060X
© Agronomy
NAAS Rating (2025): 5.20
www.agronomyjournals.com
2025; 8(12): 1007-1014
Received: 04-10-2025
Accepted: 06-11-2025

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International Journal of Research in Agronomy

Genetic analysis of quantitative traits in segregating generation of rice (*Oryza sativa* L.)

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DOI: <https://www.doi.org/10.33545/2618060X.2025.v8.i12n.4752>

Abstract

This study was undertaken to assess the variability and key genetic parameters including heritability, phenotypic and genotypic variances, genetic advance, and principal component analysis (PCA) for yield and related traits in an F_3 population of rice. Analysis of variance revealed significant differences among the 51 genotypes for all traits studied. Although phenotypic variance exceeded genotypic variance, the narrow differences between PCV and GCV across most traits indicated limited environmental influence. High GCV and PCV values were recorded for productive tillers, filled grains per panicle, and grain yield per plant. Most traits exhibited high heritability, while filled grains per panicle and plant height showed both high heritability and high genetic advance, suggesting the predominance of additive gene action and their suitability for improvement through direct selection. PCA of the seven quantitative traits showed that the first two principal components, with eigenvalues greater than one, accounted for 61.51% of the total variability. Traits such as panicle length, plant height, productive tillers, days to 50% flowering, and grain yield per plant contributed substantially to the observed divergence and were identified as major sources of variation in the population.

Keywords: Rice, heritability, genetic variance, genetic advance, principal component analysis, yield

Introduction

Rice is a major cereal crop on a global scale, acting as a primary food source in tropical and subtropical regions. As the world's population continues to grow, its demand is projected to rise in the future decades. To feed an ever-increasing population, rice production and productivity must be enhanced while utilising scarce precious resources such as land and water. Thus, enhancing productivity of the economic product will always be the main objective of plant breeders.

It is very important to understand the inheritance pattern of various polygenic traits like yield and its component traits and the influence of genetic variability before initiating a crop improvement programme. A comprehensive genetic variability assessment is necessary to guide breeding strategies effectively (Babu *et al.*, 2012) [6]. The variation present within a germplasm can be assessed using genotypic and phenotypic coefficients of variation. However, since GCV solely measures the extent of genetic diversity for a trait, it does not provide enough information on its heritability.

A trait's heritability is crucial in deciding a cultivar's responsiveness to selection (Surek and Beser). Because it indicates the level of trait transmissibility into subsequent generations, understanding heritability is critical for crop improvement based on selection. The genotypic coefficient of variation, in conjunction with heritability values, enhances potential for selection-driven genetic improvement (Burton, 1952) [11]. High heritability, coupled with considerable genetic advance, offers a stronger basis for evaluating the efficiency of genotype selection for yield-related characteristics. The success of selection for a trait is directly linked to its heritability and the extent of genetic advance relative to the mean.

It is therefore critical for any plant breeder to understand the variability in available accessions before embarking on an effective breeding programme for the crop. Consequently, this study aimed on assessing the genetic variation in the segregating population through genetic variance,

broad-sense heritability, and genetic advance estimates for various grain yield traits.

Material and Methods

The current study was conducted in *Kharif*, 2024 at Instructional farm, School of Agriculture, SR University, Warangal using fifty one F₃ rice genotypes. The plant material for this study was derived from a breeding program involving three crosses: Cross I (KNM 118 × MTU 1001), Cross II (MTU 1010 × KNM 1638), and Cross III (MTU 1010 × KNM 118). Fifty-one rice genotypes were sown in properly prepared nursery beds, and after 30 days, the seedlings were systematically transplanted following a randomized block design (RBD) with 20 × 15 cm spacing. The experiment was conducted with three replications, each consisting of three rows. Standard agronomic practices were strictly implemented to promote optimal crop growth and development.

In every replication, observations were made on five randomly selected plants of each genotype. The traits measured were grain yield and yield-related traits like days to fifty percent flowering, productive tillers, plant height in centimetres, panicle length in centimetres, filled grains per panicle, and 1000-grain weight in grams, and these are shown in Table 1. The data obtained were subjected to statistical analysis using WINDOSTAT software (version 8.1). Phenotypic and genetic coefficients of variation, heritability (broad sense), genetic advance, and genetic advance as a percentage of the mean were determined.

Computation of genetic and phenotypic variances for every trait was based on the approach of Burton (1952)^[11]. By calculating the Genotypic Coefficient of Variation (GCV) and the Phenotypic Coefficient of Variation (PCV), which are both based on Burton's formulas, a measure of genetic and phenotypic variability relative to the mean was obtained. Broad-sense heritability was determined by the method of Lush (1940)^[22] as modified by Johnson *et al.* (1955)^[18], which made it possible to estimate the portion of observed variation due to genetic factors. Besides that, the genetic advance (GA) was computed by using heritability estimates and the formula of Johnson *et al.* (1955)^[18]. This method provides a prediction of character improvement during the selection process, thus revealing the possible response to selection for each of the traits being studied.

Results and Discussion

The variance analysis (ANOVA) has shown that there was a significant difference across the F₃ genotypes for all characters evaluated, which is reported in the Table 2. This together with the genetic variation within the genotypes for the characteristics examined gives a good ground for both selection and genetic improvement. The high variability seen on the whole in the traits indicates that selection might bring about major improvements in most of these traits. These findings harmonize with the other studies like those of Adhikari *et al.* (2018)^[3], Gyawali *et al.* (2018)^[15], Sumanth *et al.* (2017)^[44], Abebe *et al.* (2017)^[1], Bandhi *et al.*, and Rashid *et al.* (2017)^[32], which all reported significant differences in yield and important yield-attributing characteristics among rice genotypes. Such results could be regarded as signposts for the opportunity to perform genetic enhancement through selection in the F₃ generation.

Evaluation of Genetic parameters

Variability

An overview of the genetic estimates of yield and associated characters in the F₃ segregating population is provided in Table

3. The presence of variation in the population is a requirement for any crop development strategy. The genotype, environment, and G×E contributed total variability, of which only the genotypic variation is heritable that plays a major role in crop improvement. Hence, to find out the true breeding value of genotypes, it is necessary to measure the variance due to various factors.

The genetic parameter estimates like phenotypic and genotypic variance and coefficients of variation (PCV and GCV) for the eight traits of the F₃ segregating population are given in Table 3. Over all traits, the phenotypic variance has always been more than the genotypic variance and the highest values have been recorded for filled grains per panicle and plant height. On the other hand, the characteristics productive tillers, panicle length, and 1000-seed weight were associated with very low phenotypic and genotypic variances. Such results are consistent with the earlier works done by Harshraj Salunkhe *et al.* (2024)^[16], Lakshmi *et al.* (2017)^[21] and Hasan *et al.* (2022)^[17], Prajapati *et al.* (2011)^[30], and Singh *et al.* (2011)^[42], who have pointed out that there was high genetic variability across these traits.

The study was able to identify a considerable range of different phenotypic coefficient of variation (PCV) values, of which the lowest was percentage 3.71% for days to 50% flowering while the highest was 24.6% for productive tillers. Very high PCV values were found for grain yield per plant (24.04%), filled grains per panicle (22.44%), and productive tillers (24.6%); these results agreed with Seneega *et al.* (2019)^[36]. On the other hand, traits like panicle length (8.06%) and days to 50% flowering (3.71%) had lower PCV values with both traits being below 10%.

GCV values also ranged from 3.51% for days to 50% flowering to 21.63% for productive tillers. It is worth noting that grain yield per plant was characterized by a high GCV of 23.4%, that was followed by productive tillers (21.63%) and filled grains per panicle (18.99%). In contrast, days to 50% flowering (3.51%) and panicle length (6.66%) showed lower GCV values that were below 10%. While on the other hand, moderate values for both PCV and GCV were observed for the remaining traits.

This research comes to the same conclusion as the studies of Lakshmi *et al.* (2017)^[21], Fathima *et al.* (2021)^[14], Bhargava *et al.* (2021)^[10], Sharma and Shanthi (2016)^[35] and Lakshmi *et al.* (2017) in terms of tillers count. Likewise, the number of filled grains per panicle observed was in agreement with the findings of Lakshmi *et al.* (2017)^[21], Singh *et al.* (2021)^[41], Fathima *et al.* (2021)^[14], Bhargava *et al.* (2021)^[10], Rukmini *et al.* (2017)^[34], Revathi *et al.* (2016)^[16], Babu *et al.* (2012)^[6], and Nayak (2008)^[25] while the outcomes for grain yield and the number of filled grains per panicle were in accordance with Abhilash *et al.* (2018)^[2]. Further, agreement was observed with the studies of Kishore *et al.* (2015)^[20], Singh *et al.* (2011)^[42], and Prajapati *et al.* (2011)^[30] for grain yield per plant. In addition, results for days to 50% flowering and panicle length confirmed Patil *et al.* (2003)^[29], Shinha *et al.* (2004)^[38], Prajapati *et al.* (2011)^[30], and Singh *et al.* (2011). On the other hand, the observations on panicle length were also consistent with the findings of Adhikari *et al.* (2018)^[3] and Kishore *et al.* (2015)^[20].

In accordance with the results of the current study, Mazid *et al.* (2013)^[23] reported high genotypic and phenotypic coefficients of variation for the number of filled grains per panicle, number of productive tillers, and grain yield per plant, while they recorded lesser values for days to 50% flowering and panicle length.

The fact that GCV and PCV values for most of the studied characters show only a small difference suggests that the

environmental impact on these characters is minimal and indicates that their expression is mainly controlled by genetic factors. The slight variation between GCV and PCV values (Figure 1) for all characters except for the filled grains per panicle, points to the fact that the phenotypic expression is mainly genetically controlled, and hence, phenotypic selection will be effective for these characters. The present observations are in agreement with the conclusions drawn by Revathi *et al.* (2016)^[33], Nandeshwar *et al.* (2010)^[24], Panwar *et al.* (2007)^[28], and Suman *et al.* (2005)^[43] from their earlier research.

The heritable component of this genetic variation is not indicated by coefficients of variation, which show the degree of genetic variability for a given characteristic as a percentage. The evaluation of genetic advance in combination with heritability allows for a much more accurate determination of this heritable component and offers a clearer view of the genetic potential for improvement through selection.

Heritability

The term heritability is used to describe the proportion of genetic variance in a trait that is responsible for the total phenotypic differences, thus allowing the distinction between hereditary and environmental impacts (Singh, 2001)^[39]. In plant breeding, the process of estimating genetic parameters including heritability is absolutely necessary for understanding the passing on of economically important quantitative traits. High heritability values suggest a greater probability that the trait is uniformly expressed across different environments which in turn increases the effectiveness of selection. Heritability estimates are indicative of the extent to which a phenotypic trait can be consistently passed on to the next generation, assisting breeders in selecting desirable characteristics with higher precision.

It has been established that the traits with high heritability attribute the major role in the expression of the trait to genetic factors and hence, phenotypic performance can be more conveniently selected based on this. On the other hand, low heritability traits reveal considerable environmental impact, thus, the likelihood of selection being ineffective is higher. The assessments of heritability that are ranked higher, especially when they are coupled with remarkable genetic advancement, provide stronger evidence for the probable good selection through the process of improvement. Parameters such as these are very important in the rice breeding programs scheduled for yield and its characters contributing to the selection of the breeding method that is the best for improving these characteristics in segregating generations.

In the present study, high estimates of heritability (68.4%-98.1%) were recorded for all the traits under investigation (Table 3; Fig. 2), indicating a predominance of genetic factors in the expression of these characters. Plant height exhibited the highest heritability (98.1%), followed by grain yield per plant (94.7%) and 1000-seed weight (90.6%). Days to 50% flowering also recorded a high heritability estimate (89.5%). Moderate to high heritability values were observed for productive tillers per plant (77.1%), filled grains per panicle (71.4%), and panicle length (68.4%). These findings are consistent with earlier reports by Priyanka *et al.* (2021)^[31], Singh *et al.* (2011)^[42], Anandrao *et al.* (2011)^[5], Prajapati *et al.* (2011)^[30], and Verma (2010)^[46], who similarly noted high heritability for yield and related traits in rice.

High heritability estimates indicate that genetic factors predominantly govern the expression of these traits, with minimal environmental influence, thereby making phenotypic performance a reliable indicator of genetic potential (Allard,

1999)^[4]. This greatly enhances the effectiveness of selection, particularly in early segregating generations where high heritability facilitates precise identification and advancement of desirable genotypes (Bello *et al.*, 2012)^[9]. Such conditions allow breeders to rely on observable phenotypic variation to accelerate improvement in complex traits.

However, heritability alone does not provide a complete prediction of the expected response to selection. For a more accurate assessment of genetic progress, heritability must be considered together with genetic advance (Johnson *et al.*, 1955)^[18]. The concurrent presence of high heritability and high genetic advance indicates predominance of additive gene action and reflects strong potential for improvement through direct selection (Prajapati *et al.*, 2011)^[30]. Hence, evaluating both parameters is essential for making informed breeding decisions, optimizing selection strategies, and enhancing genetic gain in rice and associated yield-contributing traits (Nayak *et al.*, 2008; Adhikari *et al.*, 2018)^[25, 3].

Genetic Advance

The joint consideration of heritability and genetic advance provides a more reliable indication of selection response than heritability alone. While heritability reflects the proportion of phenotypic variance attributable to genetic factors, genetic advance quantifies the expected improvement under selection pressure. Therefore, their combined interpretation offers a stronger prediction of genetic gain (Johnson *et al.*, 1955)^[18]. It is important to note that high heritability does not always correspond to high genetic advance, since non-additive gene action may limit the magnitude of improvement achievable through selection.

In the present study, the highest expected genetic gain was observed for filled grains per panicle, closely followed by plant height, indicating the predominance of additive gene action for these traits (Nandeshwar *et al.*, 2010)^[24]. Conversely, traits such as panicle length and productive tillers exhibited comparatively low genetic advance (Mazid *et al.*, 2013)^[23], suggesting that these traits may be more strongly influenced by non-additive gene effects or environmental factors (Table 3; Fig. 3). Traits that recorded high genetic advance as a percentage of the mean such as grain yield per plant, productive tillers, and filled grains per panicle are likely governed by additive genes and are therefore amenable to improvement through direct phenotypic selection. In contrast, traits like days to 50% flowering and panicle length, which exhibited lower genetic advance, may require alternative breeding strategies or evaluation across advanced generations to achieve substantial improvement.

It has been affirmed by (Panse and Sukhatme, 1967)^[27] that traits with higher heritability, as well as those with high genetic advance, are mostly controlled by additive gene action. Therefore, it would be further better if the traits with large and significant heritability plus great and considerable genetic advance were focused on since these traits would be giving out more of the additive genes as their presence would be greatly amplified. In the present study, the number of filled grains per panicle (Babu *et al.*, 2012)^[6] and plant height (Priyanka *et al.*, 2021; Singh *et al.*, 2011)^[31, 42] exhibited both high heritability and high genetic advance, offering potential for selection and further breeding. However, the yield of grain per plant showed significant heritability along with moderate genetic advancement, while other traits have high heritability but only low to moderate genetic advancement. Thus, plant height, filled grains per panicle, and grain yield per plant are mainly influenced by additive genes, and simple selection can be applied for genetic enhancement since they are responsive to it.

On the other hand, traits with high heritability but low genetic advancement signal the presence of nonadditive gene action. Selection will be less effective for these traits and the gain thus possible, will be limited. In these situations, the intermingling of superior genotypes from the segregating population, created through combination breeding methods, will be a more effective improvement strategy. Hence, for characters that are of high heritability but with low or moderate genetic advance, the breeding must be through high-tech breeding methods such as recurrent selection or genetic recombination that target the unlocking of genetic potential.

The objective of Principal Component Analysis is to determine the individual contribution and significance of all factors in variance explanation. Furthermore, it reveals how different characteristics add to variation, and the coefficients show the proportion of each variable's influence on total variance. Therefore, PCA helps breeders in selecting the traits that are key to nature and will thus expedite the process of crop improvement (Das *et al.*, 2017) ^[12]. This method essentially reduces the number of interrelated variables into a certain, fewer number of independent principal components thereby making the understanding of trait relationships clearer (Beattie & Esmonde-White, 2021) ^[7]. PCA being a major component, also helps in finding the out-standing multi-gene traits that are very important for breeding programs (Singh *et al.*, 2020) ^[40] in plant breeding.

PCA analysis was performed in this work, and Table 4 presents the eigenvalues, percent variance, and cumulative variance that were obtained. Kaiser (1960) ^[19] asserts that a principal component with an eigenvalue greater than 1 explains a larger proportion of variance contributed by each individual variable linked to that specific component. The variance linked to each component is explained by the screen plot that was created between the eigenvalues of the various principal components (Fig. 4). According to PCA analysis, the initial two principal components (PC1 and PC2) of the seven quantitative traits examined had eigenvalues greater than one collectively accounting for 61.51% of the overall variability amongst the studied traits (Table 4).

The first two principal components (PCs) together explained

more than 50% of the total variation (Figure 4) The decrease in the graph was sharp after two components and then was followed by a gradual slope, thus, suggesting that two PCs contributed most of the variability. The traits attributed to these components, such as the length of panicle, plant height, and weight of 1000 seeds (Figure 5), were among the major contributors to the total variance. These results are in confirmation with those given by Divya Mahto *et al.* (2023) ^[13] where the first two PCs accounted for a cumulative variation of 63.90% in a study on 54 derived lines of Katarni rice. In a similar way, Talekar *et al.* (2022) ^[45] reported that during the analysis of 100 rice germplasm lines, the first two principal components with eigenvalues exceeding 1 together accounted for 55.60% of the variance.

The biplot of the first two principal components showed the traits' relations and their linked genotypes (Figure 5). Among the traits studied, the number of days to 50% flowering and the number of productive tillers showed negative loadings in PC1, while the other traits had a positive contribution to this principal component. The length of each vector was an indicator of the degree of its contribution to the overall divergence with the longer vectors having the higher impact. Panicle length had the longest vector, which indicates its major contribution to overall diversity while the other traits of plant height, productive tillers, grain yield per plant, and days to 50% flowering also followed in importance.

The angle between the vectors of characters determines the correlation direction between them. A 90° angle indicates no correlation; if it is less than 90°, the correlation is positive; and if it is more than 90°, the correlation is negative. Out of the seven traits studied, grain yield per plant had a positive correlation with the number of filled grains per panicle, 1000-seed weight, productive tillers, height, and panicle length. Conversely, panicle length, 1000 seed weight, and plant height made negative contributions to the days to 50% flowering. The same trends were noted by Shanmugam *et al.* (2023) ^[37] and Palaniyappan *et al.* (2024) ^[26], which highlighted the strong association between grain yield per plant and the number of filled grains per panicle.

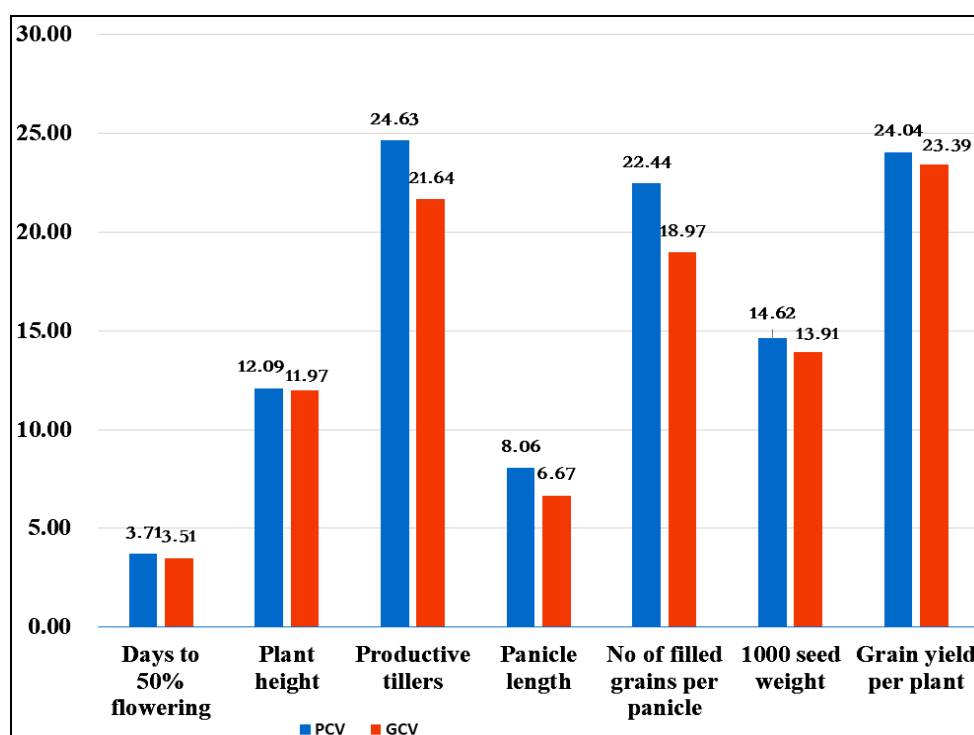


Fig 1: PCV and GCV values for yield and yield related characters

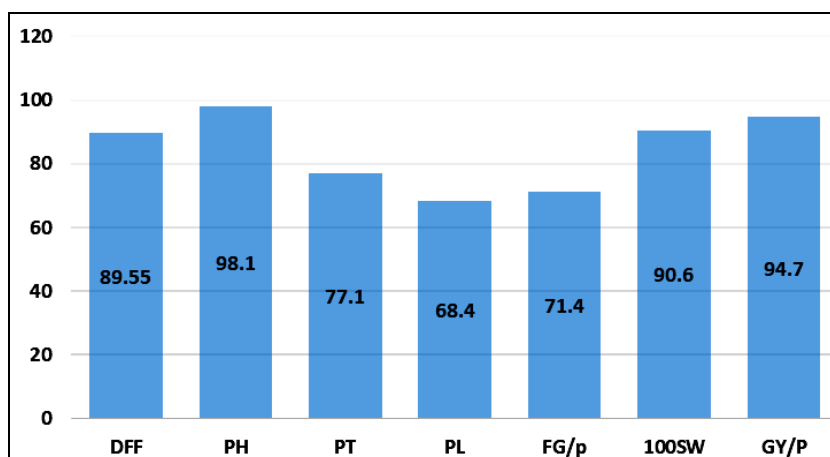


Fig 2: Graphical representation of heritability (bs) % for various traits.

DFF- Days to fifty percent flowering, PH-Plant height (cm), PL- Panicle length (cm), PT-Number of productive tillers, FG/P- Number of filled grains per panicle, 100SW - 100 Seed weight, GY/P-Grain yield per plant

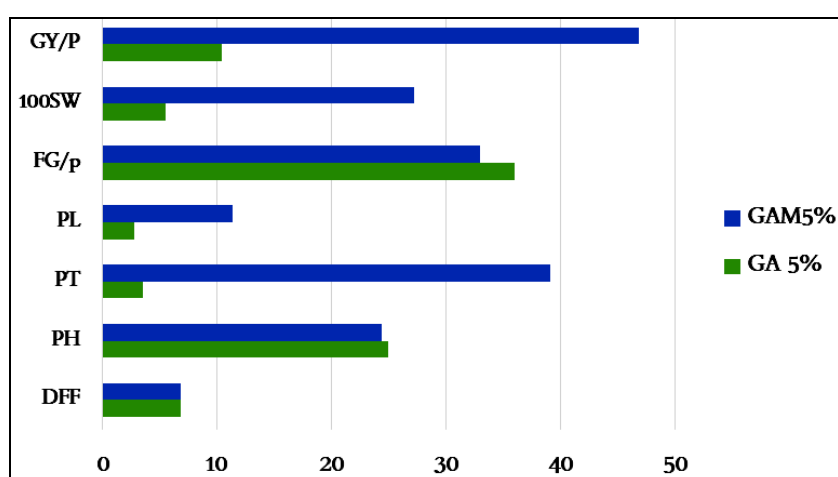


Fig 3: Graphical representation of Genetic Advance and Genetic Advance as percent of mean for various traits.

DFF- Days to fifty percent flowering, PH-Plant height (cm), PL- Panicle length (cm), PT-Number of productive tillers, FG/P- Number of filled grains per panicle, 100SW - 100 Seed weight, GY/P-Grain yield per plant

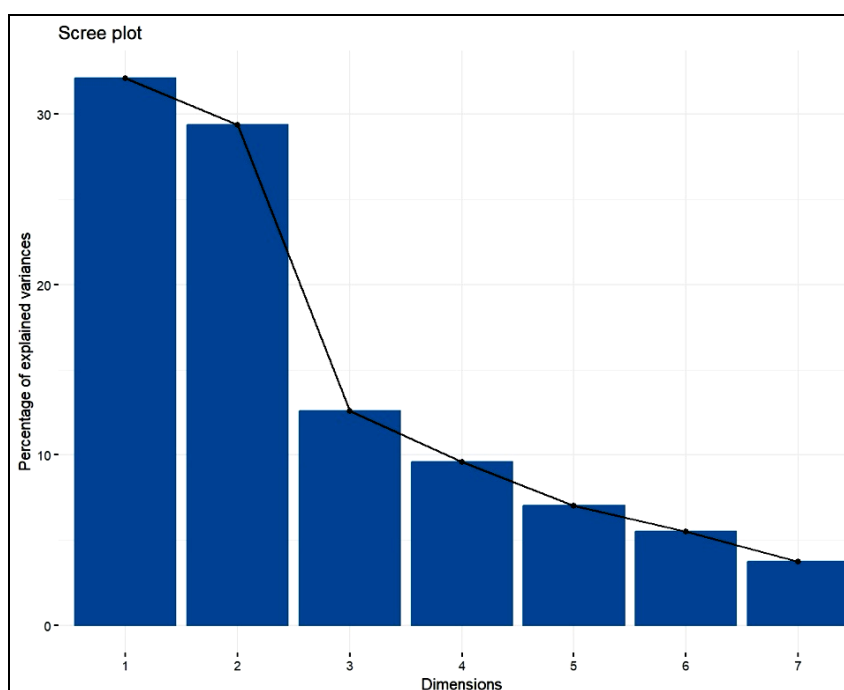


Fig 4: Screen plot representing principal components and their variations

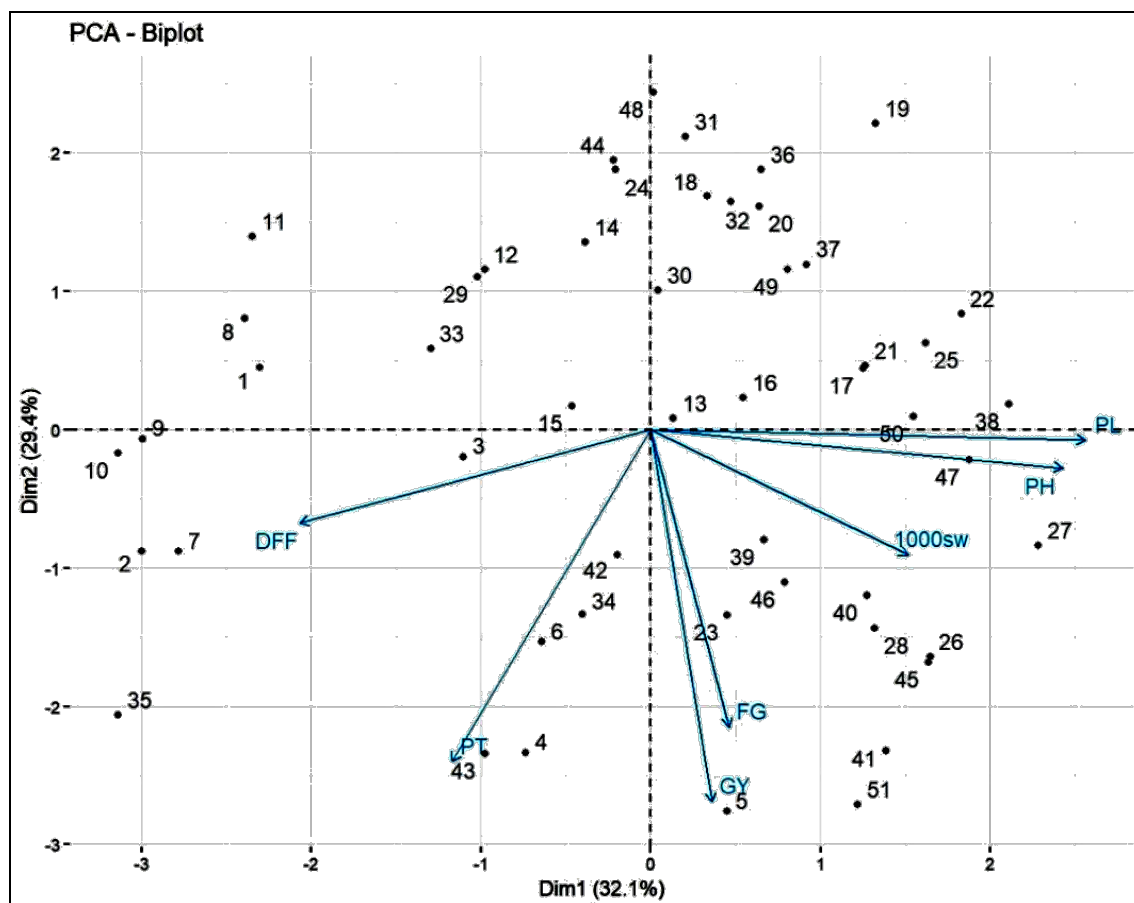


Fig 5: Biplot diagram of principal components

Table 1: List of Agro-morphological traits measured.

S. No	Trait/ Character	Description
1	Days to fifty percent flowering	The number of days from seeding to flowering of fifty percent plants in a plot
2	Plant height	The height of the plant from surface of soil to the last panicle tip
3	Productive tillers per plant	The count of tillers with panicles
4	Panicle length	The length from base of the panicle to the last spikelet tip
5	Filled grains per panicle	The count of the grains that are filled only
6	1000 seed weight	One thousand seeds were counted and weighed
7	Grain yield plant ⁻¹	Weight of grains harvested from a single plant.

Table 2: Analysis of variance of the characters under study

Trait/ Character	Replication	Treatment	Error
dof	2	50	100
Days to 50% flowering	6.37	38.69***	1.45
Plant height	4.49	451.80***	2.89
No of productive tillers per plant	1.45	13.03***	1.17
Panicle length	1.96	9.01***	1.20
No of filled grains per panicle	348.02	1455.84***	171.19
100 seed weight	4.79	25.01***	0.83
Grain yield per plant	3.26	82.96***	152.68

Table 3: Estimates of variability, heritability, genetic advance and genetic advance as per cent of mean

	PV	GV	PCV	GCV	h ² %	GA 5%	GAM5%
DFF	13.868	12.415	3.711	3.511	89.55	6.868	6.844
PH	152.333	149.636	12.089	11.974	98.1	24.959	24.430
PT	5.124	3.953	24.632	21.636	77.1	3.597	39.148
PL	3.805	2.605	8.060	6.668	68.4	2.751	11.365
FG/p	599.415	428.216	22.440	18.967	71.4	36.030	33.024
100SW	8.897	8.057	14.620	13.913	90.6	5.565	27.275
GY/P	28.675	27.148	24.040	23.392	94.7	10.444	46.886

DFF- Days to fifty percent flowering, PH-Plant height (cm), PL-Panicle length (cm), PT-Number of productive tillers, FG/P-Number of filled grains per panicle, 100SW - 100 Seed weight, GY/P-Grain yield per plant

Table 4: Eigen values, percentage of variation and cumulative percentage for principal components

	Eigenvalue	Variance Percent	Cumulative variance percent
PC1	2.25	32.13	32.13
PC2	2.06	29.38	61.51
PC3	0.88	12.58	74.09
PC4	0.67	9.61	83.70
PC5	0.49	7.04	90.73
PC6	0.39	5.51	96.24
PC7	0.26	3.76	100.00

Conclusion

The current research revealed that there was significant variability across all the traits which meant that selection could be made on the basis of the traits. It also showed that the phenotypic coefficient of variation was greater than the genotypic coefficient of variation which, in most instances, suggested the moderate influence of environmental factors, but the genetic variation still took the upper hand. Such traits as grain yield per plant, plant height as well as filled grains per panicle, together, have shown impact through high values for both PCV and GCV, thus implying their possible further improvement by selection.

The study revealed that the traits developed along such strong heritability lines, but the most yield per plant and height of the plant got genetic values that were the most, hence suggesting that these characters are mainly genetically controlled and less susceptible to external factors. Moreover, the panicles, together with plant height have shown good heritability and at the same time high genetic gain, which means that the characters can be improved easily with the use of the simple selection methods. On the other hand, traits such as panicle length and days to 50% flowering possessed high heritability but were limited by lower genetic advance; thus they may be subjected to more advanced breeding strategies or genetic interventions. The research emphasized the need to combine high heritability with large genetic advance as one of the main criteria for selection in rice breeding programs. Through PCA the main traits responsible for the whole divergence were revealed. Among these were panicle length, plant height, productive tillers, days to fifty percent flowering, and grain yield per plant, which were pinpointed as the main traits influencing total diversity by PCA. The research findings serves as a strong basis for breeding programs targeting the improvement of both yield and yield components. It is particularly recommended that the selection efforts be concentrated on traits with additive genetic control such as grain yield per plant and number of filled grains per panicle.

Conflict of interest statement

The authors declare no conflict of interest

Author Contributions

T. Soujanya^{1*} conceptualized the project, project management, planning, execution, finalizing manuscript and submission.

T. Soujanya^{1*}, Narkhede Gopal Wasudeo² were involved in conducting experiments and data analysis

D.P. Divya Vani³, and G. Harish Kumar⁴ recorded data, and were involved in preparation of the research manuscript.

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