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RESEARCH ARTICLE

Principal Component Analysis in rice (*Oryza sativa* L.) varieties for three seasons in Annamalai Nagar, an east coast region of Tamil Nadu

S.R Sruthi[1], Laleeth Kumar N[1], Kishore D[1], Johnny Subakar Ivin[2] & Y Anbuselvam[1*]

[1]Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Tamil Nadu - 608002, India

[2]Mother Terasa College of Agriculture, Mettusalai, Illuppur, Pudukkottai, Tamil Nadu - 622102, India

*Email: yanbuselvam@gmail.com

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Abstract

Principal component analysis (PCA) was used to assess genetic variability and identify key yield-contributing traits among 50 rice genotypes evaluated over three seasons under saline conditions. The study aimed to select promising donor lines for developing salt-tolerant, high-yielding cultivars suitable for coastal regions. PCA identified three principal components (PCs) that explained 73.19%, 70.34% and 64.81% of the total genetic variation in seasons 1, 2 and 3, respectively. Key plant attributes, such as grain yield per plant, panicle grain density, total tiller number, and productive tiller count, showed significant positive associations with PC1 across various growth stages, underscoring their crucial role in explaining the genetic diversity among the genotypes. Plant height, panicle length and hundred-grain weight also emerged as major contributors to variation. The PCA biplots consistently demonstrated positive correlations between grain yield and traits like panicle length, hundred-grain weight and tillering ability. In contrast, days to 50% flowering exhibited a negative association with yield. Genotypes G10, G49, G36, G41, G9, G4, G22 and G21 displayed favourable combinations of grain yield per plant, identifying them as potential donor lines for breeding programs aimed at improving rice yield and associated agronomic traits. This comprehensive PCA analysis highlights the effectiveness of the approach in capturing genotypic diversity and guiding the selection of promising germplasm for targeted trait improvement in rice.

Keywords

Rice; salinity; Principal component analysis; variability; diversity; selection

Introduction

Rice (*Oryza sativa* L.), the second most widely cultivated cereal crop, is the primary food source for 3.5 billion people worldwide, contributing up to 50% of the daily caloric intake for Asian populations (1). With the global population projected to reach 11.2 billion by 2100 (2), increasing rice production is essential to meet future food demands and ensure global food security. However, agricultural productivity is increasingly threatened by soil salinization, which affects approximately 1 billion hectares globally, exacerbated by urbanization, industrialization and rising sea levels (3).

Salinity negatively impacts rice growth and yield, particularly by affecting yield-contributing traits, making it crucial to select genotypes that exhibit tolerance to saline soil (4).

Principal Component Analysis (PCA) plays a vital role in rice breeding by evaluating genetic diversity, identifying key components, maximizing variability and ranking genotypes. This study employed PCA to assess trait correlations and genetic variability among rice varieties grown under saline conditions over three cropping seasons in Annamalai Nagar, a coastal region in Tamil Nadu affected by seawater intrusion. The goal was to identify rice varieties with salinity tolerance based on yield and related traits using PCA biplot analysis, providing valuable insights for plant breeders in selecting donor varieties for developing salt-tolerant high-yielding rice cultivars suited to coastal saline soils.

Materials and Methods

The study was conducted over three seasons, from January 2022 to June 2023, at the Genetics and Plant Breeding experimental farm of the Faculty of Agriculture, Annamalai University, Tamil Nadu. The site is located at a latitude of 11°24'N, longitude 79°44'E, and an elevation of 5.79 meters. Soil electrical conductivity (EC) was measured at the start of the experiment using a Systronics conductivity meter, with value recorded at 3.1, 3.0 and 3.1 dsm^{-1}, for seasons 1, 2 and 3, respectively.

The experimental sample included 50 genotypes sourced from the University of Agricultural Sciences, Bangalore (Table 1). Seedlings, aged 25 days, were transplanted into the main field using a Randomized Block Design (RBD) with three replications. Observations were recorded according to the Standard Evaluation System (5), with data collected from five randomly selected plants per genotype in each replication. The parameters evaluated included day to 50% flowering, plant height (cm), panicle length (cm), number of tillers per panicle, productive tillers per plant, grains per panicle, weight of a hundred seeds (g) and grain yield per plant (g).

Agronomic practices were followed as per standard recommendations based on crop requirements. Principal component analysis (PCA) was employed to identify traits contributing most to the variation among the 50 genotypes across the three seasons. Principal components (PCs) were computed using STAR and XLstat software, derived from the mean values of eight quantitative traits across the 50 genotypes.

Results and Discussion

Eigenvalues, Proportion of variance and Factor scores

Eigenvalues, Proportion of Variance Explained, and Factor scores of yield and its contributing traits for different PCs across all three seasons are provided in Table 2. In each season, the PCA identified three PCs (PC1, PC2 and PC3) with an eigenvalue greater than 1. An Eigenvalue greater than 1 indicates that the corresponding principal component accounts for more variance than any single original variable, suggesting that these three principal components capture a significant portion of the total genetic variation present among the rice genotypes studied. The cumulative percentage of variation explained by these three principal components was 73.19% in season 1, 70.34% in season 2 and 64.81% in season 3. These high percentages indicate that a substantial amount of the total genetic variation among the genotypes is represented by these three principal components. In contrast, the remaining five principal components accounted for only 26.81%, 29.66% and 29.56% of the variation in seasons 1, 2 and 3, respectively, indicating that a relatively small portion of the total genetic variation is explained by these components. A similar trend was reported in a 2021 study (6).

Table 2 illustrates the contribution of eight quantitative traits to the principal components across seasons 1, 2 and 3. The principal component analysis (PCA) conducted over the three seasons revealed differences in how various quantitative traits contributed to the genetic diversity among the rice genotypes. The analysis highlighted how each trait influenced the observed variability, its relationship with the principal components and the potential impact on genotype performance, as indicated by positive and negative loadings on the PCs. The cut-off limit for the coefficients of the principal component vectors was established based on guidelines from a study (7). Coefficients exceeding 0.3 were considered to have a significant impact, while those below 0.3 were deemed to have minimal influence on the overall variation.

Table 1. List of 50 rice genotypes used in the study

Code	Genotypes	Code	Genotypes	Code	Genotypes	Code	Genotypes	Code	Genotypes
G1	PS267	G11	AC35361	G21	Vandana	G31	AC39020	G41	B62655
G2	AC35548	G12	JBT37/89	G22	CTH-1	G32	KRH2	G42	AC35415
G3	PS360	G13	PS367	G23	PS376	G33	JBT36/169	G43	PS307
G4	AC35450	G14	PS259	G24	BPT-5204	G34	JBT36/119	G44	PS242
G5	AC36110	G15	PS91	G25	AC35187	G35	JBT36/79	G45	JBT38/116
G6	PS36	G16	AC39010	G26	S-9	G36	JBT37/29	G46	JBT36/114
G7	AC32525	G17	AC35170	G27	Dodda batta	G37	AC35406	G47	TRY 3
G8	PS366	G18	JBT38/96	G28	AC35066	G38	THANEE	G48	IR 36
G9	JBT37/85	G19	PS325	G29	JBT73/164	G39	PS329	G49	CSR 27
G10	JBT37/154	G20	AC35135	G30	AC35298	G40	AC35341	G50	ADT 46

Table 2. Eigenvalues, Proportion of Variance Explained and Factor scores of the First Three Principal Components Across Three Growing Seasons.

	SEASON 1			SEASON 2			SEASON 3		
TRAITS	**PC1**	**PC2**	**PC3**	**PC1**	**PC2**	**PC3**	**PC1**	**PC2**	**PC3**
DFF	-0.200	0.291	-0.476	0.080	0.512	0.648	0.125	0.323	-0.551
PH	-0.125	0.676	-0.235	-0.109	0.642	-0.060	-0.226	0.423	-0.457
NTPP	0.447	-0.113	-0.159	-0.470	0.219	-0.351	-0.430	0.292	0.433
NPTPP	0.430	-0.253	-0.092	-0.510	0.161	-0.157	-0.516	0.139	0.140
GPP	0.448	0.256	0.117	-0.457	0.070	0.009	-0.324	-0.535	0.003
PL	0.295	0.559	0.366	-0.375	-0.230	0.416	-0.362	-0.300	-0.488
HSW	0.210	-0.033	-0.732	-0.208	-0.353	-0.098	-0.229	0.456	0.114
GYPP	0.478	0.061	-0.041	-0.330	-0.263	0.496	-0.441	-0.171	-0.169
Eigenvalue	3.511	1.238	1.106	3.135	1.534	0.958	2.533	1.493	1.159
Proportion of Variance	0.439	0.155	0.138	0.392	0.192	0.120	0.317	0.187	0.145
Cumulative Proportion	0.439	0.594	0.732	0.392	0.584	0.703	0.317	0.503	0.648

DFF - Days to fifty percent flowering, PH - Plant height, NTPP - No. of tillers per plant, NPTPP - No. of productive tillers per plant, GPP - Grains per panicle, PL - Panicle length, HSW - Hundred seed weight, GYPP - Grains yield per plant, PC - Principal component

In season 1, the traits number of tillers per plant (0.4469), number of productive tillers per plant (0.4297), grains per panicle (0.4481) and grain yield per plant (0.4782) exhibited high positive loadings on PC1, underscoring their significant role in the observed variability. These traits are valuable for enhancing yield and yield-related components in rice breeding programs, as they are positively correlated. Plant height (0.6755) and panicle length (0.5590) showed positive loadings on PC2, indicating their positive contribution to the variability captured by this component. These findings align with previous research (8). Conversely, plant height (-0.4756) and hundred seed weight (-0.7319) displayed negative loadings on PC3, suggesting an inverse relationship with the variability represented by this component. Similar results were reported in another study (9).

In season 2, the traits panicle length (-0.3746), grain yield per plant (-0.3298), grains per panicle (-0.4572), number of tillers per plant (-0.4696) and number of productive tillers per plant (-0.5098) showed negative loadings on PC1, indicating that genotypes with higher scores on this component are likely to underperform in these desirable traits. Conversely, plant height (0.6424) and days to fifty percent flowering (0.5115) exhibited positive loadings on PC2, while hundred seed weight (-0.3531) showed a negative loading. In PC3, the number of tillers per plant (-0.3508) had a negative loading, whereas fifty percent flowering (0.6482), grain yield per plant (0.4955) and panicle length (0.4163) displayed positive loadings. These findings are consistent with previous study (8).

In season 3, the traits total tillers number (-0.43), productive tillers number (-0.5156), panicle length (-0.3624), grains per panicle (-0.3236) and grain yield per plant (-0.4407) demonstrated negative loadings on PC1, indicating these traits contribute negatively to the variability captured by this component. Grains per panicle (-0.5345) also had a negative loading on PC2, while hundred seed weight (0.4557), plant height (0.4225) and days to fifty percent flowering (0.3231) exhibited positive loadings. On PC3, days to fifty percent flowering (-0.5513), panicle length (-0.4884) and plant height (-0.4572) showed negative loadings, whereas the number of tillers per plant-(0.4332) had a positive loading. These results are consistent with findings from previous studies (10, 11).

The differing PCA results across seasons indicated that environmental factors and seasonal conditions significantly influenced trait performance, leading to varying associations between agronomic traits and yield. In Season 1, key yield-related traits such as the number of tillers per plant, grains per panicle and grain yield per plant exhibited strong positive correlations, collectively contributing to increased yield, as evidenced by their high positive loadings on PC1. However, in Seasons 2 and 3, many of these same traits showed negative loadings on PC1, suggesting that environmental stress or suboptimal growing conditions negatively impacted these traits, resulting in lower yield performance. This shift in the importance of traits highlighted the complex interactions between genotype and environment. While favorable conditions in Season 1 enhanced yield components, potential stress factors, such as a saline environment, in Seasons 2 and 3 may have disrupted these relationships.

Trait associations common across all seasons, such as the positive influence of plant height and the mixed role of flowering time, underscore the complexity of trait selection in plant breeding. Plant height consistently demonstrated a positive correlation with yield throughout all seasons, establishing it as a valuable trait for yield improvement; however, an intermediate height is recommended to prevent lodging. Days to fifty percent flowering exhibited mixed associations, with earlier flowering benefiting yield in season 1, while delayed flowering in the subsequent seasons enhanced resilience under stress conditions. Hundred seed weight consistently displayed a negative association with yield, likely due to a trade-off between seed size and seed number. Breeding programs should prioritize traits that consistently enhance yield stability, such as optimal plant height while balancing traits that may have trade-offs, such as hundred seed weight.

Across all three seasons, traits including days to fifty percent flowering, grain yield per plant, number of productive tillers per plant, plant height, number of tillers per plant, panicle length, grains per panicle and hundred seed weight emerged as significant contributors to the observed genetic diversity. Similar findings have been reported in other studies (10,12). Grain yield, grains per panicle and tillers per plant are examples of desirable traits with positive loadings on the principal components, indicating their contribution to the observed variability. In plant breeding, identifying superior genotypes for these traits may involve selecting genotypes with high scores on these principal components. Conversely, genotypes with high scores on components associated with negative loadings may perform poorly for those traits. By considering both the positive and negative loadings of traits across multiple principal components, breeders can select genotypes with desirable trait combinations, identify potential donors for specific traits and ultimately develop improved rice varieties with targeted trait enhancements.

Scree plot Analysis

The scree plot illustrated the percentage of variation accounted for by each Eigenvalue across the principal components (Fig. 1 - Fig. 3). In season 1, PC1 demonstrated the highest variation of 43.89%, with an eigenvalue of 3.51, outperforming the other PCs. This suggests that selecting genotypes based on their scores on PC1 would be beneficial for improving traits that significantly contribute to this component, namely total tiller number, grain yield per plant, grains per panicle and total productive tillers. In seasons 2 and 3, PC1 accounted for 39.19% and 31.66% of the variability, with eigenvalues of 3.13 and 2.53,

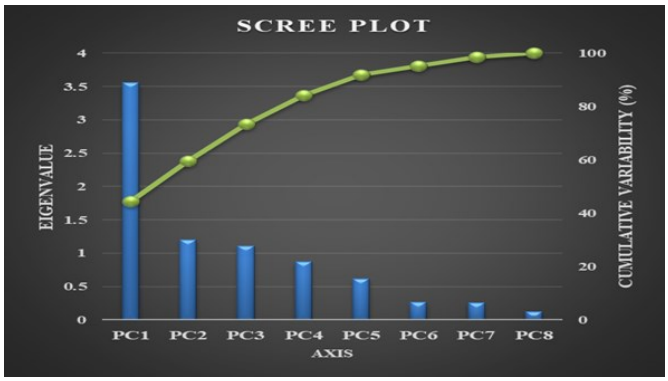

Fig. 1. Scree Plots Illustrating the Eigenvalues and Percentage of Variance Explained by Principal Components for Season 1.

Fig. 2. Scree Plots Illustrating the Eigenvalues and Percentage of Variance Explained by Principal Components for Season 2.

Fig. 3. Scree Plots Illustrating the Eigenvalues and Percentage of Variance Explained by Principal Components for Season 3.

respectively, maintaining its position as the highest among all components in both seasons. Similar findings have been reported in previous studies (11,13). PC1 was found to be the most reliable in explaining the maximum variation in the dataset across the three seasons, highlighting its significance in representing total genetic diversity. While environmental factors contributed to some variation in specific traits associated with PC1, yield-related traits such as the number of productive tillers per plant, number of tillers per plant, grains per panicle, panicle length and grain yield per plant emerged as the major contributors. Breeders can identify desirable genotypes with favorable combinations of these important yield-related traits by focusing on those with high scores on PC1, which captures a substantial portion of the total variability. In breeding initiatives aimed at enhancing rice grain yield and related components, these genotypes can be prioritized during selection and considered as potential donors.

Biplot Analysis

The biplot diagrams (Fig. 4 - Fig. 6) illustrate the distribution and nature of diversity among genotypes and quantitative traits in relation to PC1 and PC2 across all three growing seasons. The PCA biplots revealed both consistent and divergent patterns in the traits contributing most to genotypic variation.

Across all seasons, the total tillers number consistently had the longest vector (Fig. 4 - Fig. 6), indicating that it was the primary driver of divergence among the genotypes. Similar findings have been documented in other studies (14), suggesting that variation in tiller production was a key factor distinguishing the performance of different genotypes throughout the study. However, the secondary traits contributing to genotypic variations differed slightly between seasons.

In season 1, productive tillers, grains per panicle, and plant height (Fig. 4) emerged as the other major contributors to genotypic divergence, which is consistent with the results of earlier studies (15,16). In season 2, the number of productive tillers per plant and grains per panicle (15) were the next most influential traits after total tillers number (Fig. 5). In contrast, in season 3, days to fifty percent flowering and productive tillers per plant (Fig. 6) were the secondary drivers of divergence. These seasonal

variations in key traits suggest that the relative importance of different yield-related traits may have been influenced by shifting environmental or management factors. The inclusion of days to fifty percent flowering as a key trait in season 3 implies that flowering time played a role in differentiating the genotypes during that particular year. Overall, the PCA biplots highlight the multifaceted nature of the genotypic diversity present, with tillering, panicle characteristics and flowering time emerging as the primary axes of variation across the three growing seasons.

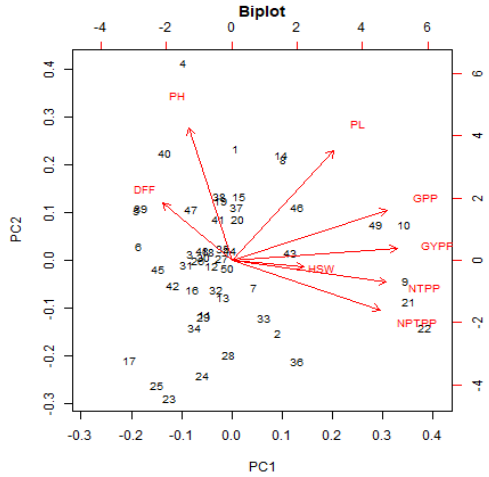

Fig. 4. PCA biplot for PCA 1 Vs PCA 2 for season 1.

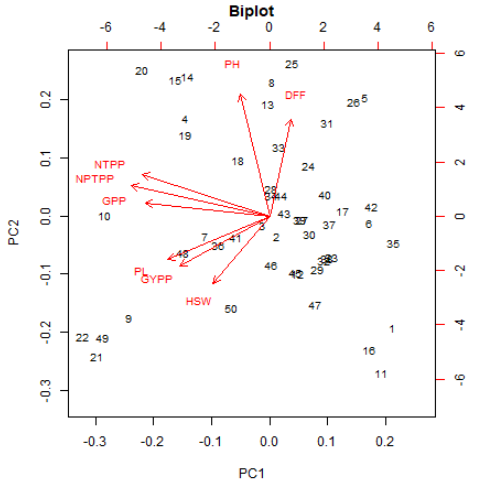

Fig. 5. PCA biplot for PCA 1 Vs PCA 2 for season 2.

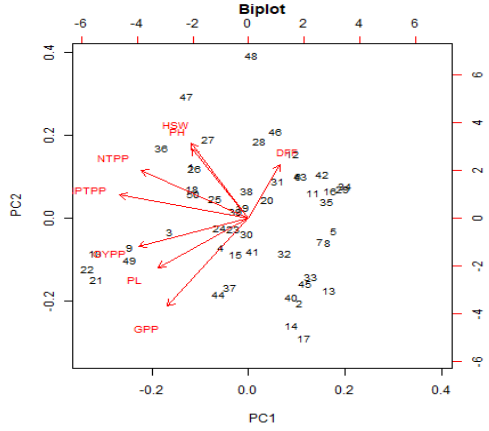

Fig. 6. PCA biplot for PCA 1 Vs PCA 2 for season 3.

The PCA biplots revealed consistent patterns in the relationships between various quantitative traits and grain yield per plant (GYPP) across the three growing seasons. In all seasons, a common set of traits showed a positive correlation with grain yield per plant, including panicle length (PL), hundred seed weight (HSW), and tillering traits such as the number of productive tillers per plant and total tillers per plant (8,17). The vectors for these traits consistently pointed in the same direction as the grain yield per plant vector, indicating a favorable association. Conversely, the duration to fifty percent flowering exhibited a negative correlation with grain yield per plant in both seasons 1 and 2, as its vector was oriented opposite to the grain yield per plant vector (17). The relationship between grains per panicle and grain yield per plant varied across seasons. In seasons 1 and 2, grains per panicle positively correlated with grain yield per plant (18). However, in season 3, the grains per panicle vector showed a slightly negative orientation relative to grain yield per plant (8). This variation suggests that while traits related to plant stature, yield components and phenology were consistently important determinants of grain yield, the specific relationships between individual traits and grain yield per plant may have been influenced by the unique environmental conditions of each growing season.

Regarding grain yield per plant, the top- performing genotypes in season 1 were G10 and G49; in season 2, G36, G41 and G9 and in season 3, G4. Genotypes G21 and G22, placed in the same quadrant and direction as grain yield per plant across seasons two and three, may be considered outstanding performers for yield. Given the positive correlation between grain yield per plant and several other traits, selecting genotypes based on this characteristic is likely to improve performance in those associated traits. The consistent identification of superior-performing genotypes across the three seasons highlights the value of PCA biplot analysis in distinguishing germplasm with favorable and unfavorable trait combinations for grain yield. This information can be used to select appropriate donor parents for future breeding efforts aimed at improving grain yield and related agronomic characteristics.

Conclusion

Principal component analyses were conducted across three seasons to identify key traits and genotypes for improvement in rice. The results highlighted that tiller production, panicle attributes and flowering time consistently contributed to genotypic diversity. Productive tillers, panicle length, and hundred-seed weight emerged as favourable as favourable yield-related characteristics. Genotypes such as G10, G49, G36, G41, G9, G4, G21 and G22 demonstrated more effective combinations of these desired traits, particularly in their ability to balance important yield components under saline conditions across multiple seasons.

The consistent superior performance of these genotypes, especially under stress-prone conditions, suggests that they may possess inherent salinity tolerance. Their ability to maintain key agronomic traits, such as tiller number, panicle length and grain yield, indicates potential physiological adaptations to salinity stress, including efficient ion regulation, osmotic adjustment and stress avoidance mechanisms. Further studies are required to confirm these adaptive traits. Therefore, these genotypes hold great promise as valuable resources for breeding programs focused on enhancing rice productivity in saline environments.

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Authors' contributions

The author YA conceived of the presented idea. The authors SR and LK carried out the experiment and wrote the manuscript with support from the authors KI and JS. All authors provided critical feedback and helped shape the research, analysis and manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None.

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